UNIVERSITY FOR DEVELOPMENT STUDIES

SCREENING AND EVALUATION OF SOME GENOTYPES OF MAIZE (*Zea mays* L.) AND THEIR F_1 HYBRIDS FOR TOLERANCE TO DROUGHT AND *Striga hermonthica* (Del.) Benth

ALHASSAN BAWA

2016

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BY

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THESIS SUBMITED TO THE DEPARTMENT OF AGRONOMY, FACULTY OF AGRICULTURE, UNIVERSITY FOR DEVELOPMENT STUDIES IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR THE AWARD OF DOCTOR OF PHILOSOPHY (Ph.D.) DEGREE IN CROP SCIENCE

MAY, 2016

Ph.D. **ALHASSAN BAWA**

DECLARATION

I, Alhassan Bawa, do hereby declare that this thesis titled "Screening and evaluation of some genotypes of maize (*Zea mays* L.) and their F_1 hybrids for tolerance to drought and *Striga hermonthica* (Del.) Benth" is the results of my own original work and that no part of it has been presented for another degree in this University or elsewhere.

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We hereby declare that the preparation and presentation of the thesis was supervised in accordance with the guidelines on supervision of thesis laid down by the University for Development Studies.

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ABSTRACT

Drought stress and striga parasitism are major constraints to maize (*Zea mays* L.) production in Northern Ghana. Two experiments were conducted to screen some genotypes of maize for tolerance to drought and *Striga hermonthica* at Nyankpala in the Guinea Savanna agro-ecological zone of Ghana. In Experiment 1, seeds were planted in pots of 0.01 m^3 volume arranged in rows on a platform in a screen house at Nyankpala. Genotypes were replicated three times in a completely randomized design. In another experiment (Experiment II), genotypes were evaluated in the field on single-row plots in three replicates using randomized complete block design. Results of screening from these two experiments showed that three of the genotypes; GUMA03-OB, KOBN03-OB and SISF03-OB were highly tolerant to drought, whilst another three genotypes, namely TAIS03, DT-STR-W-C2 and IWD-C3-SYN-F2 were highly tolerant to *Striga hermonthica*. The six genotypes stated above were crossed in complete diallel fashion to generate 30 F_1 hybrids in Experiment III. The parents and their F_1 hybrids were evaluated in Experiment IV for tolerance to drought and striga in two locations, that is, Nyankpala and Golinga under field conditions using randomized complete block design. Results on yield and other agronomic traits from field evaluation showed that highly negative significant ($P < 0.001$) GCA effect for the parent populations was observed in TAIS03, KOBN03-OB, DT-STR-W-C2 and IWD-C3-SYN-F2. For the F_1 hybrid populations, KOBN03 x DT, DT x TAIS03, TAIS03 x KOBN03, IWD x GUMA03, GUMA03 x DT, GUMA03 x SISF03 and SISF03 x TAIS03 gave the highest negative significant SCA effect for majority of the traits. Genomic DNA was extracted as reported in Experiment V with the CTAB method and polymerase chain reaction (PCR) was performed based on the common method for microsatellite markers. The PCR products were separated using 6% polyacrylamide denaturing gel. An amount of 17 microsatellites were then used to screen the parents and their F_1 progenies for tolerance to

drought and *Striga hermonthica*. The results of the study indicated that the following F_1 hybrid populations: IWD x TAIS03, IWD x GUMA03, DT x KOBN03, TAIS03 x IWD, TAIS03 x DT, TAIS03 x SISF03, SISF03 x TAIS03, SISF03 x GUMA03, GUMA03 x IWD, GUMA03 x DT and GUMA03 x KOBN03 contained the quantitative traits responsible for both drought and *Striga hermonthica* tolerance. The results of the molecular studies confirmed those from the field evaluation (Experiment IV). Therefore in drought-prone or striga-infested geographical areas like Northern Ghana, hybrid populations such as KOBN03 x DT, DT x TAIS03, IWD x GUMA03, GUMA03 x DT, GUMA03 x SISF03 and SISF03 x TAIS03 can be used for increased grain yield.

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ALHASSAN BAWA
MAY, 2016

DEDICATION

This thesis is dedicated to my late father, Afa Bawa Alhassan; my wife and children, and the entire Limam Alhassan Clan at Nyankpala in the Northern Region of Ghana.

LIST OF PUBLICATIONS FROM THIS Ph.D. WORK

(1) Bawa, A., Addai, I.K., Abdulai, M.S. and Kugbe, J.X. (2015). Evaluation of some genotypes of maize (*Zea mays* L.) for tolerance to *Striga hermonthica* (Del.) Benth in Northern Ghana. Research in Plant Biology 5 (5): 01 – 12.

(2) Bawa, A., Addai, I.K. and Abdulai, M.S. (2015). SSR markers as tools for screening genotypes of maize (*Zea mays* L.) for tolerance to drought and *Striga hermonthica* (Del.) Benth in the Northern Guinea Savanna Zone of Ghana. Research in Plant Biology 5 (5): 17 – 30.

(3) Bawa, A., Addai, I.K. and Kugbe, J.X. (2015). Evaluation of some genotypes of maize (*Zea mays* L.) for tolerance to drought in Northern Ghana. Research in Plant Biology 5 (6): 19 – 29.

(4) Bawa, A., Addai, I.K., Abdulai, M.S. and Issahaku, A. (2015). Diallel analysis and evaluation of F_1 progenies of maize (*Zea mays* L) for tolerance to drought and *Striga hermonthica* (Del.) Benth in the Guinea Savanna Agro-ecological Zone of Ghana. American Journal of Agricultural and Biological Sciences (accepted but still in press).

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LIST OF ACRONYMS

AFLP	Amplified Fragment Length Polymorphism
CBS	Central Bureau of Statistics
CTA	The Technical Centre for Agricultural and Rural Co-operation
CTAB	Hexadecyl Trimethyl Ammonium Bromide
dNTP	deoxynucleoside triphosphate
EDTA	ethylene diamine tetra acetic acid
EPA	Environmental Protection Agency
FAO	Food and Agriculture Organization
FAOSTAT	Food and Agriculture Organization Statistics
GCA	General Combining Ability
IITA	International Institute of Tropical Agriculture
PCR	Polymerase Chain Reaction
PPMED	Policy, Planning, Monitoring and Evaluation Department
QTL	Quantitative Trait Loci
RAPD	Random Amplified Polymorphic DNA
RFLP	Restriction Fragment Length Polymorphism
SARI	Savanna Agricultural Research Institute
SAS	Statistical Analysis System
SCA	Specific Combining Ability
SPSS	Statistical Package for Social Sciences
SSR	Simple Sequence Repeat
UNESCO	United Nations Education, Scientific and Cultural Organization
USDA	United States Department of Agriculture

CHAPTER ONE

GENERAL INTRODUCTION

1.1 Background

Maize (*Zea mays* L.) belongs to the tribe *Maydeae* and the family *Graminae* (*Poaceae*). The issue of the origin of maize has been a subject of debate for many years. Several schools of thought have come up regarding the origin of maize. Based on archaeological records, Ram (2011) reported tha the crop is considered to be indigenous to America, particularly Southern Mexico, and that the crop had been domesticated about 8000 years ago and does not survive in its wild form. Sauer (1993) reported that maize, also known as corn, is a native of Mesoamerica (now Mexico) and subsequently spread throughout the American continent. Maize was introduced into Africa in the 16th Century from its native Mesoamerica and it is now one of the most widely grown cereal crops in Africa. Most historians believe that corn was domesticated in the Tehuacan valley of Mexico (Brown and Darrah, 2005). Kogbe and Adediran (2003) also reported that maize is indigenous to the high valleys of the Andes in South America from where it spread to Europe, Africa and Asia through the activities of traders and explorers. Maize was domesticated in Central Mexico (Matsuoka *et al.*, 2002) between 6000 and 9000 years ago (Benz, 2000). The centre of origin for *Zea mays* has been established as the Mesoamerican region and Central America (Watson and Dallwitz, 1992). Archaeological records suggest that domestication of maize began at least 6000 years ago, occurring independently in regions of the southwestern United States, Mexico, and Central America (Mangelsdorf, 1974).

Maize is one of the oldest cultivated crops and, globally, it is the third most important cereal after wheat and rice in area and total production. It is the most important cereal food crop in Mexico, Central America, and many countries in South America and Sub-Saharan Africa. Maize is the most important cereal crop in East Africa as well as the South African Development Communities (FAO, 2011), but ranks second in terms of importance in Indonesia, Asia. The crop therefore, holds a unique position in world agriculture as a food, feed and industrial crop.

Maize is utilized directly as source of food and animal feed. In the developed world, about 70% of maize is mostly used for animal feed and only a small percentage (5%) is consumed by humans. The developing countries consume about 62% of maize as food and 34% is used as feed. The remaining proportion is used for varied industrial uses and as seed. However, maize accounts for 70% of the food consumed in Sub-Saharan Africa (FAO, 2007). The recent volatile food market and rising prices for most food crops may increase the importance of maize production. In addition, because of its productivity and wide adaptation, maize remains an important source of food with great potential to improve the livelihoods of most poor farmers in developing countries (FAO, 2011). Maize grain is used for the preparation of corn starch, corn syrup, corn oil dextrose, corn flakes, gluten, grain cake, lactic acid and acetone which are used by various industries such as textile, foundry fermentation and food industries. Maize is rapidly replacing traditional cereals such as sorghum and millet in the savannas of West and Central Africa where there is good access to fertilizer inputs and markets (Badu-Apraku and Fakorede, 2003).

According to the United Nations Food and Agriculture Organization, the world area of maize production was 176 million ha, while that of wheat and rice were 216 million ha and 184 million ha, respectively during 2012 (FAOSTAT, 2012). Compared to all other cereals, maize has the

highest average yield per unit area. Maize surpasses both wheat and rice in terms of productivity. For instance, the world maize production for 2012 was 875 million tons, while that of wheat was 606 million tons and that of rice was 635 million tons. About 70% of the world maize production area is found in developing countries. However, these countries contribute to only 49% of the world maize production (FAOSTAT, 2012). The share of Africa's maize production for 2012 was 69 million tons or about 8% of the world production.

There are many reasons that account for the low production of maize in the developing countries. A large proportion of maize in Africa is produced by resource-limited, small-scale farmers. Yields are very low because farmers are constrained by cash shortage to utilize the necessary inputs for maize production (Dawit *et al.*, 2008). Due to increased demand, maize production is spreading into marginal areas and this will likely engender risk to biotic and abiotic threats leading to minimal productivity. To achieve the growing need for maize in Africa it is necessary to boost productivity through reducing yield losses incurred through various stress factors such as diseases, pests, parasitic weeds and drought (Dagne *et al.*, 2004). In Sub-Saharan Africa, the use of agricultural inputs is extremely low resulting in poor maize yields of 1.3 ton/ha (Banziger and Diallo, 2004). Sub-Saharan African countries therefore, import approximately three million tons of maize annually to meet local demands (Pingali and Pandey, 2001; FAOSTAT, 2012). Despite poor productivity, maize producing areas are fast increasing in Sub-Saharan Africa (FOASTAT, 2012). Productivity should be enhanced through the use of improved varieties along with their production technologies for food security and import substitution (Pingali and Pandey, 2001). Maize yield in West Africa has virtually stagnated at about 1.8 tons/ha compared to 5.1 tons/ha of world average (FAOSTAT, 2012). In Central Africa, maize is cultivated on more than 3.4 million ha over a wide range of agro-climatic zones stretching from sea level to well over

2300 m in elevation (FAO, 2012). The demand for maize therefore in Sub-Saharan Africa is estimated to increase two folds by the year 2020 (Rosegrant *et al.*, 1999).

For Ghana, maize is the largest and most widely cultivated crop, accounting for 50-60% of total cereal production. It is the second largest commodity crop after cocoa (IITA, 2013), and accounts for more than 45% of the agricultural cash income among smallholder farmers in the country. Over 85% of the rural population grows maize because it fits well into the different farming systems and has great potential for increasing yield under improved management practices compared with other cereal crops (SARI, 2012). The crop has the greatest potential of combating food security challenges posed by population increase in the country due to its high yield potential, wide adaptability and relative ease of cultivation. National data indicates that production and consumption of the crop have been increasing in recent years. The current area planted to maize in Ghana stands at approximately 1 million ha. The yield and production averages are about 1.74 tons/ha and 1.65 million tons (2012 average), respectively. The per capita consumption of maize in Ghana is estimated at 44 kg/person/year (2005 estimates), and the national demand is forecast to grow at about 1.83% per annum (IITA, 2013). It is an important cereal produced in all the five agro-ecological zones of Ghana namely; Forest, Guinea savanna, Coastal savanna, Transitional zone and Sudan savanna (Obeng-Bio *et al.*, 2002). The Guinea and Sudan savannas however, have the highest potential for increased maize production and productivity due to high solar radiation, low night temperatures and low incidence of diseases (SARI, 2012). The grain, leaves, stalk, tassel and cob of maize can all be used to produce a large variety of food and non-food product. It is used for Banku, Pito, Akpele, Kenkey and Tuozaafi (FAOSTAT, 2006). Analysis based on 2006 maize consumption data in Ghana showed that the crop and foods based on it accounted for 10.8% of food expenditure by the poor,

and also 10.3% of food expenditure by all income groups. In Northern Ghana, maize stovers are used as fuel wood (SARI, 2012), and for a number of decades, maize has been used as an industrial raw material from which products such as cornflakes, oil, jam, alcohol and paper are produced.

1.2 Problem statement and justification

The maize industry plays an important role in the lives of the people of Ghana and the world at large. Notwithstanding the enormous role the maize industry plays, the industry is bedeviled with a lot of constraints. These include lack of credit facilities to farmers, soil degradation, erratic rainfall pattern and infestation caused by diseases, insect pests and parasitic weeds. In Africa, the most important limiting factors to maize production are drought, striga infestation and low soil fertility. In Ghana, the average maize grain yield is about 1.7 tons/ha as against an estimated achievable yield of about 6.0 tons/ha as a result of drought, striga infestation and low soil nutrient level, particularly nitrogen and phosphorus (MoFA-SRID, 2011).

Drought is one of the prime abiotic stresses in crop production throughout the world. It is an important climatic phenomenon, which is the second most important constraint to maize production in developing countries, after low soil fertility (Edmeades *et al.*, 1995). Maize is particularly sensitive to water stress at the reproductive stages. Crop yield losses due to drought stress are considerable since drought is the major stress affecting productivity in Africa, accounting for 70% of total crop loss (Muoma *et al.*, 2010; Ashraf, 2010). The use of genetics to improve drought tolerance and provide yield stability is an important part of the solution to stabilizing maize production. This does not imply that agronomic interventions that aim to maximize water availability at key growth stages are not critically important, since genetic

solutions are unlikely to close more than 30% of the gap between potential and realized yield under water stress (Edmeades *et al*., 2004).

In Ghana, maize production is mainly under rain-fed conditions. However, rainfall is erratic and therefore, cannot solely be relied upon for increased maize productivity. The problem of drought can be addressed either by providing supplemental irrigation to crops in water-stressed areas or by developing drought tolerant genotypes. The provision of supplemental irrigation is not economically feasible for Ghana owing to resource constraints. Plant breeding seems to be an efficient and economic means of tailoring crops to enable them grow successfully in drought-prone environments (Ashraf, 2010). Therefore, the development of drought tolerant genotypes of maize seems to be the best alternative to cope with drought stress.

Striga is a parasitic weed commonly called witch weed. It is an obligate parasite belonging to the family *Scrophulariaceae* (Parker, 2009). The witch weed is considered to be one of the major biological constraints to food production in Africa. The area infested by *Striga* species is estimated at 50 million ha, with 300 million farmers being affected, and this result in estimated losses of US$7 billion (Parker, 2009). Yield losses due to striga infestation vary from a few percentage to complete crop failure depending on crop species, variety of crop and severity of infestation. Hearne (2009) reported yield losses ranging from 35-72%. Striga infestation is a constraint to maize, sorghum and millet production. Heavy infestation with striga can render land unfit for crop production and fields have been abandoned in worst affected areas. The effects are likely to be long lasting as striga produces millions of tiny seeds that can stay viable in the soil for many years (Hearne, 2009).

In Sub-Saharan Africa, striga is probably a more serious agricultural problem than insects, birds or plant diseases (Ejeta and Butler, 1993). The problem of striga is intensifying across regions in

Sub-Saharan Africa because of deteriorating soil fertility, shortening of the fallow period, expansion of production into marginal lands with little nutrient input and an increasing trend towards continuous cultivation of one crop in place of traditional rotation and inter-cropping systems. Striga severity affects an estimated 40 million ha of land devoted to cereal production in West Africa with additional 70 million ha having moderate levels of infestation (Lagoke *et al.*, 1991). Ayongwa and Ngoumou (2001) stated that striga is the most persistent biological constraint to cereal production compared to insect pests, granivorous birds or elephant herds on rampage. Striga has been reported to cause between 10 to 100% yield losses in maize, depending on the incidence, level of infestation and distribution of the parasitic weed, the crop variety, location and cultural practices in use (Lagoke, 1986).

In Ghana, striga is a serious problem in areas north of latitude 9°30'N, which represent about 57 per cent of the total land area (Nyarko, 1986). The estimated yield losses amount to 4.1 million mega grams of grain in a year (Lagoke, 1986). The farm households in the three Northern Regions of Ghana together rank first in the production of the four major cereals in the country, namely maize, rice, sorghum and millet (PPMED, 2013), but the production of the cereals is menaced by the threat of low productivity as a result of the parasitic weed, *Striga hermonthica* (Sauerborn, 1991). According to Sauerborn (1991) records of losses caused by *Striga hermonthica* in Northern Ghana in 1991 showed that yield losses amounted to 16% for maize, 31% for millet and 29% for sorghum, representing a total economic loss of US$25 million for the three crops. Farm fields of all the districts of Northern Ghana are infested with the parasitic weed. However, Runge-Metzger *et al.* (1997) stated that the state of knowledge with respect to the severity of striga infestation, its geographical distribution in Northern Ghana and its current trend is still extremely unsatisfactory. There is the need for effective control of this parasite to

enhance higher yields of crops. Most of the current available control measures require expensive inputs. The use of host crop resistance as a component of integrated striga management seems to be the cheapest, most affordable, and most convenient for African farmers. This method is more likely to be adopted by the resource poor farmers (Debrah, 1994).

Breeding for drought and striga tolerance in maize may improve the performance of the crop even under water-stressed and/or striga-infested conditions. This could be achieved by a modification in the plant genotype. To achieve the growing need for maize in Ghana in particular, and Sub-Saharan Africa in general, it is necessary to boost productivity by reducing yield losses caused by various stress factors including drought and *Striga hermonthica*.

1.3 Objectives

Drought is a major source of grain yield decrease in cereals, especially in developing countries. For maize in the tropics, drought stress could reduce grain yield by 17–70% annually, compared with well-watered productions (Edmeades *et al.*, 1995). Research has shown that variations in drought tolerance exist in various crop species such as wheat (Guttieri *et al.*, 2001) and maize (Frova *et al.*, 1999). Hybrids of parents with more genetic diversity yield more than those of similar parents (Troyer *et al.*, 1998). Breeding to improve drought tolerance has been a challenge in maize production. This study therefore seeks to develop some genotypes of maize for tolerance to drought in Northern Guinea Savanna agro-ecological zone of Ghana. Genotypes would be screened for various morphological and physiological traits under water-stressed conditions.

Witch weed (*Striga* spp) is another major source of grain yield decrease in maize in Northern Ghana. Among the numerous species of striga that are endemic to Ghana and Africa, *Striga hermonthica* (Del.) Benth is the most widespread species affecting cereals, with maize being the most susceptible (Lagoke *et al.*, 1991). Under heavy infestation, maize is more vulnerable to striga parasitism than upland rice, sorghum and millet with high losses in excess of 90% (Efron *et al.*, 1989). Yield losses of between 70 and 90 per cent in maize have been reported by many scientists, including Olakojo *et al.* (2001). Yield losses may reach 100% on heavily infested fields (Doggett, 1995). Tolerant varieties developed for striga control have often broken down with time (Kim and Adetimirin, 1997). This is as a result of build up of more virulent striga populations, especially under continuous cropping as well as the development of new strains of striga through cross fertilization (Musselman, 1987). This study will involve evaluation of genotypes for tolerance to striga parasitism in Northern Ghana. Several methodologies may be used to develop *Striga hermonthica* tolerant lines. Conventional and molecular breeding are some of the methods that will be used in the present study. The study will involve the selection of striga tolerant genotypes under striga infested conditions.

All possible crosses in a complete diallel fashion among the selected drought and striga tolerant lines would be made, with the view to developing F_1 hybrid populations. The parental and F_1 hybrid populations would also be evaluated for yield, morphological and physiological traits under water-stressed and striga-infested conditions. The study will identify simple sequence repeat (SSR) markers (microsatellites) that are effectively linked to the quantitative trait loci (QTLs) responsible for drought and/ or *Striga hermonthica* tolerance among the parent and F_1 hybrid populations, with the view to screening the parent and F_1 hybrid populations for tolerance to drought and *Striga hermonthica*.

CHAPTER TWO

LITERATURE REVIEW

2.1 The maize crop

Maize or corn (*Zea mays* L.) is a plant belonging to the tribe *Maydeae* of the grass family *Poaceae*. Maize is a versatile crop grown over a range of agro climatic zones (Doebley, 1990). The genus *Zea* (zela) was derived from an old Greek name for a food grass. The genus *Zea* consists of four species of which *Zea mays* L. is economically important. The other *Zea* species, referred to as teosintes, are largely wild grasses native to Mexico and Central America (Doebley, 1990). The number of chromosomes in *Zea mays* is 2n = 20.

Maize is a tall, determinate, monoecious, annual C 4 plant varying in height from 1 – 4 m (DOA, 2003). It produces large, narrow, opposite leaves, borne alternatively along the length of a solid stem. The lower leaves of maize are like broad flags, 50 – 100 cm long and 5 – 10 cm wide. The stems are erect with many nodes, casting off flag-leaves at every node (DOA, 2003). Internodes can reach 20 – 30 cm. Maize is described as monoecious plant because the sexes are partitioned into separate pistillate (ear), the female flower and staminate (tassel), the male flower. It has determinate growth habit and the shoot terminates into the inflorescence bearing staminate flowers (Dhillon and Prasanna, 2001). Maize is generally protandrous, that is, the maize flower matures earlier than the female. The male (staminate) inflorescence is a loose panicle and produces pairs of free spikelets each enclosing a fertile and a sterile floret. The female (pistillate) inflorescence produces pairs of spikelets on the surface of a highly condensed rachis (central axis, or cob). The female flower is so tightly covered over by several layers of leaves to the

extent that the flowers do not show themselves easily until emergence of the pale yellow silks from the leaf whorl at the end of the ear.

The maize plant has three types of roots. These include seminal roots, adventitious and fibrous roots, and brace or prop roots. The seminal roots are developed from the radicle and persist for long period. The adventitious and fibrous roots are developed from the lower nodes of stem below ground. These are the effective and active roots of the plant. The brace or prop roots are produced by the lower two nodes of the stem above ground. The prop roots grow very rapidly and almost equally outwards and downwards. Favourable soil may allow maize root growth up to 60 cm laterally and in depth. The stem generally attains a thickness of 3 – 4 cm. The internodes are short and fairly thick at the base of the plant; become longer and thicker higher up the stem, and then taper again. The ear bearing internode is longitudinally grooved to allow proper positioning of the ear head (cob). The upper leaves in maize are more responsible for light interception and contribute relatively more to photosynthates accumulation by the maize crop.

Pollen grains per anther have been reported to range from 2000 to 7500 (Kiesselbach, 1949). Within an average of 7000 anthers per tassel and 2000 pollen grains per anther, each tassel could produce 14 x 10^6 pollen grains. In terms of the ratio of pollen grains produced per ovules fertilized, it appears that since each ear requires about 1000 pollen grains for fertilization, there are about 20,000 pollen grains per kernel in excess of what is actually needed if pollination were 100 per cent efficient (Kiesselbach, 1949). The pollen grains are very small and barely visible to the naked eye. It is very light in weight and easily carried by wind. The wind borne nature of the pollen leads to cross-pollination. However, there may be about 5 per cent self-pollination. The pollen shed is not a continuous process and usually begins two to three days prior to silk emergence and continues for five to eight days. Pollen shed stops when the tassel is too wet or

too dry and begins again when temperature conditions are favourable. Under favourable conditions, pollen grains remain viable for 18 to 24 hours. Cool temperatures and high humidity favour pollen longevity. Under optimal conditions the interval between anthesis and silking is one or two days. Under any stress situation this interval increases.

The female flower is initially smooth but protuberances soon form in rows. The basal protuberances are formed first and development advances towards the tip of the ears. The part above the attachment of the carpel develops a single sessile ovule, which consists of a nucellus with two integuments or rudimentary seed coats. The united carpels, which will form the ovary wall or pericarp of the mature kernel, grow upward until they completely enclose the ovule. The two anterior carpel (which face the ear tip) form outgrowths, which develop into the style (long threads), known as silks. The silks are elongated stigmas that look like tufts of hair, at first green and later red or yellow (DOA, 2003). Silks are covered with numerous hairs, or trichomes which form an angle with the silk where pollen grains are harboured. The silks elongate continuously until fertilization occurs. The cobs bear many rows of ovules that are always even in number. The female inflorescence or ear develops from one or more lateral branches (shanks) usually borne about half-way up the main stalk from auxiliary shoot buds. As the internodes of the shanks are condensed, the ear remains permanently closed in a mantle of many husk leaves. Therefore, the plant is unable to disperse its seeds, and instead it depends upon human intervention for seed shelling and propagation.

Fertilization occurs after the pollen grain is caught by the silk and germinates by growth of the pollen tube down the silk channel within minutes of coming in contact with a silk, and the pollen tube grows the length of the silk and enters the embryo sac in 12 to 28 hours. Pollen of a given plant rarely fertilizes the silks of the same plant (DOA, 2003). Under field conditions 97% or

more of the kernels produced by each plant are pollinated by other plants in the field. Maize kernels developed after fertilization consist of an endosperm, embryo, a pericarp and tip cap. The endosperm contains the main carbohydrates. The embryo contains the parts that give rise to the next generation, while the pericarp and tip cap enclose the entire kernel.

Gene flow from maize occurs either by pollen transfer or seed dispersal. Pollen movement is the only effective means of gene escape from maize plants (Di-Giovanni *et al.*, 1995). As maize is mainly cross pollinated, wind speed and direction affects pollen distribution. Maize pollen measuring about 0.1 mm in diameter is the largest pollen among members of the grass family and it has been reported to be disseminated by wind from a comparatively low level of elevation. Due to its large size, maize pollen settles at a rate that is approximately 10 times faster than pollen from other wind – pollinated plants (Di-Giovanni *et al.*, 1995). Maize can be crossed with teosintes to form fertile hybrids which exhibit low fitness and have little impact on gene introgression in subsequent generations. The introgression of genetic information from one plant to another is only significant if the two plants are sexually compatible and if their hybrid offspring are viable. This is not applicable in maize.

2.2 Drought

Drought, also known as water deficit, refers to any duration without rainfall which is long enough to reduce crop yield (Loffler *et al.*, 2005). In practical terms, it occurs when available soil water fails to meet the transpiration demands of a plant for a reasonable period during growth. Drought effects have not been well quantified. Several studies have focused largely on the total rainfall received within the growing season (Loffler *et al.*, 2005). The amount of

rainfall, soil water storage capacity, potential evapo-transpiration, crop phenology, and crop development stage must all be considered when assessing the impact of drought on production. Edmeades *et al.* (1999) postulated that drought was common in tropical environments, and selection for drought tolerance was one way of reducing the impacts of water on crop yield.

According to Rowland (1993), there are three categories of drought. These are meteorological, hydrological and agricultural droughts. Meteorological drought occurs when the precipitation is significantly below expectations for the time of the year and location. The primary cause of meteorological drought is inadequate rainfall leading to a protracted departure from normal availability (Farmer and Wigley, 1985). Hydrological drought occurs when the water resources used for agriculture, human and animal consumption as well as industrial purposes becomes depleted. Agricultural drought occurs when water used directly for agriculture is scarce and there is a consistently high soil moisture deficit over the growing season. Agricultural drought is based either on rainfall or on the balance between moisture supply and demand.

Drought is one of the major challenges in plant production. It affects 26% of arable area in Sub-Saharan Africa (Blum, 1988). Drought strongly affects the crop yield especially that of cereals and poses a serious threat to food security of the entire sub-continent. In water deficit conditions, plant water potential and turgor are reduced enough to interfere with normal functions (Hsiao, 1973). Annual maize yield loss due to drought is estimated to be 15% in West and Central Africa (Edmeades *et al.* 1995). Grain yield losses can even be greater if the stress coincides with flowering and grain filling period. Nesmith and Ritchie (1992) reported that maize yield can be reduced by as much as 90% if water stress occurs between a few days before tassel emergence and the beginning of grain filling. Yield losses may reach 90% under induced moisture stress from about tassel emergence stage to the end of the crop cycle of maize. Badu-Apraku *et al.*

(2005) observed yield reduction of 62% under drought conditions relative to well-watered treatment. Global food security depends on the development of crop plant with increased resistance to abiotic stresses such as drought.

The term drought resistance has long been used to refer to the ability of plants to survive drought. Drought tolerance describes all the mechanisms that tend to maintain plant survival or productivity in drought conditions. In an agricultural or horticultural context, a more drought tolerant cultivar is one that has a higher yield or marketable product in drought conditions than does a less tolerant one (Fischer and Turner, 1978). In natural eco-system, however, a drought-tolerant species is one that has the ability to survive and reproduce in a relatively dry environment. In this case drought tolerance does not necessarily rely on a high productivity. It follows, therefore, that the mechanisms favouring drought tolerance in typically agricultural monocultures may be distinct from those that evolved in natural ecosystems. Development of drought tolerant varieties is the cheapest method to overcome the problem of drought (Ashraf, 2010).

2.2.1 Effects of drought on growth, development and yield

According to Rowland (1993) water is needed for numerous essential processes during plant growth and development. It is required to keep the cells turgid, and acts as the hydrostatic support for aerial parts and pressure wedge to force roots through the soil. It also enables stomatal pores to open so allowing gaseous exchange. Transpiration of water vapour through the stomata cools leaf tissues, which could otherwise suffer heat stress during the day. Rowland (1993) reported that developmental plasticity is the ability of the plant to adapt to periods of drought by advancing more rapidly into next developmental phase.

Drought at vegetative, flowering and reproductive stages can lead to reduction in final yield. Water stress during the vegetative stage leads to reduced aerial vegetative growth in terms of height and spread. Water stress also affects the flowering stage. Flower primordial will not develop normally nor will anthesis or fertilization be fully effective. A crop can fail to achieve its yield potential if water is inadequate during the grain-filling stage (Rowland, 1993). Insufficient water in plant tissue during this stage makes it impossible for metabolites such as simple sugar and amino acids to be synthesized to the grains in adequate quantities for their conversion into more complex storage compound. The author also observed that water deficit at flowering can cause tassel blast disrupting the plant's ability to shed pollen, and can reduce the viability of the pollen itself. The contemporary high temperatures often compound the effect of moisture stress. Water stress at silking impairs extrusion of silks from the cob husk, causes desiccation of the silks and inhibits pollen tube growth, all resulting in fewer grains per cob (Rowland, 1993). Westgate and Grant (1989) reported that the response of reproductive tissues to plant water deficits varies with stage of grain development. The high sensitivity to plant-water deficits occurs in early reproductive development while sensitivity decreases as reproduction progresses.

Studies on seed germination and seedling vigour for measuring drought tolerance of some maize genotypes indicated that germination stress, germination rate stress and seedling dry matter stress indices were influenced by both genotype and moisture stress level (Elemery *et al.*, 1995; Lemcoff *et al.*, 1998). Almaghrabi (2012) observed significant differences in response to drought stress on germination of maize cultivars. Bahrami *et al.* (2012) also observed that reduction in germination with moisture deficit is attributed to lower infusibility of water through the seed coat and decreased external water potential. In general, mean germination was higher at moderate moisture than at low soil moisture conditions (Maiti *et al.*, 1996). When plants were re-watered

after a short period of water stress, leaf elongation rate was very rapid for a short time, but rate of growth after re-watering did not return to normal in severely stressed plant (Jing and Hsiao, 1987).

Cell division, though affected by water stress, is normally less sensitive than cell expansion (Sharp and Davies, 1985). In addition to simple growth inhibition, water deficit can greatly modify plant development and morphology. For example, differential sensitivity of roots and shoots (with root growth being less sensitive to water deficit) leads to large increases in the root to shoot ratio in drought (Sharp and Davies, 1985). Other effects on vegetative development include the reduction of tillering in grasses and the early termination of extension growth in perennials with the formation of dormant buds. Water stress also increases abscission of leaves and fruits. Not only does water stress decrease the size of leaves but also result in the reduction of cell expansion and cell division (Quarrie and Jone, 1977). Water stress affects reproductive development, and it is also required to stimulate floral initiation in some species. Alam (1985) pointed out that shoot elongation was reduced by water stress during vegetative period in maize. Ouattar *et al.* (1987) reported that water stress in maize decreased photosynthesis as judged by total plant dry weight and that, grain growth was more sensitive to water deficits during endosperm cell division than during the period of starch deposition. Rahman and Hassaneinn (1987) reported that fresh and dry weight decreased in maize with decreasing soil moisture.

Maximum water requirement of maize occurs during or immediately after anthesis, and that water stress during silking and tasseling are known to reduce grain yield more than at any other period (Demead and Shaw, 1960). Mayaki *et al.* (1976) also observed that maize roots penetrate deeper under conditions of moisture stress than they do when moisture is adequate. It is known that about 80 per cent of the available water in deep soil can be extracted by the roots before

stomatal regulation of transpiration begins (Ritch, 1973), and the most obvious effect of even mild water stress is to reduce growth with cell enlargement being particularly sensitive to water deficit (Hsiao, 1973). Water stress tends to advance flowering in annuals and to delay flowering in perennials. In wheat, for example, mild deficits can advance flowering by up to a week, though with a corresponding decrease in the number of spikelets and in pollen fertility and grain set (Angus and Moncur, 1977 and Morgan, 1980).

2.2.2 Avoidance of plant water deficit

There are three categories of mechanisms by which plants may avoid plant-water deficit. These are drought escape, water conservation and effective water uptake (Fischer and Turner, 1978). A plant that rapidly completes its life cycle, or at least its reproductive cycle, can escape periods of drought and grow during periods of favourable soil moisture. This mechanism is typical of the desert ephemerals that can complete their life cycles from germination to seed maturation in as little as four to six weeks. A similar, though less extreme adaptation is found in many crop plants, where the most drought tolerant cultivars are frequently those that flower and mature the earliest, thus avoiding the worst of the dry season. Many annual plants even show dynamic response of this type, flowering earlier than usual if they are subjected to water stress (Fischer and Turner, 1978). Plant adaptations that limit the rate of water loss can prevent the development of detrimental plant water deficits in two ways: They can either conserve soil water for an extended period, thus maintaining soil (and plant) water potential suitably high over a sufficient period for seed ripening, or else the reduced transpirational flux can reduce the depression of water potential, that results from the frictional resistances in the transpiration pathway. Many plants that are successful in dry habitats have no specific adaptations for controlling water loss

but rely on the development of a very deep and extensive root system that can obtain water from a large volume of soil or from a deep water table (Quarrie and Jone, 1977).

2.3 Screening for drought tolerance

Many plant scientists have conducted researches on different crops under drought conditions to develop selection criterion. For example, Bhan *et al.* (1974) reported that resistant varieties showed deeper root penetration producing heavier and more numerous primary and secondary roots than the susceptible varieties. Begg and Turner (1976) also reported that part of the reduction in osmotic pressure as a result of drought stress was due to a net increase in cell solute concentration and not just due to the loss of water from the cell. Oregan *et al.* (1993) reported in a drought study of maize that resistant genotype had a lower growth rate than the drought sensitive genotype when not stressed, but had a higher growth rate and deeper rooting than the drought sensitive genotype when stressed. The drought resistant genotype has higher relative water content throughout the period of water stress than drought sensitive cultivar. Camacho and Caraballo (1994) studied maize genotypes under drought stress in green house trial for various parameters relating to root and shoot after four weeks of emergence. Cultivars differed significantly in all growth parameters except length of root. They concluded that measurement of dry root weight was the most appropriate criterion for selection of drought tolerant maize genotypes. Petcu and Terbea (1996) evaluated maize cultivars grown in pots in a soil:sand ratio of 3:1 under water stress condition, and observed that dry matter accumulation was lower in water-stressed roots than in the control where plants were watered, and root length was shorter in the water-stressed plants than in control. Khaliq *et al.* (2000) studied wheat genotypes under field

drought condition and reported that stomatal frequency may be a useful selection criterion for increasing grain yield of wheat.

Mehdi and Ahsan (2000) evaluated 500 maize families for seedling traits in C_1 recurrent selection cycle. The study established high values of genotypic coefficient of variation (GCV) for fresh shoot and dry root weight; moderate broad sense heritability for fresh shoot weight, dry root weight and fresh shoot length; and that relative expected genetic advance (GA) was greater for fresh shoot weight and dry root weight. This could be used as selection criteria when evaluating maize genotypes at seedling stage. However, in an experiment on maize under drought stress, Mehdi *et al.* (2001) suggested that dry root weight might be more useful selection criteria, when selecting for superior S_1 families for water stress conditions. Agronomical interventions also play an important role in screening lines for drought tolerance, since genetic solutions were unlikely to close more than 30% of the gap between potential and realized yield under water stress. Campos *et al.* (2004) evaluated, under stress conditions, a set of 18 Pioneer brand hybrids and observed significant, positive genetic gains for grain yield under drought stress conditions. The largest genetic gains for grain yield were observed under conditions of full irrigation. Anthesis-to-silking interval and barrenness, especially under stress at flowering, were significantly reduced, though flowering remained the susceptible stage to drought in maize.

Hader (2006) measured the leaf parameters of maize and reported that leaf area might be a useful indirect indicator for yield improvement in maize crop. Muraya *et al.* (2006) also evaluated seven maize lines: KSTP001, KSTP003, KSTP004, KSTP005, KSTP008, E2 and E3 to study heterosis and inheritance of days to 50% flowering, cob length, number of lines per cob, hundred -grain weight, number of seeds per line, plant height, ear height, leaf angle, number of leaves per plant, leaf area index, cob diameter and grain yield. The study revealed the existence of both

additive and non-additive gene effects for all parameters. Aslam *et al.* (2006) also conducted two experiments to screen 60 maize accessions for stress tolerance with respect to relative cell membrane injury (RCI% age) and stomatal conductance. Broad sense heritability for these traits was also estimated and it was found that RCI% could be used as main selection criterion for drought tolerance in maize. Furthermore, on the basis of this selection criterion, NC-9 was found as highly water-stress tolerant, while T-7 recognized as drought susceptible. Balota *et al.* (2008) concluded that wheat cultivars with high canopy temperature depression (CTD) tend to have higher grain yield under dry, hot conditions and therefore, CTD has been used as a selection criterion to improve adaptation to drought and heat.

2.4 Physiological attributes

Cellular growth is most sensitive to water stress. Kazemi *et al.* (1978) reported genotype differences in stomata number in wheat and suggested that genotype × environment interactions would make it difficult to select for stomata number. In maize, the root weight increased whereas shoot weight decreased with water stress (Aggarwal and Sinha, 1983; Morizet *et al.*, 1983). Drought stress decreased the length and fresh weight of shoot and root in maize (Thakur and Rai, 1984). Shoot elongation was reduced by water stress during vegetative period in maize. In the green house experiment to study the effect of water stress on the vegetative and root growth of maize plants, Ramadan *et al.* (1985) found out that water stress reduced the shoot and root growth, while Hoogenboom *et al.* (1987) observed that root weight increases under moisture stress. Drought tolerant cultivars produced more dry and fresh weights of shoots compared to susceptible ones (Ashraf, 1989). Wu and Cosgrove (2000) found the root:shoot ratio of plants increased when water availability is limiting.

Maize is usually susceptible to drought around the flowering period. Edmeades *et al.* (1999) reported that drought tolerance is closely associated with a short anthesis – silking interval (ASI) and reduced kernel barrenness. Bertrain and Beck (2003) also observed that drought tolerance is associated with increased growth rates of ovaries. Drought tolerance is also closely associated with the stay-green characteristics (Sanchez and Subudhi, 2002). Drought stress delayed the silking and anthesis dates and reduced the grain filling period of each hybrid, but had little effect on the date of physiological maturity in maize (Fredrick *et al.*, 1989). According to Dai *et al.* (1990), moderate water stress inhibited the growth, development and yield of all cultivars and hybrids at different growth stages. The leaf area of resistant cultivars remained larger under drought condition. Drought at seedling stage enhanced root growth and adaptability of all cultivars. Water-stressed sorghum showed larger root:shoot ratio (Xu and Bland, 1993). Sacks *et al.* (1997) characterized the effect of water stress on cell division rates within the meristem of the primary root of maize seedlings and found that water stress caused meristematic cells to be longer and reduced the rates of cell division, per unit length of tissue and per cell, throughout most of the meristem. Terbea and Ciocazamu (1999) also studied response of some seedlings of maize inbred lines to limited water supply and reported that limited water supply in tolerant inbred lines produced a significant increase in photosynthetic rates, root length and lateral root area. Significant decrease in photosynthetic rate, root length, lateral root area and chlorophyll contents were observed in highly drought sensitive lines.

Singh (2005) studied the physiological traits associated with terminal temperature tolerance under late sowing in irrigated wheat and found a significant differential variation for physiological traits with respect to grain yield under high post anthesis temperature (> 28^{o}C) in late sowing. Hirayama *et al.* (2006) evaluated drought tolerance based on leaf temperature in

upland rice breeding. The leaf temperature of the upland rice varieties increased at relatively slower rate than that of the low land varieties. Their temperature and photosynthetic rates was highly correlated with leaf temperature measured using infra-red radiation thermometer during three years. Pandey *et al.* (2000) reported in maize that increasing moisture stress resulted in progressive less leaf area, crop growth rate, plant height, shoot dry matter and harvest index. Khan *et al.* (2001) also investigated the effects of water stress on growth and grain yield of maize cultivar YHS-202, and found that stem height, stem diameter, leaf area and days to complete flowering decreased significantly with increased water stress. Yield components, such as number of grain per cob, thousand-grain weight and yield also decreased by increased water stress.

Ti-dal *et al.* (2006) conducted an experiment to determine the effects of drought on grain yield and yield components of maize and reported that cob characteristics deteriorated and the economic yield of maize decreased significantly under drought conditions. The main factors that caused yield reduction were the decrease of kernels per ear and hundred-kernel weight. Xu *et al.* (2007) investigated the drought resistance from regenerative plants of hairy root cultures, which included plant height stress index, dry matter stress index, dry weight, total absorbing area, active absorbing area, and root:shoot ratio. They reported that there was close relationship among dry weight, dry matter stress index, leaf area, root:shoot ratio and drought resistant index.

2.5 Agronomic attributes

Any change in environmental conditions, such as drought that reduces or adversely changes growth or development is called biological stress (Levitt, 1980). According to Rowland (1993), the extent to which drought affects a growing crop is partly due to the fertility and physical

structure of the soil in which it is growing. A high nutrient status allows the crop to make good growth during periods of favourable rainfall. Root development is important. A strong, deep rooting system can tap more soil moisture in times of drought. Compacted soil resists root growth and development, and may also resist the entry of water.

As the soil dries out from the field capacity, there is an increase in the force resisting the withdrawal of water. This force is the soil moisture stress and has two components; the soil moisture tension and osmotic pressure of the solution (Wadleigh and Ageis, 1945). There is abundant evidence that growth and other processes are progressively retarded as soil water content decreases below field capacity (Hagan, 1956). In general, stress decreases number of grain per plant in maize and lack of pollen increases with increasing drought (Hall *et al.*, 1981). Grain yield will be reduced when maize plants are subjected to water stress conditions one week prior to silking, and two weeks after silking (Claassen and Shaw, 1970). The adaptation of morphological, structural, anatomical and ecological characteristics of plants has been proposed for the genetic improvement of crop plants for drought resistance in maize (Cultere *et al.*, 1977).

2.6 Crop water requirements

The crop water requirement is the amount of water that is needed to meet the evapotranspiration rate so that crops may thrive (FAOSTAT, 2001). It is the amount of water needed to meet the water loss through evapotranspiration. In order to estimate the water requirement of a crop, there is the need to measure the evapotranspiration rate. It is important to identify the growth stages of the crop, their duration and select the proper crop factor (K_c) co-efficient that need to be used.

$ET_c = K_c * ET_o$ (FAOSTAT, 2001), where ET_c = crop water requirement; K_c = crop factor and ET_o = evapotranspiration rate.

The amount of water required by a crop in its whole production period varies considerably (FAOSTAT, 2001), but for optimum productivity, maize requires about 500 to 800 mm of water per growing season, and 7.02 mm of water per day (FAOSTAT, 2001). FAO (2016) reported that the maize crop requires about 508 to 635 mm of water per growing season, and uses 50.8 mm of water per week during the vegetative and reproductive stages of growth. Maize requires the maximum amount of water during the early reproductive growth stages, which are also the most sensitive stages to water stress. When the crop does not receive enough water to meet evapotranspiration (ET_o) demands during the critical water use period, significant reductions in yield may occur. Knowledge of maize water requirements may help guides more efficient irrigation applications. Several factors including crop growth stage, maturity, crop type, weather conditions and soil type affect ET_c and irrigation decisions (FAOSTAT, 2001).

Young plants transpire less than older plants due to a smaller leaf surface area. In maize production, water stress should also be avoided during the reproductive stages (tasseling, silking and pollination). Water stress during silking can have the greatest impact on yield potential due to desiccation of the silks and pollen grains; which will result in poor pollination. Additionally, relative period of maturity of a crop also influences crop water requirements. Long-season maize will require more water over the growing season than short-season maize. Crops such as maize and sugarcane, which are relatively more sensitive to drought, also need more water than crops like millet or sorghum. The ability of the atmosphere to evaporate water is the driving force for soil water evaporation and transpiration. Daily ET_o is influenced by solar radiation, air temperature, relative humidity, and wind. High air temperatures, low humidity, and high winds

cause a large evaporative demand. Soil water holding capacity and soil water content also influence crop water requirements. Fine textured soils can hold more water than coarse textured soils. As the soil dries, it becomes more difficult for plants to extract water. At field capacity, however, plants use water at the maximum rate, but tend to use less water as the water content of the soil drops.

The crop water needs, total growing periods and sensitivity to drought of some annual crops are presented in Table 2.1. The irrigation requirements for various growth stages and the crop factor (K_c) of the maize crop are also presented in Table 2.2.

Table 2.1: Approximate values of seasonal crop water needs, total growing period and sensitivity to drought of some annual crops

Crop	Crop water need (mm/total growing period)	Total growing period (days)	Sensitivity to drought
Barley/Oats/Wheat	450-650	120-150	Low – medium
Cabbage	350-500	120-140	Medium – high
Cotton	700-1300	180-195	low
Maize*	500-800	80-110	Medium – high
Groundnut	500-700	130-140	Low – medium
Rice (paddy)	450-700	90-150	high
Sorghum/Millet	450-650	105-140	low
Soybean	450-700	135-150	Low – medium
Tomato	400-800	135-180	Medium – high

Source: FAOSTAT, 2001; *Knowledge of the seasonal water requirements of the maize crop guided the selection of the watering regimes as stated in the pot study (Experiment I) of Chapter 3

Table 2.2: Irrigation requirements by growth stages of maize and the crop factor (K_c)

Growth stage	Average water use rate (mm/day)	Total water use during stage (mm/day)	Crop factor (K_c)
Emergence	2.03	20.32	0.40
4 – leaf	2.54	45.72	0.40
8 – leaf	4.57	73.66	0.80
12 – leaf*	6.60	45.72	0.80
Early tassel*	8.13	96.52	0.80
Silking*	8.13	96.52	1.15
Blister kernel	8.13	48.26	1.15
Beginning dent	6.10	96.52	1.15
Full dent	5.08	96.52	1.00
Maturity	2.54	35.56	1.00

Source: FAO, 2016; *The vegetative and reproductive stages (from 12 – leaf to silking) of the crop development were considered in making the decision on the watering regimes of the maize plants in Experiment I of Chapter 3

2.7 The striga plant

The genus *Striga* belongs to the dicotyledonous family *Scrophulariaceae* and order *Tubiflorae*. Members of this genus are obligate annual hemi-parasitic plants. They are chlorophyllous but require a host to complete the life cycle (Musselman, 1987). An individual striga plant produces thousands of tiny dust-like seeds that can remain dormant in the soil for 15 – 20 years (Ramaiah *et al.*, 1983). Germination, attachment and haustorial formation are all dependent on striga seeds receiving chemical cues from host roots (Stewart and Press, 1990). *Striga* spp parasitize the root systems of their hosts. All *Striga* species except *Striga angustifolia* (Don.) Saldanha are dependent on a host to establish themselves, which makes them obligate parasites. Most *Striga*

species are annuals but some are perennials (Parker & Riches, 1993). The genus contains 40 species (Wolfe *et al.*, 2005), of which 28 species occur in Africa (Mohammed *et al.*, 2001). By parasitizing crop species, they can cause substantial yield losses and are therefore considered agricultural pests. In cereals three species of *Striga* are major pathogens: *Striga asiatica* (L.) Kuntze, *Striga aspera* (Willd.) Benth and *Striga hermonthica* (Del.) Benth.

Striga is limited to agro-ecosystems and endemic both in West and East Africa. It is a major pest on millet [*Pennisetum glaucum* (L.) R. Br**.],** sorghum [*Sorghum bicolor* (L.) Moench], maize (*Zea mays* L.), rice (*Oryza sativa* L.) and other cereals. Maize is the most susceptible to striga, followed by sorghum and millet (Gurney *et al.*, 1995; Kim *et al.*, 1997). *Striga hermonthica* has generally been associated more with sorghum and millet than with maize and is believed to have evolved with the former crops. Consequently, greater research efforts have already been devoted to sorghum. Maize, a high yielding crop which is a more recent introduction in the savanna of West Africa, now has a larger area devoted to its cultivation than has sorghum (Odhiambo and Ransom, 1995). Striga may not have been a problem in the traditional agricultural system but has become a problem possibly as a result of changes to the agricultural system. These changes were due to processes of agricultural intensification (shortening of fallow periods, continuous cropping, change from intercropping or crop rotations with legumes to cereal mono-cropping**)** that exceeded the carrying capacity of the environment (Kroschel, 1998).

Controlling *Striga* spp is technically difficult in view of the high number of seeds produced per plant (about 100,000) which can remain viable in the soils for up to 20 years (Parker and Riches, 1993). Also, most of the effective control technologies have been developed under high external input agriculture and are not likely to be adopted by African resource-poor farmers. There is, therefore, a need to look for simple techniques as components of the integrated striga control

package adapted to the African situation (Berner *et al.*, 1996). With the exception of *Striga angustifolia* which can possibly establish without the aid of a host, all the other *Striga* spp of agricultural importance are obligate parasites in that the seeds are only 0.2 to 0.4 mm long and can only produce a radicle up to 5 or 10 mm before seed reserves are exhausted. They must, therefore, become attached to a host root within a few days of germination. To ensure that a host root is available, they normally germinate only in response to certain substances exuded by host roots. One natural stimulant, strigol, has been identified (Cook *et al.*, 1972) but the work of Visser and Botha (1974) suggest that there is a wide range of stimulant compounds exuded by different crop species that can trigger the germination of striga seeds.

Striga hermonthica is an obligate outcrosser which occurs only on the African continent and has the greatest agricultural impact of all the *Striga* spp (Adetimirin, 1995). Developing *Striga hermonthica* seedlings can be observed on maize roots without the aid of magnifying lens at 3 weeks after maize planting. As root growth progresses, more striga seeds are intercepted, leading to an increase in the number of underground striga attachments (Adetimirin, 1995). On maize, it is found that underground striga attachments are highest at about 9 weeks after planting (WAP), followed by a reduction at 12 WAP when a number of decomposing striga was observed on maize roots.

Five major stages: germination, attachment, below-ground growth, growth after emergence and seed set, that confer special survival strategies to *Striga* species can be recognized. For dormant seeds to germinate they need to be conditioned (Kim *et al.*, 2002) and subsequently exposed to host root exudates. Striga germination is primarily triggered by a class of specific chemicals (strigolactones) exuded by host root (Lopez-Raez *et al.*, 2008). Proximity to roots is therefore crucial. Different plant species (and varieties within plant species) exude different strigolactones.

Synthetic strigolactones like GR 24 have the same effect (Johnson *et al.*, 1976). Striga germination can also be induced by the application of ethylene (Egley and Dale, 1970). Most plant species exude strigolactones, because these compounds form an essential element in the molecular dialogue between plant roots and arbuscular mycorrhizal fungi (Akiyama *et al.*, 2005). It is likely that *Striga* species have hijacked this molecular dialogue.

The next step involves the establishment of parasitic relation with a host. This happens by means of a haustorium. It is through the haustorium that the host – parasite relationship is established. The haustorium sometimes fails to complete its penetration of the cortex (Ramaiah *et al.*, 1991) and may also fail on reaching the endodermis, which provides a barrier for penetration (Saunders, 1933). The haustorium connections represent a crucial point of weakness in the host – parasite relationship. One could speculate that it is most likely that host specificity (low or high striga attachment and emergence) takes place at this stage.

Upon establishment of the haustorium, the growth of the host plant is already depressed. A large part of the negative effect of host performance due to striga occurs almost immediately after infection and attachment (Van Ast *et al.*, 2000), when the parasite interferes with host metabolism (Gurney *et al.*, 1999). Graves *et al.* (1989) found that parasite-induced reduction in host photosynthesis occurred before emergence of the parasite above ground and accounted for 80% of the predicted loss. The reduction in the mass of infected sorghum plants can exceed the mass of the parasite they support. Yield losses by striga are larger than those induced by species of the holoparasitic genus *Orobanche*. In the latter case differences in biomass between infected and uninfected host can be largely accounted for by the biomass of the parasite (Hibberd *et al.*, 1998). Press *et al.* (1990) concluded that competition for water and solutes by striga are unlikely to play a major role in determining reduction in host productivity. Apart from the direct

withdrawal of host nutrients and water, the parasite disturbs the hormonal balance in its host in order to deflect resource from host growth into its own growth (Graves *et al.*, 1989). Metabolic incompatibility was suggested as a major cause of reduction in host productivity (Press *et al.*, 1990). Rank *et al.* (2004) also reported that the toxic compounds produced by the parasite were the cause of low productivity of the host plants.

After 4-6 weeks of its life underground, striga emerges and it can flower 2-3 weeks after above-ground emergence. Severity of infestation cannot be determined accurately from count of striga numbers emerged, because under high striga pressure only 10-30% of striga on the roots emerge above the soil surface (Thalouarn and Fer, 1993). In its above-ground stage, striga has green leaves and is partly autotrophic for carbon, although data suggest that more than 50% of the carbon above-ground is from its host (Press *et al.*, 1991). Carbon fixed by striga is predominantly allocated to making new leaves, while support tissue still depends on photosynthates provided by the host (Santos-Izquierdo *et al.*, 2008). Striga produces many minute seeds. The number of mature seeds per plant may be up to 200,000 (Parker and Riches, 1993). The minute seeds do not have any seed reserves, and therefore seed germination is linked to the proximity of suitable hosts. Striga seeds can persist in the soil until appropriate hosts are available and can remain viable in the soil for a long time. Bebawi *et al.* (1984) reported that *Striga asiatica* seeds remained viable in the soil for 6 years. A population dynamics model (Van Mourik *et al.*, 2008) indicated that it is the high seed bank generated by a single mature striga plant that poses the real problem rather than actual seed longevity. Depleting seed banks through hand-pulling and removing striga plants before seed set and dispersal in infested fields remains a major challenge in striga control.

2.8 Ecology of striga

Relatively high temperatures around 30°C are known to be optimal for conditioning, germination and growth of *Striga hermonthica*. *Striga asiatica* has been shown to germinate, develop and mature on sorghum at a mean daily temperature of 22°C (Patterson, 1990). In general, both *Striga hermonthica* and *Striga asiatica* are known to thrive best under conditions of erratic or limited rainfall and may be suppressed by irrigation (Andrew, 1945). It has been suggested that in Northern Ghana frequent occurrence of *Striga hermonthica* on soils with a coarse texture and low organic matter content could be due to the fact that these soils are prone to moisture stress (Stoop, 1983). Recent results obtained in Ghana and Togo have shown that infestation of *Striga hermonthica* was positively correlated with continuous land use and with stone and gravel content, while there was negative correlation with organic matter content (Vogt *et al.*, 1991). It has been observed that intense land use can be attributed to the greater opportunity for the build-up of the striga population. However, it has also been demonstrated that striga may be suppressed to some degree by increased application of nitrogenous fertilizer (Parker and Riches, 1993).

The period required for striga seeds to remain dormant is known as 'after-ripening'. Imbibition of water by striga seeds for at least a week before exposure to stimulant is referred to as 'pretreatment', 'conditioning' or 'preconditioning'. Parker and Reid (1979) found in the laboratory that with a range of strains of *Striga asiatica* and *Striga hermonthica*, the optimum period of conditioning striga seeds varied from 1 to 5 weeks. They further observed that *Striga asiatica* responded better to conditioning at 33°C than at 23°C, while the reverse is true for *Striga hermonthica*. The biochemical processes that occur during conditioning are not yet fully understood. However, an important discovery explains that conditioning in the presence of

germination stimulant reduces the subsequent germination (Hsiao *et al.*, 1979; Pavlista *et al.*, 1979). Vallance (1950) showed that prolonged imbibition of water by striga seeds results in a steady decline in germination of *Striga hermonthica*. Reid and Parker (1979) confirmed this phenomenon with several strains of *Striga hermonthica*. The importance of this phenomenon in the pattern of development of striga infestation in the field needs a great deal of study. A suitable temperature is required for germination. Detailed work has not been done on many strains but Reid and Parker (1979) revealed a sharp fall in germination percentage below 30°C for both *Striga hermonthica* and *Striga asiatica*.

Striga is found mainly in the tropical arid and semi-arid zones of Africa, Europe and Asia, with an annual rainfall of 400 – 1000 mm. Striga occurs in areas where the dominant vegetation is natural savanna or grassland. Africa is the presumed region of origin (Wolfe *et al.*, 2005). *Striga asiatica* is the most widespread species, occurring in Africa, Asia, Australia and New Zealand (Bharathalakshmi and Jayachandra, 1979) and even in the United States of America. *Striga hermonthica* occurs mainly in Africa and is distributed throughout the semi-arid areas of northern and southern tropical Africa. *Striga hermonthica* also extends into Arabia, Angola, Namibia and Madagascar (Musselman and Hepper, 1986). In West Africa, *Striga hermonthica* is considered a weedy introduction because it does not occur in native grassland and it is widely accepted that it spreads together with sorghum to the area (Musselman *et al.*, 1988). About 35 species of this genus are believed to exist of which at least 11 are known to attack crops (Raynal-Roques, 1991). Out of these, seven are of economic importance in Africa. These include *Striga hermonthica* (Del.) Benth, *Striga asiatica* Kuntse, *Striga densiflora*, *Striga euphrasioides*, *Striga aspera* (Willd.) Benth, *Striga forbesii* (Benth) and *Striga gesnerioides* (Willd.) Vatke (Ramaiah *et al.*, 1983). *Striga hermonthica* parasitizes all of the major cereals (sorghum, maize, millet and

rice) while *Striga gesnerioides* attacks mainly cowpea (*Vigna unguiculata*) and tobacco (*Nicotiana* spp). There are also free-living members in the family *Scrophulariaceae* which do not parasitize crops. These include the Snapdragon (*Antirrhinum* species) and the weedy speedwells (*Veronica* species).

2.9 Losses caused by striga

Striga has been a major threat to the growth and production of some major cereals and legumes in the semi-arid regions of tropical Africa. The area in Africa infested by S*triga* species is estimated to be 50 million ha, with 300 million farmers being affected. This results in estimated losses of US$7 billion (Parker, 2009). Hearne (2009) reported of yield losses ranging from 35-72%. These parasitic plants thus represent one of the largest biological constraints to food production in Africa. It is likely that striga is the largest constraint to maize production, whereas for sorghum and millet striga comes second after granivorous birds. For Northern Cameroon, Ayongwa and Ngoumou (2001) stated that striga is the most persistent biological constraint to cereal production compared to insect pests, granivorous birds or elephant herds on rampage. The production of cereals in the Northern Regions of Ghana is menaced by the threat of low productivity as a result of the parasitic weed, *Striga hermonthica* (Sauerborn, 1991).

Striga causes serious economic losses to many host plants ranging from agricultural crops to wild grass species. The crops mostly affected are maize (*Zea mays* L), sorghum (*Sorghum bicolor*), millet (*Pennisetum glaucum*), cowpea [*Vigna unguiculata* (L.) Walp], tobacco (*Nicotiana tabacum* L.), sugarcane (*Saccharum officinarum* L.) and rice (*Oryza sativa*) (Mboob, 1986). The effect of the parasite on the host is manifested by the amount of carbohydrate that is removed.

According to Ramaiah and Parker (1981), when the total dry weight of *Striga hermonthica* in the root system of sorghum or maize is less than 1% of the total dry weight of the host, the host dry weight may be reduced by as much as 25%. This reduction in host weight starts initially from the shoot. The root development of the host is often significantly increased. However, reduced shoot growth eventually results in gross reduction of the whole plant system. Striga infestation is not only a biological constraint to food production in Sub-Saharan Africa but also a socio-economic problem to resource-poor farmers (Salle, 1991).

2.10 Effects of striga on growth and development of crops

The total dependence of striga on its host for organic food substances is obvious, but for the typical green-leafed species (*Striga hermonthica and Striga asiatica*) it is supposed that they could photosynthesize most of the sugars they require, once they emerge from the soil. However, studies on several species have revealed that the chlorophyll content of striga is not only low, but has an efficiency of about 20-30% of a comparable non-parasitic plant (Stewart and Press, 1990). Further investigations indicated that in *Striga hermonthica* the rate of photorespiration is very high and as a result net gain from its own photosynthesis may be very little. Using ^{13}C isotopic carbon, Press *et al.* (1987) measured the organic carbon derived from a host sorghum plant by the parasite to be around 35% of its total organic carbon content and this was even more from millet (Graves *et al.*, 1990). In *Striga hermonthica* and *Striga asiatica* the net photosynthetic value is reported to be five times lower than that observed in the host plant. Graves *et al.* (1990) again pointed out that the loss in photosynthetic efficiency by the parasite could be due to the fact that the amount of amide and amino acid needed to provide its nitrogen requirement carries with it a highly significant quantity of elaborated carbon.

The parasitic effects of striga on growth of their hosts are thought to go beyond simple removal of resources because the reduction in host growth has been shown to be enormously greater than is explained by this process. Reduction in sorghum weight by *Striga hermonthica* when the parasite was a few millimeters long was at least 30 times the weight of the parasite (Parker, 1984). Marked changes in root:shoot ratio in parasitized sorghum have been reported (Parker and Riches, 1993). At 7 weeks after planting, the root:shoot ratio of *Striga hermonthica* infested plants was 0.61 compared to 0.25 in the unparasitized plants. The shoot system remained stunted. In maize, *Striga asiatica* is reported to have a similar effect. The root:shoot ratio was 0.35 and 0.90 in healthy uninfested plants and infested plants, respectively after 10 weeks following infestation.

The main effects of parasitism is that photosynthetic capacity may be reduced to less than half of that occurring in healthy plants (Press and Graves, 1991). It is estimated that this reduction in photosynthesis in the host results in 80-85% growth reduction in infested sorghum while 20% of the damage is as a result of actual removal of carbon by the parasite (Graves *et al.*, 1989, 1990). Wylde (1991) has reported that a further parasitic effect of *Striga hermonthica* on pearl millet is a marked reduction in the amino acid content of the grain. The mechanism for reducing the photosynthetic capacity of parasitized plants is still under speculation, but the interference with the host water balance resulting in the closure of its stomata and the loss of nitrogen are suggested possibilities. Yield losses in the field can be as high as 65% in sorghum (Bebawi and Farah, 1981). Okonkwo (1966) attributed yield losses to the diversion of photosynthates, mineral salts and water from the host to the parasite.

As a root parasite, *Striga hermonthica* can affect its host in different ways, including reduction in growth and yield. Only part of the reduction in the growth of the host results from competition

for carbon assimilates, water, mineral nutrients and amino acid (Pageau *et al.*, 1998; Taylor and Seel, 1998). However, striga does not only act as an additional sink but the parasite has a strong 'toxic' or 'pathological' effect on the host (Press and Stewart, 1987; Graves *et al.*, 1990). Part of these effects is caused by the disturbed hormonal balance in striga-infected host plants, characterized by increased levels of cytokinins and gibberellins (Fros *et al.*, 1997; Taylor *et al.*, 1996). By altering the host hormonal balance, striga affects host biomass allocation, resulting in the root systems of infected plants being greatly stimulated, while the shoot is stunted and reduced (Parker and Riches, 1993). The parasite also negatively affects host photosynthesis (Smith *et al.*, 1995; Watling and Press, 2001). Parasite induced reduction in host photosynthesis has been reported as the most important mechanism of growth reduction. Graves *et al.* (1989) estimated that 80% of the decrease in host growth rate can be attributed to the impact striga has on host photosynthesis.

Furthermore, striga strongly affects the water economy of its host by its high transpiration rate and by reducing the stomatal conductance of the host plant (Gebremedhin *et al.*, 2000; Fros *et al.*, 1997; Taylor *et al.*, 1996). Leaf number and green leaf area were reduced by 10% and 34%, respectively. As fewer leaves were produced over a longer period of time, leaf appearance rate was reduced by 21%. Egley (1971) found that striga reduced shoot yields by about 70% at low nutrient level and by about 45% at the highest nutrient level. Gworgwor and Weber (1991) showed that severity of striga attack on sorghum was highest at zero N application where striga emergence was very early on sorghum followed by the low N rate and the lowest attack at the higher and moderate rates of N. In the most infertile soils striga numbers may again go down most probably due to fewer attachment sites on a malnourished host to sustain as much parasites (Ikie *et al.*, 2007).

Infection by striga can cause yield losses of a few percentages up to complete crop failure, depending on the crop variety and striga seed infestation level of the soil (Adetimirin and Aken'Ova, 2000; Rodenburg *et al.*, 2005; Van Ast *et al.*, 2000). Yield was lower when there was a higher striga infestation. Van Ast (2006) observed a proportional 4.3% increase in yield reduction per emerged striga plant in a pot experiment. However, estimating quantities in this relationship under field conditions is very far from resolved. The striga density-dependence (Rodenburg *et al.*, 2006a; Van Ast, 2006; Van Mourik *et al.*, 2008) makes it difficult to quantify the relationship between yield and striga infestation. Finally, because even a tiny number of striga plants may cause a disproportionate fall in host yield, striga counts are unreliable as indicator for yield reduction in the field (Graves *et al.*, 1989; Gurney *et al.*, 1999).

Striga reduced the height, dry matter and grain yield of maize. The reduction in height and dry matter increased with age. In a study to determine the response of maize cultivars to *Striga hermonthica*, it was found that the pattern and severity of the reductions were dependent on host genotypes. Grain yield losses are determined by the levels of resistance or tolerance of the host genotype to *Striga hermonthica* (Rodenburg *et al.*, 2005). Grain yield losses are also determined by the severity of striga infestation and by the levels of soil fertility. Highly susceptible crops or cultivars can be so severely damaged that ultimately striga growth and seed production itself is negatively affected (Kim *et al.*, 1997). Tolerant varieties suffer lower yield reduction and often produce 2 to 2.5 times the yield of susceptible varieties, especially under high infestation (Kim *et al.*, 2002). However, tolerant varieties contribute as much as or even more than susceptible varieties in the build-up of a striga seed bank. Oikeh (1996) observed that grain yield losses ranged from 10 – 100% for maize and sorghum as a result of striga infestation. In a study to compare the yield of striga-infested and striga-free experiments, Badu-Apraku *et al.* (2013)

reported that under striga-infested conditions maize yield ranged from 2537 kg/ha to 3122 kg/ha, while under striga-free conditions, grain yield ranged from 3646 kg/ha to 4227 kg/ha.

As striga is a root parasitic plant, determination of the actual infection level requires uprooting of the host plant, which is a laborious and destructive measurement. Consequently, not much is known on the relationship between soil infestation and infection level. For practical reasons, the number of above-ground striga plants is often used as an indication of parasitic pressure (Doggett, 1995). Most effects occur almost immediately following infection (Press *et al.*, 1996; Van Ast *et al.*, 2000), indicating that shortly after attachment the parasite interferes with host metabolism, ultimately resulting in yield reduction. One obvious way of influencing these relations is through the selection of resistant and/or tolerant maize cultivars. Resistance against striga reduces the infection level of a host plant, while tolerance enables a host plant to perform well, despite the parasitic infection. Host resistance is thought to be the most economical and potentially the most effective control option against root diseases and soil borne pathogens (Shew and Shew, 1994) and therefore a potentially acceptable striga control option to resource-poor farmers (Hess *et al.*, 1992; Debrah, 1994). Complete resistance or immunity against striga has not been found. This is because few striga infections already seriously harm the host plant. Resistance alone may not be enough to prevent crop losses. It is therefore recommended to direct breeding efforts towards finding cultivars that combine resistance with high levels of tolerance (Haussmann *et al.*, 2001; Rodenburg *et al.*, 2005).

2.11 Striga control methods

Several control measures have been suggested for striga. Some of the methods commonly used include cultural, biological and chemical methods as well as crop seed treatment, host plant resistance, inorganic and organic fertilizers and integrated control (Lagoke *et al.*, 1994).

2.11.1 Cultural method

The method of land preparation and time of planting can be used to effectively control *Striga* spp. Deep cultivation, to bury striga seeds, has been used to control the parasite effectively in Mali (Konate, 1986). Striga infestation can also be reduced or avoided by planting early to establish the crop before temperatures are high enough for striga especially in Africa, and planting late when rains become more continuous, to avoid the intermittent drying cycles which favour striga germination (Ramaiah and Parker, 1981). Crop rotation can also be used for combating striga. Any rotation with a non-host crop will tend to reduce the striga problem. Infestation by parasitic weeds and their virulence on host crops have always been associated with low soil fertility. It is therefore, generally believed that the application of nutrients in the form of either inorganic fertilizer or farm yard manure, reduces both the infestation of fields by striga and losses in crop yield (Parker, 1984). The use of fallow has also proved to be an effective method of striga control. The wide host ranges of the parasitic weeds include plants that are usually present in the fallow. Multiple infestation of the same field by various parasitic weeds precludes their effective control through the use of fallow.

Hand pulling and hoe weeding are the most common practices used by small-scale farmers. In Gambia, most farmers control striga by the second or late hoe weeding or hand pulling near harvesting time (Carson, 1986). Hand weeding is practised in Guinea but the result has not been encouraging. In Ghana, hoe weeding is still practised by majority of farmers (Nyarko, 1986).

Hand pulling at too early a stage may result only in breakage of the shoot below the soil and rapid re-growth may occur. Hand pulling reduces the competition between striga plants on the host root system and result in increased emergence (Ogborn, 1972). Dense infestations are not practical to hand-pull but sparse infestations should be hand-pulled shortly before flowering to protect yield and to prevent build-up of seeds. Once the crop is harvested, pulling the crop stubble will help to prevent continued growth of the parasite. Control of striga can only be achieved through the integration of various methods in a package. The use of an appropriate trap-crop, such as soybean, cotton or bambara groundnut, for one or more years in rotation with a resistant/tolerant cereal crop variety will go a long way to reduce the number of striga seeds in the soil (Berner *et al.*, 1996; Kling *et al.*, 1996).

2.11.2 Biological control

Trap and catch crops can be used as an effective control measure for striga. Both trap and catch crops induce the germination of striga seeds but whereas trap crops are not parasitized, catch crops are. Therefore, they have to be destroyed as soon as they are infected (Lagoke *et al.*, 1991). However, the limited resources available to small-scale farmers make the use of trap and catch crops unacceptable, since it involves labour and other inputs, without an immediate benefit. Soybean, cotton and bambara groundnut are some of the trap crops. When these crops are grown in rotation with a susceptible host or as an intercrop, they are reported to induce abortive germination of striga seeds with a consequent reduction in infestation (Parkinson *et al.*, 1986). Ramaiah and Parker (1981) and Greathead and Milner (1971) suggested the use of *Smicronyx* and *Ophiomiya* in India and *Eulocastra argentisparsa* in East Africa. The butterfly (*Precis orithya* Swinhoe) has also received attention both in South East Asia (Boonnitee, 1977; Mangoendihardjo and Soerjani, 1978) and in USA (Ramaiah and Parker, 1981). The larvae have

a voracious appetite for striga foliage but their specificity to *Striga* species is yet to be confirmed.

2.11.3 Chemical control and crop seed treatment

Research has shown that certain chemicals such as ethylene gas (ethephon), strigol and strigol derivatives can induce abortive germination of striga seeds in the absence of a suitable host, and therefore lead to depletion of the seed reserved in the soil. This method may be used either alone at the beginning of the season, prior to cultivation, or in combination with suitable herbicides that could kill the seedlings before attachment to the host. The use of ethylene gas has been highly efficient in USA (Eplee, 1981). However, high level of skill required for its application and the cost involved make it difficult for the small-scale farmers in developing countries to adopt this method. Methyl bromide is used (as a fumigant) on a local basis in the USA at about 200 kg/ha. But owing to its high cost, it is appropriate only to the intensive eradication programme in that country, or to the establishment of clean pots for experimental purposes. A very large number of herbicides have been tested in the USA and a number are used in various ways in the striga eradication programme (Langston *et al.*, 1979). The most important chemical/herbicide is 2, 4 – D sprayed twice as a post-emergence directed treatment in maize to kill emerged plants and prevent seed production. Oxyfluorfan as an early post-emergence directed spray has been shown to be effective in preventing striga emergence but it does not necessarily prevent attachment to the roots below the herbicide layer and the crop may still suffer striga damage. Paraquat and glyphosate may be used as late directed treatments to kill late emerging plants. Working with mixed crops where 2, 4 – D is not safe, it has been found that spot applications of ametryne, bromoxynil and linuron are effective substitutes to 2, 4 – D (Ogborn, 1972). Farmers in Sokoto State, Nigeria, have observed that soaking the crop seed in

brine or an extract of *Parkia filicoides* reduces striga infestation, while in Mali the use of nere (*Parkia biglobosa*) powder has been shown to be effective (Konate, 1986). Researchers at the National Cereals Research Institute, Nigeria have claimed some degree of success with brine and locust bean extract (Ramaiah and Parker, 1981). Hardening of maize and sorghum seeds in solutions of phenolic acids resulted in reduced stimulant exudation by the seedlings, and thus could confer increase resistance (Bharatalakshmi and Jayachandra, 1980). Though this method requires further investigation, it is unlikely that seed treatment alone will effectively control striga.

Though several classes of chemicals have been shown to illicit striga seed germination, the sorgolactones appear to be the most common and important in terms of controlling striga germination in the field (Hauck *et al.*, 1992). It has also been determined that low production of striga seed germination stimulant is inherited as a single recessive gene (Vogler *et al.*, 1996). A large number of phenolic compounds have been shown to function as haustorial initiators in striga but the active signals from host roots have not yet been identified. A simple quinone, 2, 6-dimethoxy-p-benzoquinone (2, 6 – DMBQ), though not found in root exudates have been shown to act as a strong haustorial initiating factor (Lynn and Chang, 1990). Exposure to ethylene causes striga seeds to germinate. Haustoria are only observed if the maize root produces a signal that induces its development (Ejeta *et al.*, 1999). Presence of haustoria can be detected around the growing host root at two days after ethylene treatment under a stereomicroscope (Ejeta *et al.*, 1999). In some genotypes, necrotic areas appear at striga attachment sites on the maize root. These necrotic lesions may be large, spreading up to 2 mm from the centre of attachment but most remain localized. Attached striga most often develop poorly, eventually dying on the host (Ejeta *et al.*, 1999).

2.11.4 Host plant resistance and screening for resistance/tolerance

Though some control methods as described above are available, they have not become popular at the subsistence farmers' level either because they are not practicable or are very expensive. Resistant crop cultivars on the other hand require no costly inputs. As striga incidence is influenced by soil type, fertility and rainfall; host resistance is not just the result of interaction between the host and striga, but also of their independent interaction with climatic factors. This is further complicated by the presence of physiological strains within *Striga* spp. Knowledge of physiological strains has a very important bearing in developing broad-spectrum stable resistant cultivars (Ramaiah and Parker, 1981). To date, the best understood mechanism of striga resistance is the low production of host plant root exuded compounds that are essential for striga seed germination (Lynn and Chang, 1990). Targeting the early stages of the host and parasite relationship, a laboratory procedure was developed that separates maize genotypes on their capacity to produce the exudates required for striga seed germination (Hess *et al.*, 1992). It was established that maize genotypes vary significantly in the amount and type of the germination signal they produce (Netzley *et al.*, 1988; Weerasuriya *et al.,* 1993). Maize genotypes that produce very low levels of the germination stimulants have been found to be resistant/tolerant to striga in field tests (Ramaiah, 1987; Hess *et al.,* 1992).

There are two techniques for screening for resistance/tolerance to striga. These include field and laboratory techniques. In general, field screening on naturally striga infested fields gives less consistent results because of non-uniform distribution of striga seeds in an experimental area. Deliberate artificial infestation of the experimental plots should lead to uniform striga infestation. Creation of a sick plot is thus an important requisite for reliable and consistent results. Artificial infestation of the fields could be done in several ways: broadcasting the seeds

in the beginning of the season and incorporating them by ploughing, or sowing the striga seeds with a seed drill (tractor driven or hand pushed) in rows to be planted for the test material. Both of these methods have given good results in India and Burkina Faso (Ramaiah and Parker, 1981). The criteria for evaluating the test material for striga resistance/tolerance include: number of emerged striga plants, and yield and/or agronomic expression in a sick plot. The basis for selecting against striga thus, could be no or a low number of emerged striga plants plus a higher yield. Simple laboratory techniques are very valuable in view of the difficulties encountered in field screening. A technique has been developed by Reid and Parker (1979) to identify low stimulant crop cultivars. The technique involves: pretreatment of striga seeds at about 25^{o}C for 10-14 days, growing of host crop seedlings for one or two weeks in sterilized sand pots and germinating the pretreated striga seeds with host root exudate in an incubator at 30 – 35^{o}C for 24 hours.

2.12 Diallel crossing and combining ability

The diallel crossing system is a genetic model that allows a penetrating analysis into components of genetic variation. Diallel crosses involve crossing a set of parents in all possible combinations or in a specifically defined combination (Griffing, 1956). In a complete diallel, all possible combinations between parents and their reciprocals are made. With *p* parents, the total number of families or populations would be p^2. If neither parents nor reciprocals are included in the analysis of progeny from crosses among *p* parents, the result is a half-diallel and the number of families produced is determined by the following formula: $p\ (p\text{-}1)/2$ (Griffing, 1956). Diallel analysis is therefore regarded as a special type of progeny testing. For the purpose of this study, the complete diallel was used.

Combining ability studies provide information on the genetic mechanism controlling quantitative traits and enable the breeder to select suitable parents for further improvement or use in hybrid combinations. General combining ability (GCA) has been recognized for many years as the relative performance of individuals in a similar group of organisms when crossed with a heterogeneous tester (Griffing, 1956). Specific combining ability (SCA) involves the progeny performance resulting from a particular cross as related to the performance of other particular crosses of a similar nature. It was said that a specific parental combination was desirable or undesirable and the superiority or inferiority of the cross was a result of high or low specific combining ability. General combining ability is a good estimate of additive gene action, whereas specific combining ability is a measure of non-additive (dominance) gene action.

Fisher (1918) divided the genetic variance into three components: additive, dominance and interaction components. Additive gene component is the component arising from differences between the two homozygotes for a gene, for example 'AA' and 'aa'. Dominance gene component is due to the deviation of heterozygote (Aa) from the average of the two homozygotes (AA and aa) (Fisher, 1918). This is sometimes referred to as intra-allelic interaction. Interaction or epistatic component results from an interaction between two or more genes. In crop improvement, only the genetic component of variation is important since only this component is transmitted to the next generation (Fisher, 1918). The ratio of genetic variance to the total variance, that is, phenotypic variance, is known as heritability. Thus heritability denotes the proportion of phenotypic variance that is due to genotype, that is, heritable (Fisher, 1918). Heritability estimated in this situation is known as broad sense heritability. Broad sense heritability estimates are valid when homozygous lines are studied. Additionally, the ratio of additive component of variance to the total phenotypic variance is an estimate of narrow sense

heritability. Narrow sense heritability is more important when dealing with segregating populations.

Beck *et al.* (1990) evaluated ten parents and their crosses for grain yield and plant height at six locations in Mexico. General combining ability was significant for all traits while specific combining ability was not significant for any. Brenner *et al.* (1991) also studied eight maize population and their 56 hybrids obtained by diallel crossing at Rio Pardo, Brazil in an 8×8 duplicated simple lattice design. They observed that additive (GCA) effects were more important, while reciprocal and specific combining ability (SCA) effects were important only in specific crosses. Ali (1993) used 6×6 diallel crossing system and found that GCA mean squares were highly significant for all the yield components. Furthermore, SCA mean squares were highly significant possessing more in five yield components, there by manifesting non-additive action, and in other four characters additive gene action. El-Hosary *et al.* (1994) studied GCA and SCA and their interactions in 28 F_1 hybrids of crosses among eight maize inbred lines. Both GCA and SCA were detected as significant for all traits. Singh and Mishra (1996) also observed general combining ability and specific combining ability using diallel analysis of eight inbred lines of maize for yield. Highly significant differences among the lines were recorded and general combiners were identified.

Revila *et al.* (1999) studied ten maize inbred lines in diallel fashion including reciprocals for plant height and reported of significant general combining ability and specific combining ability effects for plant height. Dubey *et al.* (2001) reported significant mean squares for hundred-grain weight. Specific combining ability variance was greater than general combining ability variance. Shreenivasa and Singh (2001) studied 7×7 half diallel cross involving relatively drought tolerant inbred lines of maize under water stress environment during the crop season. Significant

differences for general combining ability and specific combing ability effects were observed. Vacaro *et al.* (2002) evaluated twelve maize inbred lines and their crosses to estimate combining ability as source populations in breeding programmes in Brazil. Plant height and grain yield were recorded in the field experiments. The results indicated that the mean squares for general combining ability were greater than specific combining ability for all traits under study. Tabassum *et al.* (2005) evaluated 8×8 diallel for combining ability under normal and stressed conditions and reported that all traits under study were under the control of non-additive type of genes except plant height that was under the control of both additive and non-additive types of genes.

Parmar (2007) also studied genetic analysis in ten maize inbred lines and all their possible cross combinations excluding reciprocals in a diallel fashion and reported significant GCA and SCA variances on pooled basis. Akbar *et al.* (2008) evaluated combining ability and recorded GCA:SCA variance ratio exhibiting preponderance of non-additive genes for all the traits under study and found grand mean reduction in various traits. Desai and Singh (2001) conducted 7×7 half diallel crosses of maize inbred lines and reported significant differences in general combining ability and specific combining ability for plant height. Machikowa *et al.* (2011) reported that SCA were highly significant for plant height in sunflower and revealed that non-additive effects were important for plant height. Vaghela *et al.* (2011) also reported that the variance due to SCA was higher than variance due to GCA for some characters. Kumar and Sharma (2007) analyzed the gene effects using mean stomatal number and specific leaf weight of twelve populations of *Triticum aestivum* L. Additive gene effects were predominant for specific leaf weight while for stomatal number, both additive and dominance components of variance were important. Epistatic effects, particularly the additive × dominance type of interaction, were

present for both the characters. Significant heterosis was observed for some crosses as compared to the standard check. Eight genetically diverse inbred lines were crossed by Mahajan and Khera (1991) in a diallel fashion, excluding reciprocals, and the resulting 28 F_1 hybrids were evaluated at eight environments. Results indicated that additive type of gene action was involved for plant height.

Damborsky *et al.* (1994) also studied 7 inbred lines and their hybrids from a complete set of crosses and reported that grain yield was mainly conditioned by additive gene action. Dutu (1999) studied phenotypic and genotypic variance effect on grain yield in 56 simple hybrids from a diallel cross and reported that additive gene action was predominant in the inheritance of grain yield. Farshadfar *et al.* (2002) investigated the genetic properties of some physiological and agronomic characters in maize. High narrow sense heritability and additive gene action were found to be predominant for relative water loss, excised leaf water retention, seed weight and number of ears per plant. Yadav *et al.* (2003) carried out the genetic analysis according to variety cross diallel model involving eight diverse maize composites possessing various levels of tolerance to moisture stress under optimum moisture and rain-fed conditions. The variance due to dominance effect was significant for days to 50% silking and tasseling, leaf area, plant height and cob width under both moisture situations. Variance due to additive effect, dominance effect, general and specific combining ability was significant for grain yield under both irrigated and rain-fed conditions. Sayar *et al.* (2007) studied the general combining ability and specific combining ability effects in wheat and found them to be significant for traits such as deeper root length and grain yield. However, additive gene effects were predominant over non-additive effects. Broad-sense and narrow-sense heritabilities were also significant for deeper root length, confirming the importance of additive gene effects. Srdic *et al.* (2007) found that there was

inheritance of maize grain yield and grain yield components, such as number of rows of kernel, thousand-kernel weight and number of kernels per row. General and specific combining abilities were highly significant for all the observed parameters. Dominant gene effects were more significant in maize grain yield and number of kernels per row, while additive gene effects were more important for number of kernel rows and thousand-kernel weight. According to Ojo *et al.* (2007) GCA mean squares were highly significant for grain yield in maize and additive gene action was more important than non-additive gene action for grain yield. Asefa *et al.* (2008) conducted an experiment to determine the combining ability of highland maize inbred lines for ear length, hundred-kernel weight, ear height, shelling percentage and grain yield. Results indicated that the mean squares due to genotypes were significant for all traits, except for thousand-kernel weight and shelling percentage.

2.13 Screening for DNA polymorphism

Drought and striga affect virtually all aspects of maize growth in varying degrees at all stages, from germination to maturity. Tolerance to drought and *Striga hermonthica* is genetically and physiologically complicated and inherited quantitatively. Modern molecular tools and techniques can complement conventional approaches to allow breeders to effectively address priority research areas. Application of molecular-marker aided selection techniques for improvement of drought and/or striga tolerance would accelerate breeding progress by increasing selection efficiency. Polymorphism is the difference in homologous DNA sequences that can be detected by the presence of fragments of different lengths after digestion of the DNA samples in question with specific restriction endonucleases (Paterson, 1996).

The term 'Molecular breeding' is now popularly used for the utilization of molecular (DNA-based) tools, including markers, to enhance the efficiency of the breeding process. Molecular markers or genetic markers are DNA sequences associated with certain parts of the genome and they have well defined genotypes (Paterson, 1996). They can also be defined as DNA species that flag the presence or absence of particular traits (Paterson, 1996). Considering their abundance, molecular markers are powerful tools that speed and increase the precision and the effectiveness of plant breeding (Paterson, 1996). Molecular markers allow selection for traits on the basis of simple laboratory tests on a small plant tissue, rather than direct measurements of the character itself in the field. Molecular markers also showed great potential in selection and manipulation of genotypes for desirable quantitative traits loci (QTLs) that condition complex economic traits (Ejeta *et al.*, 2000). These markers detect differences in genetic information carried by two or more individuals. They are either DNA or non-DNA based. Non-DNA molecular markers are mainly isozyme and/or allozyme markers. DNA markers have the potential to aid plant breeding programmes through diverse ways, such as fingerprinting of elite genetic stocks, analysis of genetic diversity, and increasing the efficiency of selection for traits.

Among the array of DNA-based markers available to plant scientists, the ones most commonly used are simple sequence repeats (SSR), restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD) and amplified fragment length polymorphism (AFLP). Excellent reviews are available discussing the genetic bases of various DNA-based markers, the means for detecting molecular polymorphism, and the strengths and constraints associated with different markers for various applications (Karp *et al.*, 1997; Liu, 2002). The most appropriate markers for a particular application will depend on the target crop, its breeding behaviour, specific objectives of the experiment, the resolution required, and the

operational/financial constraints, if any. For example, for genetic linkage map development, any type of molecular marker may be used. However, co-dominant markers such as RFLPs, SSRs or SNPs, provide more genetic information in F_2 and backcross generations than markers detecting predominantly the presence or absence, or dominant polymorphism such as RAPDs or AFLPs. Among the different types of PCR-based DNA markers available for diverse applications in breeding, SSR markers are often preferred for simplicity and effectiveness. The SSR markers are often robust, co dominant, hyper variable, abundant, and uniformly dispersed in plant genome (Powell *et al.*, 1996a, b). Microsatellites, also known as SSR markers, have been widely used in maize genetics and breeding for its advantage of abundance in maize genome, co-dominance and a high polymorphism rate (Powell *et al.*, 1996a, b). Technical efficiency and multiplex potential of SSRs make them preferable for high throughput mapping, genetic analysis and marker aided selection. Simple Sequence Repeats (SSRs) are the DNA markers of choice for genetic analysis in maize due to their relative abundance and simple reproducible assays using agarose gel (Singh et al., 2010). High level of polymorphism at SSR loci than the use of other types of markers makes SSR markers more useful to interpret population structure results (Cho et al., 2000).

It has been reported by investigators (Semagn *et al.*, 2006a; Semagn *et al.*, 2006b; Korzum, 2003) that SSR markers require very little DNA unlike other types of molecular markers. It is important that one should select those polymorphic markers that are tightly linked to the striga and/or drought resistance QTL. In this case, polymorphism should be determined by the differences in allele sizes among the parents after allele scoring (Collard *et al.*, 2005). Simple Sequence Repeat markers are effective in detecting polymorphism as has also been reported by Korzum (2003).

CHAPTER THREE

GENERAL MATERIALS AND METHODS

3.1 Introduction

In this chapter, a brief description of the study area is provided. The chapter deals with the general details of the experiments undertaken in the 2013, 2014 and 2015 cropping seasons in the plant house of the Faculty of Agriculture, University for Development Studies, the research fields of the Savanna Agricultural Research Institute (SARI) and the Golinga Irrigation Dam. Details of the procedures adopted in the field measurements of experimental variables are also provided. Specific details of experimental design and allocation of treatments are also presented in the relevant chapters on individual experiments.

3.2 The study area

The study was conducted at Nyankpala in the Northern Region of Ghana. The experimental site is located in the Guinea Savanna agro-ecological zone of Ghana. The Guinea Savanna zone covers an area of 147,900 km^2, which is over one-third of the entire land area of Ghana (EPA, 2003). The area is characterized by high temperature and low humidity during most parts of the year. The rainfall pattern is monomodal and erratic with an annual mean of 1100 mm which mostly begins in April-May and end in October. The area is also characterized by long dry season (4-6 months) which normally takes place from November to April. Intermittent dry spells often lasting up to 2-4 weeks occur during the growing season (EPA, 2003). The rainfall,

evaporation and temperature patterns monitored at Nyankpala from January to December during the 2012, 2013 and 2014 cropping seasons are presented in Table 3.1.

Table 3.1: Rainfall, evaporation and temperature variations at experimental location from January to December during the 2012, 2013 and 2014 cropping seasons

Month	Total rain fall (mm)			Total evaporation (mm)			Mean temperature (°C)		
	2012	2013	2014	2012	2013	2014	2012	2013	2014
January	0.0	0.0	0.0	195.9	230.9	185.0	26.6	27.3	28.4
February	41.7	2.4	2.4	209.4	223.2	202.2	30.2	34.6	29.9
March	1.7	89.6	25.7	245.0	194.8	223.3	32.7	44.1	31.9
April	108.9	66.8	50.7	163.6	167.1	176.5	30.6	37.8	31.5
May	88.1	30.0	45.6	147.1	168.2	174.2	29.0	29.8	31.2
June	148.9	161.9	166.5	114.9	110.4	117.1	27.6	31.3	29.4
July*	198.8	203.8	122.9	92.3	116.6	97.2	26.1	26.7	27.9
August*	77.0	217.4	240.0	80.1	85.6	78.0	25.6	26.0	26.9
September	209.1	164.1	195.6	74.4	77.6	80.5	26.5	26.4	26.8
October	151.3	119.7	153.1	98.9	93.7	98.2	27.6	27.6	28.1
November	0.0	23.3	0.0	138.7	127.4	139.0	29.1	29.0	30.0
December	4.8	0.0	0.0	118.3	163.2	174.8	27.6	27.5	28.4

Source: SARI Annual Reports for 2012, 2013 and 2014; *Norrmal/control plants in Experiments II and IV were planted in July2013 and July 2014 respectively and harvested in November 2013 and November 2014 respectively; *Water-stressed plants in Experiments II and IV were planted in August 2013 and August 2014 respectively and harvested in December 2013 and December 2014 respectively

Rainfall, temperature and soils at the experimental sites differ significantly from those in the southern part of the country (EPA, 2003). Farmers in this area plant maize at the onset of the rains around June and harvest around September. The Northern sector of Ghana, which is mainly found in the Guinea – Sudan Savanna agro-ecological zones, is an area of prime agricultural

importance in Ghana. All national supplies of millet, sorghum, groundnut, cowpea, and soya beans and 54% of rice as well as 45% of yam and maize are produced in this region (PPMED, 1997). The area is characterized by dry monsoon winds with high risk of uncontrolled bush burning and loss of vegetative cover during the 5-6 months dry season. The cycle of uncontrolled bush burning weakens nutrient recycling for sustainable crop and livestock production. In the area, land for agricultural development has become scarce as population pressure has increased.

Nyankpala is located on latitude $9^{o}25^{1}\ 41^{11}$ N and longitude $0^{o}58^{1}42^{11}$ W in the Guinea Savanna agro-ecological zone of Ghana (SARI, 2012). The Golinga irrigation dam is located at Golinga, a suburb of Nyankpala and approximately 16 kilometers southwest of Tamale (PPMED, 1997). The experimental fields are of a middle slope, strongly disturbed, having slightly sheet erosion and well drained voltaian sandstone (parent material) soil unit described as Tingoli series. Detailed soil profile (100 + cm) study and characterization undertaken in the 1997 cropping season established it as a Ferric Luvisol (FAO/UNESCO, 1977) or Paleustalf, Clayey-Skeletal isohyperthermic (USDA) soil (PPMED, 1997).

3.3 Land preparation

The experimental areas were initially chisel ploughed and disc harrowed, after all shrubs and debris were cleared. After two weeks and with a tractor drawn disc harrow, the experimental field was disc harrowed the second time to clear all debris and also to break lumps of soil. Ridges were then constructed using a ridger. The fields were then demarcated using lines and pegs before seeds of the genotypes were planted.

3.4 Experimental designs

Five different experiments were conducted for the present study from 2013 to 2015. Experiment I was a pot study conducted in a plant house of UDS whilst experiments II, III and IV were field experiments conducted at the SARI experimental field and the Golinga Irrigation Dam site. Experiment V was a laboratory based study conducted at the Biotechnology Laboratory of SARI. The experimental designs used for experiments I, III and V were Complete Randomized Design (CRD) with three replications. However, the design used for experiments II and IV was Randomized Complete Block Design (RCBD) with three replications. In each experiment, the replications were separated from one another by a 2 m alley.

3.5 Experiment I

This experiment consisted of three components: normal, water-stressed and striga-infested trials conducted in pots at the plant house from March to May, 2013. It has been reported earlier under section 2.5 of Chapter 2 that for maximum production, maize requires 500 – 800 mm of water depending on a number of factors and that the crop requires about 7.02 mm of water per day (FAOSTAT, 2001). The 7.02 mm of water is equivalent to 7.02 litres of water applied to an area of 1 m^2 (FAO, 2016). Therefore, a 0.06 m^2 pot will receive about 0.42 litres of water for every 7.02 mm of water applied on daily basis, and for a period of one week, the 0.06 m^2 pot will receive about 2.94 litres of water. In a plant house, the rate of evapotranspiration is not as high as in the field. On the basis of the crop water requirements for maize as stated above, an amount of 2 litres of water was applied to each plant, in each of the 0.01 m^3 pots, once every week for the non-stressed treatments (control). The normal trial served as the controlled experiment that was

watered normally and kept free of striga. In the water-stressed trial, the crops were water-stressed. To mimic drought conditions, the same amount of water as mentioned above was applied, but once every two weeks to the stress treatments. For the striga-infested trial, the crops were artificially infested with seeds of *Striga hermonthica* and watered normally as in the case of the normal experiment. The study was conducted at the plant house of the Faculty of Agriculture, University for Development Studies. There were 75 plastic pots used for each of the components/trials. The pots were arranged in rows on a platform with 1 m alley between rows. Inter-row and intra- row spacing were 0.75 m and 0.40 m respectively. The plastic pots, each measuring 0.01 m^3 were filled with sterilized black soil prior to planting. The maize genotypes were obtained from Savanna Agricultural Research Institute (SARI), and some farmers from Tamale, Tolon, Kumbungu or Yendi, all in the Northern Region of Ghana. The seeds of each of the 25 genotypes of maize were treated with a solution of 2 ml Actellic EC and 85 ml dH_2O prior to planting to prevent infestation of pests as recommended by Adu *et al.* (2014). The striga seeds were collected from farms from Yendi and Gushei catchment areas in the Northern Region of Ghana. Seeds of striga were mixed thoroughly with sieved sand and deposited in the holes during planting. The ratio of the striga seed:sand mixture was 1: 99.

The experimental site was divided into three sections. Pots from one section of the site were infested with the striga seeds; one section had pots containing plants that were water-stressed (2 litres of H_2O applied every 2 weeks), whilst the other section remained non-infested and watered (2 litres of H_2O applied every week). Seeds of the same entry of maize were planted in all three sections of the site as explained above. In all, 25 genotypes of maize were used in this experiment. The genotypes include: CHFB04-OB, KPAS04, OKOMASA, KOBN03-OB, NYAZ03-Y, NYAZ04-W, GUMA03-OB, GBRM04-BA, TZE-Y-DT-STR-C4, DORKE SR,

NYAN03, TZE-W-DT-STR-C4, NYIA03, NYLA04, TAAN04, NYSW03-Y, DT-STR-W-C2, SISF03-0B, KOBN04-R, TAIS03, CHMA04, IWD-C3-SYN-F2, NYFA04, GH120 DYF/D POP and NYFA03.

The maize and striga seeds were both planted at stake on the prepared plastic pots. Three maize seeds were planted per hill and were later thinned to two per hill. The inter-row and intra-row planting distances were 0.75 m and 0.40 m, respectively. For the striga, fine sand sieved through a 250 µm sieve was used to formulate a 1% germinable striga seed-sand mixture based on pre-determined 70% purity and 65% germination of the striga seed following the procedure of IITA (1991). The sand-striga mixture was applied at approximately 2,500 germinable striga seed to each maize hole. For the normal and striga-infested components of this experiment, 2 litres of water was artificially applied to each pot once every week, whilst for the water-stressed trial, 2 litres of water was applied to each plot once every two weeks. This type of watering regime was closely observed from the beginning to the end of the experiment. Weed control and earthening up was manually carried out in all the experimental pots in the plant house using hand fork and trowel to control weeds and also to ensure aeration in the pots for proper growth and development of the crops. Basal fertilizer was applied at 2 to 3 weeks after planting at the rate of 30 kg N ha^{-1} and 60 kg P_2O_5 ha^{-1} and top-dressed with additional N at 30 kg N ha^{-1} at 4 weeks after planting.

3.5.1 Data collected

Measurements were made of growing crop parameters at the vegetative stage through destructive harvesting at 6 weeks after plant establishment (WAPE). The parameters included leaf number, shoot length, chlorophyll content, leaf area, stem girth, fresh shoot biomass, dry shoot biomass,

fresh root biomass, dry root biomass and root length. Details on how these measurements were carried out are provided in the following sections.

3.5.1.1 Leaf number and shoot length

The number of leaves per plant was counted and recorded at six weeks after planting. One plant in each plot was tagged for shoot length measurements. The tagged plants were closely monitored throughout the experimental period. Tagged plants were located within the harvest area (net plots) of each entry. A fine measuring tape was used in the measurement of the shoot length from the base of the plant to the tip of the apical leaf (i.e. flag leaf).

3.5.1.2 Chlorophyll content

The chlorophyll content was determined by measuring the relative chlorophyll concentration of three leaves of each tagged plant (lower, middle and upper leaves), and the average chlorophyll content was recorded. The measurements were done at six weeks after plant establishment. A chlorophyll meter was used to measure the chlorophyll content of leaves. Measurements were taken in the morning. The chlorophyll meter was clipped to the leaves with a slight pressure by the hand and gently released. Measurements were recorded in spad units.

3.5.1.3 Leaf length, width and area

The leaf length was determined by measuring three leaves of the tagged plants (lower, middle and upper leaves) from the bases to the tips and the average leaf length was taken. The measurements were taken at six weeks after plant establishment using a fine tape measure.

The leaf width was determined by measuring the widest portion of three leaves (lower, middle and upper leaves) of each of the tagged plants and the averages computed. The measurements were done at six week after plant establishment. The leaf lengths and leaf widths (breadths) of

the tagged plants in each plot were recorded using a meter rule. The length multiplied by the breadth provided a measured leaf area. The true leaf area was obtained by multiplying the measured leaf area by a factor of 0.75 as used by Moll and Kamprath (1977).

3.5.1.4 Fresh and dry shoot biomass

Tagged plants of each genotype were cut out at ground level. Fresh shoot biomass was taken using a fine beam balance (maximum weight of 7.2 kg) in the soil science laboratory. Plant materials were then held in brown paper envelopes and neatly arranged in a calibrated oven. The temperature of the oven was then set to a maximum and constant level of 80°C. The materials were left in the oven for 72 hours. The dry shoots were then weighed using the same balance and the dry biomass recorded. This was done at 6 weeks after plant establishment.

3.5.1.5 Fresh and dry root biomass

Tagged plant of each genotype was completely removed from the soil with the aid of a garden fork, trowel and knife, and the entire root system cut from the stem. Fresh root biomass was taken using a fine beam balance (maximum weight of 7.2 kg) in the soil science laboratory. The plant materials were then held in brown paper envelopes and neatly arranged in a calibrated oven. The temperature of the oven was then set to a maximum and constant level of 80°C. The materials were left in the oven for 72 hours. The dry roots were then weighed using the same balance and the weights recorded. This was done at 6 weeks after plant establishment.

3.5.1.6 Root length

Tagged plant of each component genotype was completely removed from the soil with the aid of a garden fork, trowel and knife, and the entire root system cut from the stem. Fresh root length was taken using a fine meter rule (maximum length of 30 cm) in the soil science laboratory.

3.5.2 Statistical analysis

The series of data collected were subjected to analysis of variance (ANOVA) using GenStat Statistical Package Edition 9. Significant difference among treatment means were separated using Fisher LSD test at 5%. Co-efficient of variation was calculated to determine the level of reliability of the experimental data and to indicate the degree/ level of variation in each set of data. Correlation analysis was run to establish relationships among parameters. All scored and count data such as drought rating, striga rating, striga count and number of leaves were transformed prior to ANOVA but they were back transformed to original values during computation of means as indicated in the tables. For visual impression and ease of understanding, summaries of findings were in some cases presented in graphs and tables.

3.6 Experiment II

This experiment consisted of three different trials or components designated as normal, water-stressed and striga-infested trials. The experiment was conducted at the experimental field of Savanna Agricultural Research Institute (SARI) from July to October, 2013. The normal trial was the controlled trial in which the plants were planted early (July 2013) and during usual time of planting maize in the study area as reported under section 3.2. The early planting of the normal trial was to ensure that the trial had enough rains for plant growth and development. The normal trial was not infested with *Striga hermonthica*. In the water-stressed trial, the genotypes were subjected to water-stressed conditions, that is, plants were planted six weeks later than the normal planting time to ensure that their growing stage coincided with the drought period in the field. According to SARI (2012), Nyankpala experiences a monomodal rain fall pattern, and that

the rainy season usually occurs between the months of May to October. The highest rainfall occurs in the months of July to September as already stated under section 3.2. In the striga-infested trial, plants were planted at the same time as the normal (control) plants, but seeds of maize were planted together with seeds of *Striga hermonthica* in each hole. The artificial infestation with striga was to ensure that the *Striga hermonthica* parasitizes with the maize plants. All agronomic practices observed in the three trials were the same as stated under section 3.5.

Pre-emergence chemical weed (other than striga) control was practised and consisted of an application of a combination of Pendimethalin [N – (1 – ethylpropyl) - 3, 4 – dimethyl –2, 6 – dinitrobenzenamine] and Gesaprim [2 – chloro – 4 – (ethylamino) – 6 – (isopropylamino) – 5 – triazine] at 1.5 lha^{-1} and 1.0 lha^{-1} a.i., respectively at planting. Where there was heavy weed growth prior to planting, Paraquat (1, 1 – dimethyl – 4, 4 – bipyridinium ion) was applied at 1.0 lha^{-1} a.i. in addition to Pendimethalin and Gesaprim. Hand weeding was also carried out to keep the plots free of weeds before striga emergence. Basal fertilizer was applied at 2 to 3 weeks after planting at the rate of 30 kg N ha^{-1} and 60 kg P_2O_5 ha^{-1} and top-dressed with additional N at 30 kg N ha^{-1} at four weeks after planting for all the experiments. All the ridged plots were earthed up once in order to maintain their integrity throughout and also bury roots of plants that were exposed due to localized erosion of soil away from the ridges.

3.6.1 Data collection

Measurements were made of growing crop parameters between flowering and physiological maturity. These parameters included plant height, days to 50% tasseling, days to 50% anthesis, days to 50% silking, anthesis-silking interval (ASI), ear height, striga count at 10 weeks after plant establishment (WAPE), striga rating at 10 WAPE and drought rating at 10 WAPE. After

physiological maturity, grain yield, hundred-grain weight and number of ears harvested per plot were then measured. Details on how these measurements were carried out are provided in the following sections.

3.6.1.1 Flowering

Plants within the net plots of each component/trial were used for the purpose of taking flowering data. Records were taken on the number of days to 50% tasseling, number of days to 50% anthesis as well as number of days to 50% silking. Records were also taken on the anthesis-silking intervals for all the genotypes within the three different trials.

3.6.1.2 Plant and ear heights

Three plants within each of the net plot were sampled (shortest, medium and tallest plants) for plant height measurements. Plant height was determined by measuring the height of each sampled plant from the base of the plant to the base of the top most leaf (i.e. flag leaf) where tassel branching occurs, and the average height recorded. A fine measuring tape was used in the measurement. The measurements were taken after ten weeks of plant establishment. The ear heights of three sampled plants (shortest, medium and tallest plants) within the net plots were measured in centimeters. Ear height was determined by measuring the ear heights of each sample plant from the base of the plant to the node bearing the upper ear, and the average ear height recorded.

3.6.1.3 Striga and drought ratings at 10 weeks after plant establishment

Data was taken on plant rating at both the striga-infested and the water-stressed trials. The intensity of drought or striga on the individual maize genotypes was assessed visually and scores attached to the various maize genotypes. The scores ranged from 1 – 5, where 5 = very intensive

drought or striga effect on the crops; 4 = intensive; 3 = quite intensive; 2 = not intensive; and 1 = intensity negligible. The implication is that a genotype that scores 1 or 2 is tolerant to drought or striga, whilst a score of 3 or higher indicates susceptibility of genotype to these biotic or abiotic stresses (Adu *et al.*, 2014).

3.6.1.4 Striga count at 10 weeks after plant establishment

Records were taken on striga count at 10 weeks after plant establishment. This was done by counting and recording the number of emerged striga plants per plot 10 weeks after plant establishment.

3.6.1.5 Plant stand, ears harvested, grain yield and hundred-grain weight

Records were taken on the total number of plants per plot after 10 weeks of plant establishment. Records were taken on the total number of ears (maize cobs) harvested per plot. Each crop was harvested by hand soon after its physiological maturity which depended on days to maturity of the various maize genotypes used in the experiments. All the harvested crops were weighed using a scale, and the weights recorded. The harvested ears were then held in open bags and dried on concrete platforms for a week. This was done to ensure complete and uniform drying of the harvested maize. The harvested cobs were then threshed in the bags, winnowed and cleaned to achieve clean grains. The grains held in open bags, were further sun dried until moisture was reduced to 14%. At this moisture level, grain weights were taken in kilograms, using an industrial scale, on a per plot basis and extrapolated to a per hectare basis.

After threshing, the grains were dried to a moisture level of 14%. Grains were sub-sampled and with the aid of a counter, hundred grains were counted and weighed in grams using an industrial scale. This was recorded as the hundred-grain weight.

3.6.2 Statistical analysis

The series of data collected were subjected to analysis of variance (ANOVA) using GenStats Statistical Package Edition 9. Significant difference among treatment means was separated using Fisher LSD test at 5%. Co-efficient of variation was calculated to determine the level of reliability of the experimental data and indication of variation in the data set. Correlation analysis was run to establish relationships among parameters. All scored and count data such as days to tasseling, days to anthesis, days to silking, ASI, striga count, drought rating and striga rating were transformed prior to ANOVA but they were back transformed to original values during computation of means as indicated in the tables. For visual impression and ease of understanding, summaries of findings were in some cases presented in graphs and tables.

3.6.3 Performance ranking of genotypes

Conjoint analysis was run to demonstrate genotype – performance ranking among the water-stressed treatments of Experiments I and II. This was to justify the selection of some genotypes to be used for diallel crossing in experiment III. Conjoint measurement was used to investigate the joint effect of a set of independent variables on an ordinal scale of measurement of dependent variable. The independent variables are typically nominal and sometimes interval scale variables. Conjoint measurement simultaneously finds a monotonic scoring of the dependent variable and numerical values for each level of each independent variable. The goal was to monotonically transform the ordinal values to equal the sum of their attribute level values. Hence, conjoint measurement was used to derive an interval variable from ordinal data. A numerical part-worth utility value is computed for each level of each attribute. Large part-worth utilities were assigned to the most preferred levels, and small part-worth utilities are assigned to the least preferred levels. The attributes with the largest part-worth utility range were considered the most important

in predicting preference. The results of the conjoint analysis are presented in Appendices 1 and 2 of this thesis.

3.7 Experiment III

Six genotypes of maize were selected from Experiments I and II as tolerant to drought and striga and were used in Experiment III. This experiment consisted of single trial conducted at the Golinga irrigation dam site from February to May during the 2014 dry season. A 6 x 6 diallel mating design was used to develop F_1 hybrids from the six selected genotypes obtained from experiments I and II. The six selected genotypes used in this experiment were: IWD-C3-SYN-F2, DT-STR-W-C2, TAIS03, SISF03-OB, GUMA03-OB and KOBN03-OB. There were 6 plots in this study. Each plot comprised twelve rows, and each row was 5 m long. Seeds of each genotype were planted on each plot. Six rows in each plot were designated as male rows whilst the remaining six rows served as the female rows. The rows were spaced 0.75 m apart. Intra-row spacing was 0.40 m. Three maize seeds were planted per hill in this study, but were later thinned to two per hill. The crops in this experiment were irrigated. Weed control and fertilizer application were carried out in the same way as stated in Experiment II.

Prior to silk production, ears of vigorously growing plants from all the female rows of all the six plots were tagged for crossing, and transparent polythene bags used to cover the selected ears to prevent unwanted pollen grains from falling into the stigma of the female reproductive organ. With the help of a water proof pollinating bags, pollen grains were collected from the male rows of one genotype at a time, to fertilize the silk of the selected ears of the five genotypes in the female rows. This process continued in a step by step manner until all the genotypes in the

female rows were successfully crossed. During the crossing process, the tassels of the male plants were gently pushed into the pollinating bag and shaked gently so that the pollen grain can fall into the bag. During the harvesting of the pollen grains from the male plants, the researcher and his assistants put on overall suits, spectacles and hand gloves to prevent body itching and contamination of pollen grains. The F_1 hybrids developed from the diallel crossing in this study were subjected to further studies in Experiments IV and V as detailed in sections 3.8 and 3.9.

3.8 Experiment IV

This experiment involved the evaluation of the F_1 hybrids and their parentals for tolerance to drought and striga. The locations of the experiment were the experimental fields of SARI and the Golinga irrigation dam. At each location, the experiment consisted of three different trials/components designated as normal, water-stressed and striga-infested trials. The experiment was carried out in 2014. The normal trial was the controlled trial in which the maize plants were planted at the normal time of planting maize in the study area and the water-stressed trial planted 6 weeks later as described under Experiment II. The striga-infested trial was planted the same time as the normal (control) trial, but infested with striga as described under Experiment II. The Experimental design and all agronomic practices observed in this experiment were similar to that of Experiment II. The 6 parents and 30 F_1 hybrids, including reciprocals that were developed from experiment III were used in this study (Table 3.2). The seeds of striga were mixed thoroughly with sieved sand and planted with maize as already described under Experiment II. All cultural practices were carried out the same way as stated under Experiment II.

Table 3.2: Parents and F_1 hybrid populations used in Experiment IV

NO.	POPULATION
1	IWD-C3-SYN-F2*
2	DT-STR-W-C2*
3	TAIS03*
4	SISF03-OB*
5	GUMA03-OB*
6	KOBN03-OB*
7	IWD × DT
8	IWD × TAIS03
9	IWD × SISF03
10	IWD × GUMA03
11	IWD × KOBN03
12	DT × IWD
13	DT × TAIS03
14	DT × SISF03
15	DT × GUMA03
16	DT × KOBN03
17	TAIS03 × IWD
18	TAIS03 × DT
19	TAIS03 × SISF03
20	TAIS03 × GUMA03
21	TAIS03 × KOBN03
22	SISF03 × IWD
23	SISF03 × DT
24	SISF03 × TAIS03
25	SISF03 × GUMA03
26	SISF03 × KOBN03
27	GUMA03 × IWD
28	GUMA03 × DT
29	GUMA03 × TAIS03
30	GUMA03 × SISF03
31	GUMA03 × KOBN03
32	KOBN03 × IWD
33	KOBN03 × DT
34	KOBN03 × TAIS03
35	KOBN03 × SISF03
36	KOBN03 × GUMA03

* = Parent population; IWD = IWD-C3-SYN-F2 and DT = DT-STR-W-C2

3.8.1 Data collection

Data were collected on growing crop parameters between flowering and physiological maturity. These parameters included plant height, days to 50% tasseling, days to 50% anthesis, days to 50% silking, anthesis-silking interval (ASI), ear height, striga count at 10 weeks after plant establishment (WAPE), striga rating at 10 WAPE, drought rating at 10 WAPE and leaf-rolling rating at 10 WAPE. After physiological maturity, grain yield, hundred-grain weight and number of ears harvested per plot were then measured. Details on how these measurements were carried out are as follows.

Data was taken on plant rating in both the striga-infested and the water-stressed trials of Experiments IV. The intensity of drought or striga on the individual maize genotypes was assessed visually and scores attached to the various maize genotypes as stated under section 3.6.1.3. Leaf-rolling rating of the water-stressed plants was also assessed through visual scoring as explained in the case of drought and striga rating. Details on how the rest of the other parameters were measured are already stated under Experiment II.

3.8.2 Diallel analysis

Data for the 6 x 6 diallel crosses obtained from two locations were analyzed using the Statistical Analysis System (SAS). For morphological traits, analysis of variance was conducted to determine significance of variability among the parents and hybrids. Mean, range, standard deviation and co-efficient of variation for each characteristic was determined using SAS version 9.1 (SAS Institute Inc., 2005). Parental accessions were selected from different maize populations. Diallel analysis was performed to calculate general combining ability (GCA) and specific combining ability (SCA) according to Griffing's (1956) method 2, model 1, using SAS

programme (GLM procedure) (Zhang *et al.*, 2005). The following model was considered for statistical analysis in experiment IV:

$$Y_{ijk} = \mu + G_i + G_j + S_{ij} + R_k + E_{ijk}$$

Where Y_{ijk} = the observed value for a hybrid between the i^{th} and j^{th} parents in the k^{th} replication; μ = population mean; G_i and G_j = GCA effect of the i^{th} and j^{th} parents; S_{ij} = SCA effect for the hybrid between the i^{th} and j^{th} parents; R_k = effect of the k^{th} replication; E_{ijk} = the error associated with the ijk^{th} hybrid (the residual) (Johnson and King, 1998). Estimation of the additive and dominance genetic variance is simple after estimating the GCA variance (σ^2_{GCA}) and SCA variance (σ^2_{SCA}) (Zhang *et al.*, 2005). The relationships are as follows:

When inbreeding coefficient (F) of parents = 0 (no inbreeding); $\sigma^2A = 4\ \sigma^2_{GCA}$ and $\sigma^2D = 4\ \sigma^2_{SCA}$.

Heritability expresses the proportion of the total variance that is attributable to the average effects of genes. Broad and narrow sense heritabilities were estimated based on the variance components in the ANOVA. Broad sense heritability values were obtained using GCA and SCA values. $H^2_b = \sigma^2_g / \sigma^2_p = 4\ \sigma^2_{GCA} + 4\ \sigma^2_{SCA} / 4\ \sigma^2_{GCA} + 4\ \sigma^2_{SCA} + \sigma^2_E$; Where H^2_b = Heritability in the broad sense; σ^2_g = total genetic variance = $4\ \sigma^2_{GCA} + 4\ \sigma^2_{SCA}$ and σ^2_p = Phenotypic variance = $4\ \sigma^2_{GCA} + 4\ \sigma^2_{SCA} + \sigma^2_E$.

Narrow sense heritability was computed from the variance components in the ANOVA for the analysis of combining ability as:

$$H^2_n = \sigma^2_A / \sigma^2_P = 4\ \sigma^2_{GCA} / 4\ \sigma^2_{GCA} + 4\ \sigma^2_{SCA} + \sigma^2_E$$

Where H^2_n = narrow sense heritability; $4\ \sigma^2_{GCA}$ = variance due to GCA; $4\ \sigma^2_{SCA}$ = variance due to SCA and σ^2_E = variance due to residual error.

3.9 Experiment V

This was a laboratory experiment conducted at the Biotechnology Laboratory of Savanna Agricultural Research Institute (SARI) from February to March, 2015 to screen the maize accessions for drought and/or *Striga hermonthica* tolerance using Simple Sequence Repeat (SSR) markers. In all, 17 SSR markers were used for the study. Prior to the laboratory experiment, a total of 36 maize parental and F_1 hybrid populations were raised under irrigated conditions during the February, 2015 dry season at SARI Technology Field. These plants served as source of material for the laboratory study. The youngest leaves from the two-week old maize plants were collected for genomic DNA extraction. Genomic DNA was isolated from all the 6 parents and 30 F_1 hybrid populations of maize, including reciprocals. The extraction of the DNA was carried out following the procedure of the CTAB method for extraction of DNA from leaves (Gawel and Jarret, 1991). Polymerase Chain Reaction (PCR) amplification of extracted DNA was then carried out. Through electrophoresis, gels were run to assess the banding pattern. The presence of bands indicated presence of drought and/or striga tolerant traits, and vice versa. Ten and seven microsatellite SSR primers that are linked to drought and striga tolerance respectively were from the umc, bnlg, phi and nc series procured from Metabion Internationa AG, Germany and used for the study.

3.9.1 DNA extraction according to Gawel and Jarret (1991)

The DNAs were extracted from the leaves of the two-week old maize plants using the CTAB method with little modification. About 200 mg of the young leaves were harvested from the seven plants in each of the 36 populations of maize and put into properly labeled separate 2 ml Eppendorf tubes containing two ball bearings each to aid proper lysis of the cells. The tubes after each harvest were placed in liquid nitrogen. The leaf samples were ground to fine powder using a

tissue lyser. This was done three times with the tubes being returned into the liquid nitrogen in-between grinding to increase the efficiency of the process. An amount of 1 ml of pre-warmed CTAB buffer (2% CTAB, 20 mM EDTA, 100 mM Tris-HCl and 1.4M NaCl) with 0.2% mercapto-ethanol (2µl/1ml of CTAB buffer) was added to each Eppendorf tube and placed in a water bath at 60°C for 1 hour. During this time the content of the tubes were mixed gently by inverting for 6-7 times. An amount of 200 µl of potassium acetate was added and put on ice for 20 min. Then, 700 µl of chloroform: Isoamyl alcohol (24: 1) was added to each tube and mixed gently by inverting, and this was left undisturbed for 5 min.

The tubes were then centrifuged at 10000 revolutions per minute (rpm) for 15 min and the middle aqueous layer transferred into properly labeled new 2 ml tubes using 1000 µl tips. The same volume of chloroform: Isoamyl alcohol as in new tubes was added, mixed gently and left undisturbed for 5 min. This was centrifuged at 10000 rpm for 10 min and the supernatant transferred into new properly labeled 1.5 ml tubes. An amount of 500 µl of ice cold isopropanol was added to get a white precipitate. For maximum precipitation of the DNA, the tubes were left over night at -20°C. The tubes were centrifuged for 5 min at 1000 rpm and the supernatant removed carefully leaving pellets of DNA. The pellets were washed twice with about 300 ml of 75% ice cold ethanol depending on pellet size, each followed by centrifugation at 15000 rpm for 5 min and allowed to air dry. About 300 ml of double distilled water was added and kept in 4°C for dissolution of the pellet. Then, 2 µl of RNAse was added to each tube to get rid of RNA in the DNA and put in an incubator at 3°C for an hour.

DNA quality check was done using agarose gel electrophoresis following the protocol of Sambrook *et al.* (1989). In determining the purity of the DNA extract, 1.0% agarose gel with (3 µl) 0.003% ethidium bromide gel red solution was prepared, and 5 µl sample DNA was

pippetted and 1 µl loading buffer (X6 bromophenol blue) added. The sample was then loaded in the wells on gel submerged in 1X TAE buffer. The sample was then run at 90 volts for 45 min. Photograph of gel was taken under UV light. The result of the gel picture that was generated from the DNA quality test is presented in Figure 3.1.

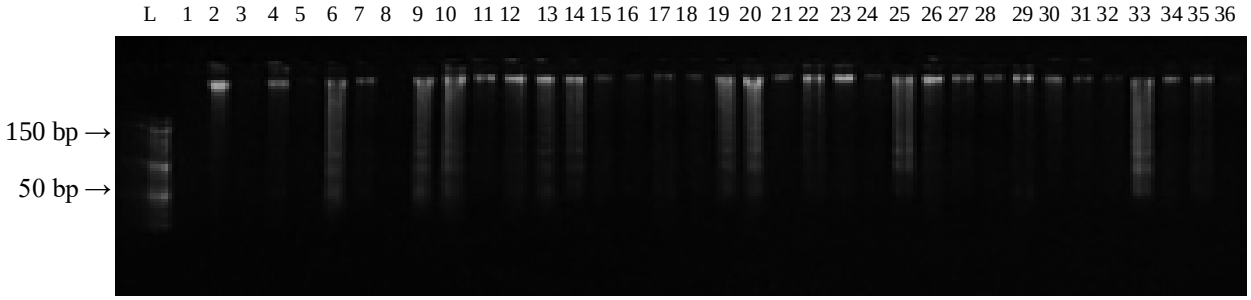

Figure 3.1: Gel picture of DNA quality test; Lanes 1-36 represent the maize genotypes as defined in Table 7.2 of Chapter 7; L represents 50 bp DNA ladder

3.9.2 PCR amplification

Polymerase Chain Reaction (PCR) was carried out in Techne Thermocyler (TC - 412) in a 10 µl reaction mixture in well – plates. PCR master mix kit (KAPA 2G Fast Ready Mix with dye) procured from KAPA Biosytems (pty) Ltd. (South Africa) was used for the amplification. The kit 2X PCR master mix containing KAPA 2G Fast DNA Polymerase (0.2 µ per 10 µl reaction), KAPA 2G Fast PCR buffer, dNTPs (0.2 mM each at 1X), $MgCl_2$ (1.5 mM at 1X), stabilizers and loading dye. Then, 5 ng/µl of genomic DNA, 1 mM of primer and 1.5 µl of premix were added to the PCR kit for DNA amplification. PCR amplification of the extracted DNAs were then carried out using the following conditions: denaturation at 94°C for 30 sec, annealing at 56°C for 30 sec and extension at 72°C for 30 sec, in a reaction volume of 10 µl (6.5 µl of ddH_2O, 5 ng/µl of DNA, 1 mM of primer and 1.5 µl of premix). The reactions were then held at 4°C until electrophoresis.

CHAPTER FOUR

SCREENING FOR DROUGHT TOLERANCE

4.1 Introduction

Maize (*Zea mays* L.) is essential for global food security. However, the overall maize production in Ghana has remained relatively low both in terms of area harvested and volume because of over reliance on rain-fed agriculture (SARI, 1996). Maize has been found to be one of the most sensitive species to water deficit or drought requiring about 508 to 635 mm of water per growing season (FAO, 2016). Maize requires the highest amount of water during the early reproductive growth stages, which are also the most sensitive stages to water stress. Significant reductions in yield may occur if the crop does not receive enough water to meet evapotranspiration (ET_o) demands during this critical stage. The factors that affect maize water requirements have already been reported under section 2.5 of Chapter 2. Water stress should be avoided during the vegetative and reproductive stages of the crop development.

Drought is an important climatic phenomenon, which is the second most important severe constraint to crop production in developing countries, after low soil fertility (Kramer, 1980). Water, being an integral part of plants plays a pivotal role in the initiation of growth, subsequent maintenance of developmental process throughout the plant's life and ultimately economy of a country. The maize crops may experience reductions in grain yield when subjected to water deficit during the critical period of crop cycle from tasseling stage to initiation of grain filling (Kramer, 1980). Crop yield losses due to drought stress are considerable. In maize, drought is the major stress affecting productivity in Africa leading up to 70% or total crop loss (Muoma *et al.*,

2010; Ashraf, 2010). Kramer (1980) reported that one-third of the world's potentially arable land suffers water shortage, and most of the crops produced are often reduced by drought. Drought is a major source of grain yield decrease in cereals, especially in developing countries. For maize in the tropics, this loss has been estimated to be around 17% annually, but may increase up to 70% under extreme conditions, compared with well-watered productions (Edmeades *et al.*, 1995). Maize grain losses due to drought in the tropics may reach 24 million tons per year, equivalent to 17% of well-watered production (Edmeades *et al.*, 1992).

Annual maize yield loss due to drought is estimated to be 15% in West and Central Africa (Edmeades *et al.*, 1995). Grain yield losses can even be greater if the stress coincides with flowering and grain-filling period. Nesmith and Ritchie (1992) reported that maize yield can be reduced by as much as 90% if drought stress occurs between a few days before tassel emergence and the beginning of grain-filling. Under induced moisture stress from about tassel emergence stage to the end of the crop cycle of maize, Badu-Apraku *et al.* (2005) observed yield reduction of 62% relative to the well-watered treatment. Yield as high as 5.0 - 5.5 metric tons per hectare have been realized by farmers using improved seeds, fertilizer, mechanization and irrigation (FAO, 2009). Over all, maize possesses extravagant variation for all traits and this variability can be easily used by the plant breeders to develop high yielding and drought tolerant genotypes for global food security. In the near future the increasing world's population will require more food, and a greater part of this food will come from maize crop (Ali and Yan, 2012). It has been estimated that more than half of the increased demand in the world food in terms of cereals as a whole will be produced by maize farmers (Yao *et al.*, 2011).

Drought tolerance is a quantitative trait whose performance is regulated by many gene loci and hence subject to multiple genotype × environment (G×E) and gene × gene interactions (epistasis)

(Campos *et al*., 2004). Although a variety of approaches have been used to alleviate the problem of drought, plant breeding, either conventional breeding or genetic engineering seems to be an efficient and economic means of tailoring crops to enable them grow successfully in drought-prone environments (Ashraf, 2010). Breeding for drought resistance/tolerance in maize may improve the performance of the crop even under water-stressed conditions and hence increase the yield of maize. The objective of the study, therefore was to evaluate a number of maize genotypes for various physiological and morphological traits with the view to selecting the promising genotypes for cultivation in drought – prone areas.

4.2 Materials and methods

The experiments were conducted at the experimental field of the Savanna Agricultural Research Institute (SARI) and at the plant house of the Faculty of Agriculture, University for Development Studies (UDS), all in Nyankpala in the Northern Region of Ghana. Two different experiments, namely Experiment I and Experiment II, were conducted for this study. Experiment I was a pot experiment conducted in a plant house while experiment II was field experiment conducted at the SARI experimental field as indicated in section 3.5. The experimental design used for experiment 1 was Complete Randomized Design (CRD) with three replications, whilst Randomized Complete Block Design (RCBD) with three replications was used for experiment II. The replications were separated from one another by a 2 m alley in each case. Specific details of the treatment structure and planting have already been reported in Chapter 3. Data were taken on several parameters such as leaf number, shoot length, chlorophyll content, leaf area, stem girth, fresh shoot biomass, dry shoot biomass, fresh root biomass, dry root biomass and root length in the case of Experiment I. For Experiment II, measurements were made of growing crop

parameters between flowering and physiological maturity. These parameters were: plant height, days to 50% tasseling, days to 50% anthesis, days to 50% silking, anthesis-silking interval (ASI), ear height, plant stand and drought rating at 10 weeks after plant establishment (WAPE). After physiological maturity, grain yield, hundred-grain weight and number of ears harvested per plot were then measured. The data collected from both experiments were subjected to analysis of variance (ANOVA) using GenStats statistical package edition 9. Significant differences among treatments were observed and treatment means were separated using Fisher LSD test at 5%. Correlation analyses were run to establish relationships among parameters. Conjoint analysis was also run to do genotype-performance ranking. This was to justify the selection of some genotypes to be used for a diallel crossing as described in Experiment III in Chapter 3. For visual impression and ease of understanding, summaries of findings were presented in graphs and tables.

4.3 Results

4.3.1 Experiment I

The analysis of variance for the parameters measured for the normal (control) trial is presented in Table 4.1. There were highly significant differences ($P < 0.001$) among the genotypes with respect to stem girth and chlorophyll content for the normal trial. There were highly significant differences ($P < 0.01$) among the genotypes with respect to number of leaves, shoot length, fresh shoot biomass, dry shoot biomass and root length for the normal plants. There were also significant differences ($P < 0.05$) among genotypes with respect to leaf area in the normal trial. There were however, no significant differences ($P > 0.05$) among genotypes with respect to fresh and dry root biomass for the normal plants (Table 4.1).

Table 4.1: Mean squares and co-efficient of variation (CV %) for vegetative traits under normal conditions

Source	df	Trait									
		No. of leaves	Shoot length (cm)	Stem girth (cm)	Leaf area (cm^2)	Chlorophyll content (spad units)	Fresh root biomass (g)	Dry root biomass (g)	Fresh shoot biomass (g)	Dry shoot biomass (g)	Root length (cm)
Replication	2	3.89^{*}	234.62^{*}	0.09^{*}	743.76^{ns}	57.20^{**}	4.72^{ns}	0.22^{ns}	260.17^{ns}	4.08^{ns}	11.50^{ns}
Genotype	24	2.04^{**}	132.65^{**}	0.12^{***}	559.73^{*}	44.75^{***}	2.79^{ns}	0.20^{ns}	717.71^{**}	8.93^{**}	32.99^{**}
Model	26	2.18^{**}	140.49^{**}	0.11^{***}	573.88^{*}	45.70^{***}	2.93^{ns}	0.20^{ns}	682.51^{*}	8.56^{**}	31.34^{**}
Error	48	0.91	54.29	0.02	291.57	10.58	3.12	0.23	320.29	3.60	13.23
CV %		12.85	13.00	10.49	15.94	9.03	57.34	68.38	38.52	38.11	22.07

*Significant at $P < 0.05$, **Significant at $P < 0.01$, ***Significant at $P < 0.001$, ^{ns} Non-significant at $P > 0.05$

The analysis of variance for the parameters measured for the water-stressed trial is presented in Table 4.2. There were highly significant differences ($P < 0.001$) among the genotypes with respect to root length, fresh root biomass, dry root biomass, fresh shoot biomass and dry shoot biomass for the water-stressed plants. There were also highly significant differences ($P < 0.01$) among the genotypes with respect to number of leaves and stem girth for the water-stressed plants. There were significant differences ($P < 0.05$) among the genotypes in terms of shoot length and leaf area for the water-stressed plants. However, there was no significant difference ($P > 0.05$) among genotypes for chlorophyll content in the water-stressed plants (Table 4.2).

Table 4.2: Mean squares and co-efficient of variation (CV %) for vegetative traits under water-stressed conditions

Source	df	Trait									
		No. of leaves	Shoot length (cm)	Stem girth (cm)	Leaf area (cm^2)	Chlorophyll content (spad units)	Fresh root biomass (g)	Dry root biomass (g)	Fresh shoot biomass (g)	Dry shoot biomass (g)	Root length (cm)
Replication	2	1.12^{ns}	19.54^{ns}	0.04^{ns}	46.01^{ns}	15.34^{ns}	0.70^{**}	0.02^{ns}	51.89^{*}	0.50^{ns}	8.45^{ns}
Genotype	24	1.54^{**}	43.56^{*}	0.04^{**}	230.97^{*}	22.73^{ns}	0.37^{***}	0.04^{***}	44.99^{***}	0.82^{***}	29.50^{***}
Model	26	1.51^{**}	41.72^{*}	0.04^{**}	216.75^{ns}	22.16^{ns}	0.39^{***}	0.04^{***}	45.52^{***}	0.79^{***}	27.88^{***}
Error	48	0.65	20.04	0.02	162.64	20.82	0.11	0.01	15.07	0.25	8.28
CV %		15.13	15.39	17.69	22.89	13.44	35.89	54.22	33.50	33.18	22.37

*Significant at $P < 0.05$, **Significant at $P < 0.01$, ***Significant at $P < 0.001$, ^{ns} Non-significant at $P > 0.05$

4.3.1.1 Vegetative traits

The effect of water-stress was assessed by comparing the parameters measured due to the stress relative to watered/normal trial. Water-stress significantly reduced all the parameters measured as compared to their counterparts in the watered (normal) regime (Table 4.3). When the normal and water-stressed treatments were compared in terms of percentage change of parameters measured, it was realized that the highest percentage reduction of 75.1% was recorded for fresh shoot biomass, whilst the lowest of 5.7% was recorded for chlorophyll content.

Table 4.3: Comparing parameters measured in the watered (normal) and water-stressed regime

Vegetative trait	Treatment		% change due to water-stress	LSD (0.05)
	Normal	Water-stressed		
Number of leaves	8^a	5^b	37.5	0.39
Shoot length (cm)	56.7^a	29.1^b	48.7	2.78
Stem girth (cm)	1.37^a	0.72^b	47.5	0.07
Leaf area (cm^2)	107.2^a	55.7^b	48.0	5.48
Chlorophyll content (spad units)	36.01^a	33.95^b	5.7	1.46
Fresh root biomass (g)	3.08^a	0.94^b	69.5	0.51
Dry root biomass (g)	0.70^a	0.21^b	70.0	0.17
Fresh shoot biomass (g)	46.46^a	11.59^b	75.1	4.71
Dry shoot biomass (g)	4.98^a	1.50^b	69.9	0.61
Root length (cm)	16.48^a	12.86^b	22.0	1.21

Traits having different letters (horizontal direction) are significantly different at the 5% level of probability

4.3.1.2 Number of leaves

When genotypes were watered regularly (normal trial), genotype, NYIA03 and NYLA04 recorded the highest of 10 leaves, whilst NYSW03-Y recorded the least of 3 leaves. The genotype NYIA03 statistically differed from NYSW03-Y, KOBN03-OB, NYAZ03-Y, NYAZ04-W, NYAN03, KOBN04-R, CHFB04-OB, TAAN04, NYFA04, TZE-W-DT-STR-C4 and GH120 DYF/D POP (Table 4.4). For the water-stressed plants, DT-STR-W-C2 recorded the highest number of leaves (7), whilst NYAZ03-Y, KOBN04-R and IWD-C3-SYN-F2 recorded the least number of leaves (4). The genotypes such as CHFB04-OB, NYAZ04-W, GUMA03-OB, NYIA03, NYSW03-Y, SISF03-OB, TAIS03, NYFA04, GH120 DYF/D POP and NYFA03 were not significantly different ($P > 0.05$) from DT-STR-W-C2.

4.3.1.3 Shoot length

Results of the study indicate that the genotype, TZE-W-DT-STR-C4 was the tallest (70.3 cm), whilst NYFA03 was the shortest (44.4 cm) for shoot length among the normal treatments. However, there was no significant difference ($P > 0.05$) among genotypes such as TZE-W-DT-STR-C4, CHFB04-OB, KPAS04, NYAZ03-Y, GUMA03-OB, NYIA03, DT-STR-W-C2, NYLA04, DORKE SR and GBRM04-BA. For the water-stressed plants, GUMA03-OB was the tallest (36.5 cm), whilst GH120 DYF/D POP was the shortest (22.3 cm). The genotypes GUMA03-OB, SISF03-OB, DT-STR-W-C2, TAAN04, TZE-W-DT-STR-C4, TZE-Y-DT-STR-C4, NYAZ04-W, KOBN03-OB, OKOMASA, KPAS04 and CHFB04-OB were statistically similar ($P > 0.05$) (Table 4.4).

4.3.1.4 Leaf area

When plants were watered regularly (normal trial), the genotype KPAS04 recorded the highest leaf area of 150.7 cm², while OKOMASA recorded the least leaf area of 87.2 cm². However, there was no significant difference ($P > 0.05$) between the genotypes KPAS04 and CHFB04-OB. For the water-stressed treatments, the genotype GUMA03-OB recorded the highest leaf area of 71.3 cm², whilst NYLA04 recorded the least of 30.8 cm². With the exception of the genotypes CHFB04-OB, NYIA03, NYLA04, IWD-C3-SYN-F2, GH120 DYF/D POP and KOBN04-R, all the other 19 genotypes were statistically at par ($P > 0.05$) (Table 4.4).

Table 4.4: Trends in number of leaves, shoot length and leaf area recorded of the genotypes during screening under pot conditions in Nyankpala in the 2013 cropping season

Genotype	Number of leaves		Shoot length (cm)		Leaf area (cm²)	
	Water-stressed	Normal	Water-stressed	Normal	Water-stressed	Normal
CHFB04-OB	6	8	30.7	65.8	45.4	136.5
KPAS04	5	7	31.0	64.9	64.6	150.7
OKOMASA	5	8	33.0	50.7	55.3	87.2
KOBN03-OB	5	7	31.2	53.5	67.8	113.4
NYAZ03-Y	4	7	27.6	61.2	51.2	95.6
NYAZ04-W	6	8	33.2	49.5	57.1	106.2
GUMA03-OB	6	9	36.5	66.2	71.3	103.7
GBRM04-BA	5	8	25.1	60.6	50.4	89.9
TZE-Y-DT-STR-C4	5	8	30.1	55.0	51.1	99.6
DORKE SR	5	9	27.8	59.6	52.6	107.5
NYAN03	5	7	28.1	58.1	56.9	118.5
TZE-W-DT-STR-C4	5	8	35.8	70.3	60.0	109.0
NYIA03	6	10	27.4	61.3	47.3	97.1
NYLA04	5	10	24.8	60.1	30.8	104.4
TAAN04	5	6	31.9	48.3	64.9	110.4
NYSW03-Y	6	3	23.1	53.2	59.5	115.9
DT-STR-W-C2	7	9	33.2	63.1	62.1	100.8
SISF03-0B	6	9	33.1	58.9	57.7	100.1
KOBN04-R	4	7	28.4	53.8	49.0	108.9
TAIS03	6	9	28.6	50.0	62.4	108.4
CHMA04	5	8	25.7	50.5	60.9	111.1
IWD-C3-SYN-F2	4	8	25.0	49.2	49.3	107.1
NYFA04	6	8	27.7	51.5	57.3	108.4
GH120 DYF/D POP	6	7	22.3	56.8	44.9	92.0
NYFA03	6	9	26.0	44.4	63.5	96.3
Mean	5	8	29.1	56.7	55.7	107.2
SEM	0.21	0.20	1.82	1.00	3.51	1.87
LSD (0.05)	1.32	1.56	7.35	12.10	20.94	28.03

SEM means standard error of mean; Measurements were made at six weeks after planting

4.3.1.5 Chlorophyll content

When plants were watered regularly, genotype KPAS04 recorded the highest chlorophyll content of 42.57 spad units, whilst CHMA04 recorded the lowest chlorophyll content of 28.13 spad units. For the water-stressed plants, the genotype TZE-Y-DT-STR-C4 recorded the highest chlorophyll content of 38.37 spad units, whilst GUMA03-OB recorded the lowest chlorophyll content of 28.77 spad units (Figure 4.1).

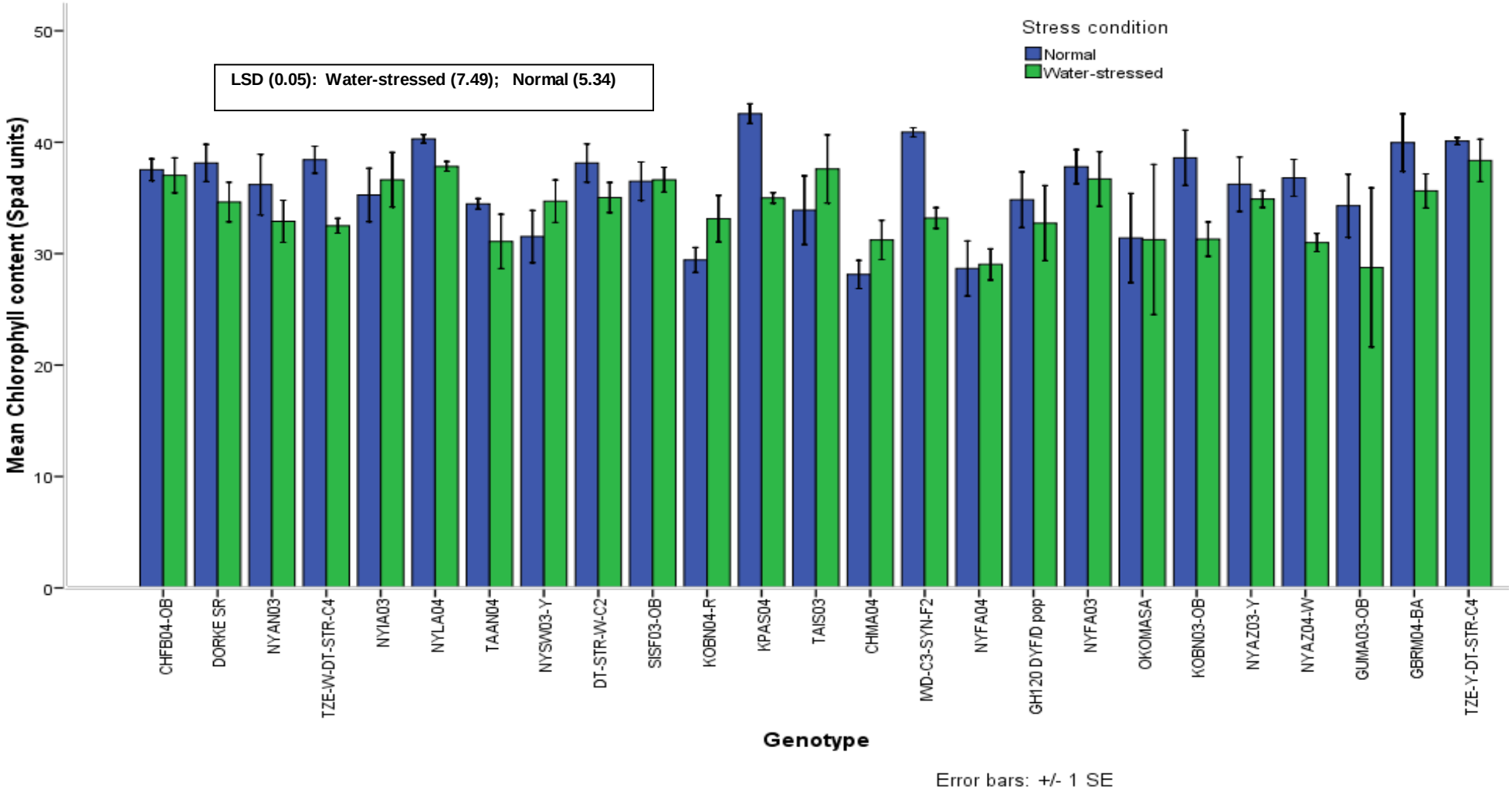

Figure 4.1: Variation in relative chlorophyll content of the genotypes for the control (normal) and water-stressed treatments; Bars represent standard error of mean; Measurements were made at six weeks after planting

4.3.1.6 Fresh root biomass

When plants were watered regularly/normally, genotype CHFB04-OB recorded the highest fresh root biomass (4.90 g), whilst TAAN04 recorded the lowest fresh root biomass (1.77 g) (Table 4.5). Genotype CHFB04-OB significantly differed ($P < 0.05$) from GUMA03-OB, GBRM04-BA and TAAN04 with respect to fresh root biomass production. For the water-stressed plants, TAIS03 and IWD-C3-SYN-F2 recorded the highest value of 1.50 g, whilst DORKE SR and DT-STR-W-C2 recorded the lowest value of 0.45 g. The genotypes such as TAIS03 and IWD-C3-SYN-F2 did not significantly differ ($P > 0.05$) from CHFB04-OB, KPAS04, OKOMASA, KOBN03-OB, NYAZ04-W, GUMA03-OB, TAAN04, TZE-W-DT-STR-C4, TZE-Y-DT-STR-C4 and NYFA04 in terms of fresh root biomass production (Table 4.5).

4.3.1.7 Dry root biomass

When plants were watered normally, genotype CHFB04-OB recorded the highest dry root biomass (1.25 g), whilst TAAN04 recorded the least dry root biomass (0.33 g). There was a statistical difference ($P < 0.05$) between CHFB04-OB and other genotypes such as KOBN03-OB, GUMA03-OB, TZE-Y-DT-STR-C4, TAAN04 and SISF03-OB for dry root biomass production. For the water-stressed treatment, the genotype NYAZ04-W recorded the highest dry root biomass (0.43 g), while DT-STR-W-C2 recorded the lowest dry root biomass (0.05 g). The genotypes such as NYAZ04-W, CHFB04-OB, KPAS04, OKOMASA, KOBN03-OB, GUMA03-OB, TZE-Y-DT-STR-C4, TAAN04, NYSW03-Y, TAIS03, CHMA04 and IWD-C3-SYN-F2 were not significantly different ($P > 0.05$) in terms of root biomass accumulation (Table 4.5).

4.3.1.8 Root length

When plants were watered normally, genotype KPAS04 recorded the highest root length of 24.05 cm, whilst IWD-C3-SYN-F2 recorded the lowest value of 10.50 cm for the normal plants. The following genotypes; KPAS04, CHFB04-OB, NYAZ04-W, NYAN03, DT-STR-W-C2, CHMA04 and GH120 DYF/D POP were not statistically different ($P > 0.05$). For the water-stressed treatments, the genotype NYSW03-Y recorded the highest root length of 19.23 cm, whilst KPAS04 and GH120 DYF/D POP recorded the lowest value of 9.40 cm. There were no significant differences ($P > 0.05$) among the genotypes such as NYSW03-Y, CHFB04-OB, KOBN03-OB, GUMA03-OB, TZE-Y-DT-STR-C4, TZE-W-DT-STR-C4, NYIA03 and TAAN04 (Table 4.5).

Table 4.5: Root growth and dry matter accumulation of the various genotypes during screening under pot conditions in Nyankpala during the 2013 cropping season

Genotype	Fresh root biomass (g)		Dry root biomass (g)		Root length (cm)	
	Water-stressed	Normal	Water-stressed	Normal	Water-stressed	Normal
CHFB04-OB	1.35	4.90	0.40	1.25	16.27	21.35
KPAS04	1.00	4.25	0.27	0.85	9.40	24.05
OKOMASA	1.17	2.93	0.27	0.73	14.23	13.07
KOBN03-OB	1.20	2.40	0.33	0.43	18.80	14.73
NYAZ03-Y	0.57	2.13	0.07	0.47	9.53	15.93
NYAZ04-W	1.33	2.40	0.43	0.53	12.57	21.30
GUMA03-OB	1.30	2.00	0.35	0.40	16.50	16.33
GBRM04-BA	0.50	1.87	0.07	0.53	9.43	14.33
TZE-Y-DT-STR-C4	1.07	2.27	0.27	0.43	17.87	16.37
DORKE SR	0.45	4.35	0.10	1.00	12.30	16.75
NYAN03	0.65	3.80	0.10	0.67	12.27	20.13
TZE-W-DT-STR-C4	1.00	3.35	0.23	0.80	15.07	13.65
NYIA03	0.50	2.17	0.13	0.50	14.80	18.03
NYLA04	0.55	4.83	0.10	1.20	9.65	16.70
TAAN04	1.40	1.77	0.25	0.33	15.65	12.60
NYSW03-Y	1.13	2.77	0.27	0.53	19.23	13.13
DT-STR-W-C2	0.45	3.57	0.05	0.83	9.70	20.03
SISF03-0B	0.85	2.03	0.20	0.43	11.40	15.57
KOBN04-R	0.70	2.83	0.10	0.63	11.23	17.73
TAIS03	1.50	3.30	0.25	0.97	10.55	14.43
CHMA04	0.90	2.70	0.30	0.87	13.50	19.47
IWD-C3-SYN-F2	1.50	3.90	0.35	0.65	10.55	10.50
NYFA04	0.97	3.43	0.20	0.67	10.83	15.47
GH120 DYF/D POP	0.55	4.45	0.10	1.10	9.40	18.40
NYFA03	0.93	2.57	0.17	0.67	10.83	11.87
Mean	0.94	3.08	0.21	0.70	12.86	16.48
SEM	0.22	0.20	0.01	0.05	0.50	0.51
LSD (0.05)	0.55	2.90	0.19	0.79	4.72	5.97

SEM means standard error of mean; Measurements were made at six weeks after planting

4.3.1.9 Stem girth

When plants were watered normally, genotype NYSW03-Y recorded the highest stem girth (1.83 cm), whilst TZE-Y-DT-STR-C4 recorded the lowest stem girth (1.13 cm). There were no significant differences ($P > 0.05$) among the genotypes such as NYSW03-Y, CHFB04-OB, OKOMASA and DT-STR-W-C2 for stem girth. For the water-stressed trial, the genotype CHFB04-OB recorded the highest stem girth of 0.93 cm, while NYLA04 recorded the lowest stem girth of 0.47 cm. There were no significant differences ($P > 0.05$) among the genotypes CHFB04-OB, KPAS04, OKOMASA, NYAZ04-W, GUMA03-OB, TZE-Y-DT-STR-C4, TAAN04, NYSW03-Y, DT-STR-W-C2, TAIS03 and NYFA04 (Table 4.6).

4.3.1.10 Fresh shoot biomass

When plants were watered normally, genotype KPAS04 recorded the highest fresh shoot biomass of 88.45 g, whilst TAAN04 recorded the least of 25.67 g. The following genotypes: KPAS04, CHFB04-OB and TZE-W-DT-STR-C4 were not significantly different ($P > 0.05$) for fresh shoot biomass production. For the water-stressed plants, genotype CHFB04-OB recorded the highest fresh shoot biomass of 20.00 g, whilst NYLA04 recorded the least of 3.95 g. There were no significant differences ($P > 0.05$) among the genotypes CHFB04-OB, GUMA03-OB, TZE-W-DT-STR-C4, TAAN04, TAIS03, CHMA04, IWD-C3-SYN-F2 and NYFA04 for fresh shoot biomass (Table 4.6).

4.3.1.11 Dry shoot biomass

When plants were watered normally, KPAS04 recorded the highest dry shoot biomass of 10.20 g, whilst NYAZ03-Y recorded the least value of 3.30 g. There were no significant differences ($P > 0.05$) among KPAS04, CHFB04-OB and TZE-W-DT-STR-C4 for dry shoot biomass

production. For the water-stressed treatments, CHFB04-OB recorded the highest dry shoot biomass of 2.80 g, whilst NYLA04 recorded the lowest of 0.45 g. The genotypes CHFB04-OB, KPAS04, TAAN04 and TAIS03 did not significantly differ ($P > 0.05$) for dry shoot biomass production (Table 4.6).

Table 4.6: Variation in stem girth, fresh shoot and dry shoot biomass of the genotypes during screening in pots in Nyankpala for the 2013 cropping season

Genotype	Stem girth (cm)		Fresh shoot biomass (g)		Dry shoot biomass (g)	
	Water-stressed	Normal	Water-stressed	Normal	Water-stressed	Normal
CHFB04-OB	0.93	1.73	20.00	85.90	2.80	8.95
KPAS04	0.87	1.57	12.27	88.45	2.60	10.20
OKOMASA	0.77	1.70	10.37	38.93	1.30	3.97
KOBN03-OB	0.70	1.47	13.73	33.27	1.83	3.77
NYAZ03-Y	0.67	1.17	9.73	28.43	1.43	3.30
NYAZ04-W	0.83	1.27	12.37	41.10	1.70	4.50
GUMA03-OB	0.87	1.40	14.07	46.00	1.70	4.37
GBRM04-BA	0.70	1.17	8.17	38.77	1.06	4.03
TZE-Y-DT-STR-C4	0.73	1.13	11.20	38.50	1.50	3.90
DORKE SR	0.67	1.30	6.67	56.35	1.00	6.35
NYAN03	0.53	1.30	9.70	53.43	1.30	5.53
TZE-W-DT-STR-C4	0.70	1.23	14.17	68.20	1.73	7.95
NYIA03	0.63	1.27	6.50	47.40	0.97	4.63
NYLA04	0.47	1.20	3.95	43.47	0.45	4.57
TAAN04	0.77	1.17	16.42	25.67	2.35	3.40
NYSW03-Y	0.87	1.83	11.73	44.40	1.47	4.97
DT-STR-W-C2	0.73	1.67	7.90	55.87	0.90	6.07
SISF03-0B	0.63	1.27	11.52	45.60	1.50	4.60
KOBN04-R	0.60	1.40	10.20	43.90	1.20	4.03
TAIS03	0.80	1.33	17.35	35.90	2.05	3.73
CHMA04	0.70	1.17	14.60	42.70	1.95	4.10
IWD-C3-SYN-F2	0.53	1.47	16.50	29.00	1.95	4.05
NYFA04	0.87	1.33	14.00	45.13	1.73	3.90
GH120 DYF/D POP	0.63	1.40	6.15	49.40	0.65	4.75
NYFA03	0.70	1.30	10.47	35.80	1.40	4.93
Mean	0.72	1.37	11.59	46.46	1.50	4.98
SEM	0.04	0.02	2.38	2.44	0.27	0.27
LSD (0.05)	0.21	0.24	6.37	29.38	0.82	3.12

SEM means standard error of mean; Measurements were made at six weeks after planting

4.3.1.12 Correlation

The correlation co-efficient among the characters were computed at phenotypic level. The association among different characters is presented in Table 4.7. The data shows that shoot length positively and highly significantly ($P < 0.001$) associated with stem girth and leaf area. The shoot length was also positively and significantly ($P < 0.05$) associated with fresh shoot biomass and dry shoot biomass. There was also positive and significant ($P < 0.01$) relation between shoot length and root length. Shoot length however, exhibited no significant correlation ($P > 0.05$) with characters such as fresh root biomass and dry root biomass.

Table 4.7: Phenotypic correlation co-efficients among vegetative traits during the 2013 cropping season

DF = 196	Stem girth	Leaf area	Fresh root biomass	Dry root biomass	Fresh shoot biomass	Dry shoot biomass	Root length
Shoot length	0.4795***	0.3887***	0.1031ns	0.1338ns	0.1217*	0.1661*	0.2149**
Stem girth		0.5179***	0.3394***	0.3886***	0.3342***	0.4215***	0.2789***
Leaf area			0.3163***	0.2740***	0.2554***	0.3112***	0.2611***
Fresh root biomass				0.8640***	0.7351***	0.7294***	0.4292***
Dry root biomass					0.6443***	0.7649***	0.4486***
Fresh shoot biomass						0.9016***	0.4072***
Dry shoot biomass							0.4367***

*Significant at P < 0.05, **Significant at P < 0.01, ***Significant at P < 0.001, ns Non-significant at P > 0.05

4.3.2 Experiment II

As in the case of Experiment I, two trials were conducted in this experiment; normal and water-stressed trials. The normal trial was the controlled trial in which the maize plants were planted at the normal time of planting maize in the study area so that the growth of plants in the field coincided with the rainy season. The early planting of the normal trial was also to ensure that the trial did not coincide with drought. In the water-stressed trial, the plants were planted six weeks later than the normal planting time to ensure that plants coincided with drought during the growth period. All agronomic practices observed in both trials were the same, except the introduction of drought stress.

4.3.2.1 Analysis of variance

The analysis of variance for parameters measured for the normal (control) trial is presented in Table 4.8. There were highly significant differences ($P < 0.001$) among the genotypes with respect to plant height, days to 50% tasseling, days to 50% anthesis, days to 50% silking, ear height and grain yield. There were highly significant differences ($P < 0.01$) among genotypes with respect to number of ears harvested per plot. However, there were no significant differences ($P > 0.05$) among genotypes with respect to anthesis-silking interval, plant stand and hundred-grain weight (Table 4.8).

Table 4.8: Mean squares and co-efficient of variation (CV %) for parameters measured for the normal trial

Source	df	Trait									
		Plant height (cm)	Days to 50% tasseling	Days to 50% anthesis	Days to 50% silking	Anthesis -silking interval	Plant stand	Ear height (cm)	Ears harvested	Grain yield (tons/ha)	Hundred-grain weight (g)
Replication	2	55.54^{ns}	2.09^{ns}	0.09^{ns}	7.24^{ns}	5.49^{ns}	7.56^{ns}	545.54^{**}	9.61^{ns}	0.27^{**}	0.002^{ns}
Genotype	24	1008.26^{***}	31.19^{***}	39.12^{***}	49.90^{***}	7.25^{ns}	7.81^{ns}	652.33^{***}	10.03^{**}	0.21^{***}	0.047^{ns}
Model	26	934.98^{***}	28.95^{***}	36.12^{***}	46.62^{***}	7.11^{ns}	7.79^{ns}	644.12^{***}	10.00^{**}	0.21^{***}	0.043^{ns}
Error	48	216.52	5.87	5.18	10.53	5.69	5.41	103.74	3.97	0.05	0.032
CV %		9.47	4.09	3.41	4.91	34.20	19.06	13.55	18.41	17.46	15.81

*Significant at $P < 0.05$, **Significant at $P < 0.01$, ***Significant at $P < 0.001$, ^{ns} Non-significant at $P > 0.05$

Similarly, the analysis of variance for parameters measured in the water-stressed trial is presented in Table 4.9. There were highly significant differences ($P < 0.001$) among the genotypes with respect to plant height, days to 50% tasseling, days to 50% anthesis, days to 50% silking, anthesis-silking interval, plant stand, ear height, ears harvested and grain yield. There were highly significant differences ($P < 0.01$) among genotypes for hundred-grain weight and drought rating.

Table 4.9: Mean squares and co-efficient of variation (CV %) for parameters measured for the water-stressed trial

Source	df	Trait										
		Plant height (cm)	Days to 50% tasseling	Days to 50% anthesis	Days to 50% silking	Anthesis -silking interval	Plant stand	Ear height (cm)	Drought rating at 10 WAPE	Ears harvested	Grain yield (tons/ha)	Hundred -grain weight (g)
Replication	2	62.56^{ns}	0.84^{ns}	30.77***	17.69**	23.09**	3.57^{ns}	136.36^{ns}	1.290*	1.08^{ns}	0.020^{ns}	0.0133^{ns}
Genotype	24	1500.84***	23.86***	51.16***	54.15***	20.25***	17.09***	723.36***	0.948**	20.94***	0.054***	0.0306**
Model	26	1390.20***	22.09***	49.59***	51.34***	20.47***	16.05***	678.19***	0.974**	19.42***	0.052***	0.0293**
Error	48	261.79	1.12	1.08	2.74	2.97	4.43	116.45	0.363	5.48	0.013	0.0132
CV %		12.53	10.86	11.65	20.52	19.52	19.60	19.60	14.43	30.81	44.20	19.25

*Significant at P < 0.05, **Significant at P < 0.01, ***Significant at P < 0.001, ^{ns} Non-significant at P > 0.05, WAPE means weeks after plant establishment

4.3.2.2 Vegetative traits

The effects of water-stress were assessed by comparing the parameters measured due to the stress relative to the watered (normal) trial (Table 4.10). When the normal and water-stressed treatments were compared in terms of percentage change of parameters measured, it was observed that grain yield recorded the highest percentage reduction of 79.3% due to the stress, whilst days to 50% silking recorded the lowest percentage reduction of 1.5% due to the stress conditions. On the contrary, anthesis-silking interval recorded a percentage increase of 66.7% as a result of the water stress conditions (Table 4.10).

Table 4.10: Comparing parameters measured in the watered (normal) and water-stressed regimes

Trait	Treatment		% change due to water -stress	LSD (0.05)
	Normal	Water-stressed		
Plant height (cm)	155.39[a]	129.15[b]	16.9	5.26
Days to 50% tasseling	59[a]	57[b]	3.4	0.69
Days to 50% anthesis	66[a]	63[b]	4.5	0.73
Days to 50% silking	67[a]	66[b]	1.5	0.86
Anthesis-silking interval	1[b]	3[a]	66.7	0.77
Plant stand	12[a]	11[b]	8.3	0.63
Ear height (cm)	75.1[a]	55.1[b]	26.6	3.90
Ears harvested	11[a]	8[b]	27.3	0.71
Grain yield (tons/ha)	3.43[a]	0.71[b]	79.3	0.07
Hundred-grain weight (g)	36.3[a]	18.8[b]	48.2	2.00

Traits having different letters (horizontal direction) are significantly different at the 5% level of probability

4.3.2.3 Plant height

Results for plant height for Experiment II are shown in Figure 4.2. Genotype NYIA03 recorded the highest plant height of 183.10 cm, whilst TZE-W-DT-STR-C4 recorded the lowest plant height of 121 cm for the normal trial. For the water-stressed plants, GBRM04-BA recorded the highest plant height of 174.73 cm, whilst NYSW03-Y recorded the lowest of 86.83 cm.

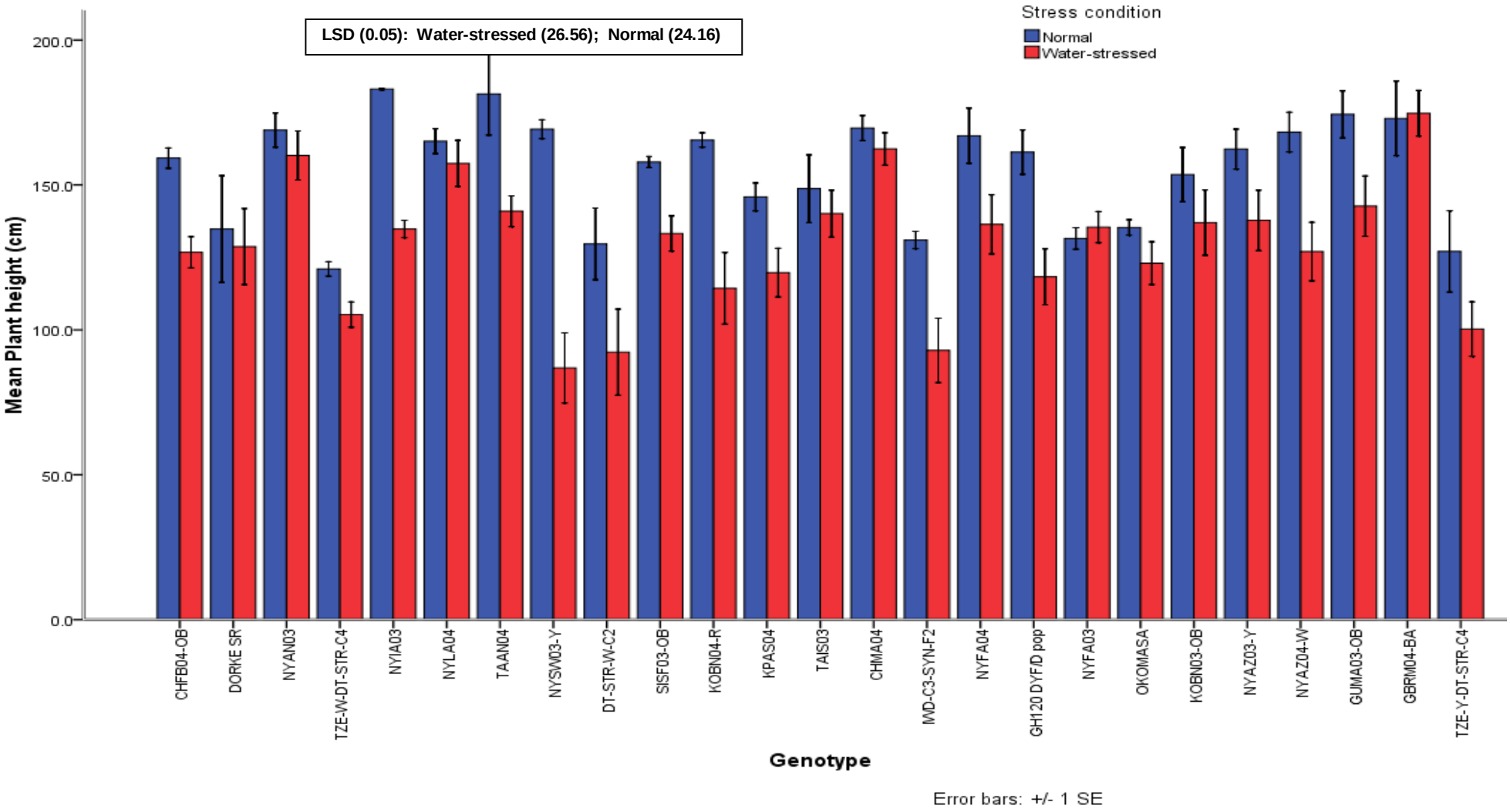

Figure 4.2: Changes in plant height of the genotypes during screening under field conditions in 2013 cropping season; Bars represent standard error of mean

4.3.2.4 Days to 50% tasseling

For the normal experiment (early planting), the genotype OKOMASA and DT-STR-W-C2 recorded the highest number of days to 50% tasseling (64), whilst TZE-W-DT-STR-C4 recorded the least number of days to 50% tasseling (51) (Table 4.11). However, there were no significant differences ($P > 0.05$) among OKOMASA, KOBN03-OB, GUMA03-OB, GBRM04-BA, DT-STR-W-C2, TAIS03, NYAZ03-Y, CHMA04, NYFA04, GH120 DYF/D POP and NYFA03. For the water-stressed plants, OKOMASA was the latest genotype in terms of number of days to 50% tasseling (64), whilst NYSW03-Y was the earliest genotype to tassel (50 days) (Table 4.11).

4.3.2.5 Days to 50% anthesis

For the normal treatments, the genotype OKOMASA was the latest genotypes to reach 50% anthesis (71), whilst TZE-W-DT-STR-C4 was the earliest (58) (Table 4.11). There were no significant differences ($P > 0.05$) among the following genotypes: OKOMASA, NYFA03, GUMA03-OB, GBRM04-BA, DORKE SR, NYAN03, DT-STR-W-C2, TAIS03, CHMA04, NYFA04, GH120 DYF/D POP, CHFB04-OB, KPAS04, KOBN03-OB and NYAZ03-Y. For the water-stressed plants, the genotypes OKOMASA and NYLA04 were the latest to attain 50% anthesis (69), while NYSW03-Y was the earliest genotype to reach 50% anthesis (54). There were no significant differences ($P > 0.05$) among OKOMASA, GBRM04-BA and NYLA04.

4.3.2.6 Days to 50% silking

For the normal planting (control/normal), the genotypes OKOMASA and DT-STR-W-C2 were the latest to produce silk (72 days), while TZE-Y-DT-STR-C4 was the earliest (58 days). There were no significant differences ($P > 0.05$) among the genotypes OKOMASA, DT-STR-W-C2, KOBN03-OB, NYAZ03-Y, GUMA03-OB, GBRM04-BA, DORKE SR, CHMA04, GH120

DYF/D POP and NYFA03. For the water-stressed plants, the genotype OKOMASA again was the latest in terms of 50% silk production (72 days), whilst TZE-Y-DT-STR-C4 was the earliest (57 days). However, OKOMASA was significantly similar ($P > 0.05$) to GBRM04-BA, NYLA04, CHMA04 and IWD-C3-SYN-F2 (Table 4.11).

Table 4.11: Trends in days to 50% tasseling, days to 50% anthesis and days to 50% silking of the genotypes during screening under field conditions in 2013 cropping season

Genotype	Days to 50% tasseling		Days to 50% anthesis		Days to 50% silking	
	Water-stressed	Normal	Water-stressed	Normal	Water-stressed	Normal
CHFB04-OB	56	60	63	66	66	68
KPAS04	57	60	62	67	64	68
OKOMASA	64	64	69	71	72	72
KOBN03-OB	57	62	64	68	68	69
NYAZ03-Y	57	60	64	68	67	69
NYAZ04-W	54	57	56	63	58	63
GUMA03-OB	57	62	65	70	67	70
GBRM04-BA	58	62	68	70	71	70
TZE-Y-DT-STR-C4	52	55	55	59	57	58
DORKE SR	57	59	65	69	67	70
NYAN03	57	59	64	67	67	68
TZE-W-DT-STR-C4	53	51	56	58	58	59
NYIA03	57	57	62	61	63	62
NYLA04	63	59	69	66	71	67
TAAN04	57	58	65	66	68	67
NYSW03-Y	50	54	54	59	59	61
DT-STR-W-C2	59	64	67	70	68	72
SISF03-0B	57	56	62	62	63	63
KOBN04-R	57	55	60	64	63	64
TAIS03	57	60	64	67	67	67
CHMA04	57	63	66	70	70	70
IWD-C3-SYN-F2	57	58	65	64	70	65
NYFA04	57	60	63	67	65	68
GH120 DYF/D POP	57	61	64	69	65	70
NYFA03	57	63	65	68	68	71
Mean	57	59	63	66	66	67
SEM	0.36	0.43	0.35	0.46	0.44	0.56
LSD (0.05)	1.74	3.98	1.71	3.74	2.72	5.33

SEM means standard error of mean

4.3.2.7 Plant stand

For the normal treatment, the genotypes NYAZ03-Y, NYAZ04-W, NYIA03 and NYFA04 recorded the highest number of plant stand of 14, whilst GH120 DYF/D POP and IWD-C3-SYN-F2 recorded the least of 9 (Table 4.12). In the water-stressed treatment, NYFA03 and NYIA03 recorded the highest number of plant stand of 14, whilst IWD-C3-SYN-F2 recorded the least number of 4.

4.3.2.8 Ear height

For the normal treatment, the genotype GBRM04-BA recorded the highest ear height of 102.3 cm, whilst DT-STR-W-C2 and IWD-C3-SYN-F2 recorded the lowest of 46.5 cm (Table 4.12). For the water-stressed treatment, GBRM04-BA recorded the highest ear height of 90.1 cm, while IWD-C3-SYN-F2 recorded the least of 28.3 cm. GBRM04-BA was not significantly different ($P > 0.05$) from the genotypes NYAN03, NYLA04 and CHMA04 in terms of ear height (Table 4.12).

4.3.2.9 Ears harvested

For the normal planting, the genotype NYIA03 recorded the highest number of ears harvested (14), whilst TZE-Y-DT-STR-C4, IWD-C3-SYN-F2, TAIS03, DORKE SR and GH120 DYF/D POP recorded the lowest number of ears harvested (8) (Table 4.12). The genotypes NYIA03, KPAS04, CHFB04-OB, NYAZ03-Y, NYAZ04-W, GUMA03-OB, GBRM04-BA, NYAN03, TAAN04, NYSW03-Y, SISF03-OB, KOBN04-R, NYFA04 and NYFA03 were not significantly different ($P > 0.05$). For the water-stressed plants, the genotype NYIA03 again recorded the highest number of ears harvested (12), whilst OKOMASA and IWD-C3-SYN-F2 recorded the least of 2. There were no significant differences ($P > 0.05$) among the following genotypes;

NYIA03, KPAS04, NYAZ03-Y, NYAZ04-W, GUMA03-OB, DORKE SR, TZE-W-DT-STR-C4, TAAN04, SISF03-OB, NYFA04 and NYFA03 (Table 4.12).

Table 4.12: Variations in plant stand, ear height, and number of ears harvested of the genotypes during screening under field conditions in 2013 cropping season

Genotype	Plant stand		Ear height (cm)		Ears harvested	
	Water-stressed	Normal	Water-stressed	Normal	Water-stressed	Normal
CHFB04-OB	12	13	56.2	73.3	8	12
KPAS04	11	13	49.5	64.0	9	12
OKOMASA	8	12	46.7	65.5	2	9
KOBN03-OB	11	12	52.8	74.8	7	11
NYAZ03-Y	11	14	57.6	78.8	10	13
NYAZ04-W	13	14	56.6	79.8	10	12
GUMA03-OB	12	12	68.7	84.2	10	11
GBRM04-BA	11	12	90.1	102.3	8	13
TZE-Y-DT-STR-C4	7	10	37.9	61.4	5	8
DORKE SR	11	10	48.8	64.0	8	8
NYAN03	11	13	75.8	98.8	8	11
TZE-W-DT-STR-C4	12	11	43.8	63.3	10	10
NYIA03	14	14	64.5	92.5	12	14
NYLA04	13	13	79.1	92.6	7	11
TAAN04	12	13	52.7	95.9	8	12
NYSW03-Y	10	13	32.1	73.6	4	12
DT-STR-W-C2	7	10	30.0	46.5	5	9
SISF03-0B	12	13	58.4	72.4	11	12
KOBN04-R	10	13	45.8	81.4	8	11
TAIS03	13	12	66.8	79.9	6	8
CHMA04	11	12	78.6	84.3	7	11
IWD-C3-SYN-F2	4	9	28.3	46.5	2	8
NYFA04	11	14	49.9	77.0	10	12
GH120 DYF/D POP	8	9	51.7	61.4	9	8
NYFA03	14	13	54.3	64.9	10	12
Mean	11	12	55.1	75.1	8	11
SEM	0.23	0.29	1.77	1.98	0.27	0.28
LSD (0.05)	3.46	3.82	17.72	16.72	3.84	3.27

SEM means standard error of mean

4.3.2.10 Anthesis – silking interval

For the normal planting, genotype NYFA03 recorded the highest anthesis-silking interval of 3 days, whilst NYAZ04-W, GUMA03-OB, GBRM04-BA, KOBN04-R, TAIS03 and CHMA04 recorded zero days for anthesis-silking interval (Table 4.13). For the water-stressed treatments, NYSW03-Y and IWD-C3-SYN-F2 recorded the highest anthesis-silking interval of 5 days, whilst NYIA03, DT-STR-W-C2, SISF03-0B and GH120 DYF/D POP recorded the least of 1 day.

4.3.2.11 Grain yield and hundred-grain weight

For the normal planting, genotype NYAZ03-Y recorded the highest grain yield of 4.81 tons/ha, whilst DT-STR-W-C2 recorded the lowest grain yield of 2.32 tons/ha. There were no significant differences ($P > 0.05$) among NYAZ03-Y, CHFB04-OB, GUMA03-OB, NYAN03, NYIA03, NYLA04, TAAN04, SISF03-OB and NYFA04. For the water-stressed plants, SISF03-OB recorded the highest grain yield of 1.74 tons/ha, whilst OKOMASA recorded the least of 0.13 tons/ha. Genotype SISF03-OB significantly ($P < 0.05$) out yielded all the other 24 genotypes (Table 4.13).

Genotype TAAN04 recorded the highest hundred-grain weight of 45 g, whilst GH120 DYF/D POP, NYANO3 and NYSW03-Y recorded the lowest of 31 g for the normal plants (Table 4.13). The following genotypes; TAAN04, CHFB04-OB, OKOMASA, KOBN03-OB, NYAZ03-Y, TZE-Y-DT-STR-C4, DORKE SR, TZE-W-DT-STR-C4, NYIA03, DT-STR-W-C2, SISF03-OB, TAIS03, CHMA04, IWD-C3-SYN-F2 and NYFA03 were not significantly different ($P > 0.05$). For the water-stressed plants, the genotype GBRM04-BA recorded the highest hundred-grain weight of 26.0 g, whilst DT-STR-W-C2 recorded the lowest hundred-grain weight of 13.3 g.

There were no significant differences ($P > 0.05$) among genotypes GBRM04-BA, KOBN03-OB, DORKE SR, SISF03-OB, KOBN04-R and CHMA04.

4.3.2.12 Drought rating

Drought rating ranged from 1 to 5. The genotypes IWD-C3-SYN-F2, NYLA04, OKOMASA, GH120 DYF/D POP, NYFA03, NYSW03-Y and CHFB04-OB recorded the highest drought rating of 5, whilst SISF03-OB, NYAZ04-W, GUMA03-OB and NYIA03 recorded the lowest drought rating of 3. There were no significant differences ($P > 0.05$) among IWD-C3-SYN-F2, NYLA04, OKOMASA, CHFB04-OB, KPAS04, NYAZ03-Y, GBRM04-BA, TZE-Y-DT-STR-C4, DORKE SR, TAAN04, NYSW03-Y, DT-STR-W-C2, TAIS03, GH120 DYF/D POP and NYFA03 (Table 4.13).

Table 4.13: Variation in anthesis-silking interval, grain yield, hundred-grain weight and drought rating of the genotypes during field screening

Genotype	Anthesis-silking interval		Grain yield (tons/ ha)		Hundred-grain weight (g)		Drought rating at 10 WAPE
	Water-stressed	Normal	Water-stressed	Normal	Water-stressed	Normal	Water-stressed plants
CHFB04-OB	3	2	0.55	4.13	17.3	39.0	5
KPAS04	2	1	0.67	3.39	16.3	33.0	4
OKOMASA	3	1	0.13	3.01	17.0	40.0	5
KOBN03-OB	4	1	0.71	3.55	22.0	38.0	4
NYAZ03-Y	3	1	0.83	4.81	18.7	38.0	4
NYAZ04-W	2	0	0.99	2.96	15.7	32.0	3
GUMA03-OB	2	0	0.99	3.89	17.3	33.0	3
GBRM04-BA	3	0	0.93	3.33	26.0	33.0	4
TZE-Y-DT-STR-C4	2	1	0.41	2.88	17.3	36.0	4
DORKE SR	2	1	0.57	2.80	23.3	39.0	4
NYAN03	3	1	0.96	3.95	17.0	31.0	4
TZE-W-DT-STR-C4	2	1	0.77	2.59	17.7	39.0	4
NYIA03	1	1	1.07	4.19	19.7	36.0	3
NYLA04	2	1	0.61	3.81	17.3	32.0	5
TAAN04	3	1	0.67	4.61	19.7	45.0	4
NYSW03-Y	5	2	0.14	2.77	17.0	31.0	5
DT-STR-W-C2	1	2	0.27	2.32	13.3	36.0	4
SISF03-0B	1	1	1.74	4.08	24.7	39.0	3
KOBN04-R	3	0	0.87	3.57	22.0	35.0	4
TAIS03	3	0	0.59	2.64	19.7	37.0	4
CHMA04	4	0	1.10	3.52	24.0	43.0	4
IWD-C3-SYN-F2	5	1	0.16	2.53	17.0	38.0	5
NYFA04	2	1	0.94	4.45	16.7	33.0	4
GH120 DYF/D POP	1	1	0.51	2.69	18.7	31.0	5
NYFA03	3	3	0.62	3.15	15.0	41.0	5
Mean	3	1	0.71	3.43	18.8	36.3	4
SEM	0.09	0.10	0.08	0.11	0.6	1.0	0.59
LSD (0.05)	1.01	1.59	0.52	0.98	6.00	9.40	0.99

SEM means standard error of mean; WAPE means weeks after plant establishment

4.3.2.13 Correlation

The correlation co-efficient among characters were computed at phenotypic level. The association among different characters is presented in Table 4.14. The data shows that grain yield positively and highly significantly ($P < 0.001$) correlated with plant height, ear height, plant stand, ears harvested and hundred-grain weight. However grain yield exhibited negative and significant correlation with four characters. These included; days to 50% tasseling, days to 50% silking, days to 50% anthesis and anthesis-silking interval.

Table 4.14: Phenotypic correlation co-efficients among ten characters in maize genotypes

DF = 196	Days to 50% tasseling	Days to 50% silking	Days to 50% anthesis	Anthesis-silking interval	Plant stand	Ear height	Ears harvested	Grain yield	Hundred-Grain weight
Plant height	-0.1967**	-0.2544***	-0.1354ns	-0.1151ns	0.1847**	0.6515***	0.2960***	0.4606***	0.1750*
Days to 50% tasseling		0.5255***	0.5469***	-0.3045***	-0.0540ns	-0.0831ns	-0.1383ns	-0.2080**	-0.0167ns
Days to 50% silking			0.7912***	0.6407***	-0.0423ns	-0.1134ns	-0.1686*	-0.2928***	-0.1423*
Days to 50% anthesis				0.3780***	-0.0575ns	-0.0644ns	-0.1627*	-0.2424***	-0.1181ns
Anthesis-silking interval					-0.0032ns	-0.0615ns	-0.0754ns	-0.1467*	-0.1439*
Plant stand						0.1982**	0.6614***	0.2379***	-0.0429ns
Ear height							0.3380***	0.5431***	0.1676*
Ears harvested								0.5071***	0.0467ns
Grain yield									0.2795***

*Significant at P < 0.05, **Significant at P < 0.01, ***Significant at P < 0.001, ns Non-significant at P > 0.05

4.4 Discussion

A clear effect of drought stress was observed on leaf development, shoot length and chlorophyll content of genotypes. The variations in these traits among genotypes from the control and those stressed may have resulted from the effect of water-stress on cell division, cell expansion and chloroplast development (Ouattar *et al.*, 1987). These authors reported that, in maize production, physiological developmental processes such as the formation and expansion of cells and development of green pigments are normally enhanced in soils with high organic matter and moisture content devoid of soil borne diseases and pests. The well watered genotypes such as KPAS04 and the water-stressed genotypes such as TZE-Y-DT-STR-C4 that produced the highest chlorophyll contents also produced the highest shoot lengths and leaf areas as reported under section 4.3 of this thesis. The plants that produced the highest chlorophyll content might have accumulated relatively more food reserves for the growth and development of more vigorous shoot and leaves. Quarrie and Jones (1977) observed that water-stress greatly affects leaf and vegetative growth. Pandey *et al.* (2000) also reported in maize that increasing moisture stress resulted in progressive reduction in leaf area. Also, according to Terbea and Ciocazamu (1999), water-stress significantly decreased chlorophyll contents and photosynthetic rate especially in highly drought sensitive genotypes. The results of the present study imply that genotypes varied in their ability to retain moisture in their tissues and have variation in their ability to resist drought.

The data of the present study indicated significant variation in the parameters measured among the water-stressed genotypes, probably as a result of inherent genetic variability of the genotypes. The drought tolerant genotypes such as GUMA03-OB, SISF03-OB, KOBN03-OB, TZE-Y-DT-STR-C4 and IWD-C3-SYN-F2 produced relatively longer shoots, broader leaves

with more chlorophyll concentration, as compared to the drought susceptible genotypes such as NYFA04. As a result of their relatively high chlorophyll concentration levels, the drought tolerant genotypes were able to undergo efficient photosynthesis to accumulate more food reserves for the development of generative organs such as leaves and stems. According to Barker *et al.* (2005), chlorophyll concentration is a measure of functional stay-green of a crop plant, and that chlorophyll plays a major role in photosynthesis which ultimately determines the crop yield. Dai *et al.* (1990) also reported that moderate water-stress inhibited the growth, development and yield of all cultivars and hybrids at different growth stages and that the leaf area of resistant cultivars remained larger under drought condition.

In general, the dry matter accumulated by crop plants positively correlates with crop yield, and could be used as a selection criterion for selection in drought studies (Mehdi *et al.*, 2001). Results of the present study showed that there were significant variations among the genotypes with respect to shoot and root dry matter accumulation. Water-stressed genotypes such as NYAZ04-W and CHF04-OB that produced relatively higher dry root and shoot biomass were considered to be more tolerant to drought conditions, whilst the stressed plants like NYLA04 and DT-STR-W-C2 that produced lower dry biomass, were relatively susceptible to the abiotic stress. The genotypes such as NYLA04, NYFA04 and NYAZ03-Y that produced relatively smaller quantities of shoot dry matter also produced lower values of chlorophyll content and therefore, are more drought sensitive. Such genotypes might not be considered by plant breeders for crop improvement programmes for drought tolerance. The water-stress condition could have caused a great reduction in moisture in such genotypes resulting in the corresponding reduction in the amount of photosynthates accumulation, which also consequently resulted in the reduction of root and shoot biomass among some of the water-stressed plants. Blum (1998) reported that efficient photosynthesis and stem reserve accumulation during the vegetative phase has a

decisive role in the production and development of root and shoot biomass, which may directly affect final yield. Some characteristics of fodder and green manure crops are that the crops produce many leaves, broader leaves, vigorous shoots that are succulent, and generally produce relatively high shoot dry matter. Well watered genotypes such as CHFB04-OB and KPAS04 recorded significantly higher root and shoot dry matter than other genotypes like NYLA04, and could be selected and further developed for use as green manure or fodder crops.

The study established a significant reduction in mean root length of water-stressed genotypes as compared to the well watered (normal) plants, and this among other factors is because of the moisture deficit which inhibited root growth and greatly modified plant development and morphology. The differences in root length of genotypes subjected to drought stress are due to variation of plant drought-resistant mechanisms associated with the individual plants. Genotypes like NYSW03-Y, KOBN03-OB, IWD-C3-SYN-F2 and GUMA03-OB that penetrated deeper into the soil, also produced longer shoots and more biomass accumulation among the stress plants and therefore, were less sensitive to drought than those genotypes like KPAS04 and GH120 DYF/D POP which produced relatively shorter roots. It is possible that the genes controlling root formation and development, among the tolerant genotypes, were stimulated by drought conditions. The deeper penetration of roots of genotypes NYSW03-Y, KOBN03-OB, IWD-C3-SYN-F2 and GUMA03-OB enabled them to draw moisture at deeper levels of soil. A number of investigators such as Matsuura *et al.* (1996) and Ramadan *et al.* (1985) made similar observations. Mayaki *et al.* (1976) however, made a contrary observation that maize roots penetrate deeper under conditions of moisture stress than they do when moisture is adequate.

Plants from the normal (early planting) treatments were taller with higher ear positions than those planted late and which coincided with drought in the field. As stated earlier in this section,

reduced moisture content of soil probably reduced the amount of photosynthates produced by water-stress plants. In this study, tolerant genotypes such as GBRM04-BA produced relatively higher plant and ear heights than IWD-C3-SYN-F2, probably because of their ability to develop vigorous and deeper root systems to draw water from the soil even at deeper levels for the development of chloroplast for effective photosynthesis to occur. Blum *et al.* (1998) confirmed this and stated that efficient photosynthesis and stem reserve accumulation during the vegetative phase plays a major role in the formation, development and growth of plant's shoot. Ali *et al.* (2011) also reported that under favourable soil and environmental conditions, maize ears are placed at higher positions on the plants, and that shorter ear heights are generally not desirable. They attributed the disadvantage of shorter ear to be crowded canopy, aeration and low transmission of sun light to the lower parts which may result in drastic reduction in yield. The study revealed that plant heights and ear heights were positively and significantly associated with grain yield (section 4.3.2.13**)**. It is possible that reduced shoots of normal or drought stress plants resulted in reduced food reserves, which consequently resulted in reduced grain yield.

There were significant variations among genotypes for number of days to flowering and number of days between anthesis and silk production among the watered and water stressed plants. The genotype NYSW03-Y that flowered relatively earlier was also more sensitive to drought as compared to those genotypes such as OKOMASA, GBRM04-BA, and IWD-C3-SYN-F2 that delayed in flowering. The premature flowering among some genotypes such as NYSW03-Y was probably due to the plant mobilizing water for the production of seed before the end of the growing season. Rowland (1993) confirmed this and stated that reduction in days to flowering among genotypes was due to the plants mobilizing water for the production of seed before the end of the growing season. Angus and Moncur (1977), and also Morgan (1980) observed that water deficits tend to advance flowering in annuals but delays flowering in perennials.

The drought stress genotypes: NYSW03-Y, IWD-C3-SYN-F2, NYLA04, OKOMASA, CHMA04, TAAN04 and GBRM04-BA which recorded relatively higher number of days between anthesis and silking might be more susceptible to drought than those genotypes such as DT-STR-W-C2, NYIA03, NYAZ04-W, GUMA03-OB and SISF03-OB that recorded lower number of days between anthesis and silking. The high daily temperature which might have resulted in low moisture content prolonged the extrusion of silk, thus delaying the days to silking in some of the studied plants. The genotypes with shortened anthesis-silking intervals like NYAZ04-W, GUMA03-OB and SISF03-OB also developed relatively longer shoots with more chlorophyll concentration, and were more tolerant to the abiotic stress (drought) as reported earlier under this section. Gonzalez *et al.* (2014) confirmed this and stated that genotypes with shortened anthesis-silking intervals (ASIs) tend to exhibit drought tolerance, whereas genotypes with long ASIs tend to exhibit less drought tolerance. In general, genotypes such as SISF03-OB, NYAZ04-W and GUMA03-OB that recorded lower number of days for anthesis, silking and anthesis-silking interval following drought also recorded higher grain yields. Such genotypes are therefore, more tolerant to drought than their counterparts. According to Edmeades *et al.* (2004) and Banziger *et al.* (1999), days to silking and anthesis-silking interval are important traits that influence maize yield under serious drought stress and these traits should be considered when selecting genotypes under drought conditions for crop improvement.

Variations in grain yield and hundred-grain weight might have been due to genotype x environment interactions and inherent genetic factors of the genotypes used in the study. The relatively high yield of plants that were planted early (field screening) to avoid drought or those that received regular water application (normal) in the case of the pot screening as compared with those planted late or stressed among other factors, is as a result of inadequate water supply during the grain-filling phase. In addition to differences in intensity of drought stress, differences

in timing of the drought stress, and more especially in drought sensitive varieties, also might have had consequences for yield or phenology (Swanton *et al.*, 2014). The genotypes SISF03-OB, NYAZ03-Y, TAAN04 and GUMA03-OB produced reduced ASI, high grain yield and hundred-grain weight from field studies. These genotypes, as stated earlier in this section, also produced relatively high shoot and root dry matter, and high chlorophyll content. These genotypes are more tolerant to water stress as compared to OKOMASA and DT-STR-W-C2. Gonzalez *et al.* (2014) reported that increased ASI, production of smaller female inflorescences, and reduced kernel production are some of the mechanisms that lead to reduced grain yield. Insufficient moisture for some of the genotypes that were stressed during the period of flowering and grain-filling (drought sensitive) could have made it impossible for metabolites such as simple sugars and amino acids to be translocated to the grains in adequate quantities for conversion into more complex storage compound. Chen *et al.* (2012) reported that the level of drought stress inhibits photosynthesis, disrupts carbohydrates metabolism and decreases kernel number and weight.

From the analysis on scoring, the study established that genotypes such as SISF03-OB, GUMA03-OB and KOBN03-OB that were rated relatively lower for drought, also produced more grain yield, hundred-grain weight, chlorophyll content, vigorous plant shoots and dry shoot and root biomass, and therefore could be more tolerant to drought than IWD-C3-SYN-F2, NYLA04 and OKOMASA that were rated significantly higher. Drought tolerant genotypes that produced vigorous shoots and higher chlorophyll concentration are more likely to produce more grain yield because of relatively easy accumulation of food reserves produced from the leaves through photosynthesis.

4.5 Conclusion

Studies from Experiment I (pot experiment) indicated that genotypes SISF03-OB, GUMA03-OB, TAAN04, TAIS03, NYAZ04-W, TZE-Y-DT-STR-C4, KOBN03-OB and NYSW03-Y produced the best results with reference to number of leaves, shoot length, stem girth, leaf area, chlorophyll content, fresh root biomass, dry root biomass, fresh shoot biomass, dry shoot biomass and root length. These eight genotypes were considered to be more tolerant to drought than their counterparts in the pot studies.

For Experiment II (field experiment), genotypes SISF03-OB, NYIA03, GUMA03-OB, DORKE SR, TZE-W-DT-STR-C4, NYFA04, KOBN04-R, KOBN03-OB and CHMA04 produced the best results with reference to parameters such as drought rating, grain yield, number of ears harvested, hundred-grain weight, plant height, ear height, days to 50% tasseling, days to 50% anthesis, days to 50% silking and anthesis-silking interval. These nine genotypes were also considered to be more tolerant to drought than their counterparts from the field screening studies.

In general, therefore genotypes GUMA03-OB, KOBN03-OB and SISF03-OB were drought tolerant from both pot and field studies. They produced relatively lower drought rating, more grain yield, bigger kernels, higher dry shoot and root biomass, higher chlorophyll content and reduced anthesis-silking interval. These three genotypes are considered to be very tolerant to drought according to the pot and field screening.

The cultivation of one or more of the above listed genotypes, especially GUMA03-OB, KOBN03-OB and SISF03-OB or their crosses in drought prevalent areas would result in increment in grain yield.

CHAPTER FIVE

SCREENING FOR STRIGA TOLERANCE

5.1 Introduction

Striga hermonthica (Del.) Benth is one of the major biological constraints to food production in Sub-Saharan Africa, and it is probably a more agricultural problem than insects, birds or plant diseases (Ejeta and Butler, 1993). Bawa *et al.* (2015) reported that the problem of striga infestation has intensified across regions in Sub-Saharan Africa for a number of reasons, including: deteriorating soil fertility, shortening of the fallow period, expansion of production into marginal lands with little nutrient input and an increasing trend towards continuous cultivation of one crop in place of the traditional rotation and inter-cropping systems. It is likely that striga is the largest constraint for maize production, whereas for sorghum and millet, striga comes second after granivorous birds (Ejeta and Butler, 1993).

The area infested by *Striga* spp is estimated to be 50 million ha, with 300 million farmers being affected in Africa. This results in estimated losses of US$7 billion (Parker, 2009). The effects are likely to be long lasting as striga plants produce millions of tiny seeds that can stay viable in the soil for many years. Yield losses due to striga infestation vary from a few per cent up to complete crop failure depending on crop species, crop variety and severity of infestation. Hearne (2009) reported yield losses ranging from 35-72%. Striga severely affects an estimated 40 million ha of land devoted to cereal production in West Africa alone, with additional 70 million ha having moderate levels of infestation (Lagoke *et al.*, 1991).

In Ghana, striga is a serious problem in areas north of latitude 9º30'N, which represent about 57 per cent of the total land area (Nyarko, 1986). The estimated yield losses amount to 4.1 million mega grams of grain in a year. The farm household systems in the northern sector of Ghana rank first in the production of the four major cereals in the country; namely maize, rice, sorghum and millet (Bawa *et al.*, 2015). But the production of the cereals is menaced by the threat of low productivity as a result of the parasitic weed, *Striga hermonthica* (Del.) Benth (Sauerborn, 1991). According to Sauerborn (1991) records of losses caused by *Striga hermonthica* in Northern Ghana in 1988 showed that yield losses amount to 16% for maize, 31% for millet and 29% for sorghum, representing a total economic loss of US$25 million for the three crops. Under heavy infestation, maize is more vulnerable to striga parasitism than upland rice, sorghum and millet with high losses in excess of 90 per cent (Efron *et al.*, 1989).

Striga infestation can cause yield losses of 20 – 100 per cent in maize, driving some farmers to give up cultivation of the crop entirely. Farm fields of all the districts of Northern Ghana are infested with the parasitic weed. However, Runge-Metzger *et al.* (1997) stated that the state of knowledge with respect to the severity of striga infestation, its geographical distribution in Northern Ghana and its current trend is still extremely unsatisfactory. *Striga hermonthica* had generally been associated more with sorghum and millet than with maize and is believed to have evolved with the former crops. Consequently, greater research efforts had already been devoted to sorghum. Maize, a high yielding crop which is a more recent introduction in the savanna of West Africa, now has a larger area devoted to its cultivation as compared to sorghum. Generally, maize is more susceptible to striga than sorghum and millet (Odhiambo and Ransom 1995). Maize is most susceptible to striga probably due to the fact that the crop did not co-evolve with the parasite, followed by sorghum and millet (Kim *et al.*, 1997).

Maize possesses extravagant variation for all traits and this variability can be easily used by the plant breeders to develop high yielding and striga tolerant genotypes for global food security. Breeding for striga tolerance in maize would improve growth and yield of maize under striga infested conditions (Bawa *et al.*, 2015). The objective of the study was to evaluate maize genotypes for various physiological and morphological traits under striga infested conditions with the view to selecting the promising genotypes and their crosses for cultivation in striga infested areas for increased grain production.

5.2 Materials and methods

Two experiments were conducted at the experimental field of the Savanna Agricultural Research Institute (SARI) and the plant house of the Faculty of Agriculture, University for Development Studies, all in Nyankpala in the Northern Region of Ghana. Experiment I was a pot experiment conducted in a plant house, whilst experiment II was a field experiment conducted at the SARI experimental field. Complete Randomized Design (CRD) and Randomized Complete Block Design (RCBD) were used for experiment I and experiment II, respectively. Specific details of the treatment structure and planting on this topic have already been reported in Chapter 3.

Data were taken on several parameters including leaf number, shoot length, stem girth, chlorophyll content, leaf area, fresh shoot biomass, dry shoot biomass, fresh root biomass, dry root biomass, and also root length in the case of Experiment I. For Experiment II, measurements were taken of plant height, days to 50% tasseling, days to 50% anthesis, days to 50% silking, anthesis-silking interval, ear height, plant stand, striga rating at 10 weeks after plant establishment (WAPE), striga count at 10 WAPE, number of ears harvested per plot, grain yield and hundred-grain weight. These data were subjected to analysis of variance (ANOVA) using

GentStat statistical package edition 9. Significant differences among treatment means were separated with Fisher LSD test at 5%. Co-efficient of variation was calculated and correlation analysis was also run to establish relationships among parameters. Conjoint analysis was also run to do genotype-performance ranking to justify the selection of some genotypes to be used for a diallel crossing as described in Experiment III in Chapter 3. For visual impression and ease of understanding, summaries of findings were presented in graphs and tables.

5.3 Results

5.3.1 Experiment I

The analysis of variance for number of leaves, shoot length, stem girth, leaf area, chlorophyll content, fresh root biomass, dry root biomass, fresh shoot biomass, dry shoot biomass and root length under the normal (control) conditions is presented in Table 5.1. There were highly significant differences ($P < 0.001$) among the genotypes for stem girth and chlorophyll content. There were also highly significant differences ($P < 0.01$) among the genotypes with respect to number of leaves, shoot length, fresh shoot biomass, dry shoot biomass and root length. There were significant differences ($P < 0.05$) among genotypes with respect to leaf area in the normal trial. However, there were no significant differences ($P > 0.05$) among the genotypes with respect to fresh and dry root biomass.

Table 5.1: Mean squares and co-efficient of variation (CV %) for vegetative traits for the normal trial

Source	df	Trait									
		No. of leaves	Shoot length	Stem girth	Leaf area	Chlorophyll content	Fresh root biomass	Dry root biomass	Fresh shoot biomass	Dry shoot biomass	Root length
Replication	2	3.89^{*}	234.62^{*}	0.09^{*}	743.76^{ns}	57.20^{**}	4.72^{ns}	0.22^{ns}	260.17^{ns}	4.08^{ns}	11.50^{ns}
Genotype	24	2.04^{**}	132.65^{**}	0.12^{***}	559.73^{*}	44.75^{***}	2.79^{ns}	0.20^{ns}	717.71^{**}	8.93^{**}	32.99^{**}
Model	26	2.18^{**}	140.49^{**}	0.11^{***}	573.88^{*}	45.70^{***}	2.93^{ns}	0.20^{ns}	682.51^{*}	8.56^{**}	31.34^{**}
Error	48	0.91	54.29	0.02	291.57	10.58	3.12	0.23	320.29	3.60	13.23
CV %		12.85	13.00	10.58	15.94	9.03	57.34	68.38	38.11	38.11	22.07

*Significant at P < 0.05, **Significant at P < 0.01, ***Significant at P < 0.001, ^{ns} Non-significant at P > 0.05

The analysis of variance for number of leaves, shoot length, stem girth, leaf area, chlorophyll content, fresh root biomass, dry root biomass, fresh shoot biomass, dry shoot biomass and root length under striga-infested conditions is presented in Table 5.2. There were highly significant differences ($P < 0.001$) among genotypes with respect to number of leaves, fresh shoot biomass and root length. There were highly significant differences ($P < 0.01$) among the genotypes with respect to stem girth, fresh root biomass, dry root biomass and dry shoot biomass. There were significant differences ($P < 0.05$) among the genotypes with respect to shoot length and leaf area. There were however, no significant differences ($P > 0.05$) among genotypes for chlorophyll content.

Table 5.2: Mean squares and co-efficient of variation (CV %) for vegetative traits under striga-infested conditions

Source	df	Trait									
		No. of leaves	Shoot length	Stem girth	Leaf area	Chlorophyll content	Fresh root biomass	Dry root biomass	Fresh shoot biomass	Dry shoot biomass	Root length
Replication	2	0.52^{ns}	71.09^{ns}	0.05^{ns}	1012.95^{*}	65.95^{*}	8.23^{ns}	0.56^{ns}	1096.79^{**}	19.84^{*}	13.38^{ns}
Genotype	24	5.47^{***}	241.68^{*}	0.15^{**}	576.74^{*}	33.56^{ns}	8.42^{**}	1.31^{**}	498.42^{***}	10.95^{**}	22.73^{***}
Model	26	5.09^{**}	228.56^{*}	0.14^{**}	610.29^{*}	34.05^{*}	8.41^{**}	1.25^{**}	544.44^{***}	11.64^{***}	22.01^{***}
Error	48	1.74	114.71	0.05	299.07	20.01	3.13	0.47	148.06	4.12	5.82
CV %		16.75	21.54	22.57	24.31	14.05	52.30	75.83	36.41	41.46	18.88

*Significant at $P < 0.05$, **Significant at $P < 0.01$, ***Significant at $P < 0.001$, ^{ns} Non-significant at $P > 0.05$

5.3.1.1 Vegetative traits

The effect of striga was assessed by comparing the measurements made of any trait under striga-infested and striga free conditions. In comparing the normal (striga free) and striga-infested plants in terms of percentage change, it was observed that the mean leaf area of the striga infested plants was reduced by 33.6%, whilst the mean dry shoot biomass was reduced by 2%. However, mean dry root biomass of the striga-infested plants recorded a percentage increment of 22.2% relative to the striga free plants (Table 5.3).

Table 5.3: Treatment means of the striga-infested and normal plants for various vegetative traits

Vegetative trait	Treatment		% change due to striga infestation	LSD (0.05)
	Normal	Striga-infested		
Number of leaves	8[a]	7[b]	12.5	0.39
Shoot length (cm)	56.7[a]	49.7[b]	12.4	2.78
Stem girth (cm)	1.37[a]	1.02[b]	25.6	0.07
Leaf area (cm^2)	107.1[a]	71.1[b]	33.6	5.48
Chlorophyll content (spad unit)	36.01[a]	31.83[b]	11.6	1.46
Fresh root biomass (g)	3.08[a]	3.38[a]	8.9	0.51
Dry root biomass (g)	0.70[b]	0.90[a]	22.2	0.17
Fresh shoot biomass (g)	46.46[a]	33.42[b]	28.1	4.71
Dry shoot biomass (g)	4.98[a]	4.88[a]	2.0	0.61
Root length (cm)	16.06[a]	12.78[b]	20.4	1.21

Traits having the same letters (horizontal direction) are not significantly different at the 5% level of probability

5.3.1.2 Shoot length

When plants were not infested with striga, genotype TZE-W-DT-STR-C4 was the tallest (70.3 cm), whilst NYFA03 was the shortest (44.4 cm) for shoot length. There were no significant differences ($P > 0.05$) among the following genotypes; TZE-W-DT-STR-C4, CHFB04-OB, KPAS04, NYAZ03-Y, GUMA03-OB, NYIA03, DT-STR-W-C2, NYLA04, DORKE SR and GBRM04-BA (Table 5.4). Genotype IWD-C3-SYN-F2 was the tallest (59.1 cm), whilst TZE-Y-DT-STR-C4 was the shortest (39.1 cm) when plants were infested with striga.

5.3.1.3 Stem girth

Among the striga-free plants (normal), the genotype NYSW03-Y recorded the highest stem girth of 1.83 cm, whilst TZE-Y-DT-STR-C4 recorded the lowest of 1.13 cm. There were no significant differences ($P > 0.05$) among the following genotypes: NYSW03-Y, CHFB04-OB, OKOMASA and DT-STR-W-C2 (Table 5.4). For the striga-infested treatments, genotype SISF03-OB recorded the highest stem girth (1.60 cm), whilst NYSW03-Y recorded the lowest (0.53 cm). There were no significant differences ($P > 0.05$) among the genotypes SISF03-OB, TAIS03 and IWD-C3-SYN-F2.

5.3.1.4 Leaf area

Among the normal plants, the genotype KPAS04 recorded the highest leaf area (150.7 cm^2), while OKOMASA recorded the lowest leaf area (87.2 cm^2). There was no significant difference ($P > 0.05$) between genotypes KPAS04 and CHFB04-OB (Table 5.4). Among the striga-infested, the genotype SISFO3-OB recorded the highest leaf area of 97.6 cm^2, while NYSW03-Y recorded the lowest leaf area of 33.1 cm^2.

Table 5.4: Shoot length, stem girth and leaf area of genotypes during screening under green house conditions in 2013

Genotype	Shoot length (cm)		Stem girth (cm)		Leaf area (cm²)	
	Striga-infested	Normal	Striga-infested	Normal	Striga-infested	Normal
CHFB04-OB	57.4	65.8	1.03	1.73	87.5	136.5
KPAS04	54.9	64.9	0.90	1.57	82.3	150.7
OKOMASA	50.7	50.7	0.83	1.70	68.0	87.2
KOBN03-OB	43.9	53.5	0.90	1.47	74.4	113.4
NYAZ03-Y	51.3	61.2	0.70	1.17	59.9	95.6
NYAZ04-W	49.9	49.5	1.10	1.27	76.8	106.2
GUMA03-OB	58.0	66.2	1.00	1.40	69.2	103.7
GBRM04-BA	48.3	60.6	0.97	1.17	74.7	89.9
TZE-Y-DT-STR-C4	39.1	55.0	0.85	1.13	63.1	99.6
DORKE SR	58.3	59.6	1.00	1.30	73.0	107.5
NYAN03	53.3	58.1	1.00	1.30	85.0	118
TZE-W-DT-STR-C4	54.5	70.3	0.80	1.23	67.6	109.0
NYIA03	57.7	61.3	1.07	1.27	68.8	97.1
NYLA04	57.1	60.1	1.10	1.20	86.1	104.4
TAAN04	40.3	48.3	0.95	1.17	68.9	110.4
NYSW03-Y	17.9	53.2	0.53	1.83	33.1	115.9
DT-STR-W-C2	51.7	63.1	1.00	1.67	58.7	100.8
SISF03-0B	51.4	58.9	1.60	1.27	97.6	100.1
KOBN04-R	47.5	53.8	1.00	1.40	83.1	108.9
TAIS03	46.2	50.0	1.53	1.33	72.6	108.4
CHMA04	54.7	50.5	1.10	1.17	76.5	111.1
IWD-C3-SYN-F2	59.1	49.2	1.25	1.47	49.4	107.1
NYFA04	44.1	51.5	1.10	1.33	73.5	108.4
GH120 DYF/D POP	40.2	56.8	1.03	1.40	48.9	92.0
NYFA03	55.4	44.4	1.13	1.30	79.6	96.3
Mean	49.7	56.7	1.02	1.37	71.1	107.1
SEM	1.77	1.00	0.04	0.02	3.5	1.8
LSD (0.05)	17.58	12.10	0.38	0.24	28.39	28.03

SEM means standard error of mean; Measurements were made at six weeks after planting

5.3.1.5 Chlorophyll content

Results on relative chlorophyll content are shown in Figure 5.1. Genotype KPAS04 recorded the highest chlorophyll content of 42.57 spad units, whilst CHMA04 recorded the lowest chlorophyll content of 28.13 spad units for the normal plants. For the striga-infested plants, the genotype TAIS03 recorded the highest chlorophyll content of 38.87 spad units, whilst NYSW03-Y recorded the lowest chlorophyll content of 25.33 spad units.

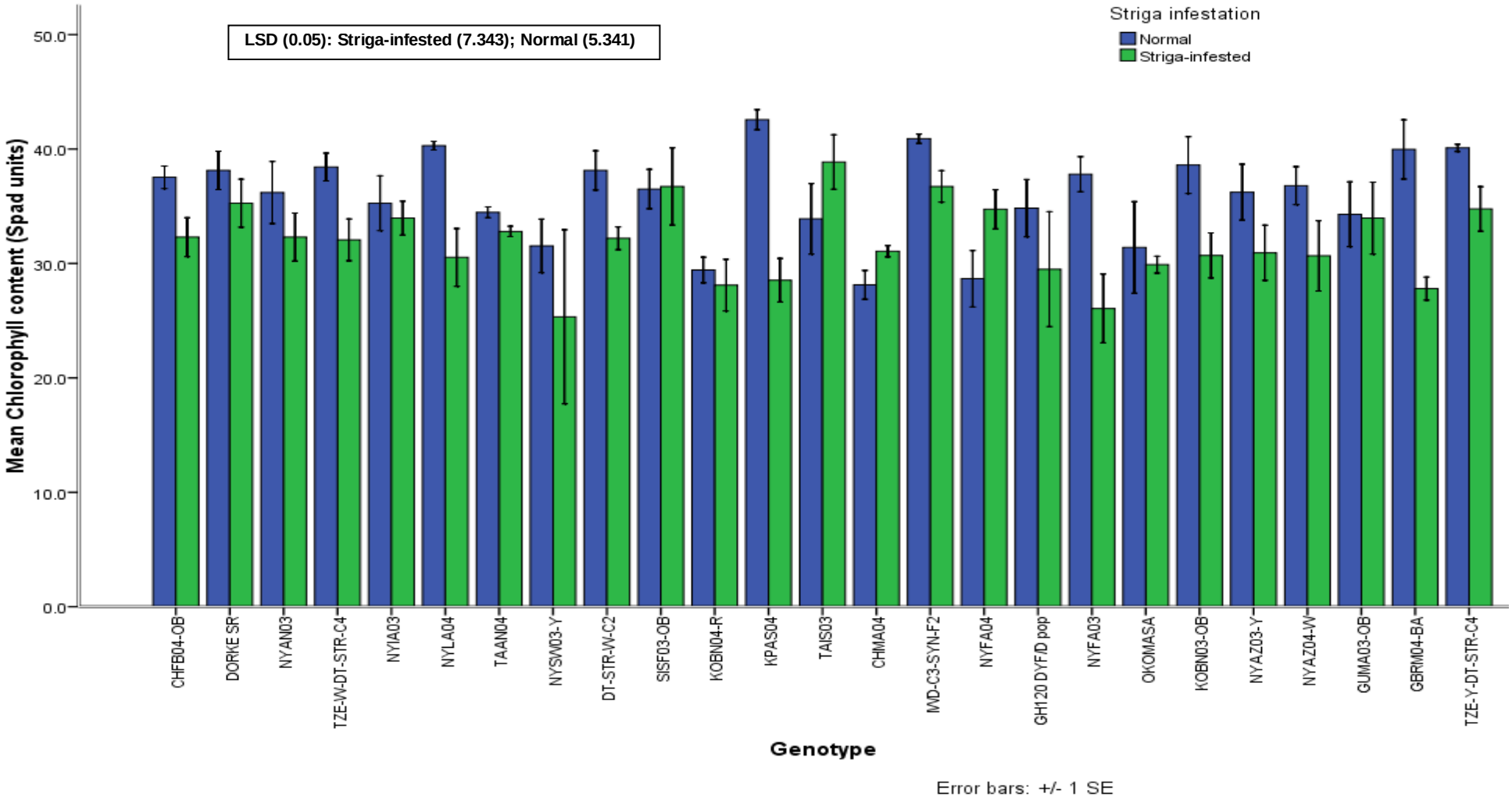

Figure 5.1: Changes in chlorophyll content of the genotypes at six weeks after planting during screening under green house conditions in 2013; Bars represent standard error of mean

5.3.1.6 Fresh root biomass

For the normal treatments, genotype CHFB04-OB recorded the highest fresh root biomass of 4.90 g, whilst TAAN04 recorded the lowest of 1.77 g (Table 5.5). For the striga-infested plants, SISF03-OB recorded the highest fresh root biomass of 7.53 g, whilst NYSW03-Y recorded the lowest of 1.02 g. The genotype SISF03-OB did not significantly differ ($P > 0.05$) from TZE-Y-DT-STR-C4, TAIS03, CHMA04 and IWD-C3-SYN-F2 in terms of fresh root biomass (Table 5.5).

5.3.1.7 Dry root biomass

For the normal plants, the genotype CHFB04-OB recorded the highest dry root biomass of 1.25 g, whilst TAAN04 recorded the lowest of 0.33 g. Among the striga-infested plants, the genotype SISF03-OB recorded the highest dry root biomass of 2.67 g, while NYSW03-Y recorded the lowest dry root biomass of 0.09 g. The genotype SISF03-OB was statistically similar ($P > 0.05$) to the genotypes TAIS03, CHMA04, IWD-C3-SYN-F2 and GH120 DYF/D POP (Table 5.5).

5.3.1.8 Root length

For the normal plants, the genotype KPAS04 recorded the highest root length of 24.05 cm, whilst NYFA03 recorded the lowest of 11.87 cm. The genotypes KPAS04, CHFB04-OB, NYAZ04-W, NYAN03, DT-STR-W-C2, CHMA04 and GH120 DYF/D POP were not significantly different ($P > 0.05$). For the striga-infested plants, the genotype SISF03-OB recorded the highest root length of 17.79 cm, whilst GBRM04-BA recorded the lowest of 7.26 cm. There were no significant differences ($P > 0.05$) among genotypes SISF03-OB, CHFB04-OB, GUMA03-OB, DORKE SR, NYIA03, TAIS03, IWD-C3-SYN-F2 and NYFA04 (Table 5.5).

Table 5.5: Root biomass accumulation and root length of genotypes during screening under green house conditions in 2013

Genotype	Fresh root biomass (g)		Dry root biomass (g)		Root length (cm)	
	Striga-infested	Normal	Striga-infested	Normal	Striga-infested	Normal
CHFB04-OB	4.56	4.90	1.06	1.25	17.62	21.35
KPAS04	3.60	4.25	0.60	0.85	12.30	24.05
OKOMASA	1.68	2.93	0.38	0.73	8.92	13.07
KOBN03-OB	3.78	2.40	0.80	0.43	13.02	14.73
NYAZ03-Y	2.10	2.13	0.36	0.47	13.48	15.93
NYAZ04-W	2.31	2.40	0.45	0.53	12.72	21.30
GUMA03-OB	4.38	2.00	0.83	0.40	14.28	16.33
GBRM04-BA	1.29	1.87	0.18	0.53	7.26	14.33
TZE-Y-DT-STR-C4	4.83	2.27	1.17	0.43	11.31	16.37
DORKE SR	3.38	4.35	0.74	1.00	15.48	16.75
NYAN03	2.40	3.80	0.42	0.67	12.26	20.13
TZE-W-DT-STR-C4	1.62	3.35	0.23	0.80	10.79	13.65
NYIA03	4.38	2.17	1.11	0.50	16.62	18.03
NYLA04	4.41	4.83	0.90	1.20	10.77	16.70
TAAN04	2.22	1.77	0.51	0.33	11.31	12.60
NYSW03-Y	1.02	2.77	0.09	0.53	9.00	13.13
DT-STR-W-C2	1.59	3.57	0.36	0.83	11.67	20.03
SISF03-0B	7.53	2.03	2.67	0.43	17.79	15.57
KOBN04-R	1.83	2.83	0.35	0.63	9.36	17.73
TAIS03	5.73	3.30	1.86	0.97	15.15	14.43
CHMA04	4.76	2.70	1.57	0.87	13.72	19.47
IWD-C3-SYN-F2	5.76	3.90	1.78	0.65	16.20	10.50
NYFA04	2.06	3.43	0.84	0.67	14.64	15.47
GH120 DYF/D POP	4.62	4.45	2.09	1.10	12.06	18.40
NYFA03	2.74	2.57	1.25	0.67	11.82	11.87
Mean	3.38	3.08	0.90	0.70	12.78	16.06
SEM	0.20	0.20	0.06	0.05	0.52	0.51
LSD (0.05)	2.91	2.90	1.13	0.79	3.96	5.97

SEM means standard error of mean; Measurements were made at six weeks after planting

5.3.1.9 Number of leaves

For the normal plants, NYIA03 and NYLA04 scored the highest number of 10 leaves, whilst NYSW03-Y scored the least number of 3 leaves. The genotypes, DORKE SR and TZE-W-DT-STR-C4 recorded the highest number of 9 leaves, whilst TZE-Y-DT-STR-C4, KOBN03-OB, NYAZ03-Y, KOBN04-R and CHMA04 recorded the least number of 6 leaves for the striga-infested plants (Table 5.6). There were no significant differences ($P > 0.05$) among the genotypes NYIA03, OKOMASA, GUMA03-OB, GBRM04-BA, TZE-W-DT-STR-C4, DORKE SR, NYLA04, DT-STR-W-C2, SISF03-OB, TAIS03, IWD-C3- SYN-F2 and NYFA03.

5.3.1.10 Fresh shoot biomass

For the normal plants, genotype KPAS04 had the highest recorded fresh shoot biomass of 88.45 g, whilst TAAN04 recorded the lowest of 25.67 g fresh shoot biomass. The genotypes KPAS04, CHFB04-OB and TZE-W-DT-STR-C4 were not significantly different ($P > 0.05$) for the trait. Among the striga-infested plants, the genotype TAIS03 recorded the highest fresh shoot biomass of 63.78 g, whilst NYSW03-Y recorded the lowest fresh shoot biomass of 7.00 g. There were no significant differences ($P > 0.05$) among genotypes TAIS03, NYIA03, SISF03-OB and GH120 DYF/D POP (Table 5.6).

5.3.1.11 Dry shoot biomass

Among the normal plants, the genotype KPAS04 recorded the highest dry shoot biomass of 10.20 g, whilst NYAZ03-Y recorded the lowest dry shoot biomass of 3.30 g. There were no significant differences ($P > 0.05$) among KPAS04, CHFB04-OB and TZE-W-DT-STR-C4. For the striga-infested plants, SISF03-OB recorded the highest dry shoot biomass of 9.12 g, whilst NYSW03-Y recorded the lowest of 0.63 g. The genotypes SISF03-OB, NYIA03, TAIS03,

CHMA04, IWD-C3-SYN-F2, GH120 DYF/D POP and NYFA03 did not significantly differ ($P > 0.05$) (Table 5.6).

Table 5.6: Leaf production and shoot biomass accumulation of genotypes during screening under green house conditions in 2013

Genotype	Number of leaves		Fresh shoot biomass (g)		Dry shoot biomass (g)	
	Striga-infested	Normal	Striga-infested	Normal	Striga-infested	Normal
CHFB04-OB	8	8	41.32	85.90	5.32	8.95
KPAS04	8	7	37.44	88.45	5.34	10.20
OKOMASA	8	8	14.88	38.93	2.88	3.97
KOBN03-OB	6	7	38.10	33.27	5.18	3.77
NYAZ03-Y	6	7	23.14	28.43	3.16	3.30
NYAZ04-W	7	8	31.00	41.10	3.87	4.50
GUMA03-OB	8	9	30.99	46.00	3.75	4.37
GBRM04-BA	7	8	11.04	38.77	2.61	4.03
TZE-Y-DT-STR-C4	6	8	26.22	38.50	3.69	3.90
DORKE SR	9	9	40.70	56.35	5.70	6.35
NYAN03	7	7	24.76	53.43	3.22	5.53
TZE-W-DT-STR-C4	9	8	33.12	68.20	4.83	7.95
NYIA03	8	10	47.16	47.40	6.75	4.63
NYLA04	7	10	33.36	43.47	5.31	4.57
TAAN04	7	6	29.07	25.67	4.08	3.40
NYSW03-Y	7	3	7.00	44.40	0.63	4.97
DT-STR-W-C2	8	9	33.78	55.87	4.11	6.07
SISF03-0B	8	9	57.81	45.60	9.12	4.60
KOBN04-R	6	7	26.04	43.90	3.33	4.03
TAIS03	7	9	63.78	35.90	7.83	3.73
CHMA04	6	8	39.34	42.70	6.18	4.10
IWD-C3-SYN-F2	8	8	40.05	29.00	6.48	4.05
NYFA04	7	8	27.68	45.13	4.52	3.90
GH120 DYF/D POP	8	7	45.75	49.40	7.68	4.75
NYFA03	7	9	32.00	35.80	6.78	4.93
Mean	7	8	33.42	46.46	4.88	4.98
SEM	0.11	0.20	2.31	2.44	0.28	0.27
LSD (0.05)	1.56	2.17	19.98	29.38	3.33	3.12

SEM means standard error of means; Measurements were made at six weeks after planting

5.3.1.12 Correlation

The correlation co-efficient between characters were computed at phenotypic level. The association among different characters is presented in Table 5.7. The data showed that shoot length positively and highly significantly ($P < 0.001$) associated with stem girth and leaf area. Shoot length also positively and significantly ($P < 0.01$) correlated with root length. However shoot length exhibited no significant correlation ($P > 0.05$) with three characters, namely; fresh root biomass, dry root biomass and fresh shoot biomass.

Table 5.7: Phenotypic correlation co-efficients among vegetative traits of maize genotypes

DF = 196	Stem girth	Leaf area	Fresh root biomass	Dry root biomass	Fresh shoot biomass	Dry shoot biomass	Root length
Shoot length	0.4795***	0.3887***	0.1031ns	0.1338ns	0.1217ns	0.1661*	0.2149**
Stem girth		0.5179***	0.3394***	0.3886***	0.3342***	0.4215***	0.2789***
Leaf area			0.3163***	0.2740***	0.2554***	0.3112***	0.2611***
Fresh root biomass				0.8640***	0.7351***	0.7294***	0.4292***
Dry root biomass					0.6443***	0.7649***	0.4486***
Fresh shoot biomass						0.9016***	0.4072***
Dry shoot biomass							0.4367***

*Significant at P < 0.05, **Significant at P < 0.01, ***Significant at P < 0.001, ns Non-significant at P > 0.05

5.3.2 Experiment II

5.3.2.1 Analyses of variance for traits

The analyses of variance for the traits measured under normal (control) conditions are presented in Table 5.8. There were highly significant differences ($P < 0.001$) among the genotypes with respect to plant height, days to 50% tasseling, days to 50% anthesis, days to 50% silking, ear height and grain yield for the normal trial. There were highly significant differences ($P < 0.01$) among genotypes with respect to number of ears harvested per plot in the normal trial. However, there were no significant differences ($P > 0.05$) among genotypes with respect to anthesis-silking interval, plant stand and hundred-grain weight in the normal trial.

Table 5.8: Mean squares and co-efficient of variation (CV %) for vegetative traits under normal conditions

Source	df	Trait									
		Plant height (cm)	Days to 50% tasseling	Days to 50% anthesis	Days to 50% silking	Anthesis –silking interval	Plant stand	Ear height (cm)	Ears harvested	Grain yield (tons/ha)	hundred–grain weight (g)
Replication	2	55.54^{ns}	2.09^{ns}	0.09^{ns}	7.24^{ns}	5.49^{ns}	7.56^{ns}	545.54^{**}	9.61^{ns}	0.27^{**}	0.002^{ns}
Genotype	24	1008.26^{***}	31.19^{***}	39.12^{***}	49.90^{***}	7.25^{ns}	7.81^{ns}	652.33^{***}	10.03^{**}	0.21^{***}	0.047^{ns}
Model	26	934.98^{***}	28.95^{***}	36.12^{***}	46.62^{***}	7.11^{ns}	7.79^{ns}	644.12^{***}	10.00^{**}	0.21^{***}	0.043^{ns}
Error	48	216.52	5.87	5.18	10.53	5.69	5.41	103.74	3.97	0.05	0.032
CV %		9.47	4.09	3.41	4.91	34.20	19.06	13.55	18.41	17.46	15.81

*Significant at ($P < 0.05$), **Significant at ($P < 0.01$), ***Significant at ($P < 0.001$), ^{ns} Non-significant at ($P > 0.05$)

The analyses of variance for traits measured under striga-infested conditions are presented in Table 5.9. There were highly significant differences ($P < 0.001$) among the genotypes with respect to days to 50% tasseling, days to 50% anthesis, days to 50% silking, plant stand and striga rating of the striga-infested trial. There were highly significant differences ($P < 0.01$) among the genotypes with respect to plant height, anthesis-silking interval and ears harvested per plot of the striga-infested trial. There were significant differences ($P < 0.05$) among genotypes for hundred-grain weight in the striga-infested experiment. There were however, no significant differences ($P > 0.05$) among the genotypes for ear height, grain yield and striga count in the striga-infested trial.

Table 5.9: Mean squares and co-efficient of variation (CV %) for vegetative traits under striga-infested conditions

Source	df	Trait											
		Plant height (cm)	Days to 50% tasseling	Days to 50% anthesis	Days to 50% silking	Anthesis-silking interval	Plant stand	Ear height (cm)	Ears harvested	Striga count at 10 WAPE	Striga rating at 10 WAPE	Grain yield (tons/ha)	hundred-grain weight (g)
Replication	2	146.78**	2.89^{ns}	0.17^{ns}	5.32^{ns}	1.97^{ns}	0.52^{ns}	54.02^{ns}	0.12^{ns}	17.61*	0.00^{ns}	0.04^{ns}	0.078^{ns}
Genotype	24	461.47**	24.72***	24.94***	37.76***	6.50**	7.95***	324.75^{ns}	9.86**	7.00^{ns}	0.95***	0.09^{ns}	0.041*
Model	26	437.26**	23.04***	23.03***	35.26***	6.15*	7.38***	303.92^{ns}	9.11**	7.82^{ns}	0.88**	0.08^{ns}	0.044*
Error	48	201.32	2.78	2.09	3.18	2.85	1.98	197.16	3.61	5.46	0.32	0.06	0.024
CV %		10.23	2.89	2.23	2.67	18.48	10.79	21.44	16.96	28.87	19.90	35.94	17.90

*Significant at ($P < 0.05$), **Significant at ($P < 0.01$), ***Significant at ($P < 0.001$), ^{ns} Non-significant at ($P > 0.05$)

5.3.2.2 Vegetative traits

The effect of striga on vegetative growth and yield was assessed by comparing the performance of the traits under striga-free environment and striga-infested plots. Mean grain yield recorded the highest percentage reduction of 48.1% as a result of the striga-infestation. There was no significant difference ($P > 0.05$) between the striga free and striga-infested plots for number of ears harvested per plot. However, anthesis-silking interval increased by 50.0% as a result of the striga infestation (Table 5.10).

Table 5.10: Treatment means of the striga-infested and normal plants for various traits

Trait	Treatment mean		% change due to striga infestation	LSD (0.05)
	Normal	Striga-infested		
Plant height (cm)	155.39[a]	138.65[b]	10.8	5.26
Days to 50% tasseling	59[a]	58[b]	1.7	0.69
Days to 50% anthesis	66[a]	65[b]	1.5	0.73
Days to 50% silking	67[a]	67[a]	0.0	0.86
Anthesis-silking interval	1[b]	2[a]	50.0	0.77
Plant stand	12[b]	13[a]	7.7	0.63
Ear height (cm)	75.17[a]	65.49[b]	12.9	3.90
Ears harvested	11[a]	11[a]	0.0	0.71
Grain yield (tons/ha)	3.41[a]	1.77[b]	48.1	0.20
Hundred -grain weight (g)	36.3[a]	27.4[b]	24.5	2.00

Traits having the same letters (horizontal direction) are not significantly different at the 5% level of probability

5.3.2.3 Plant height

For the normal plants, genotype NYIA03 recorded the highest plant height of 183.10 cm, whilst TZE-W-DT-STR-C4 recorded the least of 121 cm for the normal plants (Table 5.11). However, the genotype NYIA03 did not significantly differ ($P > 0.05$) from CHFB04-OB, NYAZ03-Y,

NYAZ04-W, GUMA03-OB, GBRM04-BA, NYAN03, NYLA04, TAAN04, NYSW03-Y, KOBN04-R, CHMA04, NYFA04 and GH120 DYF/D POP. Among the striga-infested plants, the genotype CHMA04 recorded the highest plant height (160.03 cm), whilst GH120 DYF/D POP recorded the lowest of 117.87 cm. Genotype CHMA04 did not significantly differ ($P > 0.05$) from CHFB04-OB, KOBN03-OB, NYAZ03-Y, NYAZ04-W, GUMA03-OB, GBRM04-BA, DORKE SR, NYAN03, NYIA03, NYLA04, TAAN04, TAIS03 and NYFA04 (Table 5.11).

5.3.2.4 Days to 50% tasseling

Among the normal treatments, variety OKOMASA and DT-STR-W-C2 recorded the highest number of 64 days to 50% tasseling, whilst TZE-W-DT-STR-C4 recorded the lowest of 51 days. However, there were no significant differences ($P > 0.05$) among OKOMASA, KOBN03-OB, GUMA03-OB, GBRM04-BA, DT-STR-W-C2, TAIS03, NYAZ03-Y, CHMA04, NYFA04, GH120 DYF/D POP and NYFA03. For the striga-infested, genotype GBRM04-BA recorded the highest number of 67 days to 50% tasseling, whilst TZE-Y-DT-STR-C4, TZE-W-DT-STR-C4 and NYSW03-Y recorded the lowest of 53 days, and there was a significant difference ($P < 0.05$) between GBRM04-BA and the other 24 genotypes (Table 5.11).

5.3.2.5 Days to 50% anthesis

For the normal plants, variety OKOMASA recorded the highest number of 71 days to 50% anthesis, whilst TZE-W-DT-STR-C4 and TZE-Y-DT-STR-C4 recorded the lowest number of 58 days. However, there were no significant differences ($P > 0.05$) among the following genotypes: OKOMASA, NYFA03, GUMA03-OB, GBRM04-BA, DORKE SR, DT-STR-W-C2, CHMA04, GH120 DYF/D POP, KOBN03-OB and NYAZ03-Y (Table 5.11). For the striga-infested plants, the genotype GBRM04-BA recorded the highest number of 72 days to 50% anthesis, whilst

TZE-W-DT-STR-C4 recorded the lowest of 58 days. The genotype GBRM04-BA significantly differed ($P < 0.001$) from the other 24 genotypes.

Table 5.11: Trends in plant height, days to 50% tasseling and days to 50% anthesis of the genotypes during field screening in the 2013 cropping season

Genotype	Plant height (cm)		Days to 50% tasseling		Days to 50% anthesis	
	Striga-infested	Normal	Striga-infested	Normal	Striga-infested	Normal
CHFB04-OB	149.13	159.27	58	60	67	66
KPAS04	132.77	145.87	58	60	66	67
OKOMASA	131.10	135.33	62	64	67	71
KOBN03-OB	138.53	153.57	58	62	65	68
NYAZ03-Y	147.83	162.37	58	60	65	68
NYAZ04-W	149.73	168.23	55	57	66	63
GUMA03-OB	142.67	174.35	60	62	68	70
GBRM04-BA	152.53	172.97	67	62	72	70
TZE-Y-DT-STR-C4	118.83	127.07	53	55	62	58
DORKE SR	138.40	134.80	58	59	66	69
NYAN03	149.83	168.93	58	59	65	67
TZE-W-DT-STR-C4	119.33	121.00	53	51	58	58
NYIA03	144.33	183.10	58	57	65	61
NYLA04	156.03	165.10	61	59	69	66
TAAN04	150.53	181.37	59	58	65	66
NYSW03-Y	131.43	169.23	53	54	59	59
DT-STR-W-C2	129.53	129.67	57	64	64	70
SISF03-0B	130.63	157.90	58	56	65	62
KOBN04-R	132.10	165.50	57	55	64	64
TAIS03	150.03	148.70	57	60	63	67
CHMA04	160.03	169.63	59	63	67	70
IWD-C3-SYN-F2	125.90	131.00	57	58	62	64
NYFA04	144.27	167.00	58	60	65	67
GH120 DYF/D POP	117.87	161.33	57	61	63	69
NYFA03	122.77	131.53	57	63	65	68
Mean	138.65	155.39	58	59	65	66
SEM	2.96	2.50	0.34	0.43	0.49	0.46
LSD (0.05)	23.29	24.16	2.74	3.98	2.37	3.74

SEM means standard error of mean

5.3.2.6 Days to 50% silking

Among the normal plants, OKOMASA and DT-STR-W-C2 recorded the highest number of days to 50% silking (72), while TZE-W-DT-STR-C4 and TZE-Y-DT-STR-C4 recorded the least number of 59 days to 50% silking. There were no significant differences ($P > 0.05$) among the following genotypes: OKOMASA, DT-STR-W-C2, CHFB04-OB, KPAS04, KOBN03-OB, NYAZ03-Y, GUMA03-OB, GBRM04-BA, DORKE SR, NYAN03, NYLA04, TAAN04, TAIS03, CHMA04, NYFA04, GH120 DYF/D POP and NYFA03. Among the striga-infested plants, the genotype GBRM04-BA recorded the highest number of 75 days to 50% silking, while NYSW03-Y recorded the least of 59 days to 50% silking. However, there was no significant difference ($P > 0.05$) between the genotypes GBRM04-BA and NYLA04 (Table 5.12).

5.3.2.7 Anthesis – silking interval

For the normal plants, NYFA03 recorded the highest anthesis-silking interval of 3 days, whilst NYAZ04-W, GUMA03-OB, GBRM04-BA, KOBN04-R, TAIS03 and CHMA04 recorded zero days for anthesis-silking interval. However, the genotype NYFA03 was not significantly different ($P > 0.05$) from CHFB04-OB, NYSW03-Y and DT-STR-W-C2. For the striga-infested plants, the genotype OKOMASA recorded the highest anthesis-silking interval of 5 days, whilst NYSW03-Y and TZE-Y-DT-STR-C4 recorded zero days for the trait (Table 5.12).

5.3.2.8 Plant stand

For the normal plants, genotypes NYAZ03-Y, NYAZ04-W, NYIA03 and NYFA04 recorded the highest number of plant stand of 14, whilst GH120 DYF/D POP and IWD-C3-SYN-F2 recorded the least number of 9. The genotypes NYAZ03-Y, NYAZ04-W, NYIA03 and NYFA04 significantly differed ($P < 0.05$) from that of TZE-Y-DT-STR-C4, DORKE SR, DT-STR-W-C2,

GH120 DYF/D POP and IWD-C3-SYN-F2. For the striga-infested genotypes, NYAZ03-Y, SISF03-0B, GBRM04-BA and NYIA03 recorded the highest number of plant stand (15), whilst GH120 DYF/D POP recorded the least number of 9 (Table 5.12).

Tale 5.12: Plant stand, days to silking and anthesis-silking interval of genotypes during field screening in the 2013 cropping season

Genotype	Days to 50% silking		Anthesis-silking interval		Plant stand	
	Striga-infested	Normal	Striga-infested	Normal	Striga-infested	Normal
CHFB04-OB	68	68	1	2	14	13
KPAS04	68	68	2	1	14	13
OKOMASA	72	72	5	1	13	12
KOBN03-OB	67	69	2	1	14	12
NYAZ03-Y	66	69	1	1	15	14
NYAZ04-W	68	63	2	0	14	14
GUMA03-OB	70	70	2	0	13	12
GBRM04-BA	75	70	3	0	15	12
TZE-Y-DT-STR-C4	62	59	0	1	10	10
DORKE SR	67	70	1	1	10	10
NYAN03	67	68	2	1	12	13
TZE-W-DT-STR-C4	60	59	2	1	13	11
NYIA03	67	62	2	1	15	14
NYLA04	73	67	4	1	14	13
TAAN04	67	67	2	1	13	13
NYSW03-Y	59	61	0	2	14	13
DT-STR-W-C2	66	72	2	2	12	10
SISF03-0B	67	63	2	1	15	13
KOBN04-R	67	64	3	0	14	13
TAIS03	66	67	3	0	14	12
CHMA04	68	70	1	0	14	12
IWD-C3-SYN-F2	65	65	3	1	10	9
NYFA04	67	68	2	1	14	14
GH120 DYF/D POP	65	70	2	1	9	9
NYFA03	68	71	3	3	12	13
Mean	67	67	2	1	13	12
SEM	0.51	0.56	0.02	0.10	0.34	0.29
LSD (0.05)	2.93	5.33	0.56	1.59	2.31	3.82

SEM means standard error of mean

5.3.2.9 Ear height

For the normal plants, genotype GBRM04-BA recorded the highest ear height of 102.30 cm, whilst DT-STR-W-C2 recorded the lowest ear height of 46.50 cm. However, there were no significant differences ($P > 0.05$) among GBRM04-BA, NYAN03, NYIA03, NYLA04 and TAAN04. For the striga-infested plants, the genotype TAIS03 recorded the highest ear height of 84.93 cm, while DT-STR-W-C2 recorded the lowest ear height of 48.49 cm (Table 5.13).

5.3.2.10 Ears harvested

The results indicated that genotype NYIA03 recorded the highest number of 14 ears harvested per plot, whilst TZE-Y-DT-STR-C4, GH120 DYF/D POP, DORKE SR, TAIS03 and IWD-C3-SYN-F2 recorded the lowest number of 8 ears harvested for the normal plants (Table 5.13). Genotypes NYIA03, KPAS04, CHFB04-OB, NYAZ03-Y, NYAZ04-W, GUMA03-OB, GBRM04-BA, NYAN03, TAAN04, NYSW03-Y, SISF03-OB, KOBN04-R, NYFA04 and NYFA03 were not significantly different ($P > 0.05$) (Table 5.13). For the striga-infested plants, genotypes CHFB04-OB and NYIA03 recorded the highest number of 14 ears harvested per plot, whilst IWD-C3-SYN-F2 recorded the least number of 8 ears harvested. There were no significant differences ($P > 0.05$) among genotypes CHFB04-OB, KPAS04, KOBN03-OB, NYAZ03-Y, NYAZ04-W, GUMA03-OB, TZE-W-DT-STR-C4, NYIA03, NYLA04, NYSW03-Y, DT-STR-W-C2, SISF03-OB, TAIS03 and NYFA04 (Table 5.13).

5.3.2.11 Hundred-grain weight

The genotype TAAN04 recorded the highest hundred-grain weight of 45 g, whilst NYANO3, NYSW03-Y and GH120 DYF/D POP recorded the lowest hundred-grain weight of 31 g for the normal plants (Table 5.13). The genotypes TAAN04, CHFB04-OB, OKOMASA, KOBN03-OB, NYAZ03-Y, TZE-Y-DT-STR-C4, DORKE SR, TZE-W-DT-STR-C4, DT-STR-W-C2, SISF03-OB, TAIS03, CHMA04, IWD-C3-SYN-F2 and NYFA03 were not significantly different ($P > 0.05$). For the striga-infested plants, the genotype CHMA04 recorded the highest hundred-grain weight of 33.3 g, whilst KOBN04-R, NYSW03-Y and NYAN03 recorded the lowest of 21.3 g. There were no significant differences ($P > 0.05$) among genotypes CHMA04, CHFB04-OB, KPAS04, KOBN03-OB, NYAZ03-Y, NYAZ04-W, GBRM04-BA, TZE-Y-DT-STR-C4, DORKE SR, TZE-W-DT-STR-C4, NYIA03, TAAN04, DT-STR-W-C2, SISF03-OB, IWD-C3-SYN-F2, NYFA04 and GH120 DYF/D POP (Table 5.13).

Table 5.13: Ear height, ears harvested and hundred-grain weight of genotypes during field screening in 2013 cropping season

Genotype	Ear height (cm)		Ears harvested		Hundred-grain weight (g)	
	Striga-infested	Normal	Striga-infested	Normal	Striga-infested	Normal
CHFB04-OB	70.32	73.31	14	12	32.0	39.0
KPAS04	58.50	64.00	12	12	28.3	33.0
OKOMASA	60.22	65.53	9	9	22.3	40.0
KOBN03-OB	61.94	74.77	12	11	27.0	38.0
NYAZ03-Y	66.26	78.83	13	13	31.7	38.0
NYAZ04-W	74.88	79.77	13	12	31.3	32.0
GUMA03-OB	83.38	84.23	11	11	24.7	33.0
GBRM04-BA	73.32	102.30	9	13	25.3	33.0
TZE-Y-DT-STR-C4	51.16	61.39	9	8	29.3	36.0
DORKE SR	65.06	64.00	9	8	27.0	39.0
NYAN03	68.31	98.82	10	11	21.3	31.0
TZE-W-DT-STR-C4	60.77	63.32	13	10	29.7	39.0
NYIA03	80.71	92.54	14	14	29.3	36.0
NYLA04	82.28	92.60	11	11	25.0	32.0
TAAN04	64.94	95.90	11	12	32.3	45.0
NYSW03-Y	54.89	73.63	13	12	21.3	31.0
DT-STR-W-C2	48.49	46.50	11	9	26.7	36.0
SISF03-0B	55.94	72.42	13	12	27.0	39.0
KOBN04-R	64.66	81.37	9	11	21.3	35.0
TAIS03	84.93	79.93	12	8	24.7	37.0
CHMA04	75.72	84.27	11	11	33.3	43.0
IWD-C3-SYN-F2	58.89	46.52	8	8	32.7	38.0
NYFA04	62.00	77.03	13	12	28.7	33.0
GH120 DYF/D POP	56.82	61.39	9	8	28.0	31.0
NYFA03	52.88	64.93	9	12	24.0	41.0
Mean	65.49	75.17	11	11	27.4	36.3
SEM	2.05	1.98	0.37	0.28	0.5	0.7
LSD (0.05)	23.05	16.72	3.12	3.27	8.0	9.4

SEM means standard error of mean

5.3.2.12 Grain yield

Genotype NYAZ03-Y recorded the highest grain yield of 4.81 tons/ha, whilst DT-STR-W-C2 recorded the lowest of 2.32 tons/ha among the normal plants (Figure 5.2). For the striga-infested genotypes, NYAZ03-Y recorded the highest grain yield of 2.80 tons/ha, whilst NYSW03-Y recorded the lowest of 1.04 tons/ha. The following genotypes; NYAZ03-Y, CHFB04-OB, KPAS04, KOBN03-OB, NYAZ04-W, TZE-W-DT-STR-C4, TAAN04, DT-STR-W-C2, TAIS03, IWD-C3-SYN-F2 and NYFA04 did not significantly differ ($P > 0.05$).

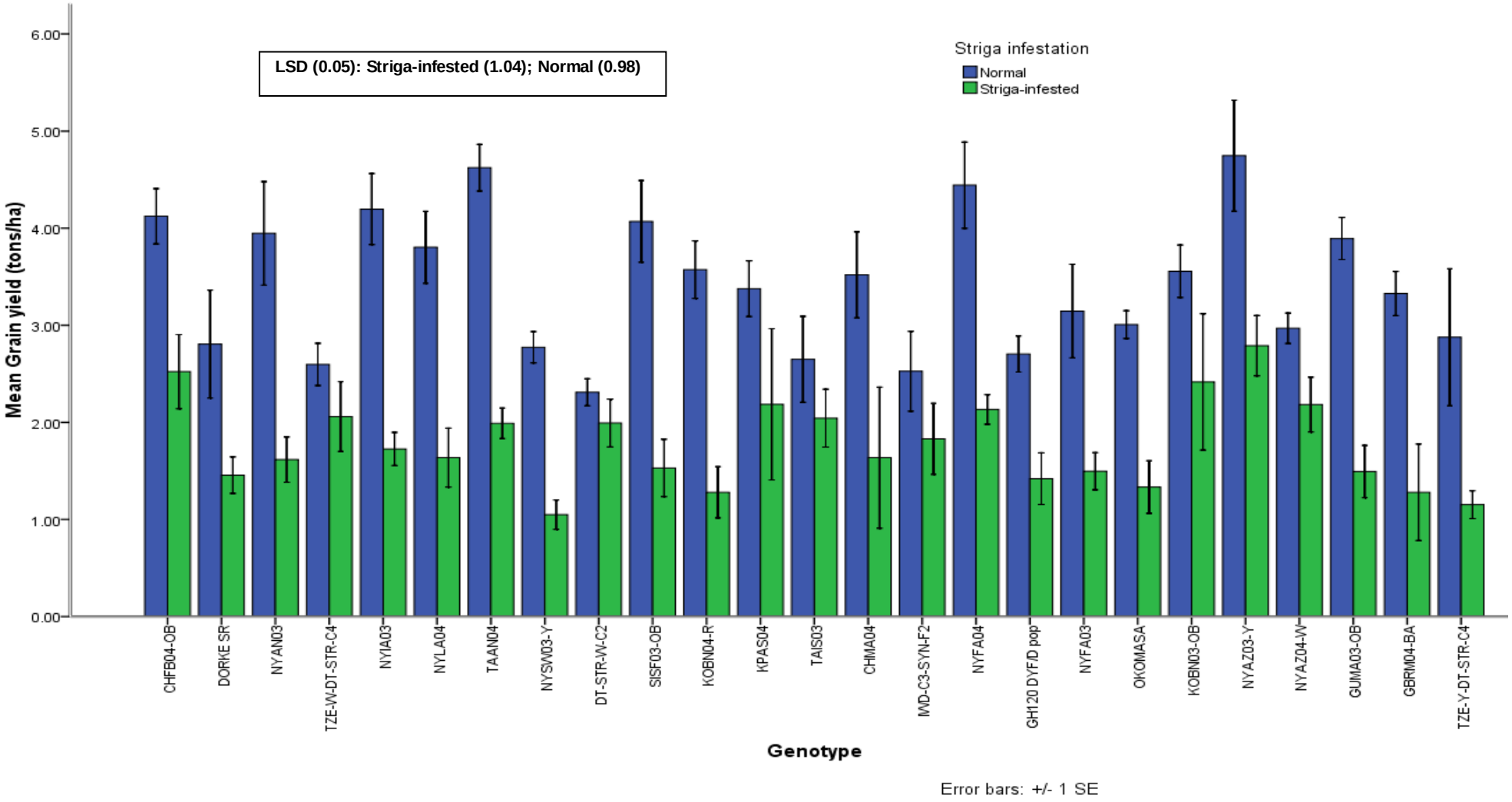

Figure 5.2: Grain yield of striga-infested and normal (non-infested) genotypes at harvest during field screening in the 2013 cropping season; Bars represent standard error of mean

5.3.2.13 Striga rating and striga count

The genotypes GH120 DYF/D POP, TZE-W-DT-STR-C4 and NYIA03 recorded the highest number of 5 striga plants emerging per plot, whilst KPAS04 and DORKE SR recorded zero striga emergence among the striga infested genotypes (Figure 5.3). However, the genotypes GH120 DYF/D POP, NYIA03, CHFB04-OB, OKOMASA, GUMA03-OB, GBRM04-BA, NYAN03, NYLA04, DT-STR-W-C2, SISF03-OB, KOBN04-R, TAIS03, CHMA04, NYFA04 and NYFA03 did not significantly differ ($P > 0.05$).

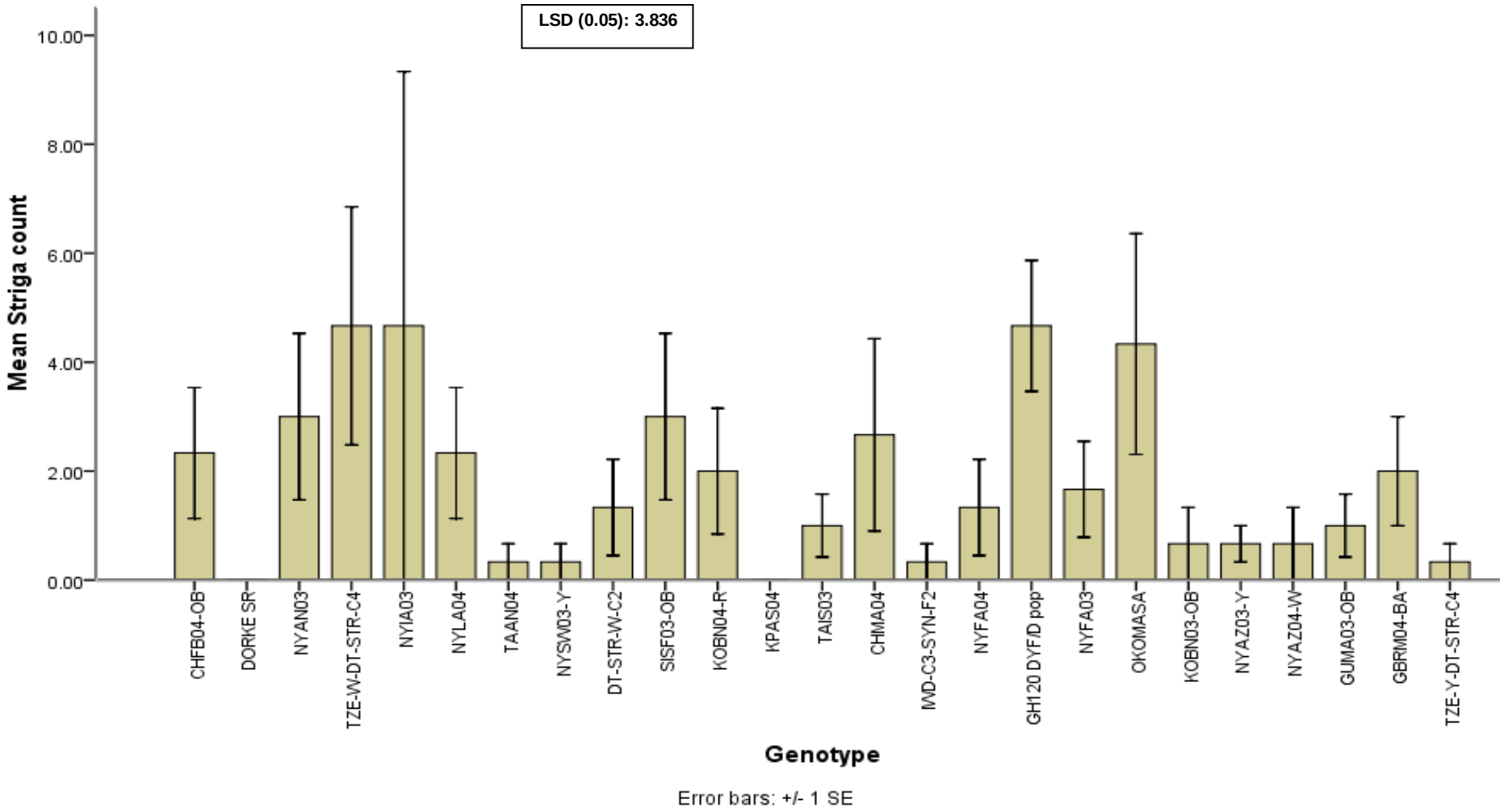

Figure 5.3: Variations in striga count among genotypes during field screening in 2013 cropping season; Bars represent standard error of mean

For striga rating, genotypes GH120 DYF/D POP, KOBN04-R, NYAZ03-Y and OKOMASA recorded the highest rating of 4, whilst IWD-C3-SYN-F2 and TAIS03 recorded the lowest rating of 2 (Figure 5.4). There were no significant differences ($P > 0.05$) among genotypes GH120 DYF/D POP, KOBN04-R, NYAZ03-Y, OKOMASA, KOBN03-OB, NYIA03, NYSW03-Y, DT-STR-W-C2, SISF03-OB, CHMA04, NYFA04 and NYFA03.

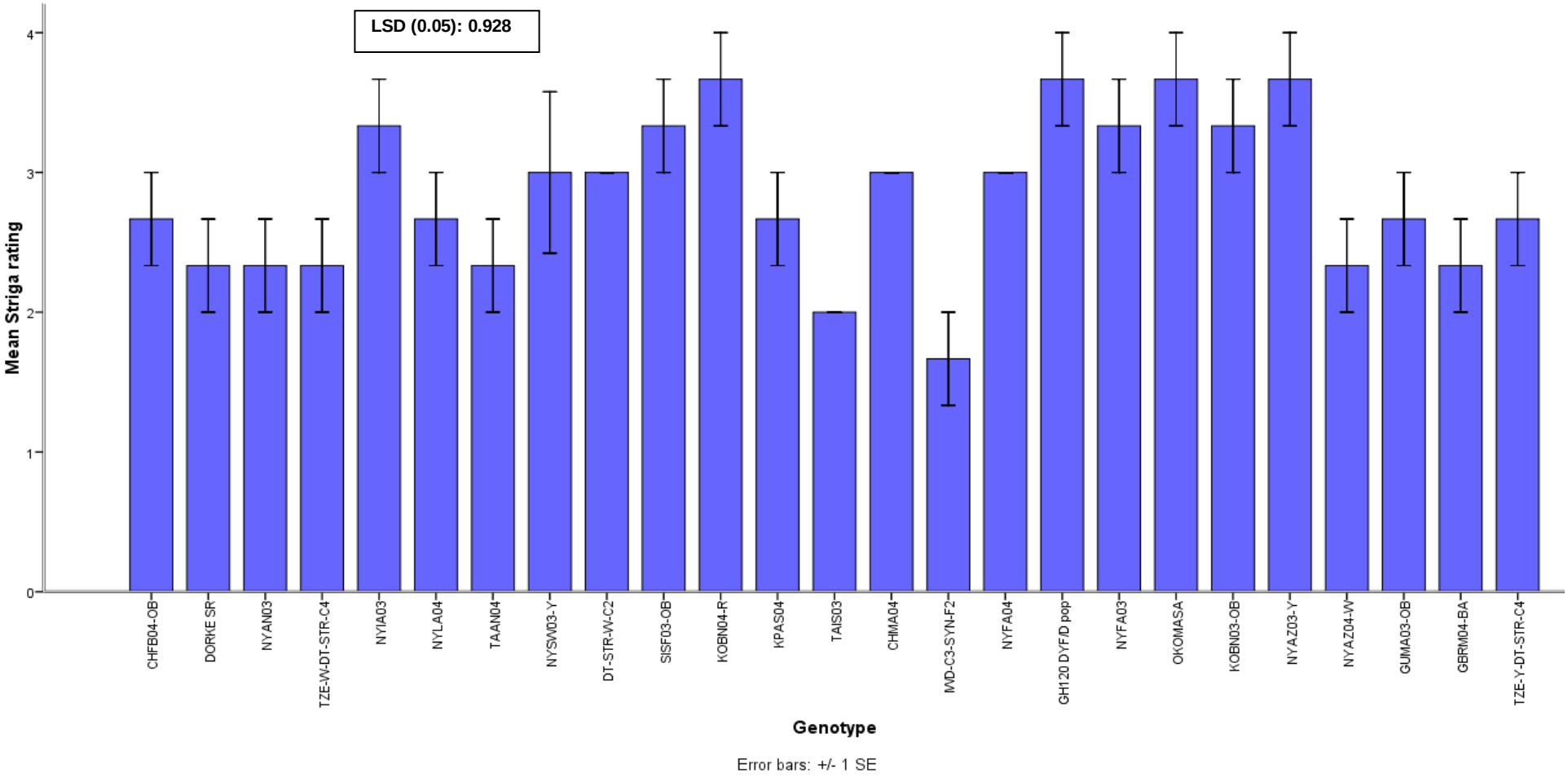

Figure 5.4: Variations in striga rating among genotypes during field screening in 2013 cropping season; Bars represent standard error of mean

5.3.2.14 Correlation

The correlation co-efficient between the characters were computed at phenotypic level and is presented in Table 5.14. The data shows that grain yield positively and highly significantly ($P < 0.001$) associated with plant height, ear height, plant stand, ears harvested and hundred-grain weight. However, grain yield exhibited negative but highly significant ($P < 0.001$) correlation with days to 50% silking and days to 50% anthesis. There was also negative but significant association ($P < 0.05$) between grain yield and anthesis-silking interval.