MEGA –ENVIRONMENT IDENTIFICATION FOR SOYBEAN [*GLYCINE MAX* L. MERRILL] IN ZAMBIA

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LUSAKA

DECLARATION

I **Pride Cheelo** do declare that this work is my own and that to the best of my knowledge, the works of other persons utilized in this dissertation have been duly acknowledged. The work documented in this thesis has not been previously presented or submitted for similar purposes.

Signature

Cheelo Pride Date

APPROVAL

This dessertation of Pride Cheelo was approved as fulfilling part of the requirements of the award of the degree on Masters of Science in Plant Breeding and Seed Systems by the University of Zambia.

Examiner's name **Signature** **Date**

DEDICATION

I am dedicating this work to my late father Mr. Noah Cheelo. The unrelanting dedication you had towards me has made me who I am today. Your words of wisdom are greatly missed.

ABSTRACT

Soybean is one of the most important cultivated crops in the world with about 6% of the world's arable land dedicated to its production. Compared to other major food crops, soybean experienced the highest percentage of yearly increases in production area over the period 1968 to 2013 from 29 million ha in 1968 to 102 million ha in 2008. Despite these high increases in the global perspective, Zambia is currently producing less than 0.01% of the global production, producing 261,063 metric tonnes in 2013. This is despite the fact that Zambia has vast arable land ideal for crop cultivation including soybean. Efforts are being made to improve the production trends in the country through many avenues among which is the introduction of new varieties. This effort has been concentrated in agro ecological region II of Zambia. There are no region specific adapted soybean varieties in Zambia. The current study was carried out in the 2013/2014 agricultural season to define soybean mega environments in two (2) agro ecological regions of Zambia. The study had 15 soybean varieties grown at four (4) locations in the two agro ecological regions of Zambia under rainfed conditions. The sites included GART, Kabwe, Msekera and Masumba. The trials were laid out in a Randomised Complete Block Design with four replications. The parameters which were collected were days to 50% flowering, plant height at harvest, pods per plant, seed size and computation of yield. Data analysis was done using Genstat version 16 and GGE biplot. The results showed the existence of three mega environments namely Kabwe/Msekera, GART and Masumba. Kabwe was found to be the most ideal environment for soybean production with Masumba being the worst. Kabwe was also the most descriminating location for testing of genotypes. Masumba was descriminating but not ideal. The genotypes yield mean score was 1239 Kg/ha and TGX 1988-22F was the highest yielding genotype with mean of 1517 kg/ha and the lowest was TGX 1835-10E with 418 kg/ha. In terms of variability in accordance to GGE biplot, Safari was the most variable and the most stable was TGX 1988-22F. Therefore, the study concluded that the best genotype for general adaptability was the variety TGX 1988-22F which was ideal across all the locations as it was high yielding and stable. Six genotypes had yield which was below the mean performance of the genotypes across all the locations; these were Lukanga, TGX 1835-10E, TGX 1830-20E, TGX 1988-18F, TGX 1987-23F and TGX 1987-11F. The mega environment Kabwe/Msekera had TGX 1988-22F as the winning genotype, GART had safari and Masumba had Magoye.

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CHAPTER ONE

1.0 INTRODUCTION

Soybean *(Glycine max L. Merrill)* is one of the most important cultivated crops in the world with about 6% of the world's arable land dedicated to its production (Hartman et al., 2011). It is among the most important oil crops in the world that together with rape seed, oil palm and sunflower account for 75% of edible oil seed production (FAO, 2013). The crop has the highest protein content (40%) among food legumes and second only groundnuts in oil content at 20% (Hartman et al., 2011). Its importance in domestic and international trade cannot be overemphasised especially for countries with enough land for expansion and improved varieties for improved productivity (Mcfarlane and O'connor, 2014, siteresources.worldbank.org). Southern Africa is generally a net importer of soybean apart from Zambia (Technoserve, 2011), which also only utilizes 6% of its land for crop production.

1.1 World Production

Compared to other major food crops, soybean has experienced a high percentage of yearly increases in world production area over a 40 year period, from 29 million ha in 1968 to 97 million ha in 2008 (Hartman et al., 2011). The world soybean production as of 2013 was at 268 million metric tonnes (Soystats, 2013). The leading producing countries of Soybean in the world are Brazil, United States of America and Argentina, producing 81% of world production (Soystats, 2013). The seven top soybean producing countries namely Brazil, United States of America, Argentina, China, India, Paraguay and Canada accounted for 94% of world production in 2012 (Soystats, 2013).

The increases in production of soybean are being fueled by the growth of edible oil consumption in the developing countries (FAO, 2013). This has hence made oil crop production among the most vibrant agricultural activities.

1.2 Soybeans Production in Africa

Soybean production in Africa was by 2008 at 1.4 million tonnes (Tefera, 2011). This level of production was actually the lowest in comparison to other continents of the World in 2008. The production level did not change much in response to the growth in the poultry industry which had reached a 30% annual growth rate on the continent between 2003 and 2008 (IITA, 2016***).*** Despite some improvements, Africa was still producing less than 1% of the world production by 2013 (FAO, 2014). The top three producers of soybean in Africa were, South Africa (948,000 T), Nigeria (679,000 T) and Zambia (214,179 T) accounting for about 50% of Africa's production (FAO, 2014). The productivity has been among the major bottlenecks to increased production with most small scale farmers still producing less than 1 tonne per hactre (IITA, 2016**).** The countries with the highest productivity in africa are Egypt (3.06 T/ha), Ethiopia (2.25 T/ha), South Africa (2.08 T/ha) and Zambia (2.08 T/ha) (FAO, 2014). The other countries have an average productivity of less than 2 tonnes per hectare.

1.3 Soybean production in Zambia

Soybean production was estimated at 170,076 metric tonnes in Zambia in the year 2000 (FAO, 2014). By the year 2013 soybean production for Zambia was reported at 261,063 metric tonnes (FAO, 2014). The information shows that there was an increase in the production of soybean in the country in the period 2000 to 2013. The increase was substantial though failed to meet the combined national and regional demand.

Zambia is among the countries in the Southern African region considered to have high potential for soybean production (Gasparri et al., 2015). This potential has not been utilised to expand soybean production and productivity. Production has remained concentrated in the agro-ecological region II of Zambia. The other two agro-ecological regions, I and III have had minimal contributions to the national soybeans output This has mainly been due to the challenging environmental conditions like soil acidity and temperature prevailing in these regions for which no specific soybean varieties have been developed.

1.4 Justification of the Study

This study was carried out to understand the existence of soybean mega environments and also identify genotypes with specific and general adaptability in two agro-ecological regions of Zambia. The knowledge gained would help to improve production and productivity by

way of promoting specific varieties to specific environments in which productivity is enhanced. Indeed, this differential adaptation would define areas which have a similar genotype response and also identying genotypes which would perfom well in the different mega environments.The information would also help rationalise soybean variety testing through identification of environments that discriminate varieties adequately to realize specific and general adaptation .

1.5 Research Objectives

The main objective of this study was to identify the existence of soybean mega environments in Zambia. The specific objectives were to:

1. Identify the most ideal soybean testing environment in Zambia.
2. To determine the adaptation of new soybean lines (IITA), to identify high yielding stable lines.

1.6 Research Hypothesis

This study was based on the premise that soybean varieties grown are suitable for any environment, hence can be grown anywhere in Zambia.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Taxonomy

Soybean belong to the family leguminosae, subfamily papilionideae, and the genus *Glycine*. *Glycine* is composed of two subgenera, *glycine* and *soja* (Smith and Hamel, 1999). The cultivated soybean, *Glycine max* (L.) Merrill and its wild counterpart *Glycine soja* are now classified as species of the sub genus *soja* of the genus *Glycine* (Hymowitz , 1970) *Glycine max* and *Glycine soja* are diploid (2n=40). The genus of *Glycine* is characterised of tri foliate leaves, flowers inserted singly at each node of the raceme, a five toothed calyx with the upper pair of teeth not well united, a glabrous corolla with long clawed petals, a keel which is longer than the seeds and estrophilate seed (Smith and Hamel, 1999; Hymowitz, 2008).

2.2 Crop history

The beginnings of the domestication of soybean may never be exactly known except that the plant was first probably domesticated successfully in the eastern half of north China (Hymowitz & Shurtleff, 2005). The Soyinfocentre (Soyinfocenter, 2014) provides a robust list of biographies on the history of soybean. The main areas of contention on soybean have much to do with the years of domestication than much on the areas of origin.

There is rather an unanimous agreement by scientists that soybean originated in China though some small differences on the exact areas exist. This was mainly due to what the researcher considered as of primary importance in their study. For instance Alphonse de Candolle a French botanist whose interest was to find the soybean area of origin by gathering evidence of the wild progenitors and also the growth of the crop under wild conditions concluded that the area of origin was South East Asia (Hymowitz, 1970). Nicholai Vavilov on the other hand gave primary importance to finding regions displaying a maximal diversity of primary varieties or centres of botanical diversity (Singh, 2009). In 1926 Vavilov concluded that there were eight world centres where virtually all cultivated plants had originated and he ascribed soybean to the South Eastern Asia centre basically the same area specified by de Candolle (Soyinfocenter, 2014). The two scientists however differ on the exact locations as Vavilov tended to point a more northerly part than the traditional South East Asia region.

As concerning the years of domestication; legends exist claiming the use of soybean for medicinal purposes as early as 2838 BC during the reign of the legendary emperor Shen Nung (Soyinfocenter, 2014; Acquaah, 2005). This information is believed to be contained in Shen Nung's supposedly publication the Pen Ts'ao Kang Mu (Hymowitz, 1970). Further historical analysis has revealed that the emperor Shen Nung is a mythical and fabricated figure that was created most probably by Han historians (Hymowitz and shurtleff, 2005). However the geographical and historical evidence gathered by Hymowitz (1970) lead to the most widely held theory concerning the origin of soybean that it emerged as a domesticate in the eastern half of north China in about the 11th century BC (early Chou dynasty) (Hymowitz, 1970; Soyinfocenter, 2014).

From its area of origin; soybean began its dissemination to the rest of the world such that by the 16th century AD, it was being grown and used in most Asian countries like Japan, India, Burma, Korea, Nepal, the Philippines, Thailand and Vietnam (Hartman et al., 2011). In the 18th century, soybean was being grown in some countries in Western Europe and the United States of America (Hartman et al., 2011; Acquaah, 2005).

According to existing records, soybean was first cultivated in Africa in Egypt in the year 1858 (Shurtleff and Aoyagi, 2009; Soybeanafrica.com*).* Soybean from its inception in Africa in 1858 was by 2009 being cultivated in all apart from 5 countries namely Namibia, Eritrea, Mauritania, Djibouti and Cape Verde (Shurtleff and Aoyagi, 2009).

Though it has been generally known that soybean was introduced in Zambia in the 1930s (Muliokela, 1997), the earliest available evidence by the Soyinfo centre point that soybean was first cultivated in Zambia in 1910 (Soybeanafrica.com; Soyinfocenter, 2014*).*

2.3 Plant development

Soybean is very responsive to environmental conditions and the main climatic factor affecting its yield is photoperiod, which in turn influences the temperature and water availability (Mundstock and Thomas, 2005). Cultivated soybean is adapted to a wide range of latitudes from 52 degrees north to 50 degrees south and to a range of seasonal durations from about 90 to 180 days (Smith and Hamel; 1999). The discussion on the developmental stages is based on the scale by Fehr and Caviness (1971)**.**

Seeds of most soybean plants imbibe water rapidly following planting (Smith and Hamel, 1999). Under optimum temperature and moisture, the plants would emerge within 5 to 14 days (www.soybeanmanagement.inf). The germination of soybean is epigeal, meaning that the hypocotyl is active and pulls the cotyledons above the ground during growth. The radical emerges from the seed in 1 to 2 days after planting. Downward growth of the primary root is rapid and by the 4^{th} or 5^{th} day, the first secondary roots emerge about 5 cm behind the primary root apex, while at about the same time, the cotyledons emerge growing rapidly to be pulled out of the soil (Purcell et al., 2014). After the emergence of the cotyledons, further growth of the seedling and the plant before flowering involves the formation of trifoliate leaves (Fehr and Caviness 1971**).**

Table 1: A description of the vegetative (V) and reproductive (R) growth stages in soybean

Stage	Description
V1	Completely unrolled leaf at the unifoliate
V2	Completely unrolled leaf at the first node above the unifoliate node
V3	Three nodes on the main stem beginning with the unifoliate node
R1	One flower at any node
R2	Flower at node immediately below the uppermost node with a completely unrolled leaf
R3	Pod 0.5 cm long at one of the uppermost nodes with a completely unrolled leaf
R4	Pod 2 cm long at one of the four uppermost nodes with a completely unrolled leaf
R5	Seeds beginning to develop at one of the uppermost nodes with completely unrolled leaf
R6	Pod containing full –size green seeds at one of the four uppermost nodes with a completely unrolled leaf
R7	Pods are yellowing; 50% of leaves are yellow and the crop is at physiological maturity
R8	95% of pods are brown and this is the optimal to harvest to avoid shattering

Source : Fehr and Caviness, 1971

The reproductive stages in soybean are represented by flowering, podding and seed development. In the reproductive stages, a difference should be recognised between indeterminate and determinate cultivars. Indeterminate cultivars begin flowering when about half the nodes on the main stem have developed and flowering proceeds upward on the plant as additional nodes are produced (Acquaah, 1999). Therefore, flowers, pods and seeds development are more advanced on the bottom portion of the main stem than on the top. For the determinate cultivars on the other hand, flowering frequently does not occur until all the nodes on the main stem have developed; which means flower, pod and seed development are similar throughout the plant (Smith and Hamel, 1999). The period between planting and flowering is primarily dependant on two things, temperature and daylength (Pederson, 2007).

Soybean is a qualitative short day plant and must receive a certain day length or less so that developmental timing is optimal for the location (Avila et al., 2013).

2.4 Soybean growth requirements

2.4.1 Temperature

Soybean is a C_3 plant, a category of plants that fix CO_2 initially into three carbon sugars via the carboxylation of ribulose-1, 5-bisphoshate (RuBP) (Smith and Hamel, 1999). Soybean grows best at temperatures between 20 ^oC and 30 ^oC (Avila et al., 2013). It is therefore a sub-tropical plant which thrives in the above temperature range mostly found in the sub tropics. There exists an inverse relationship between temperature and soluble carbohydrate concentration in leaves (Smith and Hamel, 1999). Photosynthesis increases with increasing temperature to between 35 to 40 ^{o} C and then begins to decline, while respiration usually continues to increase with temperature above the optimum for photosynthesis which is typical of all C_3 plants when photorespiration sets in (Wingler et al., 2000; Boote et al., 2005). The greatest number of pods per plant is obtained under mild temperature conditions having a day/night temperature combination of 26/14 ^oC with the optimal temperature being 26 ^oC (Avila et al., 2013; Boote et al., 2005). Temperatures above 40 ^oC during the vegetative stage reduce growth and hastens flowering. High temperatures during the reproductive phase can cause reductions in seed number and seed weight (Avila et al., 2013). On the other hand, cold regions where the temperature is equal or less than 10 ^oC makes the vegetative growth become small or null while production is affected by an upset in the carbohydrate partitioning rising as a result of decreased growth in some sink organs like seed embryos (Hamantaranjani et al., 2014).

2.4.2 Solar radiation

Solar radiation acts as an energy source for photosynthesis in crop production. The light spectrum duration and quality besides the radiation intensity are determinants of morphological and phenotypic responses striking in soybean such as plant height, induction of flowering and ontogeny (Avila et al., 2013). Soybean is a qualitative short day plant, and for it to flower require only when the daily exposure to the light was reduced below a certain critical duration (Avila et al., 2013). It is therefore that, since different latitudes receive different amounts of radiation in a year, adaptation of different cultivars varies across latitudes.

2.4.3 Soil moisture

Water participates in nearly all physiological and biochemical processes in plants, comprising 90 % of their mass (Souza et al., 2013). Water is responsible for the thermal regulation of the plant, acting both to maintain the cooling and heat distribution and provides the mechanical support to the plant (Souza et al., 2013). Under rainfed conditions, the seasonal water used for soybean can range from about 309 to 825 mm of water where the growing season ranges from 100 days at low altitudes to up to 190 days in the higher altitudes (Smith and Hamel, 1999, Das, 2003). Water availability is important in all the periods of soybean development; germination, emergence and flowering grain filling period (Avila et al., 2013). A seasonal water use pattern is that water use rate is generally low during the germination and seedling stages due to partial canopy cover and with a large portion of the water lost due to soil evaporation (FAO, 2015). When the plant moves into the rapid stage from V3 to VN, there is a rapid increase in water use and research carried out by Das (2003) found that rainfall during this phase plays a crucial role in the development of the crop and ultimately affects its yield. The discussion on water availability and the physiological and biochemical responses of soybean will be broken down into three components; root related traits, shoot related traits and flowering, podding and seed filling.

Root growth is affected by drought if they are affected during the later stages of vegetative stages or the early reproductive stages (R1 to R2) as there is an increase in root growth (Manavalan et al., 2009). The increase in the root growth is as a result of the shift in the carbohydrate partitioning balance in favour of roots in order for them to reach deeper moisture zones (Souza et al., 2013). Manavalan et al., (2009) concluded that if a plant develops a large root system during its early vegetative growth, it would be in an excellent position to maintain turgor under drought conditions later on in its life.

Shoot growth is affected in that shoots of water stressed plants have decreased photosynthetic surface area caused by decreased leaf enlargement and hastened leaf senescence (Smith and Hamel, 1999). The V4 stage presents a very unique scenario in soybean development relative to water stress as reported by Kron et al., (2008) on their studies of the developmental window on soybean who concluded that at V4, if water stress is subjected; the crop showed increased tolerance to water shortages in later growth stages

Yield as measured by the weight of seeds is reduced most by stress occurring during early formation and pod filling stages. Water stress during early reproductive growth (flowering and pod set) reduces yield usually as a result of fewer pods and seeds per unit area (Manavalan et al., 2009). Abscission of flowers, pods and seeds of water stressed plants and as well as the later decrease in seed size maybe be partially a response to water stress due to its effect on photosynthesis which affects the concentration of assimilates in the vegetative pools (Smith and Hamel, 1999).

Another aspect in soybean growth which is affected by moisture stress is nitrogen fixation. The water deficit promotes the accumulation of nitrogenous compounds in the shoot of the soybean plant causing a feedback reduction in fixation of N_2 (King and Purcell, 2005).

2.4.4 Nutrient requirements

Soybean genotypes have been found to tolerate specific pH within a given range (Jandong et al., 2011). Soybean is very sensitive to low pH, the stature of plants has been known to be affected below the pH of 4.0 (Uguru et al., 2012). Exchangeable aluminium in low pH soils is reported to be the major problem of growing soybean plants (Munns et al., 1981). Apart from addressing the acidity problem, it is important however not to deny plants of phosphorus especially in soils very low in phosphorus since phosphorus deficiency decrease whole plant photosynthate as it is important in improving plant height and leaf area of soybean and also improves soybean yield if applied with Potassium in appropriate quantities (Xiang et al., 2012, Khaswa et al., 2014).

Soybean has three main sources of nitrogen for its growth and production; nitrogen fixation by Bradyrhizobium, Nitrate and Ammonium in the soil and from applied nitrogenous fertilizers (Wood et al., 1993; Salvagiotti et al., 2008). Despite these sources, it is necessary to apply N fertlizers especially in locations with some greater environment limitations to improve yield (Wood et al., 1993). However, care should be taken not to apply beyond the soil requirement as it may affect the biological nitrogen fixation and not have meaningful gains to the crop (Wilson et al., 2014).

The micro nutrient requirement is similar to most green plants though soybean need additional Mo and Fe to make nitrogenase and leghaemoglobin (Hedarzade et al., 2016).

2.5 Genotype by Environment Interactions in Crop Adaptation

Genotype by environment interaction is the change in the relative performance of a character of two or more genotypes measured in two or more environments (Bowman, 1972, Haldane, 1946). Genotypes by environment interactions are ascribed to differences of sensitivity, which means that a given environmental difference affects some genotypes more than others (Falconer, 1981). Another important idea by Falconer (1981) is that some genotypes are more sensitive than others to environmental differences implying that environmental variance is a property of the genotype, but the source of the variation is environmental and not genetic. Henceforth, Information on variety stability to varied environments is very important in isolating genotypes which are responsive to better environments and maintain satisfactory yields under poor management (Brar et al., 2010).

Biometricians and breeders have over the years tried to find best ways of how to better understand G by E and how to improve genotypes in its presence. The initial way which was realised and used to deal with G x E was stratification of environments for which the breeder is dealing with and this did not prove very successful as G x E still existed within a micro environment (Eberhat and Russell, 1966). Among the earliest works which elucidated clearly on genotype by Environment interaction is a paper by Allard and Bradshaw (1964). Based on the realisation of the existence of G x E interactions even after stratification of environments, they concluded that there are two types of environment variations which exist, predictable and unpredictable and the later being the one which is important for selection of stable varieties. The discourse of Allard and Bradshaw (1964) did not however try out a parametric approach on how to resolve the issues of stability. The earliest known work on handling of genotype by environment interactions was by Yates and Cochran (1938). They proposed a methodology using linear regression models to compare the performance of a set of varieties evaluated in multiple sites and years in which for each variety, a regression of their mean was obtained regarding the overall mean of all varieties in each site per year. The regression model developed by Yates and Cochran (1938) did not initially receive a lot of attention until its use by Finlay and Wilkinson (1963) according to Lin and Thomson (1975). Finlay and Wilkinson (1963) proposed a methodology using linear regression to compare the performance of a set of barley varieties tested on different locations in different years. The method involved comparing a list of sampled varieties by way of computing a linear regression of individual yield on the mean yield of all varieties for the location and season.

They concluded that they had two very important parameters to determine the stability of varieties, the regression coefficient and the variety mean yield over all environments. Another prominent development on the regression approach of determination of genotype stability was by Eberhat and Russell (1966). In trying to resolve the aspect of genotype by environment interaction and genotype stability, they stated that a variety in an experiment should be regressed on an environmental index and that a function of the squared deviations from the regression is an estimate of the stability parameter. They therefore developed the second stability parameter, the deviation from regression.

Other breeders like Shukla (1972) and Francis and Kennenberg (1978) used variants of the linear regression model in their efforts to determine genotype stability.

The multiplicity of the regression based stability statistics brought a lot of confusion and Lin et al., (1986) decided to analyse the relationship of nine stability parameters. They concluded that all the statistics investigated represented three different concepts of stability; (1) if the genotype's among environment variance is small, (2) if the genotype response to the environment is parallel to the mean response of all genotypes in the trial and (3) if the residual Mean Square (MS) from the regression model on the environmental index is small.

The next aspect which was assessed was the heritability of the stability parameters if they were to be of use for selection. It was found after fitting the stability parameters to the additive model that the variance of genotypes across environments and that the years within locations MS for a genotype averaged over locations (fourth stability parameter) types of stability were heritable hence useful (Lin and Binns, 1990).

A turning point however came after the realisation that regression models assumed that genotypes have linear response to changes in the environments. A second approach of handling genotype x environment interaction by way of models taking into account of multiplicative effects was now pursued (Das et al., 2012). The two most famous methods that came from this approach are the Additive Main effects and Multiplicative Interaction (AMMI) by Zobel et al., (1988) and Genotype and Genotype by Environment interaction biplots (Yan and Kang, 2003).

AMMI partitions the GE interactions matrix into individual genotypic and environmental scores (Yan and Hunt, 2001; Zobel et al., 1988). AMMI only subjects the genotype by environment component to single value decomposition in genotype evaluation. Singular

Value Decomposition (SVD) is the process of decomposing a two way table (matrix) into two component matrices or simply said is the reverse process of matrix multiplication (Yan and Kang, 2003). Although genotype by environment is an important issue in cultivar evaluation, it must be emphasised that cultivar evaluation must be based on both genotype and genotype by environment simultaneously (Yan and Hunt, 2001). Another issue is that AMMI constructed biplots are plots of additive affects versus multiplicative effects and arguments are that it does not have the core properties of the biplots such as the inner product property (Yan; 1999 unpublished manuscript).

A multiplicative model that overcomes some of the disadvantages of AMMI is the sites regression model (SREG) which is used to study the combined effects of genotyp**e** and genotype by environment (GGE) (Setimela et al., 2007). This model expresses the empirical mean of the i^{th} genotype in the j^{th} environment as a sum of linear (additive) components, a sum of bilinear (Multiplicative) components hence combining the effects of genotypes (G) and genotype by environment and a residual error . The SREG model is able to predict the crossover and the non crossover interaction and this property makes it useful in simultaneously finding subsets of locations and genotypes hence finding homogenous locations thereby improving breeding efficiency (Gupta et al., 2013). It is important to note that these interactions are difficult to define without graphically presenting the data (Yan et al., 2001) and hence the SREG based GGE biplots are constructed (Setimela et al., 2007, Gupta et al., 2013).

GGE refers to genotype main effect (G) plus genotype by environment interaction (GE) and it is the part of variation which is relevant to genotype and test site evaluation (Yan and Kang, 2006). The GGE biplot model keeps G and GE together and partitions this mixture into two multiplicative terms (Yan and kang, 2003). The procedure developed by Yan and kang, (2003) allows an environment-centred matrix containing the GGE data to be subjected to singular value decomposition (SVD); each element in the matrix being estimated using the following equation:

$$E\,(Yij) = \beta_{j} + \sum \lambda_{k} Y_{ik}\, \delta jk$$

where *E (Yij)* is the expectation of genotype i in environment j; μ is the general mean; βj represents the environment main effect; K is the number of principal components (PC) needed to provide an adequate description of G + GE; λk is a proportionality constant or

singular value for the *k*th PC (PCk); and *γik* and *δjk* are the ith genotype score and the jth environmental score, respectively, for PCk. Singular Value Decomposition was achieved by providing a scaling factor *f* to obtain alternative genotype (*ikfik k n* = l g) and environment (*jkfjk k m* = l -1d) scores.

The SVD allowed G × E table of means to be displayed in a plot having n points for the genotypes plus m points for the environments.

2.5.1 Mega Environment

A mega environment is defined as a subset of locations that consistently share the best set of genotypes and the regions are relatively homogenous with similar biotic and abiotic stresses and cropping system requirements (Yan and Rajcan, 2002). The pattern of genotype response allows partitioning of test sites into mega environments and ideal environments based on their discriminating ability (Tukamuhabwa et al., 2012). Environment identification and characterisation is important in plant breeding in order to rationalise resources and confine genotype testing to sites which will give informative data thereby facilitating a rapid response to selection. The mean location performance and the mean genotypic yields though important in showing performance differences do not show the most important aspects of multi environment trials data. Multi environmental trials data analysis must address four major issues according to Yan and kang (2003).These four issues are:

1. The presence of mega- environments:
2. Cultivar evaluation within each mega environment:
3. Test environment evaluation within each mega environment and
4. Investigations of the causes of the genotype by environment Interactions.

2.6 Genotype x environment interactions in soybean adaptation

Many aspects of genotype x environment interactions have been widely studied in soybean. Some of the aspects studied are comparison of the discriminating powers of GGE to the AMMI model in soybean selection (Amira et al., 2013), the effects of genotype by environment on soybean agronomic traits (Zhe et al., 2010), stability of Isoflavine content (Murphy et al., 2009), genotype by environment and stability for grain yield and nutritional quality (Gurmu et al., 2009) and stability across several soil pH environments (Jandong et al., 2011).

Soybean nutritional factors like oil and protein have been studied for stability due to their importance in human nutrition (Zhe et al., 2010). Genotype by environment studies done have shown that oil and protein in soybean are affected by the environment and the genotype by environment interaction (Gurmu et al., 2009).

Though several traits have been studied in the genotype by environment trials (Zhe et al., 2010, Ngalamu et al., 2013), yield was found to be the most sensitive trait to genotype by environment interactions and efforts to resolve this have received attention from researchers in an attempt to assess the adaptability and stability of soybean . For instance Zhe et al., (2010) in their stability study found that repeatability of yield was lower than protein and oil.

Appropriate analysis of the yield response in the genotype by environment studies allows environment characterization (Tukamuhabwa et al., 2012 and Ashraf et al., 2010). For instance in the study by Amira et al., (2013) to compare the discriminating powers of GGE to the AMMI in soybean, yield was used. The findings were that GGE is more effective and informative than AMMI in mega-environment analysis and genotype by environment evaluation. GGE biplot in soybean has also been found to demonstrate an ability to provide information on genotypes and environments simultaneusly in evaluation of yield and other traits (Murphy et al., 2009 and Zhe et al., 2010).

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Zambia agro ecological regions description

Zambia is located on the African Sub continent between latitude 8-18^{o} S and longitudes 22-33^{o} E and covering an area of 752,620 km^{2}, which is 2.5% of the African continent (Muliokela, 1997; Saasa, 2003). It is a country with three agro ecological zones which are characterised by differences on climatic conditions most important of which is the amount of rainfall received annually (Muliokela, 1997). The other climatic parameters which are notable in these agro ecological regions are temperature, soil characteristics and the vegetation type.

Region I comprises the valley areas of the country and lies between 300 and 900 m above sea level. The annual rainfall received in this area is low not exceeding 800 mm with relatively high mean temperatures of 38^{o}C received in october. Region 2 is the most agricultural active region receing between 800 mm to 1000 mm of annual rainfall. The elevation of this region is between 900 and 1300 meters above sea level. The mean daily temperatures during the growing season range between 23-25^{o}C. Most of the national soybean production in Zambia is done in region II. The last region is region 3 at an elevation ranging between 1100-1700 meters above sea level and receives above 1000 mm of rainfall per year. The average monthly temperature in the growing season is 16 ^{o}C. This region has a soil acidity set back in agricultural production. Table 2 below shows the soil characteristics of the three agro ecological regions of Zambia and their limitations to crop production.

Table 2: Soils in the agro ecological regions and thier limitations to crop production

Region	General Description of Soils	Limitations
Region I	Loamy and clay with course to fine tops	Slightly acidic to alkaline. Minor fertility limitations
	Reddish course sandy soils	Low pH, available water and nutrient capacity reserve
	Poorly drained sandy soils	Severe wetness, acidic and low fertility
	Shallow and gravel soils in rolling to hilly areas	Not suitable for cultivation
Region II	Moderately leached clayey to loamy soils	Low nutrient and water holding capacity
	Slightly leached soils	Slight to moderate acidity. Heavy textured soils
	Course sandy loams in large dambos	Impefectly to poorly drained. Limitations due to wetness
	Sandy soils on kalahari sand	Medium to strong acidity, course textured top soil, low water holding capacityand nutrient capacity.
Region III	Red brown clayey loamy soils	Very strong acidity and highly leached
	Shallow and gravel soils	Limited depth
	Clayey soil, red in colour	Fewer limitation but moderately leached
	Poorly to very poorly drained flood plain soils	Variable texture and acidity
	Course sandy soils in pan dambos on kalahari sand	Very strong acidity

Source: Compiled from Bunyolo. A, Chirwa. B and Muchinda M. Agro ecological and Climatic conditions in Muliokela. S (ed), 1997: Zambia Technology handbook, Ministry of Agriculture Food and Fisheries, Lusaka

3.2 Experimental sites

The multi environment trials were carried out in the 2013/2014 agricultural season at four locations described in Table 3 and shown in Figure I below.

Table 3: Experiment sites description

Location Name	Coordinates	Agro ecological region	Altitude (M)
Masumba	13.22 S, 31.93 E	I	546
Golden Valley Agriculture Research Trust (GART)	14. 50 S, 28.10 E	II	1139
Kabwe Research Station	14.39 S, 28.49 E	II	1176
Msekera Research Station	13.38 S, 32.34 E	II	1032

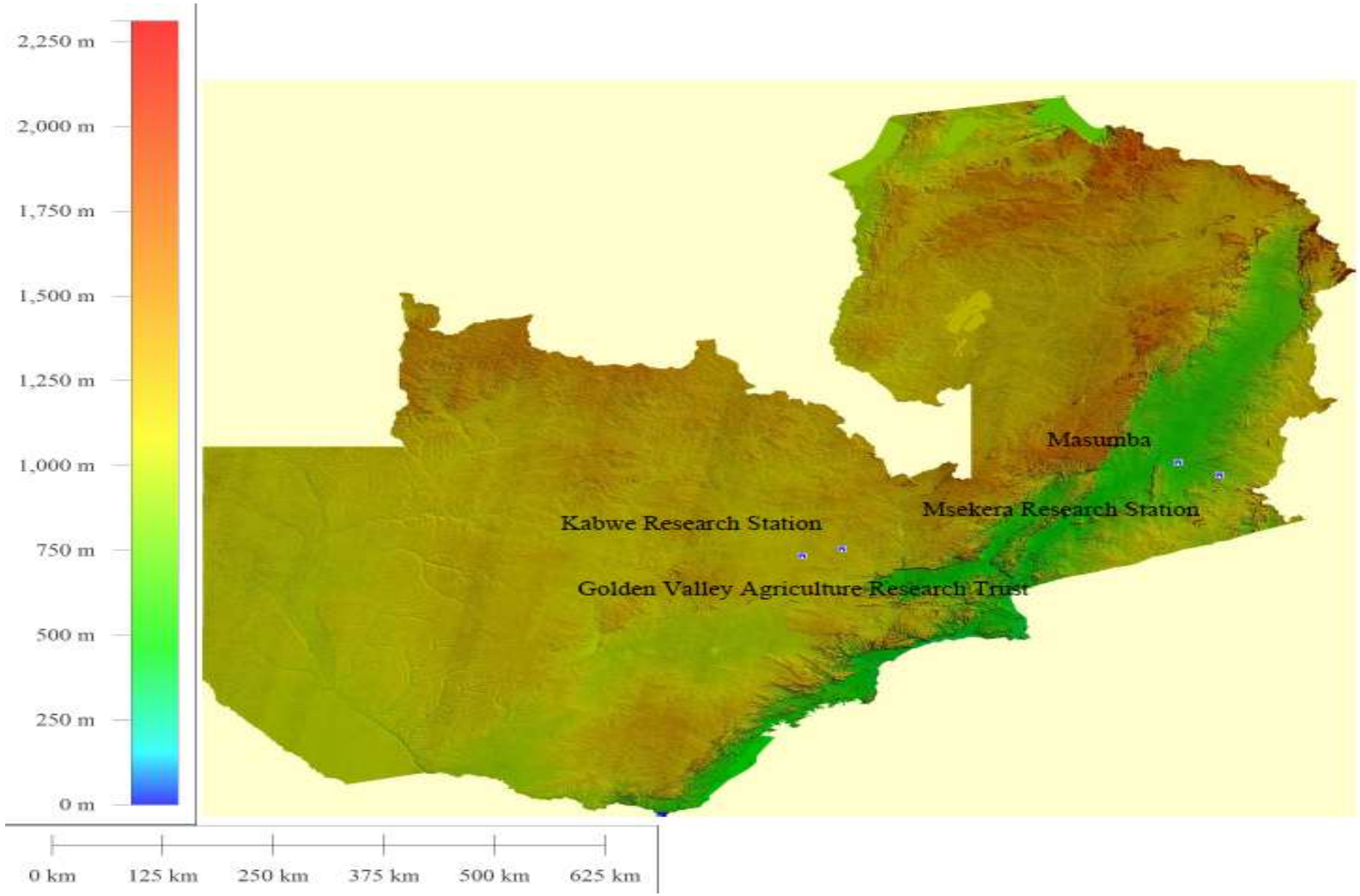


Figure 1: Map of Zambia Showing the Trial Locations

Composite soil samples were collected at the 4 locations upto a depth of 30 cm and soil analysis was done at the University of Zambia soil science laboratories. The soil analyis results are indicated in Table 4 show that the locations had relatively similar soil texture of sandy loam in three locations, Masumba, Msekera and Golden Valley Research Trust (GART) while one location (Kabwe) had loamy sands. The pH range for the locations was between 5.52 and 5.95. The locations varied on NPK and the trace nutrients.

Table 4: Soil analysis results for the four (4) trial locations

Location	pH	N	Organic Matter	P	K	Na	Ca	Mg	Cu	Fe	Mn	Zn	S	Sand	Clay	Silt	USDA
	0.01M	0.01M	Walkley and Black	Bray 1	Amm Acetate					DTPA			Acetate	Hydrometer			Texture
	$CaCl_2$	$CaCl_3$	%	mg/kg	cmol/kg					mg/kg			mg/kg	%			Class
Kabwe	5.52	0.063	0.56	15.21	0.17	0.05	1.83	0.57	0.14	6.44	6.43	0.58	14.79	80	6	14	Loamy sand
GART	5.95	0.07	1.92	7.56	0.66	0.08	6.50	2.47	3.24	3.38	6.26	0.92	17.75	64	16	20	Sandy loam
Msekera	5.63	0.08	2.40	12.27	0.90	0.10	10.00	2.25	0.64	9.46	8.03	0.74	13.81	70	10	20	Sandy loam
Masumba	5.52	0.07	3.52	1.99	0.43	0.06	6.83	1.51	0.97	6.92	9.61	0.55	12.82	64	12	24	Sandy loam

Climatic conditions namely rainfall and temperature were recorded and aggregated on a monthly basis. The data for three locations; Masumba, Kabwe and Msekera was obtained from the Zambia Meterology Department, while the data for Golden Valley Agriculture Research Trust was obtained from the research station. The recorded data is tabulated in Table 5. The highest amount of rainfall was recieved at Msekera (1097.7 mm). The other locations recieved 642.8 mm (Masumba), 601.2mm (GART) and 583.3 mm (Kabwe). The mean temperatures for the locations were 32.88^{o}C (Masumba), 29.5 ^{o}C (Msekera), 23.12 ^{o}C (kabwe) and 24.24 ^{o}C (GART).

Table 5: Mean Monthly meteorological data for the four locations over the study period

Month	Location	Mean temp(^{o}C)	Total Monthy Rainfall (mm)
December	Masumba	35.6	106.9
	Msekera	31.6	143.1
	Kabwe	24.9	191.7
	GART	25.2	307.6
J**anuary**	Masumba	31.8	246.3
	Msekera	28.5	306.5
	Kabwe	23.5	204.2
	GART	25.1	69.2
February	Masumba	31.8	214.1
	Msekera	28.5	407.8
	Kabwe	22.95	97
	GART	24.4	99.4
March	Masumba	33	75.5
	Msekera	30.1	216.8
	Kabwe	22.95	88.4
	GART	24.1	65.1
April	Masumba	32.2	0
	Msekera	28.8	23.5
	Kabwe	21.3	2
	GART	22.4	60.2

3.3 Experimental design

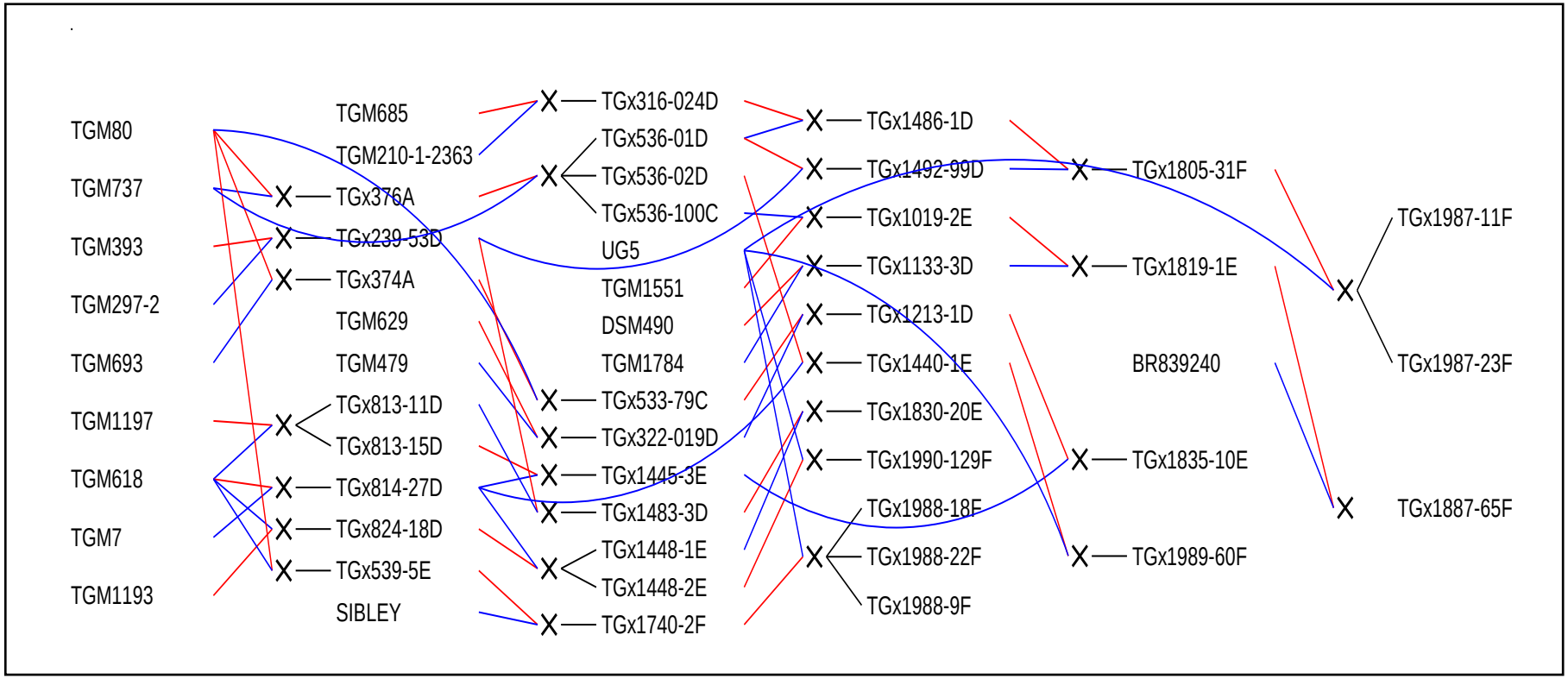
The experimental material consisted of 15 genotypes of soybean (Table 6). These were obtained from the International Institute of Tropical Agriculture and the Zambia Agricultural

Research Institute (ZARI). The pedigree of the IITA genotypes is presented in Figure 2 below.

Table 6: List of genotypes used in the trial and their assigned codes

Genotype	Genotype Assigned Code	Source
TGX 1740-2F	G 1	IITA
TGX 1830-20E	G 2	IITA
TGX 1835-10E	G 3	IITA
TGX 1887-65F	G 4	IITA
TGX 1904-6F	G 5	IITA
TGX 1987-11F	G 6	IITA
TGX 1987-23F	G 7	IITA
TGX 1988-9F	G 8	IITA
TGX 1988-18F	G 9	IITA
TGX 1988-22F	G 10	IITA
TGX 1989-60F	G 11	IITA
TGX 1990-129F	G 12	IITA
Magoye	G 13	ZARI
Safari	G 14	SeedCo
Lukanga	G 15	ZARI

***The IITA lines were obtained from a pool recommended for Zambian trials under the USAID funded feed the future project**.



The blue and red line show the parents which were crossed to produce a corresponding line from the left to the right.

Figure 2: Pedigree diagram for the IITA genotypes used in the study

The treatments (genotypes) were arranged in a Randomised Complete Block Design with 4 replications at each location. Each plot consisted of 4 rows of 6 meters long. An interrow spacing of 50cm and intrarow spacing of 5cm were used.

Planting was done at different times depending on the onset of the rains while weeding was done by hand as and when required. Fertilizer application consisted of basal dressing with Compound 'D' (N= 10, P_2O = 20, K_2O = 10, S = 6-8) at a rate of 200kg/ha . There was no innoculum applied in all the trials.,

3.4 Data collection and analysis

Data collection started when the crop had reached 50% flowering and others at maturity. Table 7 below show the parameters measured and the procedure followed during data collection.

Table 7: Parameters measured and the procedure during data collection

Parameter	Procedure
Days to 50% flowering	Counting of plants which had flowered per plot of each genotype was done and each plot which reached 50% was recorded
Plant Height	10 plants were randomly selected from the net plot. Measurements were taken from the ground to the tip of the plant . and the average was recorded
Number of Pods Per Plant	5 plants were randonmly sampled from the net plot and all the pods on each were counted then the average calculated and recorded.
Number of Plants at harvest	Plant stand count was taken for the net plot (two roles) just prior to harvesting.
100 seed weight	Randomly sampled 100 seeds in sets of 3 were taken from each net plot harvest and weighed. The average was calculated and recorded.

Analysis of the data was through analysis of variance using Genstast version 16. The model used was a random effects model, where genotypes and locations were considered as random factors. GGE biplot (Yan et al., 2000) was applied for grain yield data to determine the genotype by environment interactions, Genstat version 16 was used.

CHAPTER FOUR

4.0 RESULTS

4.1 Analysi of variance

Table 8 presents the analysis of variance for all variables considered in the study. There were significant (p=0.05) differences among locations with respect to yield, days to 50% flowering, Plant height, 100 seed weight and pods per plant. Significant (p=0.05) differences were also obtained among genotypes with respect to yield, days to 50% flowering, plant height and 100 seed weight. There were also significant (p=0.05) interactions genotype x environments differences for yield, days to 50% flowering, plant height and 100 seed weight

Table 8: Combined Analysis of Variance (ANOVA) for all the variables in the study conducted during the 2013/2014 season in Zambia

Source of Variation	Degrees of Freedom	Yield	D_50% flowering	Plant_Height	100 Seed_W	Pods Per Plant
Location	3	16158777**	289.54**	5358.09**	140.46**	24379.20**
Reps/Location	12	415793	2.63	121.93	3.21	365.72
Genotypes	14	1192617**	232.72**	880.56**	38.82**	477.30
Location * Genotypes	42	472487*	10.77*	124.13	9.30*	736.10
Error	167	128231	3.28	63.87	2.67	459.60
Total	238					

Note * and ** indicates statistical significance at the 0.05 and 0.01 levels of probability respecitively

4.1.1 Grain yield

The yield data is presented in Table 9. The table presents the three aspects of the study; the location means, genotypes means and the interaction of the genotype and the locations. The location with the highest yields (kg/ha) was Kabwe at (1978 kg/ha) and the lowest at Masumba (798 kg/ha). Yields at GART and Msekera fell between those ones reported above, each significantly lower than level at Kabwe but significantly (p=0.05) higher than level at Masumba.

The mean grain yield for the genotypes evaluated in the study showed that genotype TGX 1988-22F was the highest yielding (1517 kg/ha). Genotype TGX 1835-10E gave the lowest yield (418 kg/ha). Five genotypes namely Lukanga, TGX 1835-10E, TGX 1830-20E, TGX 1988-18F, TGX 1987-23F and TGX 1987-11 yielded below the overall mean yield of the trial.

Significant (p=0.05) interactions were observed between genotypes and locations (Table 9). These differential responses in sense are manifested through inconsistencies in the rankings as the best yielding genotype at GART, Safari (1731 kg/ha), was not among the top best five at Masumba and Msekera, while one of the lowest yielding, genotype TGX 1987-23F (1610 kg/ha), in Kabwe was the second best yielding (1205 kg/ha) in Msekera. This change in ranking is observed for all genotypes, except TGX 1835-10E that showed consistently low yields, being in the lowest three genotypes in all the four locations.

Table 9: Genotype yield for and across the locations

	Locations				
Genotypes	**GART**	**Masumba**	**Msekera**	**Kabwe**	**Mean**
TGX 1740-2F	1412	751	1267	2003	1358
TGX 1830-20E	1064	842	669	1228	951
TGX 1835-10E	594	388	478	213	418
TGX 1887-65F	1239	611	1414	2316	1395
TGX 1904-6F	1419	1238	1001	2262	1480
TGX 1987-11F	798	850	890	1834	1093
TGX 1987-23F	1008	1205	420	1610	1060
TGX 1988-9F	852	809	1078	2364	1276
TGX 1988-18F	1465	417	719	2121	1180
TGX 1988-22F	1309	807	1340	2610	1517
TGX 1989-60F	1396	1172	944	2076	1397
TGX 1990-129F	1389	1107	1392	2124	1503
Magoye (check)	991	1164	1109	2459	1431
Safari (check)	1731	236	1061	2409	1359
Lukanga (check	1640	372	630	2047	1172
Mean	1220	801	958	1978	1239
Lsd	A (locations=135.9) x B (Genotypes=263.1) = A x B = 526.2				
CV (%)	A (locations) x B (Genotypes) =A x B = 30.4				

4.1.2 Days to 50% flowering

Days to 50% flowering results are presented in Table 10. There were significant (p=0.05) differences for location, genotype and genotype by environment interaction differences (p= 0.05) on the variate days to 50% flowering. The earliest flowering was at Masumba (50.82 days) and latest flowering was at Kabwe (56.05 days). Flowering at Msekera and GART was intermediary (53.90 and 52.67 days respectively).

The genotype Lukanga had the shortest days to 50% flowering of 46.94 days while TGX 1887-65F had the longest days to 50% flowering mean of 60.44 days. The other genotypes showed significant (p=0.05)differences relative to the pairs involved.

Significant (p=0.05) interactions represent differential response of the genotypes to the locations i.e genotype TGX 1887-65F failed to maintain its relative ranking from one location to another , it had the longest days to 50% flowering mean for the locations , Msekera (63.5 days) and Masumba (57.75 days) but was second (2^{nd}) at GART (60.75 days) and third (3^{rd}) at location Kabwe (59.75 days). The genotype TGX 1830-20E had the longest days to 50% flowering for the locations GART (61 days) and Kabwe (61.75 days) but was second for the locations Masumba (57days) and Msekera (59.75 days).

Table 10: Genotypes days to 50% flowering for and across the locations

	Locations				
Genotypes	**GART**	**Masumba**	**Msekera**	**Kabwe**	**Mean**
TGX 1740-2F	49.00	47.00	48.00	56.25	51.00
TGX 1830-20E	61.00	57.00	59.75	61.75	59.88
TGX 1835-10E	54.50	57.00	53.50	54.75	54.94
TGX 1887-65F	60.75	57.75	63.50	59.75	60.44
TGX 1904-6F	54.50	51.25	55.25	59.50	55.12
TGX 1987-11F	52.50	50.75	54.75	50.75	53.69
TGX 1987-23F	55.75	52.75	57.00	60.50	56.50
TGX 1988-9F	53.75	52.50	53.75	56.50	54.12
TGX 1988-18F	49.00	43.50	49.75	52.25	48.62
TGX 1988-22F	51.00	52.75	53.50	57.50	53.69
TGX 1989-60F	49.25	47.75	52.75	55.00	51.19
TGX 1990-129F	52.50	50.25	54.00	56.25	53.25
Magoye (check)	51.00	50.00	51.00	56.00	52.00
Safari (check)	49.25	47.00	50.25	49.50	49.00
Lukanga (check	46.25	45.00	48.00	48.50	46.94
Mean	52.67	50.82	53.90	56.05	53.36
Lsd	A (locations=0.65) x B (Genotypes=1.26) = A x B = 2.53				
CV (%)	A (locations) x B (Genotypes) = A x B = 3.4				

4.1.3 Location and genotype effect on 100 seed weight

Significant (p=0.05) location, genotype and location x genotype differences for 100 seed weight were realised from the analysis of variance (Table 8). The analysis of the results is elaborated in Table 11 below.

The analysis of the location results show that Masumba had the highest 100 seed mean weight of 14.61 grams, then Msekera (13.40 g) followed by Kabwe (12.40 g) and the least weight recorded was at GART (11.22 g).

The evaluation further showed that the genotype TGX 1988-18F had the highest 100 seed mean weight of 15.97 grams and Magoye had the lowest with 10.89 grams. Eight (8) genotypes of the 15 genotypes in the trial had 100 seed mean weights below the mean weight of all the genotypes (12.90 g). The genotypes which had a 100 seed weight above the mean were TGX 1987-11F (13.97 g), TGX 1988-18F (15.97 g), TGX 1988-22F (13.09), TGX-1989-60F (14.17 g), TGX 1990-129F (13.28 g), Safari (15 g) and Lukanga (14.76 g)

Significant (p=0.05) interactions were observed between genotypes and locations with respect to 100 seed weight. The results show differential responses are manifested through inconsistencies in the relative rankings of the genotypes across the locations. The results for instance show Safari to have the highest 100 seed weight at the locations Kabwe (16.25 g), Msekera (16.17 g) and GART (14.50 g) but was the 5th lowest in Masumba (13.08 g). On another aspect is the genotype TGX 1835-10E which perfomed consistenly below average in all the locations except one; it was the highest (tie with Safari) at GART (14.50 g) but could not maintain its ranking and was lowest in Masumba (8.97 g).

Table 11: 100 seed weight of the genotypes for and across locations

	Locations				
Genotypes	GART	Masumba	Msekera	Kabwe	Mean
TGx 1740-2F	10.75	15.00	11.97	11.25	12.24
TGx 1830-20E	9.75	12.25	12.75	9.25	10.99
TGx 1835-10E	14.50	8.97	11.30	11.50	11.57
TGx 1887-65F	9.25	10.77	13.95	12.00	11.49
TGx 1904-6F	10.25	13.87	13.70	11.00	12.05
TGx 1987-11F	11.25	16.75	14.65	13.25	13.97
TGx 1987-23F	9.00	13.25	12.05	10.75	11.26
TGx 1988-9F	9.75	17.50	13.25	11.00	12.87
TGx 1988-18F	14.50	19.50	14.62	15.25	15.97
TGx 1988-22F	9.50	16.25	13.60	13.00	13.09
TGx 1989-60F	11.50	17.75	13.68	13.75	14.17
TGx 1990-129F	11.25	15.75	13.12	13.00	13.28
Magoye (check)	8.50	12.25	13.07	9.75	10.89
Safari (check)	14.50	13.08	16.17	16.25	15.00
Lukanga (check	14.00	16.25	13.80	15.00	14.76
Mean	11.22	14.61	13.40	12.40	12.90
Lsd	A (locations=0.59) x B (Genotypes=1.12) A x B = 2.28				
CV (%)	A (locations) x B (Genotypes) = A x B = 12.7				

4.1.4 Plant height at harvest

Plant height at harvest results are shown in Table 12. The significant results (p=0.05) for the locations analysis show that the tallest plants were at GART (69.08 cm) and the shortest at Msekera (46.66 cm). The other two locations Kabwe (58.79 cm) and Masumba (52.67 cm) had plant heights which were signifcant shorter than GART but significantly taller than Msekera.

The genotypes had significant (p=0.05) differences for plant height at harvest and the results showed that the genotype with the highest mean for plant height across the locations was TGX 1887-65F (66.11 cm). Some of the genotypes with taller plants above the mean were TGX 1988-9F (61.07 cm), TGX 1990-129 (61.08 cm) and TGX 1740-2F (64.15cm). The genotype TGX 1835-10E had the shortest plants at harvest with a mean hieght of 37.60 cm.

Significant interactions (p=0.05) were observed from the analysis of plant height at harvest. The relative ranking of the genotypes varied across the locations for instance the genoype TGX 1987-11F failed to maintain its relative ranking from one location to another , for instance, it had the second tallest plants (77.75 cm) at GART, then ranked third at Masumba (61.00 cm), 6^{th} at Msekera (46.98 cm) and was 10^{th} at Kabwe (61.63 cm). Apart from the genotype TGX 1835-10E which had consistently shorter plants across the locations, the other shorter genotype TGX 1835-20E varied its relative ranking across the locations with being the 7^{th} shortest at GART (69.25 cm), third shortest at Masumba (44.25cm), 6^{th} shortest at Msekera (45.30 cm) and fifth shortest at Kabwe (55.55 cm).

T**able 12**: Genotypes plant height at harvest for and across the locations

	Locations				
Genotypes	**GART**	**Masumba**	**Msekera**	**Kabwe**	**Mean**
TGx 1740-2F	74.50	62.00	56.30	63.80	64.15
TGx 1830-20E	69.25	44.25	45.30	55.55	53.59
TGx 1835-10E	44.75	37.75	32.30	35.58	37.59
TGx 1887-65F	74.00	55.25	67.85	67.32	66.11
TGx 1904-6F	75.75	50.25	43.27	71.55	60.21
TGx 1987-11F	77.75	61.00	46.98	60.80	61.63
TGx 1987-23F	68.00	57.00	44.30	62.42	57.93
TGx 1988-9F	75.00	51.75	46.88	70.68	61.07
TGx 1988-18F	72.25	52.50	48.25	64.22	59.31
TGx 1988-22F	79.75	59.75	51.15	66.23	64.22
TGx 1989-60F	68.00	66.75	43.80	61.08	59.91
TGx 1990-129F	74.75	59.50	48.77	61.30	61.08
Magoye (check)	63.00	41.50	42.55	44.55	47.90
Safari (check)	63.00	46.50	41.80	53.37	51.17
Lukanga (check	56.50	44.25	40.48	43.40	46.16
Mean	69.08	52.67	46.67	58.79	56.80
Lsd	A (locations=2.88) x B (Genotypes=5.58) = A x B = 11.72				
CV (%)	A (locations) x B (Genotypes) = A x B = 14.7				

4.1.5 Pods per plant at harvest

The pods per plant data is presented in Table 13. The table presents the location means, genotypes means and the interaction of the genotype and the locations. The analysis of variance in table 8 however showed only significant (p=0.05) for locations with respect to pods per plant at harvest. The location which recorded the plants with the highest number of pods per plant was Kabwe (65.5) and the lowest was at Msekera (19.5). The location GART (56.8) was significantly (p=0.05) lower than Kabwe and higher than Masumba and Msekera. The location Masumba (40.6) was significantly higher than Msekera but lower than GART and Kabwe.

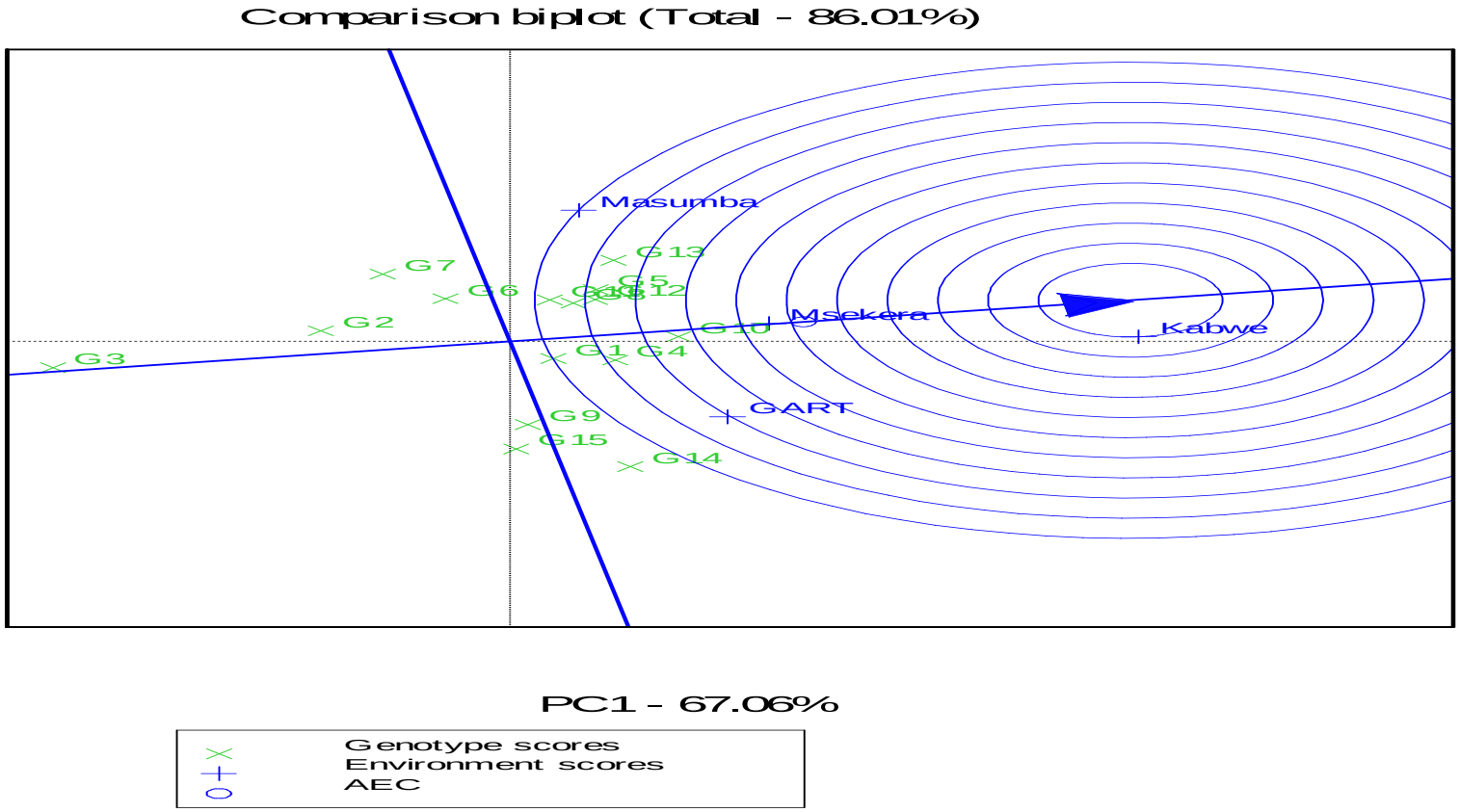
Table 13: Genotypes number of pods per plant for and across locations

	Locations				
Genotypes	**GART**	**Masumba**	**Msekera**	**Kabwe**	**Mean**
TGx 1740-2F	60.20	25.90	16.30	64.60	41.80
TGx 1830-20E	69.60	35.10	18.40	57.80	45.20
TGx 1835-10E	86.00	42.60	24.50	31.30	46.10
TGx 1887-65F	47.20	40.80	17.00	78.00	45.70
TGx 1904-6F	70.90	34.70	17.80	36.50	40.00
TGx 1987-11F	43.20	32.00	22.60	76.60	43.60
TGx 1987-23F	52.30	36.50	17.60	73.90	45.10
TGx 1988-9F	49.70	36.80	24.40	58.10	42.20
TGx 1988-18F	53.90	38.30	16.10	116.00	56.10
TGx 1988-22F	57.00	59.90	21.60	81.90	55.10
TGx 1989-60F	56.10	48.80	25.10	72.90	50.70
TGx 1990-129F	45.60	46.50	16.90	70.70	44.90
Magoye (check)	52.60	51.70	25.40	70.90	50.10
Safari (check)	58.50	45.10	14.80	42.60	40.20
Lukanga (check	49.60	34.90	14.40	51.10	37.50
Mean	56.80	40.60	19.50	65.50	45.60
Lsd	A (locations=7.73) x B (Genotypes=14.96) = A x B = 29.94				
CV (%)	A (locations) x B (Genotypes) = A x B = 46.8				

4.2 Interactions between genotypes and locations for grain yield.

From the additional analysis of the interactions between genotypes and locations for grain yield using GGE biplot method, the following results were observed.

Figure 3 presents the ranking of the genotypes relative to the ideal . The average environment is represented by the centre of the concentric circles (Jadong et al., 2011). The average environment has the average coordinates of all test environments and Average Environment Axis is the line that passes through the average environment and the biplot origin (Yan and Tinker, 2006). This average environment projected the average performance of the target environment (Yan and Kang, 2003). The environment closest to the centre of the concentric circles is the most representative of the locations. The present study showed Kabwe to be the most representative location followed by Msekera while Masumba was the least representative of the test sites.



***The Average Environment Axis (AEA) is the line running from left to right with an arrow at the centre of the concentric circles of the biplot.**

Figure 3: Environmental ranking of the genotypes

4.2.1 Discriminating ability determination

Figure 4 below shows the scatther plot which represents the genotypes discriminating ability. The lengths of the environment vectors on the vector view biplot approximates the standard deviation within each location, which is the measure of their discriminating ability (Yan and Tinker, 2006). The study found kabwe with the longest environment vector hence being the most discriminating location followed by Masumba and the least was Msekera.

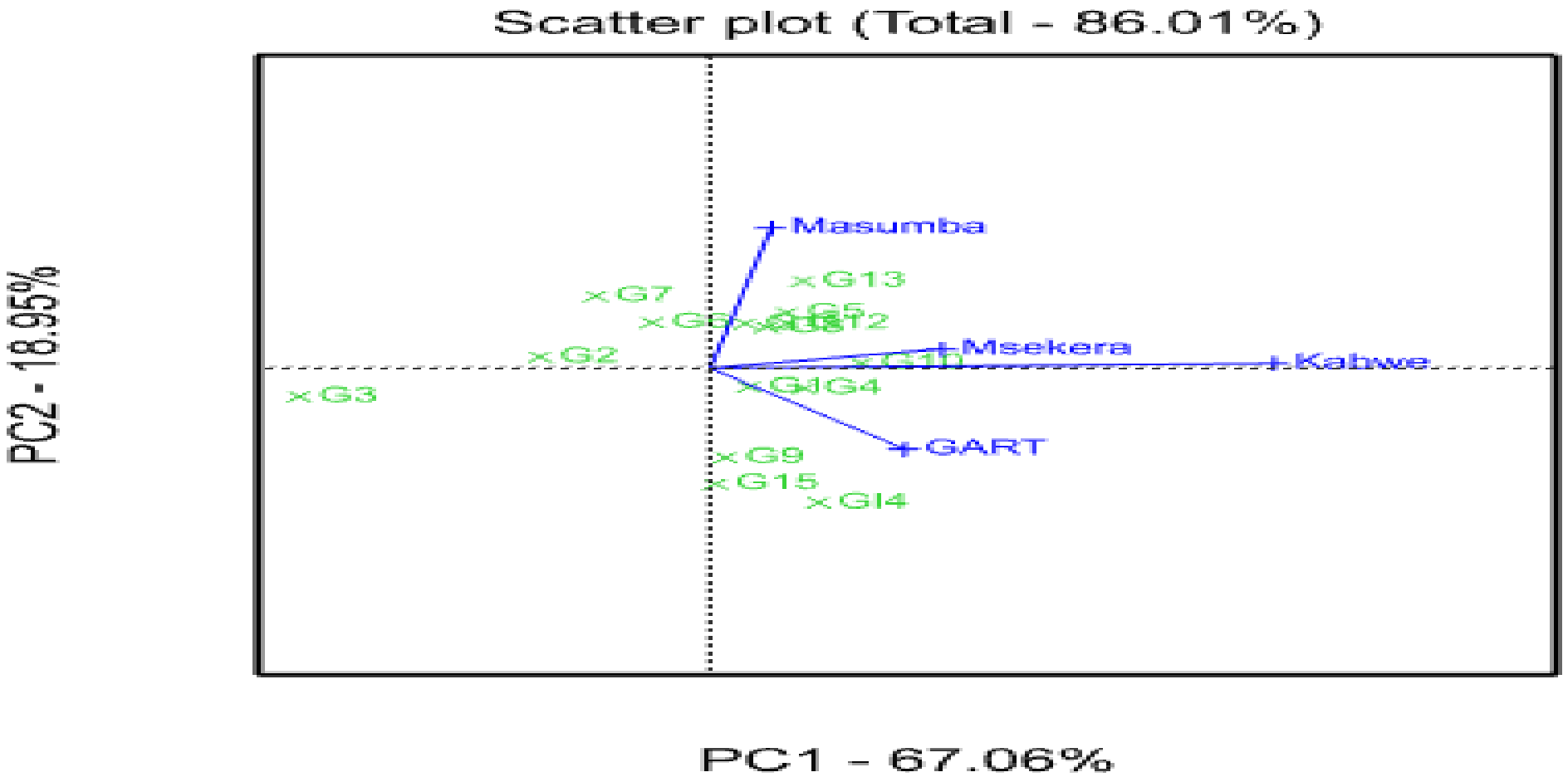


Figure 4: Vector view GGE biplot showing the discriminating abilities of the locations

4.2.2 Ideal test environment identification

Based on the results of Figure 3 and 4, Kabwe was identified to be the most ideal test location for soybeans since it was both discriminating and representative of the test environments/locations. Msekera according to Figure 3 is relatively more representative compared to GART and Masumba but is not discriminating as shown by the length of the environment vectors (Figure 4), hence making it not an ideal test location among the locations studied. Masumba and GART were discriminative location as shown by the lengths of the environment vectors (Figure 4) but were not representative as per their position on the concentric circles from the average environment (Figure 3).

4.2.3 Yield stability

The results in Figure 5 below are a depiction of the mean perfomance of the genotypes across the locations and their stability. The single arrowed line called Average Environmental Coordinate (AEC) Abscisca points to higher mean seed yield across locations. Therefore, the projections of the genotype markers on this line approximates their yield; hence the results showed that TGX 1988-22F had the highest mean and the genotype with the lowest mean was TGX 1835-10E. The thick perpendicular line to the AEC Abscisca is the Average Environmental Coordinate Ordinate (AEO) which points to greater variability in both directions (Brar et al., 2010). The projections of the genotype markers in figure 5 showed that Safari was the most variable genotype. The results also showed the genotype TGX 1835-10E to have been non responsive as observed by the fact that it lies exactly on the AEC abscisca which is a zero point for the average environment coordinate. Based on the projections described above, the results showed that TGX 1988-22F is the most stable genotype across all the locations.

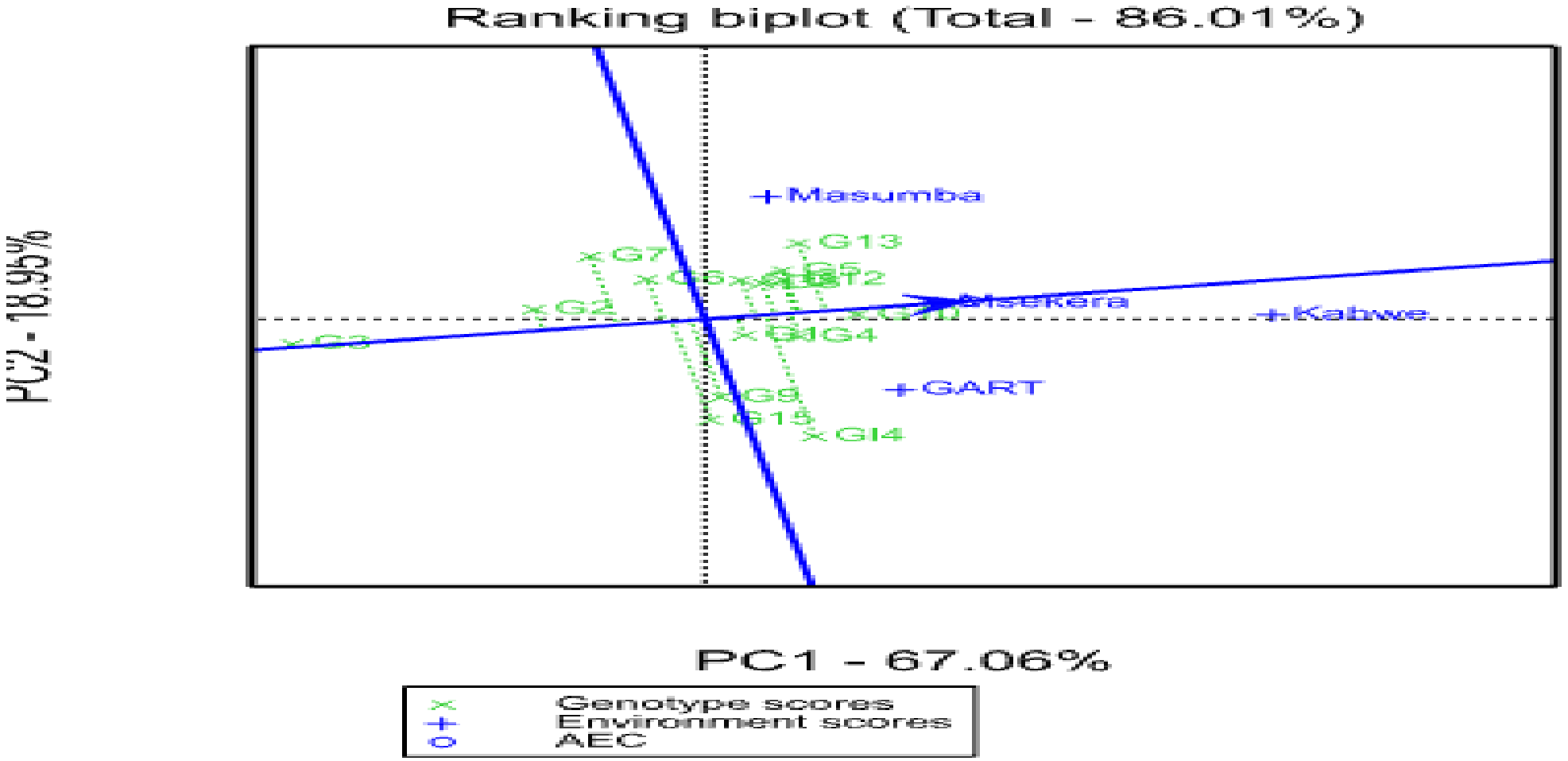


Figure 5: Average Environmental Coordinate View showing genotype variability

4.2.4 Mega Environment Identification

Figure 6 below is a scatther plot which shows the analysis indication of mega environments which were identified and the high perfoming genotypes in each of those locations. A polygon was drawn on genotypes that are furthest from the biplot origin so that all the other genotypes are contained within the polygon. Then perpendicular lines to each side of the polygon are drawn starting from the biplot origin (Yan and Tinker, 2006). Based on the interpretations of the polygon view on the biplot; the genotypes on the vertices are either the worst or the best yielding genotypes (Brar et al., 2010). The perpendicular lines in the polygons are equality lines between adjacent genotypes (Yan and Tinker, 2006). Therefore the study results show that for the locations Kabwe and Msekera, TGX 1988-22F (G10) was the best genotype, Safari (G14) was the best for GART and Magoye (G13) was the best performer for Masumba.

Also based on the GGE principle that any number of environments/locations with the same "winning" genotype form a mega environment, the results in Figure 6 show 3 mega environments. The mega environments were Kabwe/Msekera, GART and Masumba.

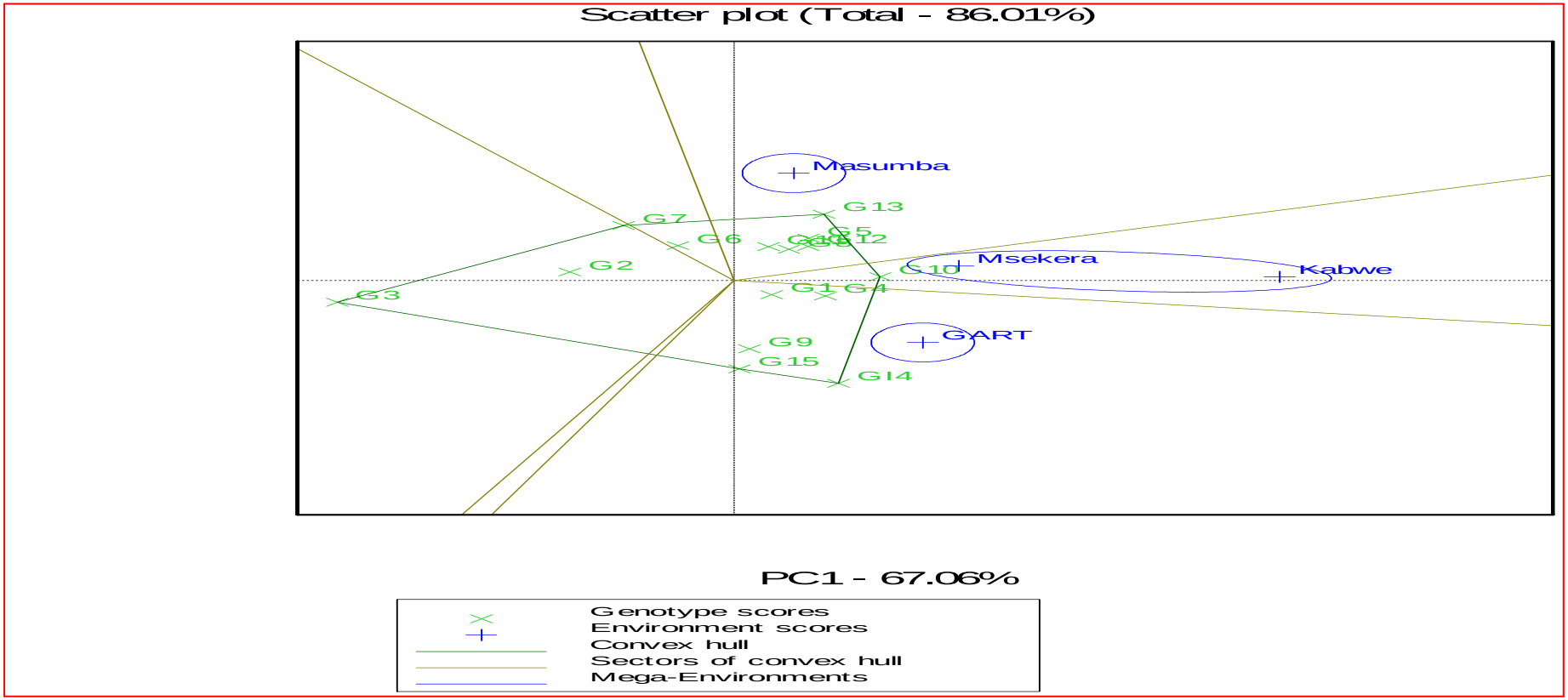


Figure 6: The GGE biplot showing the mega environments and also"which won where pattern"among the genotypes

CHAPTER FIVE

5.0 DISCUSSION

5.1 Morphological Characteristics

Plant height varied among locations and genotypes with the character being influenced by location as testified by the significant genotype x location interactions. The significant differences among locations can be attributed to the individual and combined effects of edaphic and climatic factors. These results are contrary to what Khaswa et al., (2014) reported that areas with relatively high P tended to have taller soybeans plants. GART in this study had one of the lowest level of soil P but had the tallest plants. Similarly the highest rainfall recorded was at Msekera but this location had the shortest plants. Hartman et al., (2011) noted that drought is among the major causes of reduced growth and also led to yield loss in soybeans. Current study results do not confirm the effect of low soil moisture as shortest plants were at Msekera that had the highest rainfall. The differences in ambient temperature at the locations during planting is the only plausible cause for the differences in plant height among the locations. GART had season temperature high of 25.2 ^{o}C compared to Msekera and Masumba that had of 31.6 ^{o}C and 35.5 ^{o}C , respectively. Temperature have been found to affect plant growth (Thuzar et al., 2010) and specifically high temperatures have been known to affect photosynthesis by way of damaging the photosystem ii found in the thyloid membranes of the chloroplasts, thereby reducing availability of photoassimilates needed for good growth (Hermantaranjani et al., 2014).

The differences observed among genotypes for plant height could be partly due to genetic differences and indeed to differential response to locational factors. The genotype differences behavior for soybeans attributed to inherent genetic factors and hereditary variation of the cultivars was found in the soybeans study by Kandil et al., (2012).

The other morphological trait studied was days to 50 % flowering. There were significant differences among locations and among genotypes for 50% flowering. Indeed, significant interactions were observed between genotypes and locations. The location Masumba had the shortest days to 50 % flowering while on the other hand, Kabwe had the longest days to 50% flowering. The soybean could have flowered early in Masumba due to the high temperatures

consistently recorded at the location during the farming season. These temperatures were seconded by temperatures at Msekera. Soybean is a thermo sensitive crop and its growth rate and blooming dates are affected by temperature from germination onwards (Junior et al., 2015). Avila et al., (2013) reported that temperatures above 30 degrees celsius during the vegetative stage hastens flowering.

5.2 Yield and yield components

The results showed significant differences for location and genotypes for the yield and the yield component seed size. There were however only significant differences for locations on the pods per plant. There are supposedly many reasons for the differences observed in yield since yield is a quantitative trait hence interplay of many factors are responsible for the differences (Herdaizade et al., 2016).

The locations in the study had major temperature differences over the growing season. The recorded high temperatures at Masumba followed by Msekera could be attributed to the lower yields (Avila et al., 2013; Boote et al., 2005) at these locations. Such temperatures induce heat stress that adversely affect soybean yields (Thuzar et al., 2010). Temperature requirements for soybean like in many other crops differ according to the stage of plant growth. Hemantaranjan et al., (2014) found that general crop yields are predicted to decrease approximately 10% for every one-degree increase in temperature above the optimum. Studies in cereals have also found that heat stress induces decrease of the duration of developmental phases leading to fewer organs, smaller organs, reduced light perception over the shortened life cycle and perturbation of the processes related to carbon assimilation (Stone, 2001.; Puteh et al., 2013). In the current study Masumba and Msekera had fewer numbers of pods compared to Kabwe and GART. Indeed temperatures at Masumba and Msekera were significantly higher than those at GART and Kabwe. These results are in agreement with Avila et al., (2013) who found that to obtain the greatest number of pods, soybeans needs mild temperatures of up to 26 degrees celsius and higher temperatures were found to reduce the number of pods, while still when above 30^{o}C reduce growth and hastens flowering during the vegetative stage and cause reductions in seed number and seed weight during the reproductive phase.

The observed 100 seed weight at Masumba, against the emerging negative effect of temperature on growth and development of soybeans suggest that enhanced flowering while

associated with reduced organs, seed weight was not negatively affected. Masumba and Msekera had the heaviest seeds. This could be attributed to sufficient photo assimilates available to the reduced sink (pods per plant) in the two locations. This assertion is in agreement with Liu et al., (2010) whose findings suggest that there is an increase in the seed size in the presence of reduced pod load in soybean. The results could be attributed to the internal mechanism that moderate the final seed size in soybean (Liu et al., 2010). The photosynthate would therefore have allowed optimal pod filling hence the highest weight. The relationship of the reduction of number of pods to the yield is consistent with other findings who reported that reduction of pods will directly lead to the reduction in yield since number of pods is one of the most crucial soybean yield components (Stone, 2001).

5.3 Characterisation of the Environments

The highly significant differences contributed by the environment indicate that Zambia is highly variable from location to location. The results are in agreement with the findings by Setimela.et al., (2007). These results justify the need for carrying out multi environment trials in the country for the genotypes. Besides the locations, there were significant differences among the genotypes which would suggest that genotypes are favoured by specific locations. The specificity of soybean genotypes to specific locations is consistent with the findings of Tukamuhabwa et al., (2012). The genotype by environment interactions showed significant differences for almost all the traits under study apart from pods per plant. The significant genotype by environment interactions especially on yield justified a study for mega environment identification. The study identified three mega environments in the two agro ecological regions studied. The existence of more than one mega environment in Zambia was also found in the maize studies by Setimela et al., (2007).

In essence all environments are useful provided they are discriminative as they can be used to select superior genotypes (Yan and Kang, 2003 and Yan and Tinker, 2006).

5.4 Characterisation of the genotypes

The check varieties Safari and Lukanga did not have a good overall mean performance relative to Magoye despite not having significant differences. Both varieties performed very well at Golden Valley Agricultural Trust (GART) and Kabwe research station. Among the reasons why these varieties performed very well could be the ideal environment conditions

for the two sites. The two genotypes (Lukanga and Safari) are not self nodulating (not promiscuous) hence the fact that they were not inoculated with rhizobium would explain their poor performance in poor environments in Msekera and Masumba.

The performance of IITA lines followed a particular pattern with regard to their pedigree. All the varieties had a bushy growth habit relative to the checks though similarities were more common to closely related genotypes. Genotypes TGX 1830-20E and TGX 1835-10E had poor germination across all locations. Despite the lower plant populations recorded, there was no compensatory growth observed for the above genotypes. These genotypes were the worst performing genotypes in the trials and ultimately the yield (Table 9). Their poor performance was more to their genotype as compared to the environment as shown in the GGE biplot analysis (Figure 5). The results showed that the two were least responsive genotypes to the environment. The other closely related genotypes which performed in a similar pattern were TGX 1987-11F and TGX 1987-23F, the genotypes performed consistently poorly across all the locations. The two genotypes are very closely related to TGX 1887-65 (Figure 2). The good performing genotypes TGX 1740-2F, TGX 1988-18F and TGX 1988-22F have close descent relations relative to the other genotypes in the trial. Very closely related to the above high performing three is TGX 1990-129F.

Though some of the IITA lines have been released in other countries as promiscuous soybean lines (Tefera, 2011), their performance in Zambia was not consistent to their performance elsewhere i.e. TGX 1835-10E and TGX-20E. The only IITA promiscuous variety which has been released in other countries and was able to perform well was TGX 1740-2F. The poor performance of the genotype. TGX 1835-10E was also found by other researchers (Ikeogu and Nwofia, 2013).

CHAPTER SIX

6.0 CONCLUSIONS

The study was carried out to identify the existence of soybean mega environments in two agro ecological regions of Zambia. The objective was achieved with the realisation of three mega environments in the two agro ecological regions studied. The mega environments identified were Kabwe/Msekera, GART and the last one was Masumba. The mega environment Kabwe/Msekera had TGX 1988-22F as the winning genotype, GART had safari as the winning genotype with genotypes TGX 1740-2F, TGX 1887-65F, TGX 1988-18F and Lukanga. Masumba recorded Magoye as the winning genotypes with four other genotypes showing good perfomance at the location, these genotypes were TGX 1904-6F, TGX 1990-129F ,TGX 1988-9F and TGX 1989-60F. The other genotypes viz TGX 1835-10E, TGX 1830-20E, TGX 1988-18F, TGX 1987-23F and TGX 1987-11F perfomed poorly across all locations. This shows that the genotypes are not suitable for the studied Zambian locations.

In the specific objective of identifying the environments capable of descriminating yield differences between the genotypes. The most descriminating and representative environment was identified and also the worst environment was identified. The most descriminating environment was kabwe and the worst environment was Masumba. Kabwe can therefore be recommended in cases were there is a resource constraint to be used as the sole site to carry out a soybean yield trial. On the other hand if there is need to reduce on the number of genotypes to be progressed in a multi environment trial, the site Masumba can be used for culling poor perfoming genotypes.

Characterisation of the perfomance of soybean and relating to the environments was done and achieved in the study. Perfomance of the genotypes varied across the locations mainly due to the environmental condition temperature and also due to the inherent genotype characteristics. The trial established that most of the yield variance in soybeans was due to the environment variance component. Thus it was possible to determine and group the locations from most suitable which was Kabwe, GART, Msekera and the worst location was Masumba. The inherent genetic perfomance of the genotypes was determined by a comparative reference of the field perfomance across and within locations of the genotypes to their pedigree information. Closely related lines had a similar response pattern in most of the traits studied.

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