STABILITY AND GENOTYPE BY ENVIRONMENT ANALYSIS FOR QUALITY, YIELD AND YIELD COMPONENTS OF SOYBEAN [*Glycine max* (L.)] LINES

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DECLARATION AND RECOMMENDATION

Declaration

I declare that this thesis is my original work and has not been presented before in any institution.

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Recommendation

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DEDICATION

This thesis is dedicated to my late father Mr. Ayub Njoroge and my mum Mrs. Dorcas Nyokabi Njoroge as well as my dear wife Minneh Muthoni, our children Grace Wanjiku, Charles Njoroge and Dorcas Nyokabi.

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ABSTRACT

Soybean [*Glycine max* (L.) Merrill.] Breeders' prefer genotypes with high grain yield along with high oil and protein content. Soybean in Kenya is important in the manufacture of feed, food and natural resource management. Availability of high yielding and stable varieties is among the constraints that limit adoption and production of soybean in Kenya. The objectives of the study were to determine the performance of fifteen soybean genotypes in five environments, the broad sense heritability for yield and its components as well as determine stable genotypes for yield, oil and protein content. A randomised complete block design was used for the study. Combined analysis of variance was done to get the performance of the genotypes. Broad sense heritability was estimated by variance component method. Additive main effects and multiplicative interactions (AMMI) then genotype and genotype plus environment (GGE) bi-plots were used to determine stable genotypes. The analysis of variance indicated environments, genotypes and genotype by environment interactions to be highly significant ($P < 0.01$) for traits studied. The mean seed yield was 1267.8 kg ha^{-1}. Genotype Nyala gave the highest seed yield of 1600.9 kg ha^{-1} while DPSB 3 (TGX 1835-10E) gave the lowest yield of 661.7 kg ha^{-1}. The mean oil content ranged from 166.0 g kg^{-1} - 219.0 g kg^{-1} for genotypes DPSB 19 and 931/5/34, respectively. The mean protein content ranged from 352.0 g kg^{-1} for genotype 931/5/34 to 403.0 g kg^{-1} for genotype DPSB 19 (TGX 1740-2F). Broad sense heritability was low for protein and oil content, pods per plant, number of branches, seed yield, and high for 50% flowering, plant height, number of seeds per pod and number of nodes per plant. Seed yield was positively correlated to oil content and negatively correlated to protein content while plant height was positively correlated to nodes per plant. Genotypes EAI 3600 and SBH 4/6/6 had stable yields above the mean while genotypes SBH 4/4/4, SBH 7/1/1, 1/12/9 and Gazelle were stable in yield and oil content. Because these genotypes are high in seed yield and oil content, they could be directly grown by farmers in the test environments or used in breeding programmes to develop new varieties.

Key words: Soybean, genotype by environment, stability, heritability.

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LIST OF ABBREVIATIONS AND ACRONYMS

AFLP	Amplified Fragment Length Polymorphism
ANOVA	Analysis of Variance
FAO	Food and Agricultural Organization
G × E	Genotype by environment
GoK	Government of Kenya
GTZ	German Technical Corporation
KARI	Kenya Agricultural Research Institute
KALRO	Kenya Agricultural and Livestock Research Organization
m.a.s.l.	Metres above sea level
MoA	Ministry of Agriculture
SAS	Statistical Analysis Software
SBH	Soybean Hybridization
DPSB	Dual Purpose Soybean
TGX	Tropical *Glycine* crosses
b_i	regression coefficient
Sd_i^2	deviation from regression mean square
IPCA	Interaction Principal Components Axis
GGE	Genotype Plus Genotype and Environment
PCA	Principal Component Analysis
AMMI	Additive Main Effects and Multiplicative Interactions
AEA	Average Environment Axis
AOE	Average Ordinate Environment axis
DUS	Distinctiveness, uniformity and stability
MET	Multi-environment Trials
MC	Moisture Content
RIL	Recombinant inbred line

CHAPTER ONE

1.0 Introduction

Soybean (*Glycine max* L.) is a legume classified in the genus *Glycine.* Soybean occupies an important position among grain legumes due to its economic importance (Dugje *et al.,* 2009) and high protein supplement (Agwu *et al.,* 2008). Importance soybean is due to its extraordinary qualities. It contains about 37-42% high quality protein, 29% carbohydrate and 17-24% oil, comprising 85% poly-saturated fatty acid with two essential fatty acids (linoleic and linolenic acid) and 6% ash, (Antalina, 2000; Balasubramaniyan and Palaniappan, 2003). Soybean meal is rich in phosphorous (P), calcium (Ca) and iron (Fe) (Ogoke *et al.,* 2003). In the international world trade market, soybean is ranked first among major oil crops such as rapeseed (*Brassica napus* L.), groundnut (*Arachis hypogea* L.), sunflower (*Helianthus annus* L.), linseed (*Linum usitassimum*), sesame (*Sesamum indicum* L.) and safflower (*Carthamus tinctorius* L.) (Chung and Singh, 2008). Soybean grows in a wide range of agro-ecological zones in Kenya and it contributes to food security, alleviation of poverty and has potential to contribute to bio-fuel energy (Chianu *et al.,* 2008).

The spread of soybean from South East Asia has been mainly due to its adaptability and predominant use as a food crop, feed, medicinal plant and as an industrial crop (Alghamdi, 1991). In Kenya most of the soybean goes to the animal feed industry (Tinsley, 2009). Crop yield fluctuates due to stability links of varieties to different growing seasons or environments. Environment is the sum total of external conditions which influence growth and development of an organism (Allard, 1960), and the performance of genotypes vary across environments (Tyagi and Khan, 2010). The different attributes of the environment include temperature, moisture supply, soil pH, humidity and light among others (Yau *et al.,* 1991). Inconsistent genotypic responses to environmental factors from location to location and year to year are a function of genotype by environment (G × E) interactions. Cultivar crossover interactions, and genotypic rank changes across environments are of importance in plant breeding and may slow down the selection process (Abdalla *et al.,* 1997). Identification of yield-contributing traits and knowledge of G × E interactions and yield stability are important for breeding new cultivars with improved adaptation to the environmental constraints prevailing in the target environments (Tyagi and Khan, 2010). Quantitative gene expression is subject to modification by environment and therefore expression of phenotype on genotype depends on environment (Kang, 1998). The development of new cultivars involves breeding of cultivars that are high yielding, tolerant and resistant to biotic and

abiotic stresses (Rao *et al*., 2002). Stable genotypes with traits that are resistant to certain biotic and abiotic stresses such as soybean mosaic virus, soybean rust (*Phakopsora pachyrhizi*), pH, water stress and nematodes among many others, have been developed and hence These stable genotypes are an important source of genes in a soybean breeding programme the need for search of such genotypes prior to setting up a breeding programme. Long term value of a genotype depends not only on its absolute productivity or the possession of some other desirable traits but also on its ability to maintain sufficient levels of these traits under different environmental conditions (Dejan *et al.,* 2008). While estimating heritability of components of a simple physiological yield model using final harvest data, Ntare and Williams (1998) reported that information on heritability and G × E interactions of integrated physiological traits linked with yield was vital to develop valuable selection scheme to improve yield of groundnut across environments. Heritability among traits differ within a population, heritability estimates of varying traits in addition to genetic correlation estimates among traits can be used to identify selection plans that maybe more effective than direct selection scheme (Rebetze *et al.,* 2002). Rajnesh *et al.* (2010) reported high broad sense heritability estimates for dry matter weight per plant and high genetic advance for number of pods per plant and plant height. Seed yield maybe increased by considering these traits having a good association between certain agronomic characters and seed yield. Availability of improved statistical tools to analyze and understand G × E interactions has now made it possible to develop improved cultivars for target environments and needs of the client based selection integrated with traditional plant breeding (Kang, 1998).

1.1 Statement of the Problem

Soybean varieties in Kenya have been released and recommended on the basis of yield performance across environments yet the concept of stable varieties has been overlooked over the years. Further, soybean yields are low and usually not consistent across the environments as shown by yields of 560 kg ha^{-1} in Eastern and 1100 kg ha^{-1} in Western Kenya (Chianu *et al.,* 2008). About 30% of Kenyans suffer from protein energy malnutrition (PEM) suggesting a need for a good supply of quality protein in the diet (Kwena and Baliddawa, 2012). Unlike most other protein-rich foods, soybeans can store for 2-3 years at room temperature without deterioration in food value (KARI report, 2005). Currently, about 6000-7000 tonnes of soybean are being produced in Kenya against an annual demand of 50,000 MT (Tinsely, 2009). The deficit is met through imports from external sources mainly

Uganda, Malawi, Argentina and Brazil. Climate variability is an important source of risk in soybean production since it affects yield variation and often leads to yield losses (Molua, 2009). Climate change heightens farm risks by influencing crop growth and development leading to reduced yields (Adams *et al.,* 1998). Effects from climate change may lead to increased frequency and severity of adverse weather events which would likely impact negatively on soybean production. This means it may be useful to select for stable soybean genotypes across environments to mitigate against reduced soybean production. Stable genotypes with the desired traits are useful as parents in a breeding programme. Heritability studies make the breeding process more efficient and focused as it allows for utilisation of the most appropriate breeding scheme.

1.2 General Objective

To improve soybean yields across different environments by identifying stable and high yielding genotypes in Kenya.

1.3 Specific Objectives

(i) To determine the response of soybean genotypes in terms of grain yield, days to flowering, days to harvest maturity, plant height, number of pods plant^{-1}, number of seeds pod^{-1}, number of branches plant^{-1}, number of nodes plant^{-1}, seed weight, oil and protein content in different environments.

(ii) To determine the broad sense heritability estimates of yield and yield components of the soybean genotypes.

(iii) To identify stable soybean genotypes in yield, oil and protein content and adaptable across different environments.

1.4 Hypotheses

(i) There is no uniformity in response in terms of yield and yield components among soybean genotypes in different environments.

(ii) There is no uniformity in heritability estimates for yield and yield components in soybean.

(iii) Soybean genotypes do not differ significantly in their stability and adaptability across different environments.

1.5 Justification

In Kenya soybeans production is done under rain fed conditions. There is considerable year to year variation in monthly rainfall often exceeding 100%. According to Tinsley (2009) there are substantial lulls in rains during the crops growing season that will stress the crops and reduce potential yields between years. Kenya is not immune to the impacts of climate change which is a change in the statistical properties of the climate system when considered over long periods of time regardless of cause (Hourton, 2001). The variation and unpredictability of rainfall patterns would make a change in climate that would necessitate to a change in varieties adapted to particular regions. Lack of consistent supply of high yielding varieties has been cited among the constraints that limit adoption of large scale production of soybeans in Kenya (Chianu *et al.,* 2008). This makes it necessary to develop stable varieties that can withstand changes in the environment. There is therefore need to initiate search for stable genotypes that are of high quality, adaptable and have stable agronomic traits. Identification of stable genotypes would reduce the need to produce new varieties in rapid succession thus reducing related breeding costs.

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CHAPTER TWO

LITERATURE REVIEW

2.0 Origin and botany of Soybean

Soybean [*Glycine max* (L.) Merr.] is a major legume crop worldwide that originated from Asia and has been grown for thousands of years (Tinsley, 2009). Cultivated soybean is believed to have been derived from a wild progenitor, *Glycine ussuriensis*, which occurs in East Asia. The plant was first domesticated in the 11th Century in North East China. The genus *Glycine* has two subgenera-*Soja* and *Glycine*. The subgenus *Soja* consists of two species: *Glycine max* (2n = 2x = 40), the cultivated species, and *Glycine soja* (L.) Sieb or *G. ussuriensis* (2n = 2x = 40), a wild species. These two species can be crossed and generate a fertile progeny. There are fifteen wild species of soybean of which *G. tabacinia* and *G. tomentella* have polyploidy forms (including 2n = 4x = 80) (Acquaah, 2009). Soybean is a sub-tropical plant grown in a wide range of ecological zones ranging from the equator to 52^{o} N.

Soybean is self-pollinated although < 1.0% natural cross-pollination occurs (Poehlman, 1987). Flowering is affected by temperature changes within the approximate range of 10-30^{o}C. Increasing temperature within this range hasten flowering and reducing temperature delays flowering (Poehlman, 1987). In a study involving backcross derived soybean isolines for three maturity genes E_1, E_2, and E_3 it was reported that reproductive development periods prior to and after flowering can be affected by the same gene in different directions (McBlain *et al*., 1987). Flowering was delayed 14.4, 5.4 and 2.7 days and 16.0, 6.6 and 5.5 days in controlled photoperiod and planting date experiments by E_1, E_2, and E_3, respectively. Maturity was delayed 16.1, 7.1 and 4.3 days and 10.8, 10.6 and 5.8 days in controlled photoperiod and planting date field experiments by E_1, E_2, and E_3, respectively. Morphological diversity exists, but the soybean plant generally grows 90-120 cm in height with the first leaves simple and opposite and all other leaves alternate and trifoliate (Norman, 1978).

Soybean grown for grain is classified into 13 maturity classes, ranging from 000, 00, 0 and roman numerals I to X. The 000 group consists of the earliest maturing cultivars while the X group consists of the latest maturing cultivars. Groups' 000-IV are considered indeterminate, while groups V-X are determinate cultivars (Acquaah, 2009). The maturity groups are assigned based on maturity data collected at Urbana (40^{o}07′N), Stoneville

(33°25′N), or Isabela (18°30′N). The time of maturity is affected by both the length of the photoperiod and temperature. Maturity group 000 is adapted to the highest latitudes generally greater than 49°N while maturity group X is adapted to very low latitudes of less than 15°N (Verma and Shoemaker, 1996). The group (X) is adapted to short days of the tropical regions on either side of the equator (Alliprandini *et al.,* 2009).

2.1 Soybean and Nitrogen Fixation

Symbiosis between leguminous plants and soil bacteria (rhizobia) is of considerable environmental and agricultural importance (Ogutcu *et al.,* 2009). Rhizobia are responsible for an estimated 180 x 106 tons per year of biological nitrogen fixation worldwide, which is equivalent to generation of resource equivalent to USD 160-180 billion (Saghal *et al.,* 2003). Fitting legume species into crop rotations is highly recommended to reduce the need for an expensive chemical nitrogen fertilizer that increases the total cost of production (Yusuf *et al.,* 2009). Soybean farming is one of the most cost effective ways in which small holder farmers can maintain soil fertility and yet reap other benefits like increased incomes (Osunde *et al.,* 2003). Biological nitrogen fixation has the advantage of being environmental friendly and therefore ideal for sustainable agriculture (Qi Cheng, 2008). Effectiveness in fixing atmospheric nitrogen makes soybean have little or no demand on soil nitrogen and actually spares the same for the subsequent crop in rotation or the companion crops in an intercrop. The biomass from soybean is also an important source of feed, green manure and mulch (Chianu *et al.,* 2008). Sanginga *et al.* (2003) estimated that soybean can fix between 44-103 kg N ha^{-1}. This can reduce the need for expensive and environmentally damaging nitrogen fertilizer (Zhang *et al.,* 2003). Nodulation and nitrogen fixation in soybean occurs effectively if other mineral elements such as Phosphorus (P), Potassium (K) and Sulfur (S) are present in the soil necessitating their constant addition in form of fertilizers to boost soil mineral nutrient level (Mugendi *et al.,* 2010). However, when using grain legumes that are traditionally grown in large parts of sub-Saharan Africa, a substantial part of the legume nitrogen fixed from the atmosphere is usually removed from the field through harvested grains and/or stover often resulting in marginally positive or even negative nitrogen balances (Vanlauwe *et al.,* 2003). This makes researchers make do with green manure legumes of which none or little harvested products are removed from the field (Vanlauwe *et al.,* 2003) e.g. *Mucuna pururiens* in West Africa (Verteeg *et al.,* 1998) or *Sesbania sesban* tree fallows in East Africa (Sanchez and Jama, 2002).

2.2 Importance of Soybean

Some soybean varieties mature early and are drought tolerant hence a food security crop. Soybean grains serve as raw materials in livestock feed industries, human food manufacturing outfits, edible vegetable oil processing industries, and recently as a source of bio-energy (Myaka *et al.,* 2005). Small scale home processing of soybean into various products also creates employment and enables households to increase their access to cash income thereby effectively contributing to poverty reduction (Chianu *et al.,* 2008). Studies indicate that consumption of soybean reduces cancer, blood serum cholesterol, osteoporosis and heart disease (Birt *et al.,* 2004). Soybean is also appropriate for people with lactose intolerance and it is known to ease the symptoms of menopause. People who suffer from digestive problems or diabetes also stand to benefit from soybean-based food (Greenberg *et al.,* 1998).

2.3 Global Soybean Production

Soybean is the world's leading source of oil and proteins (Fedaku *et al.,* 2009). The other sources are cotton seed (*Gossypium hirsutum*), sunflower seed (*Helianthus annus*), rapeseed *(Brassica napus*) and groundnuts (*Arachis hypogea* L.). Soybeans accounts for 90% of USA oilseed production (USDA, 2008). In 2011, soybean represented 56% of world oilseed production, and 33% of those soybean were produced in the United States. (http://www.soystats.com/2012). The nine major world producers in 2011 were United States of America (33%), Brazil (29%), Argentina (19%), China (5%), India (4%), Paraguay (3%), and Canada (2%) (http://www.soystats.com/2012). Increased use of biotechnologically modified planting materials such as roundup ready soybeans has had higher soybean yields and greater tolerance to soybean diseases and pests in USA, Argentina and Brazil (Jagwe and Nyapendi, 2004).

Soybean restores fertility of marginal soils (Nkhuzenje *et al.,* 2002) and this makes the crop suitable for production in Africa. Africa is a very small producer of soybeans compared to USA, South /Latin America and Asia. Africa accounts for 0.4-1% of total world production of soybean. Uganda (17%), South Africa (15%) and Zimbabwe (8%) are the main producers but Nigeria accounts for 50% of Africa's production. This was just 0.3 % of world production in 2003 (Chianu *et al.,* 2008).

2. 3.1 Soybean Production in Kenya

In Kenya vision 2030 policy document, agriculture has been identified as one of the sectors which will contribute to the pillar for economic growth. In Kenya soybean can grow at 0-2200 metres above sea level (m.a.s.l.) and rainfall regime of 300-1200mm (KARI, 2005). Western Kenya is leading in production accounting for almost 50% of total small holder planted area and production in 2003 when Butere/Mumias and Bungoma accounted for 80% of total soybean production in western province (Chianu *et al.*, 2008). Central and western provinces accounted for about 11-12% of total small holder production of soybean in 2003. Nyanza province accounts for 11-15% of Kenya land area potentially suitable to soybean cultivation. At County level, Uasin Gishu, Trans-Nzoia and Bungoma Counties account for the largest proportion of land potentially good for soybean production in Kenya (Chianu *et al.,* 2008).

During the five year period of 2009-2013 Kenya soybean production averaged 2770 tonnes annually with the highest production observed in 2011 when 4335 tonnes were produced (FAOSTAT, 2015). Depending on the agro-ecological zones, soybean varieties recommended by the GTZ SBP project (1993-1998) were expected to yield 0.6-1.9 tons ha^{-1} in the farmers' fields. Soybean production in Kenya is estimated at 5,000 tonnes per annum which does not meet the demand necessitating an estimated importation of 50,000-100,000 tonnes annually (Karuga and Gachanja, 2004).

2.4 Yield Components of Soybeans

Yield variation of cultivars across locations and years is associated with changes in number of seeds per unit area has been reported in soybean suggesting that yield component is largely determined during the period that begins from flowering to pod setting (Eglin, 1998). Exposure of soybean to extended photoperiods increased the number of nodes per plant and improved node fertility thus increasing the number of pods and seeds produced per unit area (Kantolic and Safler, 2005). Extension of the photo period by 1.5, 3, 4.5 or 6 hours reduced the average seed weight and these varied among the cultivars and the treatments. While investigating the effect of plant population on four legumes on yield and its components, Ayaz *et al*. (2004) reported that seed yields were positively correlated to number of pods and seed m^{-2} for all the species studied. Branches per plant were reduced nearly six fold as plant population increased. Although variation in yield was species dependent, in all species number of pods m^{-2} and seeds m^{-2} could be used as primary criteria

for selection in a breeding program. Seed size traits in soybean i.e. length, width and thickness and their corresponding ratios play a crucial role in determining seed appearance, quality and yield (Xu *et al.,* 2011). The number of pods, seed weight and seed number are the most important yield components of soybean. Leaf area index (LAI), Leaf area duration (LAD) and dry matter accumulation during the reproductive stage influence yield components (Xiaobing *et al.,* 2005).

2.5 Soybean Breeding in Kenya

Soybean germplasm evaluation started in 1993 under the GTZ project with 96 local and imported soybean varieties, which were tested for yields and management requirements, seed colour and height (Nassiuma and Wasike, 2002). The imported varieties were from regions that are similar to Kenya in latitude, but not necessarily in altitude such as Nigeria, Zimbabwe, Zambia and Ecuador on the basis of high yields. With the increasing demand for soybeans, it was prudent to evaluate the available varieties rather than embark on a crossing programme. In Kenya, the trials are conducted for the purpose of evaluating the performance of the final set of genotypes to allow the breeder to make a decision as to which genotype to release as a cultivar. The trials, referred to as advanced yield trials, are conducted for several years at different locations, using more replications than the preliminary trials (Acquaah, 2009).

2.6 Genotype by Environment Interaction

Genotype by environment (G × E) interaction has been defined as the differential performance of genotypes across environments to achieve the same relative performance in different environments (Baker, 1988). Genotype by environment interaction is a function of genotypic, phenological and physiological traits of varieties (Nachit *et al.*, 1992). Genotype by environment interaction describes the differential performance of genotypes across environments. The term G × E interaction commonly refers to yield variation that cannot be explained by the genotype main effect (G) or the environment main effect (E) (Rubio *et al*., 2004). Different statistical methods have been used to analyse multi-environment trials involving several cultivars to determine the nature of interactions. The reference model is the two-way analysis of variance (ANOVA) model with interaction. For a measured variate, $Y_{ge,}$ the model is written as:

$$E[Y_{ge}] = \mu + \alpha_g + \beta_e + \alpha\beta_{ge}$$

Where;

E [Y_{ge}] is the expectation of performance for genotype *g* grown in environment *e*, μ is the general mean , α_g is the genotype main effect, β_e is the environment main effect and $\alpha\beta_{ge}$ is the effect of the interaction between genotype and environments (Leflon *et al.,* 2005). Knowledge of the pattern and magnitude of G × E interaction and stability analysis is important for understanding the response of different genotypes to varying environments and for identification of stable and widely adapted and unstable but specifically adapted genotypes (Fekadu *et al.,* 2009).

In an experiment evaluating five soybean genotypes planted in six time periods over a two year period of 2000 and 2001, Alghamdi, (2004) concluded that G × E interaction plays a significant role in the success of any breeding program for development of genetically adapted to wide range of environments. The result of combined analysis of variance indicated that genotypes, years, sowing dates and their interactions were significant for seed yield and seed weight per plant. The mean squares due to environments, genotypes and G × E interaction were highly significant among the two traits indicating that genotypes respond differently with the environments. The highly significant differences detected among the tested genotypes, suggested the presence of genetic variability among the cultivars for the two agronomic traits. He also observed that the highest performing genotype was not stable hence selecting the best genotypes cannot be based upon the means alone, but the stability of these genotypes should be examined and that seed yield by itself may not be the best criteria for selection.

In an experiment to evaluate ten soybean genotypes (BAU-23, BS-12, BS-15, TGX-843, C.O.-1, AGS-160, Jupitar, BS-60, SAU-LUIZ and Sohag as a check) evaluated at different dates in Bangladesh in 1992-1993, Paul *et al*. (2003) considered five sowing dates in specific plots as single environments and observed twelve characters specifically days to 80% germination, plant height, number of pods per plant, number of seeds per pod, seed yield per plant, seed weight and harvest index. The results indicated that there was significant G × E interaction (linear) and deviation from regression (non-linear) for this trait. Most of the genotypes germinated early in first sowing and all genotypes were late in the fifth sowing. In all sowing dates, line BS-15 took minimum days to germinate (7.33) and the line TGX-843 took maximum days (8.73). Plant height was influenced by genotype, environment and G × E interaction.

Ahmed and Abdella, (2009) evaluated 19 locally developed sunflower (*Helianthus annus*) and an introduced one (Hysun, 33) in two consecutive seasons (2003/04 and 2004/05)

in order to estimate stability of performance for seed yield under irrigation. The G × E interaction was highly significant suggesting that the hybrids performed differently across environments for yield leading to the assessment of stability of performance for each of the twenty hybrids to identify hybrids with superior yields. The results indicated that hybrids Salih and Ka99 x 17 as most likely adapted hybrids to favourable environmental conditions for the yield was high, b_i above unity and Sd_i not significantly different from zero. The hybrids were below average in stability and thus sensitive to environmental changes and hence could be recommended for favourable environments. Bearing in mind that most climate–change scenarios suggest an increase in drought potential in many areas of the world, Dodig *et al.* (2008) examined relationships among agronomic traits and some drought indices with grain yield as influenced by genotype and environment. In a four year experiment, 100 cultivars and landraces of bread wheat (*Triticum aestivum* L.) from different countries were tested under three watering regimes. The additive main effects and multiplicative interaction (AMMI) models were used to study effects of G × E. The combined analysis of variance showed that 34.7% of the total variation in grain yield was explained by differences among genotypes, 32.5% by differences among treatments, and 2.2% by differences among years and 30.7% by G × E interaction. In this study, interactions between genotypes and years accounted for the largest portion of the total variance for G × E (51.5%) followed by year × treatment interactions (30.6%), genotype × year × treatment interactions (11.1%) and genotype × treatment interactions (5.8%).

2.7 Stability Evaluation

Stability is the ability of a genotype to have always the uniform yield regardless of environmental effects (Becker, 1981; Babic *et al.*, 2006). Several studies (Spraque and Federer, 1951; Federer and Sculli, 1993; Helms, 1993) concluded that genotypes of broad adaptability generally had a lower yield while those genotypes of a high yield had narrow adaptability. Generally a stable genotype will perform better than average across environments; such a type will respond to the richer environments, but will also do well in poorer environments. High yield stability usually refers to a genotype's ability to perform consistently, whether at high or low yield levels, across a wide range of environments (Annicchiarico, 2002). The ultimate reason for differential stability among genotypes and for differential results from various test environments is non-repeatable G × E interactions (Yan and Hunt, 2002). The yield and stability are regulated by different genes that provide tandem

selection for traits with simultaneous difficulties due to their inverse correlation (Babic *et al.*, 2006). There are several methods of assessing stability which include partitioning of variance, regression analysis, non-parametric analysis and multivariate techniques.

2.7.1 Analysis of Variance

Analysis of variance is commonly used for a mixed model, that is, fixed genotypes and random environments. The stability may be assessed by averaging of the variance components determined by pair-wise combination involving the genotype in question with every genotype in the trial and by determining the contribution of a genotype to the G × E interaction (Singh, 2005). In all the measures, the larger the estimate for a genotype the poorer is its general agronomic stability or adaptation (Singh, 2005). A combined analysis of variance detects G × E interactions when cultivars are evaluated in different environments. However, it does not describe the different responses of the individual cultivars to environment (Ngeve, 1993).

2.7.2 Multivariate Analysis

In multivariate techniques, yield data from G × E is subjected to pattern analysis which makes parallel use of classification and ordination techniques to present the maximum variation from G × E matrices in a few dimensions. The additive main effects and multiplicative interaction model (AMMI) is a hybrid analysis that combines additive and multiplicative components of the two way data structure. The additive portion is separated from interaction by ANOVA. The interactive principal analysis (IPCA) which provides a multiplicative model, then is applied to analyze the interaction effect from the additive ANOVA model (Mohammadi *et al.,* 2007). AMMI adjusted data with increased predictive precision can be analyzed further by methods of pattern analysis to study behavior of groups of environments and genotypes. AMMI adjusted data shows clear trends than analyses of raw data (Gauch and Zobel, 1996; Adugna, 2007; Sadeghi *et al.*, 2011). Holcomb *et al.* (1977) used the AMMI method to verify the *indica- japonica* grouping of rice (*Oryza sativa*) entries within and among countries. Bartual *et al.* (1985) also used multivariate analysis to classify 125 soybean lines into groups on the basis of physiological maturity, seed quality and productive traits to determine which groups were better suited to specific ecological conditions and found out that late maturing varieties belonging to maturity group III showed best adaptation to the ecological conditions of the area when soybeans were sown at early planting dates. Adguna, (2007) used the multivariate approach (AMMI model) to confirm

results obtained from three univariate stability models in stability of sorghum genotypes. The AMMI analysis of variance for grain yield of the 15 genotypes in the eight environments revealed that 73.8% of the total sum of squares was attributable to environmental effects, 5.9% to genotype effects and the remaining 20.3% was due to G × E effects. There were inconsistencies with the univariate stability estimates but the AMMI model was better for portioning the G × E into causes of variation. Mwamburi and LaBonte, (2010) used multivariate analysis, in this case to select AFLP molecular markers associated with β-carotene in sweet potatoes. They used cluster analysis (Macharo *et al.,* 2004), discriminant analysis and logistic regression (Uen *et al.,* 2007; Du *et al.,* 2009). Logistic regression selected 8 markers less than that were associated with β-carotene content compared to discriminant analysis.

The concept of stability is often overlooked when breeders look for genotypes that yield well across a number of environments and years. This kind of approach is acceptable if there is no G × E interaction but more often than not, the interaction is there (Fedaku *et al.,* 2009). Some genotypes can have high yield in few environments and very low yield in other environments and hence the knowledge of the pattern and magnitude of G × E and stability is important for understanding the response of different genotypes to varying environments and for identification of stable and widely adapted genotypes. The information is important for breeding cultivars with improved adaptation to the environmental constraints prevailing in the target environments. Bekheit (2000), evaluated fifteen soybean genotypes during three seasons under three sowing dates. The results showed that high yielding genotypes were more likely to have low stability and vice versa low yielding genotypes tend to have high stability at different environments. Selection of genotypes based on the highest yielding genotypes appeared less stable than the average of all lines (Gebeyehu and Assefa, 2003). It can be concluded that soybean breeders should consider environmental conditions and general stability as a criteria for selecting high yielding genotypes (Alghamdi, 2004).

2.8 Heritability in Soybeans

In a breeding program, the response to selection, and hence its efficiency, depends on the ability to predict the genotype from the observation of the phenotype. A number of molecular techniques will make it possible to select directly on the basis of the genotypic values as indicated by the presence of a suitable marker, or by the expression of the desirable allele(s) (Oyoo *et al.,* 2010). Currently most plant breeding programs still depend on how

closely the phenotype is a measure of the genotype, and this in turn depends on the magnitude of environmental effects, number of observations and size of genetic variance (Al-Yassin *et al.*, 2005). In the case of quantitative traits, a measure of the relationship between genotype and phenotype is the heritability (Al-Yassin *et al.*, 2005).

In crop breeding, only the additive genetic component of variation is important since only the genetic component is transmitted to the next generation. The extent of contribution of genotype to the phenotypic variation to a trait in a population is ordinarily expressed as the ratio of the genetic variance to the total variance. Broad sense heritability is normally higher than narrow sense heritability since it estimates heritability on the basis of all genetic effects (Poehlman, 1987). Broad sense heritability denotes the proportion of phenotypic variance that is due to genotype (Singh, 2005) as given below:

$$H^2 = \frac{\delta^2 g}{\delta^2 p} = \frac{\delta^2 g}{(\delta g + \delta^2 e)}$$

Where: H^2 = broad sense heritability; $\delta^2 g$ = variance due to genotype; $\delta^2 e$ = variance due to the environment; $\delta^2 p$ = variance due to the phenotype.

The environmental variance is dependent on the conditions of culture or management: more variable conditions reduce the heritability; more uniform conditions increase it. Hence, a heritability value stated for any character should be understood to refer to a particular population under particular conditions (Falconer, 1985).

There are various methods of calculating heritability such as variance component method, parent off-spring regression method and molecular-marker based (Mousseau *et al.*, 1998) among others and therefore the values obtained by the various methods differ slightly. For the variance component method, heritability uses the statistical procedure of ANOVA. Heritability is described on a single plant basis, a plot or entry mean basis (Walter, 1987). The equation used in calculation of heritability on entry-mean basis is as indicated below:-

$$H^2 = \frac{\delta g}{\frac{\delta^2 e}{rt} + \frac{\delta^2 ge}{t} + \delta g}$$

Where: H^2 = broad sense heritability; $\delta^2 e$ = experimental error; $\delta^2 g$ = genetic variance; $\delta^2 ge$ = genotype by environment interaction; r = number of replicates; t = number of test environments.

The parent-offspring regression method is based on several assumptions: the trait of interest has diploid Mendelian inheritance; the population from which the parents originated is randomly mated; the population is in linkage equilibrium; parents are non-inbred; and

there is no environmental correlation between the performance of parents and offspring. The heritability estimate is computed by first obtaining the parent and offspring means. Cross products of the paired values are used to compute the covariance (Acquaah, 2009). A regression of offspring on mid parent value is then calculated as follows:

$$h^2 = \mathrm{b_{op}} = \frac{\delta^2 \mathrm{A}}{\delta^2 \mathrm{P}}$$

Where:

b_{op} = the regression of the offspring on mid-parent value

$\delta^2 A$ = the additive variance

$\delta^2 P$ = the phenotypic variance

Incase only one parent is known or relevant;

$$b = \frac{1}{2}\left(\frac{\delta^2 A}{\delta^2 P}\right)$$

Where:

$h^2 = 2\ b_{op}$

In an experiment involving 25 soybean genotypes in Islamabad, Malik *et al*. (2006) using the component method observed high heritability in seed weight, days to maturity, days to flowering completion, days to pod initiation, leaf area, days to 50% flowering, oil contents and protein content respectively indicating the additive type of gene action. Moderate heritability (0.67, 0.65, 0.68, 0.67 and 0.65) was noted for pods per plant, branches per plant, unfilled pods per plant, and shattered pods per plant and grain yield per plant. Ramteke *et al*. (2010) in a trial composed of 92 genotypes observed high heritability for days to maturity, days to 50% flowering, plant height, oil and protein content implying these characters would respond to any intense selection exercise and would result in improvement in soybean for these characters.

2.9 Soybean Oil and Protein

Soybeans are desired as a valuable source of protein and oil. The major factors affecting soybean quality are protein and oil contents, the chemical components of protein and oil and seed appearance (Liu *et al.,* 1995). Protein is used for feed and food while the oil is incorporated into food, feed and some industrial applications such as bio-diesel. Protein and oil percentages in soybean, while influenced by genotype and environment, averages about 40% and 20%, respectively (Clemente and Cahoon, 2009). There is an inverse relationship between total protein and oil contents in soybean where 1% reduction in total oil

lead to 2% increase in total protein content. The regulation of carbon flux during embryogenesis is impacted by both genetics and environment (Swchender *et al.*, 2003). The location of seeds on the plant can impact carbon flux during embryogenesis with pods positioned at the top of the plant having seeds with higher percentage of protein and lower oil content than those positioned at the bottom (Bennett *et al*., 2003). Application of nitrogen at various stages of growth has not proven effective in improving the protein and oil concentration in soybean (Schmitt *et al.,* 2001) but hydroponic trials indicate that external sources of nitrogen can increase soybean protein concentration. Soybean dependent on nitrogen fixation, produced seeds with a protein content of 35% while those supplemented with 6 mM of potassium nitrate (KNO_3) gave seeds with 41% protein (Paek *et al.,* 1997). A supply of 30 mM of KNO_3 increased the protein content by 28% in a soybean cultivar that exhibited normal seed protein content (Nakasathien *et al.,* 2000). These trials indicate the potential for increasing protein quantity by increasing nitrogen availability to the plant (Bennett *et al.*, 2003).

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CHAPTER THREE

PERFORMANCE OF SOYBEAN [*Glycine max* (L.) Merrill] GENOTYPES FOR AGRONOMIC AND QUALITY TRAITS ACROSS DIFFERENT ENVIRONMENTS

Abstract

Soybean [*Glycine max* (L.) Merrill] is one of the important legume oil crops that grow in tropical, sub-tropical and temperate climates. The study was conducted in five environments to evaluate soybean [*Glycine max* (L.) Merrill] genotypes for agronomic traits, quality, yield and yield components. There were significant (P <0.01) effects due to genotype and genotype × environment interaction for flowering, maturity, plant height, number of pods^{-1}, nodes plant^{-1}, number of seeds pod^{-1}, seed yield, seed weight, oil and protein content. Variety Nyala produced the highest yield of 1600.9 kg ha^{-1} while low yield was observed on variety DPSB 3 at 661.7 kg ha^{-1}. Yield was significantly and positively associated with seed weight (r = 0.58*) and oil content (r = 0.68**) but negatively correlated to protein content (r = 0.67**). The mean oil content ranged from 166.0 g kg^{-1} for genotype DPSB 3 to 219.0 g kg^{-1} for genotype 931/5/34. Mean protein content was between 352.0 g kg^{-1} and 403.0 g kg^{-1} for genotype 931/5/34 and DPSB 19, respectively. Protein content was significantly ($P \leq 0.01$) and negatively correlated to seeds pod^{-1} and oil content. High oil content was observed in all genotypes at Nakuru West while high protein content was observed at Njoro A in all genotypes except SBH 7/1/1 and SBH 4/4/4.

3.0 Introduction

Soybean [*Glycine max* (L.) Merrill] is one of the important legume oil crops that grow in tropical, sub-tropical and temperate climates (Amira *et al.,* 2013). It grows well in maize growing areas in the tropics (Ojo, 2003). The demand for soybean is likely to increase as the crop has the potential to improve dietary quality of human food and animal feed worldwide (Hartman *et al.*, 2011). Multi-environment trials are conducted to identify high yielding varieties and ecologies that best represent the target environment (Yan *et al.,* 2001). The interaction between genotypes and environments results in significant influences of environment on the performance of genotype (Gauch and Zobel, 1997). Differential response of genotypes across environments aid breeders to select genotypes for specific environments and those that are widely adapted (Arslanoglu and Aytac, 2010). While evaluating genotype × environment interaction (G × E) for iron (Fe) deficiency, Naeve and Rehm (2006) observed significant G × E for yield, with soil factor creating a larger impact than year to year

variation. In a study involving ten soybean genotypes, Paul *et al*. (2003) revealed significant G × E for germination, plant height, number of pods plant^{-1}, number of seeds pod^{-1}, seed yield plant^{-1}, seed weight and harvest index (HI). Due to varying regional ecological conditions, there is need to test genotypes in order to detect environmental effects and identify specific or non-specific adaptable genotypes.

Evaluation of eight soybean genotypes across environments over two years showed variable response for plant height, first pod height, pods plant^{-1}, seeds pod^{-1}, seed weight seed yield and isoflavones content (Hoeck *et al.,* 2000; Karasu *et al.,* 2009). At seed development stage, high temperatures decrease total amounts of accumulated isoflavones (Caldwell *et al.,* 2005, Lozovaya *et al.,* 2005; Murphy, 2007). In a study involving 35 genotypes across 10 environments over two years in 2005 and 2006, Murphy *et al.* (2009) demonstrated that isoflavone content is influenced by the environment and also observed significant effects due to genotypes, environments and G × E interactions for total isoflavone content. Primomo *et al.* (2002) investigated influence of environment on soybean fatty acids and found significant genotype × year interaction for all fatty acids. The objective of this study was to determine the response of soybean genotypes for grain yield, days to flowering, days to harvest maturity, plant height, number of pods plant^{-1}, number of seeds pod^{-1}, number of branches plant^{-1}, number of nodes plant^{-1}, seed weight, oil and protein content in five environments.

3.1 Materials and Methods

3.1.1 Experimental Sites

The study was conducted in Njoro (0^{o} 20′S, 35^{o} 56′E) at early and late planting (Njoro A and Njoro B), Eldoret (0^{o} 35′N and 35^{o}18′E), Nakuru West (0^{o} 33’S and 36^{o} 0’E) and KALRO-Lanet (0^{o}18′S and 36^{o} 09′E). Njoro [2185 metres above sea level (m.a.s.l.)] is situated about 200 km West of Nairobi in Nakuru County. Njoro experiences an average daily minimum temperature of 9.5^{o}C and maximum temperature of 24.2^{o}C with an average precipitation of 1032 mm (average of 20 years 1992-2012 weather station number 903502). The soils are mollic andosols in eco-zone III (Jaetzold *et al.,* 2010). Eldoret (2154 m.a.s.l.) is located in Uasin Gishu County (FAO/UNESCO, 1994) and the soils are predominantly acidic (pH 4.7) rhodic ferrasols that are low in organic matter and deficient in nitrogen (N) and phosphorus (P). KALRO-Lanet is 16 Km South East of Nakuru town at an altitude of 1920 m.a.s.l. Rainfall pattern in Lanet is bimodal with an annual mean of 800 mm. The minimum

and maximum temperatures are 10^{o}C and 26^{o}C (http://www.kalro.org). Nakuru West is elevated to an altitude of 2003 m.a.s.l. and is on wind ward side overseeing Lake Nakuru.

3.1.2 Genotypes evaluated

Fifteen soybean genotypes were used in this study. Eight genotypes were developed through hybridization between early and medium maturing genotypes and introduced germplasm (SBH lines). Genotype EAI 3600, a medium maturing variety was used as a check. Genotype TGX 1835-10E (DPSB 3) was introduced from Nigeria and is known to be resistant to Asian soybean rust (*Phakospora pachyrrhizi)*. Genotypes TGX 1895-33F (DPSB-8) and TGX 1740-2F (DPSB-19) are promiscuous with indigenous nodulating bacteria and have high biomass traits that can aid in improvement of poor soils.

3.1.3 Experimental procedure

The seed bed was disc ploughed once and disc harrowed twice in order to achieve a tilth suitable for planting soybean. Planting was done on 13th June 2011 at Njoro(Njoro A), 22nd June at Nakuru West, 8th July 2011 at Lanet, 14th June 2011 at Eldoret and on 15th July 2011 at Njoro in the late planting (Njoro B). The experiment was laid out in a randomized complete block design (RCBD) with three replicates. At each location, the genotypes were planted in plots measuring 3 m × 2.7 m. Seeds were planted at an average depth of 5 cm at a seed rate of 75 kg ha^{-1} and spaced at 45 cm between rows and 10 cm within row. At planting time Diamonium phosphate fertilizer (DAP) was applied by placing and mixing with soil in the furrow to supply 22 kg of N ha^{-1} and 57.5 kg of P ha^{-1}. Immediately after planting, a pre-emergent herbicide (*Metribuzin*) was applied at the rate of 360 g ha^{-1}. Soybean seedlings were thinned to leave a space of about 10 cm within the row when the soybean had the first trifoliate leaf fully open. Weeding was done manually when weeds appeared after the effect of the herbicide waned off. Foliar fungal diseases were controlled by application of *Tebuconazole* at the rate of 250 g ha^{-1} weekly. This was done at flowering until the crop was at stage R7 (Fehr and Caviness, 1977).

3.1.4 Data collected

Time to flowering was taken at stage R2 when 50% of the plants had at least one open flower while plants were considered mature at stage R8 when 95% of the pods had changed colour from yellow to brown (Fehr and Caviness, 1977). Mean plant height at maturity was determined from five randomly selected plants from each plot by measuring

from ground level to the tip of stem. The number of nodes plant^{-1}, number of pods plant^{-1} and number of branches plant^{-1} were determined from five randomly selected plants from the four center rows. The mean of twenty randomly selected pods were counted and considered as the number of seeds pod^{-1}. The weight of 100-seeds was observed from a sample of 100 seeds from each treatment. Oil and protein content was estimated from soybean seeds using Near Infra-red Refractometer (NIR) grain analyzer (Infratec ^{TM} 1241 Grain Analyzer ISW 3.20: Foss Analytical AB, SE-2632 21 Hoganas, Sweden).

3.1.5 Data analyses

Bartlett's test was used to determine the homogeneity of variances between environments to determine the validity of the combined ANOVA. The combined ANOVA was done to estimate the effects of genotype, environment and genotype × environment interaction for yield, yield components and quality components using the SAS software (SAS institute version 8.1) proc GLM procedure. The genotypes were considered as fixed while the environments were considered random. The model for the experiment used was

$$Y_{ijkl} = \mu + E_i + RE_{(j)i} + G_k + GE_{ki} + \mathcal{E}_{ijkl}$$

Where:

μ is the general mean, E_i is effect due to the i^{th} environment, $RE_{(j)i}$ is effect due to the j^{th} replicate in the i^{th} environment, G_k is effect due to the k^{th} genotype in the j^{th} replicate, GE_{ik} is the effect of the k^{th} genotype in the i^{th} environment, $\mathcal{E}_{ijkl}$ is the random error effect due to the j^{th} replicate of the k^{th} genotype in the i^{th} environment.

Means for main effects were separated using Least Significant Difference (LSD) at ($P < 0.05$) using the following formula (Gomez and Gomez, 1984).

$LSD_{0.05} = t_{0.05}\sqrt{2ems/r}$

Where: ems = variance due to error; r = replicates

3.2 Results

3.2.1 Combined analyses of variance

The combined analysis of variance indicated that there were significant ($P < 0.01$) effects due to genotype (G), environment (E) and genotype × environment (G×E) interactions for all traits (Table 3.1). The highest yield (Table 3.2) was observed on the cultivar Nyala (1600.9 kg ha^{-1}) whose performance was not significantly different from that of SBH 7/1/1. Genotype Nyala produced 14% more grain yield than the check genotype EAI 3600.

Genotype 931/5/34 (47.1) had the highest number of pods plant^{-1} which was not significantly different from those of genotypes SBH 3/8/4/1 and SBH 6/6/6/2. The number of pods plant^{-1} was least in the check genotype EAI 3600 (32.5). There was limited variation in the number of pods plant^{-1} as 66.7 % of the genotypes had high number of pods plant^{-1} and were not significantly different from each other. The highest number of seeds pod^{-1} was recorded for genotypes SBH 10/5/6, SBH 1/12/9, SBH 7/1/1, SBH 4/4/4, SBH 4/6/6, SBH 6/6/6/2, DPSB 8, 931/5/34 and SBH 3/8/4/1. These were not significantly different from those of the check genotype. Genotype DPSB 3 had least number of seeds pod^{-1}, lowest seed weight and oil content (166.0 g kg^{-1}). It took longest time to flower (100.9 days) and mature (194.2 days). Although it produced most branches (7.2) plant^{-1} it had the least grain yield (661.7 kg ha^{-1}). Grain yield varied among the genotypes and environments (Table 3.2). Oil content ranged from 219.0 g kg^{-1} as observed on genotype 931/5/34 to 166.0 g kg^{-1} as detected on genotype DPSB 3 (Table 3.2). The check genotype had an oil content of 200.2 g kg^{-1} which was not significantly ($P > 0.01$) different from those of genotypes SBH 10/5/6, SBH 7/1/1 and SBH 4/4/4. Genotype 931/5/34 had the highest oil content which was 4.7% more than that of the check genotype.

Genotype DPSB 19 was earliest in flowering (74 days) and maturity (141 days). The latest maturing genotype (DPSB 3) flowered in 101 days and matured in 194 days. Significant ($P < 0.01$) differences were observed in plant height among the genotypes which ranged from 55.3 cm for genotype 931/5/34 to 95.8 cm for genotype DPSB 8. Genotype DPSB 8 also had a high number of seeds pod^{-1} and number of nodes plant^{-1}. The shortest genotype (931/5/34) was observed to have the same number of seeds pod^{-1} as the tallest genotype (DPSB 8) which had 2.4 seeds pod^{-1}. However, genotype 931/5/34 had significantly ($P < 0.01$) lower number of nodes plant^{-1} at 12.3 compared to DPSB 8 which had 16.3 nodes plant^{-1}.

Table 3.1. Mean squares for seed yield and yield components and other traits of fifteen soybean [*Glycine max* (L.)] evaluated in Njoro, Lanet, Eldoret and Nakuru West in 2011.

Source of Variation	df	Flowering (days)	Maturity (days)	Plant height (cm)	Pods plant^{-1} (No.)	Seeds Pod^{-1} (No.)	Branch Plant^{-1} (No.)	Nodes Plant^{-1} (No.)	Yield (Kg ha^{-1})	Seed weight (g)	Oil content (g kg^{-1})	Protein content (g kg^{-1})
Env. (E)	4	1120.60 **	10411.87**	6458.81**	6203.01**	0.43**	36.42**	94.15**	4983331.16**	97.68**	134.68**	649.34**
Reps (Env.)	10	8.71	67.96	70.25	120.93	0.04	1.40	1.64	77842.17	1.62	0.81	6.88
Genotype (G)	14	714.72**	3774.52**	2996.69**	339.60**	0.21**	6.68**	59.85**	933486.56**	71.41**	6.98**	26.31**
G × E	56	30.24**	142.55**	439.69**	251.51**	0.08**	1.45**	8.64**	227898.57**	5.53**	0.97**	4.65**
Error	140	4.91	36.75	37.41	48.97	0.04	0.48	1.24	50436.56	1.81	0.39	3.02
CV %		2.64	3.72	8.72	17.83	8.79	12.64	8.29	17.71	9.85	3.23	4.61
R^2		0.95	0.95	0.94	0.86	0.62	0.83	0.90	0.86	0.87	0.94	0.88

** Significant (P < 0.01).

Table 3.2 Mean of yield, quality and other agronomic traits of fifteen soybean [*Glycine max* (L.)] genotypes evaluated in Njoro, Lanet, Eldoret and Nakuru West in 2011.

Genotype	50% Flower (d)	Harvest maturity (d)	Plant height (cm)	Number of pods plant $^{-1}$	Number of seeds pod^{-1}	Number of branches plant^{-1}	Number of nodes plant^{-1}	Seed yield (kg ha^{-1})	Oil content (g kg^{-1})	Seed weight (g)	Protein content (g kg^{-1})
SBH 10/5/6	79.00	158.20	87.37	35.25	2.38	5.37	15.68	1303.46	204.70	13.33	365.80
SBH 1/12/9	79.80	155.27	78.07	40.58	2.35	5.37	14.44	1434.70	196.30	12.60	370.30
SBH 7/1/1	79.60	162.53	87.88	39.43	2.38	5.00	16.84	1543.95	201.30	12.87	367.70
Gazelle	89.27	168.47	81.60	32.88	1.99	5.69	14.81	1327.53	198.90	17.47	360.90
SBH 4/4/4	79.20	156.73	85.65	33.85	2.39	4.55	15.08	1367.42	202.60	12.80	368.50
SBH 10/2/3	83.07	154.20	60.47	39.80	2.29	5.69	11.43	1124.93	196.60	14.47	387.70
SBH 4/6/6	82.60	153.80	62.08	37.25	2.31	5.89	11.12	1289.49	197.30	14.40	384.10
Nyala	84.30	174.53	60.73	46.12	2.21	5.52	13.42	1600.87	194.80	17.60	372.00
EAI 3600	83.20	155.80	66.25	32.57	2.43	5.63	11.36	1375.19	200.20	14.13	377.60
SBH 6/6/6/2	80.60	151.13	57.77	43.21	2.30	5.52	11.34	1197.65	192.10	12.20	378.50
DPSB 8	91.67	185.07	95.84	37.47	2.43	4.89	16.25	1414.82	179.60	12.33	380.30
DPSB 19	74.00	140.53	59.64	37.85	2.25	4.32	12.48	807.91	170.10	10.67	402.80
931/5/34	93.07	188.93	55.33	47.13	2.43	5.89	12.32	1323.33	218.80	16.67	352.01
DPSB 3	100.93	194.20	57.16	39.05	2.14	7.20	13.75	661.73	165.90	10.47	391.70
SBH 3/8/4/1	80.60	147.33	56.84	46.35	2.31	5.36	11.12	1243.46	191.80	12.93	389.80
Mean	84.05	163.12	70.18	39.26	2.30	5.46	13.43	1267.76	194.10	13.66	376.60
CV%	2.64	3.72	8.71	17.83	8.79	12.64	8.29	17.71	3.23	9.85	4.61
$LSD_{(0.05)}$	1.60	4.38	4.41	5.05	0.15	0.49	0.80	162.12	0.45	0.97	1.25

The means for number of branches plant^{-1} were significantly different. Although genotype DPSB 3 produced the least grain yield, this genotype was observed to have the highest number of branches plant^{-1} (7.2). Genotype DPSB 19 had the least number of branches plant^{-1}(4.3) and had a low yield of 807.9 kg ha^{-1} compared to the check. Protein content was highest (403.0 g kg^{-1}) in genotype DPSB 19. This was not significantly different from that of DPSB 3 (392.0 g kg^{-1}). The lowest protein content of 352.0 g kg^{-1} was observed on genotype 931/5/34. This was lower by 6.8% that of the check genotype EAI 3600 (378 g kg^{-1}).

3.2.2 Comparison of traits across environments

The mean values of traits studied differed significantly across the five environments. However, there were no significant differences in the performance of some traits in certain environments. Days to flowering were not significantly different between Nakuru west and Lanet (Table 3.3). The mean numbers of pods plant^{-1} were not significantly different in Njoro A, Njoro B and Lanet (Table 3.6). The number of seeds pod^{-1} was not significantly different in Nakuru West and Lanet (Table 3.6) while the mean seed yield was not significantly different in Njoro A and Lanet (Table 3.5). There were no significant differences observed in seed weight at Nakuru West, Njoro A and Njoro B (Table 3.8). Oil content was highest at Nakuru West (229.0 g kg^{-1}) while Njoro (A and B) expressed the least oil content at 182.0 and 179.0 g kg^{-1}, respectively (Table3.7). The mean protein content was not significantly different in Njoro A and B (Table 3.7). The least mean protein content (311.0 g kg^{-1}) was expressed by genotypes at Nakuru West (Table 3.7). Mean days to maturity, plant height and nodes plant^{-1} were significantly different among environments.

Generally the genotypes evaluated flowered and matured late in Njoro A with a mean of 91.2 and 182.2 days, respectively (Table 3.3). However, the genotypes flowered slightly earlier at Lanet than in Nakuru West at 79.2 and 79.6 days respectively. Genotypes took longer to mature at Lanet than in Nakuru West by 20 days. Plant height and number of nodes plant^{-1} were higher in Njoro and Lanet but were lower in Nakuru West and Eldoret (Table 3.4 and 3.5). The check genotype had a mean height of 66.3cm which was lower than the overall mean plant height (70.2 cm) by 5.6%. Generally, soybean genotypes produced more branches plant^{-1} in Njoro than in the other test environments. An average grain yield of 895.5 kg ha^{-1} was realized in Nakuru west which was the least among all environments (Table 3.5). The

Table 3.3. Means of days to flowering, days to harvest maturity and plant height of soybean [*Glycine max* (L.)] genotypes evaluated in Njoro, Lanet, Eldoret and Nakuru West in 2011.

	Days to flowering						Days to maturity					
			Nakuru	Njoro					Nakuru	Njoro		
Genotype	Eldoret	Lanet	West	A	B	Mean	Eldoret	Lanet	West	A	B	Mean
SBH 10/5/6	82.00	75.00	75.33	85.33	77.33	79.00	142.00	162.00	136.33	181.67	169.00	158.20
SBH 1/12/9	84.00	75.67	74.67	87.67	79.00	79.80	133.33	157.67	137.67	184.67	163.00	155.27
SBH7/1/1	4.00	75.67	74.00	87.67	76.67	79.60	141.67	173.33	139.00	184.00	174.67	162.53
Gazelle	93.33	82.00	82.67	103.67	84.67	89.27	153.33	165.67	145.00	196.67	181.67	168.47
SBH 4/4/4	81.33	75.00	75.67	87.33	76.67	79.20	142.00	157.33	137.33	181.67	165.33	156.73
SBH 10/2/3	83.00	79.67	78.00	88.33	86.33	83.07	136.00	163.00	137.00	170.00	165.00	154.20
SBH 4/6/6	84.00	79.33	77.67	88.33	83.67	82.60	137.00	159.00	137.00	159.00	177.00	153.80
Nyala	85.67	81.33	80.00	92.00	81.67	84.30	165.67	166.00	164.00	195.00	182.00	174.53
EAI 3600	83.00	80.33	79.00	89.67	84.00	83.20	138.67	162.67	137.33	176.67	163.67	155.80
SBH 6/6/6/2	83.67	75.67	76.33	87.00	80.33	80.60	134.00	165.00	133.33	161.67	161.67	151.13
DPSB 8	92.67	83.67	91.00	102.00	89.00	91.67	185.33	183.00	165.33	208.00	183.67	185.07
DPSB 19	75.67	70.33	74.00	80.67	69.33	74.00	127.33	145.00	129.33	159.67	141.33	140.53
931/5/34	96.00	84.00	92.67	98.00	94.67	93.07	188.00	189.33	179.00	196.67	191.67	188.93
DPSB 3	103.33	95.00	88.00	104.33	114.00	100.93	191.00	193.33	172.00	216.67	198.00	194.20
SBH 3/8/4/1	83.33	75.67	75.33	88.33	80.33	80.60	136.00	145.67	133.67	160.33	161.00	147.33
Mean	86.33	79.22	79.62	91.22	83.84	84.05	150.09	165.87	145.55	182.15	171.91	163.12
C.V.% 2.6							C.V.% 3.7					
LSD[a] 3.666							LSD[a] 10.057					
LSD[b] 3.576							LSD[b] 9.7					

LSD [a]- for comparing any two genotypes means across environments.
LSD [b] - for comparing genotypes means within the same environment.
C.V. % - coefficient of variation across environments.

Table 3.4. Mean of plant height and number of branches per plant of soybean [*Glycine max* (L.)] genotypes evaluated in Njoro, Lanet, Eldoret and Nakuru West in 2011.

	Plant height (cm)						Number of branches Plant^{-1}					
			Nakuru	Njoro					Nakuru	Njoro		
Genotype	Eldoret	Lanet	West	A	B	Mean	Eldoret	Lanet	West	A	B	Mean
SBH 10/5/6	64.47	94.93	60.40	99.40	117.67	87.37	5.13	4.80	4.80	7.13	5.00	5.37
SBH 1/12/9	60.80	98.07	61.47	107.20	62.80	78.07	5.07	4.60	4.67	7.27	5.27	5.37
SBH7/1/1	64.80	96.13	59.00	104.40	115.07	87.88	5.80	3.53	4.40	6.87	4.40	5.00
Gazelle	63.13	78.20	57.93	105.67	103.07	81.60	5.40	5.00	3.53	7.67	6.86	5.69
SBH 4/4/4	64.67	89.33	56.20	105.60	112.47	85.65	3.80	4.00	4.13	6.67	4.10	4.55
SBH 10/2/3	47.13	56.47	58.60	65.93	74.20	60.47	3.93	6.00	5.67	6.80	6.06	5.69
SBH 4/6/6	50.00	61.00	60.47	61.60	77.33	62.08	4.80	6.00	5.27	7.27	6.13	5.89
Nyala	47.40	51.07	63.20	63.73	78.27	60.73	5.60	5.20	4.07	7.73	5.00	5.52
EAI 3600	47.87	66.00	67.00	69.00	81.40	66.25	4.73	5.60	5.13	6.87	5.80	5.63
SBH 6/6/6/2	53.60	54.87	63.87	56.13	60.40	57.77	4.93	5.33	6.00	6.20	5.13	5.52
DPSB 8	63.60	102.81	76.13	110.87	125.73	95.84	3.40	4.67	4.07	6.13	6.20	4.89
DPSB 19	42.47	69.33	61.13	56.67	68.60	59.64	3.07	4.40	4.67	4.60	4.87	4.32
931/5/34	50.33	54.40	53.27	58.20	60.47	55.33	4.47	6.07	5.33	8.26	5.33	5.89
DPSB 3	52.47	56.80	60.13	45.87	70.53	57.16	6.27	6.00	6.73	8.40	8.60	7.20
SBH 3/8/4/1	57.40	54.40	56.07	54.67	61.67	56.84	4.93	4.87	5.13	6.60	5.27	5.36
Mean	55.34	72.26	60.99	77.66	84.64	70.18	4.75	5.07	4.91	6.96	5.60	5.46
CV% 8.7							C.V.% 12.6					
LSD[a] 10.156							LSD[a] 1.185					
LSD[b] 9.874							LSD[b] 1.114					

LSD [a]- for comparing any two genotypes means across environments.
LSD [b] - for comparing genotypes means within the same environment.
C.V. % - coefficient of variation across environments.

Table 3.5. Means of number of nodes plant^{-1} and yield of soybean [*Glycine max* (L.)] genotypes evaluated in Njoro, Lanet, Eldoret and Nakuru West in 2011.

	Number of Nodes $^{-1}$						Yield in Kg ha^{-1}					
			Nakuru	Njoro					Nakuru	Njoro		
Genotype	Eldoret	Lanet	West	A	B	Mean	Eldoret	Lanet	West	A	B	Mean
SBH 10/5/6	13.93	16.73	11.27	19.67	16.80	15.68	1222.80	1748.80	912.30	1370.00	1263.00	1303.46
SBH 1/12/9	11.20	17.80	11.80	20.67	10.73	14.44	1204.30	1932.10	920.40	1495.10	1621.60	1434.70
SBH 7/1/1	13.53	18.67	12.47	20.87	18.67	16.84	1492.00	1975.30	942.00	1542.00	1768.50	1543.95
Gazelle	13.13	15.07	11.20	18.40	16.27	14.81	1197.50	2179.00	959.20	827.80	1474.10	1327.53
SBH 4/4/4	14.13	16.27	11.67	17.40	15.93	15.08	1217.30	1668.50	918.50	1459.90	1572.80	1367.42
SBH 10/2/3	10.93	11.13	10.93	12.73	11.40	11.43	812.30	1804.90	682.70	997.50	1327.10	1124.93
SBH 4/6/6	10.73	11.07	10.53	11.87	11.40	11.12	943.80	1933.90	1070.40	1156.80	1342.60	1289.49
Nyala	13.53	12.00	11.60	15.73	14.22	13.42	1165.40	1992.60	1229.00	1237.70	2379.60	1600.87
EAI 3600	11.27	10.87	11.13	12.27	11.27	11.36	1125.90	2036.40	1129.60	1205.60	1378.40	1375.19
SBH 6/6/6/2	11.20	10.80	11.27	12.80	10.40	11.34	1085.80	1538.90	871.60	800.00	1692.00	1197.65
DPSB 8	13.53	18.80	11.07	18.00	16.87	16.25	927.20	1816.10	873.50	1919.10	1538.30	1414.82
DPSB 19	10.40	14.33	11.80	13.73	12.13	12.48	675.30	1175.90	768.50	246.90	1172.90	807.91
931/5/34	12.47	12.20	12.33	13.53	11.06	12.32	1293.20	1930.80	587.73	1569.10	1235.80	1323.33
DPSB 3	14.13	12.53	13.33	13.73	15.00	13.75	1055.00	792.60	887.00	827.80	124.70	661.73
SBH 3/8/4/1	12.13	10.93	11.27	11.53	9.73	11.12	1184.00	1778.40	680.90	937.70	1636.40	1243.46
Mean	12.42	13.94	11.79	15.53	13.45	13.43	1106.79	1753.62	895.56	1147.66	1435.19	1267.76
CV% 8.3							CV% 17.7					
LSD^{a} 1.815							LSD^{a} 368.9					
LSD^{b} 1.797							LSD^{b} 362.5					

LSD ^{a}- for comparing any two genotypes means across environments.
LSD ^{b} - for comparing genotypes means within the same environment.
C.V. % - coefficient of variation across environments.

Table 3. 6. Means of number of pods plant^{-1} and number of seeds pod^{-1} of soybean [*Glycine max* (L.)] genotypes evaluated in Njoro, Lanet, Eldoret and Nakuru West in 2011.

	Number of Pods Plant^{-1}						Number of Seeds Pod^{-1}					
			Nakuru	Njoro					Nakuru	Njoro		
Genotype	Eldoret	Lanet	West	A	B	Mean	Eldoret	Lanet	West	A	B	Mean
SBH 10/5/6	26.33	39.60	18.13	44.53	47.67	35.25	2.30	2.32	2.43	2.27	2.57	2.38
SBH 1/12/9	35.47	46.80	20.20	46.87	53.60	40.58	2.17	2.45	2.39	2.25	2.52	2.35
SBH 7/1/1	35.60	45.33	17.47	44.73	54.00	39.43	2.08	2.25	2.56	2.25	2.75	2.38
Gazelle	29.20	48.80	17.07	28.73	40.60	32.88	1.93	1.95	2.23	2.10	1.75	1.99
SBH 4/4/4	26.80	36.53	16.33	43.93	45.67	33.85	2.27	2.45	2.57	2.28	2.40	2.39
SBH 10/2/3	24.93	51.80	24.40	42.86	55.20	39.80	2.13	2.57	2.27	2.08	2.25	2.29
SBH 4/6/6	33.47	46.73	21.47	41.53	43.07	37.25	2.13	2.58	2.42	2.10	2.33	2.31
Nyala	39.73	51.20	18.07	59.47	62.47	46.12	2.08	2.28	2.43	1.97	2.27	2.21
EAI 3600	32.20	34.53	21.13	38.27	36.73	32.57	2.33	2.52	2.48	2.20	2.63	2.43
SBH 6/6/6/2	37.06	40.93	30.40	55.87	51.80	43.21	2.08	2.37	2.48	2.27	2.28	2.30
DPSB 8	17.80	45.73	16.80	50.50	56.53	37.47	2.35	2.23	2.43	2.68	2.43	2.43
DPSB 19	23.93	52.67	26.60	28.53	57.53	37.85	2.03	2.53	2.30	2.18	2.20	2.25
931/5/34	24.87	52.47	34.13	82.73	41.47	47.13	2.23	2.38	2.58	2.31	2.48	2.43
DPSB 3	25.60	30.40	31.07	77.20	31.00	39.05	2.33	2.00	2.40	2.35	1.62	2.14
SBH 3/8/4/1	44.20	54.27	34.00	49.53	49.73	46.35	2.07	2.33	2.45	2.28	2.43	2.31
Mean	30.45	45.18	23.15	48.99	48.47	39.26	2.17	2.34	2.43	2.23	2.32	2.30
CV% 17.8							CV% 8.8					
LSD^{a} 11.841							LSD^{a} 0.3269					
LSD^{b} 11.297							LSD^{b} 0.3268					

LSD ^{a}- for comparing any two genotypes means across environments.
LSD ^{b} - for comparing genotypes means within the same environment.
C.V. % - coefficient of variation across environments.

Table 3.7. Mean values of oil and protein content of fifteen soybean [*Glycine max* (L.)] genotypes evaluated in Njoro, Lanet, Eldoret and Nakuru West in 2011.

	Oil content g kg^{-1}						Protein content g kg^{-1}					
Genotype	Eldoret	Lanet	Nakuru West	Njoro A	B	Mean	Eldoret	Lanet	Nakuru West	Njoro A	B	Mean
SBH 10/5/6	215.0	197.3	229.3	189.3	192.3	204.7	355.3	385.7	314.3	386.7	387.0	365.8
SBH 1/12/9	189.0	199.0	229.7	189.7	174.0	196.3	374.6	369.3	313.3	385.7	408.3	370.3
SBH 7/1/1	193.0	198.7	231.0	191.0	192.7	201.3	390.7	377.0	311.7	378.0	381.0	367.7
Gazelle	195.0	199.3	233.3	185.0	181.7	198.9	363.0	360.3	308.3	379.3	393.3	360.9
SBH 4/4/4	202.0	198.7	233.3	186.3	192.6	202.6	391.0	372.3	311.3	385.7	382.0	368.5
SBH 10/2/3	205.7	194.3	223.7	179.0	180.3	196.6	380.0	400.0	314.7	433.0	411.0	387.7
SBH 4/6/6	206.7	195.7	222.3	182.3	179.7	197.3	373.0	398.3	311.3	418.3	419.3	384.1
Nyala	184.3	199.3	221.0	186.0	183.3	194.8	395.3	371.3	309.7	399.3	384.3	372.0
EAI 3600	204.7	200.7	224.0	185.0	186.7	200.2	377.3	379.7	311.3	415.7	404.0	377.6
SBH 6/6/6/2	198.0	187.7	229.3	176.7	172.7	192.1	367.3	385.7	307.3	416.7	417.3	378.5
DPSB 8	175.0	179.7	201.0	170.0	172.3	179.6	391.7	390.7	314.3	406.0	398.7	380.3
DPSB 19	164.3	173.0	194.3	161.3	157.3	170.01	414.0	398.7	315.7	451.3	434.3	402.8
931/5/34	215.3	222.7	256.0	207.0	193.0	218.8	342.0	359.3	305.7	368.7	385.0	352.0
DPSB 3	159.0	163.7	192.3	159.7	155.0	165.9	415.7	404.6	309.3	420.7	408.0	391.7
SBH 3/8/4/1	188.6	183.3	227.7	181.7	177.7	191.8	391.7	402.0	311.7	436.3	407.3	389.8
Mean	193.0	192.9	222.9	182.0	179.4	194.1	381.5	383.6	311.3	405.3	401.4	376.6
CV% 3.2							CV% 4.6					
LSD[a] 1.047							LSD[a] 2.923					
LSD[b] 1.0123							LSD[b] 2.805					

LSD [a]- for comparing any two genotypes means across environments.
LSD [b] - for comparing genotypes means within the same environment.
C.V. % - coefficient of variation across environments.

Table 3.8. Mean of seed weight of fifteen soybeans [*Glycine max* (L.)] genotypes evaluated in Njoro, Lanet, Eldoret and Nakuru West in 2011.

	100-seed weight(g)					
				Njoro		
Genotype	Eldoret	Lanet	Nakuru West	A	B	Mean
SBH 10/5/6	12.33	14.67	13.67	12.67	13.33	13.33
SBH 1/12/9	8.33	14.00	13.33	12.333	15.00	12.6d
SBH7/1/1	11.33	14.33	14.00	12.33	12.33	12.87
Gazelle	13.67	20.00	17.00	18.33	18.33	17.47
SBH 4/4/4	11.67	13.67	13.33	12.33	13.00	12.8
SBH 10/2/3	10.33	18.00	14.67	16.00	13.33	14.47
SBH 4/6/6	10.67	17.67	14.00	15.33	14.33	14.4
Nyala	17.67	19.67	15.33	17.67	17.67	17.60
EAI 3600	11.33	17.67	13.33	15.00	13.33	14.13
SBH 6/6/6/2	8.33	14.33	13.67	12.33	13.67	12.20
DPSB 8	12.67	12.33	12.67	12.00	12.00	12.33
DPSB 19	9.00	12.33	11.67	10.33	10.00	10.67
931/5/34	14.67	19.67	16.33	18.00	14.67	16.67
DPSB 3	10.67	11.00	12.33	10.67	7.67	10.47
SBH 3/8/4/1	9.00	14.33	14.00	12.67	14.67	12.93
Mean	11.44	15.58	13.86	13.88	13.55	13.66
CV% 9.9						
LSD[a] 2.165						
LSD[b] 2.177						

LSD [a]- for comparing any two genotypes means across environments.
LSD [b] - for comparing genotypes means within the same environment.
C.V. % - coefficient of variation across environments.

numbers of pods plant^{-1} were not significantly different at Njoro A and B at 48.99 and 48.47, respectively (Table 3.6) while Nakuru west had the least pods plant^{-1} (23.2). Although Eldoret had the least number of seeds pod^{-1}(2.2), there was low variation within and among the sites (Table 3.6) for this trait. The least number of seeds pod^{-1} was observed for genotype Gazelle across the test sites.

The genotype mean oil content was highest in Nakuru West (223.0 g kg^{-1}) while Njoro, Eldoret and Lanet gave lower oil content than the trial mean of 194.0 g kg^{-1} (Table 3.7). On the contrary, genotypes tested at Nakuru west expressed the least protein content at 311.0 g kg^{-1} while all other sites had higher protein content than the mean of 377.0 g kg^{-1}. Seasonal effects also had influence on the soybean genotypes with respect to days to flowering and maturity, plant height and grain yield. The mean days to flowering and harvest maturity (Table 3.3) were more in Njoro A than in Njoro B. Soybean genotypes were taller and had higher yield in Njoro A than in Njoro B (Table 3.4 and 3.5). The highest mean seed weight was observed at Lanet while the least was observed at Eldoret. Nakuru West and Njoro A and B gave seed weight which was not significantly different from the trial mean of 13.7 g (Table 3.8). Genotype DPSB 3 had the least weight of 7.7 g which was observed on the late planted crop (Njoro B).

The mean plant height ranged from 55.3 to 95.8 cm (Table 3.4). Genotype DPSB 8 was the tallest in all environments and had the highest number of nodes plant^{-1} in Eldoret, Lanet and Nakuru. However, the performance of this genotype in terms of grain yield was highest in Lanet and Njoro A (Table 3.5). Although genotype 931/5/34 was the shortest, its height was not significantly different from genotypes SBH 6/6/6/2, DPSB 19, DPSB 3 and SBH 3/8/4/1 (Table 3.4).

The number of branches plant^{-1} was least at Eldoret (4.8) and highest (7.0) at Njoro in early planted crop (Njoro A) [Table 3.4]. The check genotype, EAI 3600 had a mean of 5.6 branches plant^{-1} across all environments which were not significantly different from the overall treatment mean of 5.5. Variety Nyala and genotype SBH 7/1/1 had the highest yield across the environments and also had high number of branches at Eldoret, Lanet and Njoro A (Table 3.5). Genotype SBH 7/1/1 had a mean of 18.7 nodes plant^{-1} at Lanet and late planted crop (Njoro B). The highest mean number of nodes plant^{-1} (Table 3.5) was observed at Lanet (13.90), Njoro A (13.9), Njoro B (13.5) and least at Nakuru West (11.8). Mean seed yield (Table 3.5) was high at Lanet (1153.6 kg ha^{-1}), Njoro A (1147.7 kg ha^{-1}) Njoro B (1435.2 kg ha^{-1}) and least at Nakuru West at 895.6 kg ha^{-1}.

There was genotypic variation in the number of pods plant^{-1} within and across environments (Table 3.6). The genotypes evaluated at Njoro (A and B) produced an average 49 and 48.5 pods plant^{-1}, while the genotypes had the least number of pods plant^{-1} (23.2) at Nakuru west (Table 3.6). Oil content was highest in Nakuru West and least in Njoro A (Table 3.7). An oil content of 200.2 g kg^{-1} was observed for genotype EAI 3600 which was 3% above the mean oil content of 194.0 g kg^{-1} across all environments. Genotype 931/5/34 recorded the highest oil content in all the environments. The highest oil content (256.0 g kg^{-1}) was recorded at Nakuru West and least (153.0 g kg^{-1}) in the late planted soybean (Njoro B). Genotype DPSB 3 had least oil content in all environments. Its oil content was highest at Nakuru west and least in the late planted crop (Njoro B).

Protein content was high (405.0 g kg^{-1}) in genotypes evaluated at Njoro A. Genotype DPSB 19 had the highest protein content in the seed across the five environments with the highest protein content (451.0 g kg^{-1}) observed at Njoro A (Table 3.7). Least protein content was observed in genotype 931/5/34 across all environments. In contrast, the protein content of 377.0 g kg^{-1} was observed in genotype EAI 3600. Other genotypes that had higher protein content than the mean were DPSB 3, SBH 3/4/4/1, SBH 10/2/3, SBH 4/6/6, DPSB 8 and SBH 6/6/6/2. Variety Gazelle was leading in 100-seed weight (20 g) at Lanet while genotype DPSB 3 expressed least seed weight (7.7 g) in the late planted soybean in Njoro (Njoro B). Variety Nyala maintained superiority in this trait across all five environments (Table 3.8). The least mean seed weight (15.6 g) was observed at Lanet. Genotype Nyala, Gazelle and genotype 931/5/34 had the highest mean seed weight at 17.6 g, 17.5 g and 16.6 g, respectively. The least mean 100-seed weight (11.4 g) was observed in Eldoret (Table 3.8) while Nakuru West, Njoro A and Njoro B observed non-significantly different mean values from each other at 13.9, 13.9 and 13.6 g, respectively.

3.2.3 Correlation coefficients among soybean agronomic and quality traits

Yield was significantly and positively correlated to 100-seed weight (r = 0.58*) and oil content (r = 0.68**) but negatively correlated to protein content (r = -0.67**). Though not significant, there was negative correlation between seed yield and number of branches plant^{-1}, harvest maturity and 50% flowering (Table 3.9). Harvest maturity was positively and significantly correlated to 50% flowering (r = 0.91**) and branching (r = 0.55**) while plant height was positively correlated to nodes plant^{-1}(r = 0.88**) and negatively correlated to pods plant^{-1} (r = 0.56*). Oil content was significantly and positively correlated to 100-seed

weight (r = 0.66**) and yield (r = 0.68**) but negatively correlated to the protein content. Seed weight was negatively correlated (r = -0.63*) to protein content (Table 3.9).

3.3 Discussion

Genotypes are selected in the test environments with a goal of identifying those genotypes that have superior performance in future target environments (Helms and Hammond, 2006). The study compared the performance of fifteen genotypes across five environments in a multi-environment trial. It is clear that there were genotypic effects and G × E interactions suggesting that the environments influenced the performance of soybean genotypes. The effect due to environments indicates that there were diversity in the genotypes and environments. The significant ($P < 0.01$) G × E interaction further demonstrated the variability among genotypes and test environments. However, contribution to the total sum of squares differed among the traits. Studies elsewhere have observed significant presence of G × E interactions in soybean data collected across environments (Amira *et al.,* 2013, Bueno *et al.,* 2013). Kumar *et al.* (2010) while evaluating rice (*Oryza sativa*) mutants indicated significant G × E interaction for plant height, days to 50% flowering, panicle length, panicle number plant^{-1} and grain yield. There was significant G × E interaction for days to 50% flowering and harvest maturity. All genotypes observed had a higher yield at Lanet than in any other environment probably because the environmental conditions favoured soybean production. The environmental factors that contributed to lower yields in the other environments could have been acidity in Eldoret, low soil moisture content in Nakuru west and low night/day temperatures at Njoro.

The components of yield in soybean include number of plants per unit area, size of the seed, number of pods plant^{-1} and number of seeds pod^{-1} (Liu *et al.,* 2010). Yield was variable among the genotypes across the environments (Table 3.5). Genotype Nyala yielded highest across the environments and this could be attributed to its medium maturity period (Table 3.3), high seed weight and high number of pods plant^{-1} (Table 3.2). Seed size is an important quality aspect in some products. It is necessary to have large seed size of >200 mg seed^{-1} with high protein and sugar content for production of soymilk, tofu and miso, while natto production needs small seed size of < 80 mg seed^{-1} with high protein and sugar content (Cicek *et al.,* 2006). Despite there being a positive correlation between the number of pods, primary branches plant^{-1} and seed yield in soybean (Malhorta *et al.,*1971), genotype DPSB 3 with the highest number of branches across the environments had the least yield (Table 3.4).

Table 3.9. Pearson correlation coefficients for agronomic and seed quality traits in soybean [*Glycine max* (L.)] based on data observed across five environments in 2011.

Agronomic and quality traits		50% flowering	Harvest maturity	Plant height	Pods plant^{-1}	Seeds Pod^{-1}	Branches	Nodes plant^{-1}	Yield	100 seed weight	Oil content
Harvest maturity	(d)	0.91**									
Plant height	(cm)	-0.11	0.08								
Pods plant^{-1}	(No.)	0.10	0.17	-0.56*							
Seeds pod^{-1}	(No.)	-0.28	-0.11	0.22	0.09						
Branches plant^{-1}	(No.)	0.74**	0.55*	-0.45	0.16	-0.37					
Nodes plant^{-1}	(No.)	0.09	0.35	0.88**	-0.34	0.04	-0.28				
Yield	(kg ha^{-1})	-0.24	-0.01	0.48	0.07	0.37	-0.34	0.32			
100-seed weight	(g)	-0.16	0.23	-0.07	0.16	-0.22	0.14	-0.09	0.58*		
Oil content	(g kg^{-1})	-0.18	-0.05	0.14	0.09	0.38	-0.09	0.03	0.68**	0.66**	
Protein content	(g kg^{-1})	-0.16	-0.36	-0.39	-0.01	-0.16	-0.02	-0.42	-0.67**	-0.63*	-0.82**

*** Significant at P < 0.01; *Significant at P < 0.05.*

The relationship between yield and the number of primary branches (Table 3.9) was non-significant, weak and negative. The low seed yield could be attributed to low 100-seed weight and low number of seeds pod (Table 3.6 and 3.8). Genotype DPSB 3 was developed with the intention of producing high biomass and grain to address soil fertility issues and its probable most of the photosynthates were apportioned to vegetative growth rather than seed filling. DPSB 3 had low yield and took long to mature and hence could not be recommended for production in any of the environments studied. The genotype may be recommended for lower altitudes where it's warmer. Although the genotypes yield mean was higher than the 600 kg ha^{-1} obtained by small scale farmers in the tropics (FAO, 2004), none of the genotypes attained the potential of 3000-3600 kg ha^{-1} (Verde *et al.*, 2013).

The genotypes varied in their plant height within and across the environments. Genotypes at Eldoret had the least mean plant height which could be attributed to the high soil pH (4.7) which is lower than pH 6.0 suitable for soybean production (Okogun *et al.*, 2004). Genotype 931/5/34 was generally shortest across the environments while genotype DPSB 8 was tallest. Plant height, seed yield, seed coat cracking and some types of disease resistance in soybean and other plant species are economically important traits that are polygenic, complex and controlled in a quantitative manner (Oyoo *et al.*, 2010; Alcivar *et al.*, 2007; Kassem *et al.*, 2006) influenced by genetics and environment. Plant height in this study was negatively correlated to pods $plant^{-1}$ but positively correlated to nodes $plant^{-1}$. This observation disagrees with that of Ngalamu *et al.* (2013) who had observed significant correlation of plant height with number of seeds pod^{-1} and but agrees with the observation on non-significant correlation with 50% flowering, number of branches $plant^{-1}$ and seed yield. The mean plant height range observed in the current study agrees with studies done by Aditya *et al.* (2011) and Karasu *et al.* (2009). The differences in height imply that there was significant genetic variability for this trait among genotypes tested. Plant height and seed weight largely influence the harvest index and are among the yield related traits in soybean (Wang *et al.*, 2004).

In soybean the number of pods and fullness of pods are the most important criteria for seed yield (Arslanoglu and Aytac, 2010). However, pods $plant^{-1}$ cannot be considered in isolation but with other traits such as seeds pod^{-1} and seed weight. In the current study, genotype Nyala had high yield due to the high number of pods $plant^{-1}$ and high seed weight. Genotypes SBH 6/6/6/2, 931/5/34 and SBH 3/8/4/1 with similar number of pods $plant^{-1}$ as Nyala gave lower yield most likely due to their low seed weight (Table 3.2). Genotype SBH

7/1/1 also gave high yield and this could be attributed to its high number of pods plant^{-1}, high number of seeds pod^{-1}(Table 3.6), medium maturity (Table 3.3) and plant height (Table 3.4). The pods plant^{-1} and yield results disagree with those of Ojo, (2003) who observed a higher range of pods plant^{-1} and yield. The differences could be attributed to the genotypes tested and environments used in the studies.

Oil content was significantly different among the genotypes. The oil content varied among genotypes across the environments (Table 3.7). The contribution to the total sum of squares was attributed to the environment (52%), genotype (36.5%) and genotype × environment (5%). The oil content was affected more by the environment and the genotype and less by G × E interactions effects implying the trait is polygenic and controlled quantitatively. Genotypes 931/5/34/ and DPSB 3 had high and low oil content, respectively across the environments. This could be attributed to the low G × E interaction on the trait. The range in oil content within the SBH lines did not differ significantly within environments implying that the lines were not genetically diverse. Optimum growth conditions are required during seed filling for oil in soybean seed to accumulate during this growth stage with a maximum rate occurring thirty days after flowering (Wilson, 2004). The genotypes mean oil content was highest at Nakuru West and this was probably due to the higher temperatures experienced at this site as modified by the lower altitude. This phenomenon is well displayed by genotype 931/5/34 (Table 3.7). Wilson, (2004) observed that under controlled conditions, oil percentage increased in response to increase in mean daily temperature. Cuniberti *et al.* (2004); Yaklich and Vineyard, (2004) had observed similar effects of temperature on oil content. However, Ojo *et al.* (2002) observed that high temperature tended to increase protein content with little or no effect on oil content. The protein and oil content are influenced by both genotype and environment cues (Clemente and Cahoon, 2009).

Protein content in the current study varied among the genotypes and the variation was attributed to environment (69.9%), genotypes 9.9% and G × E (7.0%). The high protein content at Njoro and the low protein content observed at Nakuru West could be attributed to environmental conditions. Njoro is cooler than Nakuru West as attributed to altitude. The inverse relationship between oil and protein content exists, typically a 15% reduction in total oil content leads to a 2% increase in protein content (Clemente and Cahoon, 2009). The negative correlation of oil and protein indicates that selection for high protein content in a variety is indirectly selecting for low oil content. Protein and oil content were genotype specific and were affected by environmental factors and this agrees with observation made

by Popovic *et al.* (2012). Seed size is denoted by the seed weight. Seed size was significantly and negatively correlated to protein content but positively and significantly correlated to oil content. However, the relationship between seed weight and oil content was weak and could not be used as criteria for selection of high oil content (Table 3.9).

3.4 Conclusion

Environments and G × E interaction play a significant role in the performance of genotypes in a particular environment. There was significant G × E interaction for all traits studied raising the need to carry out multi-environment trials to get region specific genotypes for economic production of soybeans. Variety Nyala may be recommended for production in Nakuru West while genotype SBH 7/1/1, Gazelle, and DPSB 8 maybe recommended for Eldoret, Lanet and Njoro, respectively. Genotype DPSB 19 was early maturing and gave the highest protein content but gave poor grain yields. Genotype 931/5/34 had the highest oil content across the environments with yields above the trial mean. The two genotypes could be used to improve protein and oil content in other high yielding genotypes. Genotype SBH 7/1/1 showed promising yields and oil content above the mean. This genotype may be recommended as a candidate for evaluation in the national performance trials.

3.5 References

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CHAPTER FOUR

STABILITY AND ADAPTABILITY OF AGRONOMIC TRAITS OF SOYBEAN [*Glycine max* (L.) Merrill]

Abstract

Soybean [*Glycine max* (L.) Merrill] is an important legume valued for its protein and oil content raising the need to develop soybean genotypes that are consistent in production under varying environmental conditions. The nature and magnitude of heritability helps to determine the best method to use in selection of traits and the choice of donor parents in a breeding programme. The objective of the study was to determine stability and adaptability of grain yield, protein and oil content of fifteen soybean genotypes by additive main effects and multiplicative Interaction (AMMI) analysis and genotype and genotype plus environment (GGE) biplots. The study further sought to estimate broad sense heritability of agronomic traits by variance component method. The study was conducted at Eldoret (0^{o} 35′N and 35^{o}18′E), Lanet (0^{o}18′S and 36^{o} 09′E), Nakuru west (0^{o} 33'S and 36^{o} 0'E) and Njoro (0^{o} 20′S, 35^{o} 56′E) in 2011. Genotype Nyala, a medium maturing genotype, was adapted to Nakuru west, Njoro B and Lanet while genotype SBH 7/1/1 was adapted to Eldoret and Njoro A. AMMI analysis identified genotypes EAI 3600 and SBH 4/6/6 as stable for yields with means above the mean yield of 1267.8 kg ha^{-1} while genotypes SBH 4/4/4, SBH 7/1/1, SBH 1/12/19 and Gazelle were stable for yield and oil content. Genotype DPSB 19 was stable for protein content. It also had high protein content (400.2 g kg^{-1}). Heritability estimates of the traits studied ranged from 0.17- 0.79%. Broad sense heritability was low for protein content, seed yield, number of branches plant^{-1} and pods plant^{-1}. Heritability was medium for oil content but high for days to 50% flowering, days to harvest maturity, plant height, and seeds pod^{-1}, number of nodes plant^{-1} and seed weight. High heritability implies low contributions of environments to phenotypic variance and therefore it would be easier for the breeder to make selections of superior genotypes for various purposes.

4.0 Introduction

Soybean [*Glycine max* (L.) Merrill] is increasingly becoming an important food and cash crop in the tropics due to its nutritional qualities and adaptability to various growing environments (McKevith, 2005). Soybean is valued worldwide for its high oil and protein contents (Marega *et al.,* 2001) and is used for manufacturing edible oil, feed and food (Wilcox and Shibles, 2001). Chemical composition of soybean seed is given priority by the

processors (Zilic *et al.*, 2009). Composition of protein varies with the genotype and can be substantially affected by the environment (Dukic *et al.*, 2010). Due to their importance, evaluation of genotypes under different environments for their stability in oil and protein should be a priority in any soybean breeding programme. -

Analysis for stable genotypes is valuable and important as an efficient tool for agronomists and breeders. Stability analysis helps identify and make choice of superior performing genotypes that are suited to a given set of agro-ecological zones (Jadong *et al.*, 2011). Stability analysis has been done in different crops using different methods. Additive main effects and multiplicative interaction analysis (AMMI) has become popular for stability analysis because it combines additive components for the principle genotype effects and environments, with multiplicative components for the effects that involve G × E interactions (Oliveira *et al.*, 2006). The AMMI method has been employed on G × E studies in maize (Ajibade *et al.*, 2002), wheat (Kaya *et al.*, 2002) and soybean (Tukamuhabwa *et al.*, 2011). Stable genotypes though not necessarily high in yield provide soybean growers with stable yields despite the different soybean growing environments with a range of edaphic and weather factors.

The AMMI analysis eradicates the "noises" of the G × E interaction and concentrates only on "standard" of this interaction (Oliveira *et al.*, 2006). While evaluating superior soybean genotypes using genotype main effect plus genotype by environment interaction effect (GGE), Yan and Rajcan (2002) found that selection for yield of seed on its own was a simple and highly effective strategy in the initial stages of soybean breeding. Genotype main effect plus genotype × environment interaction effect (GGE) biplot graphically displays G × E interaction data and this facilitates cultivar evaluation on the basis of multi-environment (MET) data. The GGE biplot identifies the ideal genotype as one having highest average value of all genotypes and be totally stable and thus is not affected by G × E interaction (Yan and Tinker, 2006)

Yield in soybeans is a complex quantitative character and an integrated function of a number of component traits and selection for yield in isolation may not be much rewarding unless other yield attributing traits are taken into consideration (Aditya *et al.*, 2011). A thorough understanding of yield traits such as heritability, genetic and environmental effects should be studied in detail prior to initiating a breeding programme (Sabu *et al.*, 2009).

Heritability in the broad sense is the amount to which a character is controlled by genetics (Falconer and Mackay, 1996). According to Graham and Welch, (1996) estimation of

heritability for a trait is more important than just knowing the number of genes that is involved in the expression of that trait because the latter is an important tool for measuring progress in crop improvement. However, Thangavelu and John (1997) observed that heritability estimates alone cannot provide sufficient information for genetic improvement that would result from selection of best individual crops suggesting the need for additional information. A multi-environment trial can be used for it allows the partitioning of a character on the basis of how it is influenced by genotype, environment and the extent of G × E interaction (Falconer and Mackay, 1996). The less G × E interaction on the character the more it is controlled by the genetic constitution and the more control a breeder has to improve the trait. Narrow sense heritability is the extent to which a trait can be passed from generation to generation by genes (Falconer and Mackay, 1996). The higher the narrow sense heritability the more likely a character will be passed on from parent to offspring. A cultivar with high heritability for desired traits is preferred for it can be improved more quickly (Nyquist, 1991). High environmental effect on genotypes reduces the heritability and makes genetic studies difficult. Heritability for seed protein and oil were reported as 0.89 and 0.84, respectively in F_5-derived recombinant inbred lines (RIL) from a high × low protein mating (Chung *et al.,* 2003). Heritability estimates of soybean seed protein and oil are high, notably in populations that have substantial differences in seed protein or oil (Chung *et al.,* 2003). High heritability in such kind of soybean populations implies that simple selection would be a sufficient scheme for achieving genetic gain (Phansak, 2010). Breeders make selections based on phenotypic traits that are controlled by genetic and environmental components.

The objective of the study was to identify adaptable and high yielding genotypes for specific environments and stable genotypes that can be grown across environments for yield, oil and protein content. Further, heritability estimates for quality traits and agronomic traits were determined.

4.1 Materials and Methods

4.1.1 Experimental Sites

The study was conducted at Njoro (0° 20′S, 35° 56′E) for early and late planting (denoted as Njoro A and Njoro B, respectively), Eldoret (0° 35′N and 35°18′E), Nakuru West (0° 33’S and 36° 0’E) and KALRO-Lanet (0°18′S and 36° 09′E). Njoro (2185 m.a.s.l.) is situated about 200 km West of Nairobi in Nakuru County. The site experiences an average daily minimum temperature of 9.5°C and maximum temperature of 24.2°C with an average

precipitation of 1032 mm (average of 20 years 1992-2012 weather station number 903502). The soils are mollic andosols in eco-zone III (Jaetzold *et al.*, 2010).

Eldoret (2154 m.a.s.l.) is located in Uasin Gishu County (FAO/UNESCO, 1994), and the soils are predominantly acidic (pH 4.7) rhodic ferrasols that are low in organic matter and deficient in nitrogen (N) and phosphorus (P). KALRO-Lanet is 16 Km South East of Nakuru town at an altitude of 1920 m.a.s.l. Rainfall pattern in Lanet is bimodal with an annual mean of 800 mm. The minimum and maximum temperatures are 10^{o}C and 26^{o}C (http:// www. kalro. org). Nakuru West is elevated to an altitude of 2003 m.a.s.l. and is on wind ward side overseeing Lake Nakuru.

4.1.2 Genotypes

Fifteen soybean genotypes were used in this study. Eight genotypes which were developed by hybridization (SBH lines) were early to medium in maturity. Genotypes Nyala, Gazelle and EAI 3600 were medium maturing varieties and variety EAI 3600 was used as a check. Genotype TGX 1835-10E (DPSB 3) was introduced from Nigeria and is reported to be resistant to Asian soybean rust (*Phakospora pachyrrhizi)*. Genotypes TGX 1895-33F (DPSB-8) and TGX 1740-2F (DPSB-19) are promiscuous with indigenous nodulating bacteria and have high biomass, traits that can aid in improvement of poor soils.

4.1.3 Experimental procedure

The seed bed was prepared to a tilth suitable for planting soybean seed. Planting was done on 13th June 2011 at Njoro for the early planting (Njoro A), 22nd June at Nakuru West, 8th July 2011 at Lanet, 14th June 2011 at Eldoret and on 15th July 2011 at Njoro for the late planted crop (Njoro B). The experiment was laid out in a randomised complete block design (RCBD) with three replicates. In all locations, plots measured 3 m × 2.7 m. The seeds were planted at a seed rate of 75 kg ha^{-1} at a spacing of 45 cm × 10 cm. At planting time Diamonium phosphate fertilizer (DAP) was applied by placing it in furrows and mixing with soil in order to supply 22 kg of N ha^{-1} and 57.5 kg of P ha^{-1} before placing the seed. Covering of the seeds was done before the application of a pre-emergent herbicide (*Metribuzin*) at the rate of 360 g ha^{-1}. Weeding was done manually when weeds appeared after the effect of the herbicide waned off. Foliar fungal diseases were controlled by application of *Tebuconazole* at the rate of 250 g ha^{-1} weekly at flowering until the crop was at stage R7 (Fehr and Caviness, 1977).

4.1.4 Data collected

Time of flowering was taken at stage R2 when 50% of the plants had at least one open flower, while plants were considered mature at stage R8 when 95% of the pods had changed colour from yellow to brown (Fehr and Caviness, 1977). Mean plant height at maturity was determined from 5 randomly selected plants from each plot by measuring from ground level to the tip of the main stem. The number of nodes plant^{-1}, number of pods plant^{-1} and number of branches plant^{-1} were determined from a five plant sample from the four center rows. The mean of twenty randomly selected pods were opened, seeds counted to determine the number of seeds pod^{-1}. The seed weight was determined by weighing 100 seeds sample from each treatment. Oil and protein content of the seed was estimated using near-infrared reflectance (NIR) whole grain analyzer (Infratec ^{TM} 1241 Grain Analyzer ISW 3.20: Foss Analytical AB, SE-2632 21 Hoganas, Sweden).

4.1.5 Data analysis

Yield stability, yield components, protein and oil content and genotype adaptability among the 15 soybean genotypes was analyzed using an additive main effects and multiplicative interaction (AMMI) model using GenStat 13th edition statistical software (VSN international, Ltd 2010) as indicated below.

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^{n'} \lambda_n \alpha_{in} \gamma_{jn} + \theta_{ij}$$

Where Y_{ij} is the mean yield of ith genotype in the jth environment; μ is the general mean; g_i is the ith genotype effect; e_j is the jth location effect; λ_n is the eigen value of the PCA axis n; α_{in} and γ_{jn} are the ith genotype jth environment PCA scores for the PCA axis n; θ_{ij} is the residual; n´ is the number of PCA axes retained in the model. The number of PCA axes retained is determined by consideration of F-test of significance (Gauch 1988).

Genotype and Genotype plus Environment (GGE) biplots were additionally used to display stability and adaptability of the genotypes. The combined data analysis was done using the SAS statistical software version 8.1. The mean squares were used to estimate broad sense heritability as described by Walter, (1987). The variance component method was used to calculate broad sense heritability by applying the equation on entry means basis as indicated below (Fehr, 1989).

$$H^2 = \frac{\delta^2 g}{\frac{\delta^2 e}{rt} + \frac{\delta^2 ge}{t} + \delta^2 g}$$

Where;

H^2 = heritability, $\delta^2 e$ is experimental error, $\delta^2 g$ is genetic variance, $\delta^2 ge$ is variance due to genotype by environment interaction, r is number of replicates and t is number of test environments

4.2 Results

4.2.1 Yield adaptability and stability

The ANOVA indicated that specific genotype and environment combinations were significantly ($P < 0.01$) different. The results from ANOVA by AMMI had divided the main effects of treatments into genotype, environment and G × E interactions (Table 4.1). There were highly significant ($P < 0.01$) differences among the components. The environment contributed 44.0% of the variation while the genotypes (G) and the G × E interaction accounted for 28.1% and 27.9% of the variation, respectively (Table 4.1). The IPCA score of the fifteen genotypes in 5 environments indicated that about 66% of the genotypes were highly interactive (Table 4.2). The four high yielding genotypes according to the yield means were Nyala (1601 kg ha^{-1}), SBH 7/1/1(1544 kg ha^{-1}), SBH 1/12/9 (1435 kg ha^{-1}) and DPSB 8 (1415 kg ha^{-1}) (Table 4.2). The least yielding genotype was DPSB 3. Other low yielding genotypes were DPSB 19 and SBH 10/2/3 producing 808 and 1125 kg ha^{-1}, respectively. Based on the first IPCA, the most interactive genotypes were DPSB 3 with interaction score of -28.8 and Nyala with an interaction score of 17.23. The least interactive genotype was DPSB 8 with an interactive score of 0.49. The other less interactive genotypes were SBH 4/4/4, SBH 4/6/6 and SBH 1/12/9. The GGE biplot [Fig.4.1 (a)] indicated that genotype SBH 7/1/1, and Nyala were the nearest to the ideal genotype for yield while DPSB 19 and DPSB 3 were the least associated with the ideal genotype. Analysis by AMMI determined the best four genotypes in yield per environment (Table 4.3). Gazelle and EAI 3600 were the best two genotypes at Lanet while Nyala and SBH 7/1/1 were best performers for Njoro B. Genotype DPSB 8 and 931/5/34 were superior at Njoro A while SBH 7/1/1 and EAI 3600 gave the best yield at Eldoret. At Nakuru West, genotypes Nyala and SBH 7/1/1 registered best performance. The later genotypes had best grain yields at Lanet and Nakuru West.

Table 4.1. AMMI analysis for yield of 15 soybean genotypes evaluated across five environments in 2011.

Source of variation	Degrees of freedom	Mean square
Treatments	74	622004**
Genotype	14	923121**
Environments	4	5065090**
Block	10	101141
Interactions	56	229361**
IPCA 1	17	314981**
IPCA2	15	325906**
IPCA3	13	117664**
Residuals	11	97393
Error	140	53788
Total	224	-

***Significant at P < 0.01*

Genotype SBH 7/1/1 was in the top three genotypes in all environments and genotype Nyala ranked first in two out five environments. Genotype EAI 3600, the check genotype, was placed second in two out of the five environments. Genotype SBH 10/5/6 was among the best four genotypes at Eldoret only (Table 4.3).

The GGE biplot showed genotypes that were stable in yield and adaptable [Fig.4.1 (b)]. The first principle component is represented on the x-axis and the higher the value along its length, the higher the productivity of a given genotype in terms of yield. The first principle component was very important and accounted for 52.25% of the variation in stability and the two principle components explained 71.8% of the variation. The 2nd principal component is represented on the y-axis and the further from the average environment axis (AEA) line the genotype is placed, the lower the stability in yield. The AEA line (with a single arrow) passes through the origin and the average coordinates of the environment (AEC) represented by a small circle.

The stability analysis showed that genotype SBH 4/4/4 had the shortest vector indicating that it had the most stable yield while genotype 931/5/34 had longest vector suggesting that it was the least stable [Fig. 4.1(b)]. The order of genotype stability in descending order was SBH 4/4/4, Gazelle, SBH 1/12/9, SBH 6/6/6/2, SBH 10/2/3, DPSB 3, DPSB 8, SBH 10/5/6, SBH 7/1/1, DPSB 19, EAI 3600, SBH 4/6/6, SBH 3/8/4/1, Nyala and 931/5/34. Genotype Nyala was the most adaptable at Nakuru west, Njoro B and Lanet while EAI 3600, genotype Gazelle and SBH 4/6/6 had good performance in the same environment.

Genotype SBH 7/1/1 was the most adaptable genotype to Eldoret and Njoro A environments while SBH 1/2/19 and SBH 4/4/4 gave good yields in these environment.

Table 4. 2. Mean seed yield (kg ha^{-1}) and Interaction Principal Component Axis (IPCA) scores for 15 soybeans genotypes evaluated across five environments in 2011.

Genotype	Genotype mean yield (kg ha^{-1})	IPCA 1	IPCA 2	IPCA 3
SBH 10/5/6)	1303	-6.6448	-5.4367	0.8741
SBH 6/6/6/2	1198	6.7862	8.4653	6.5740
DPSB 8	1415	0.4982	-19.2481	8.0822
DPSB 19	808	2.5775	15.4596	4.2702
931/5/34	1323	-5.2747	-14.7096	-5.5063
DPSB 3	660	-28.8156	11.3142	6.0144
SBH 3/8/4/1	1243	6.5759	2.3849	-1.7210
SBH 1/12/9	1435	1.4815	-7.1336	1.1503
SBH 7/1/1	1544	1.0449	-5.4754	2.5177
Gazelle	1308	3.3330	9.3407	-17.0816
SBH 4/4/4	1302	1.0057	1.5485	4.9685
SBH 10/2/3	1125	3.9994	-2.8099	-6.1595
SBH 4/6/6	1290	-1.0609	-0.2970	-5.4123
Nyala	1601	17.2451	6.0809	8.6099
EAI 3600	1375	-2.7518	0.5162	-7.1808

Table 4. 3. The first four AMMI selections of soybean genotypes per environment based on yield and oil content in five environments in 2011.

Environment	Mean yield (kg ha^{-1})	Score	1	2	3	4
a) Based on yield						
Lanet	1754	6.32	Nyala	SBH 7/1/1	DPSB 8	SBH 1/12/9
Njoro B	1435	29.04	Nyala	SBH 7/1/1	Gazelle	SBH 3/8/4/1
Njoro A	1148	-7.29	DPSB 8	931/5/34	SBH 7/1/1	SBH 1/12/9
Eldoret	1107	-15.69	SBH 7/1/1	EAI 3600	Nyala	SBH 10/5/6
Nakuru west	896	-12.38	Nyala	Gazelle	SBH 7/1/1	EAI 3600
b) Based on oil content (g kg^{-1})						
Njoro A	182.0	0.6919	931/5/34	SBH 7/1/1	SBH 4/4/4	SBH 10/5/6
Lanet	192.9	0.4581	931/5/34	SBH 7/1/1	SBH 4/4/4	SBH 10/5/6
Nakuru West	223.0	0.1876	931/5/34	Gazelle	SBH 1/12/9	SBH 4/4/4
Njoro B	179.4	0.1648	931/5/34	SBH 10/5/6	SBH 7/1/1	SBH 4/4/4
Eldoret	193.0	-1.5025	931/5/34	SBH 10/5/6	SBH 4/6/6	SBH10 /2/3

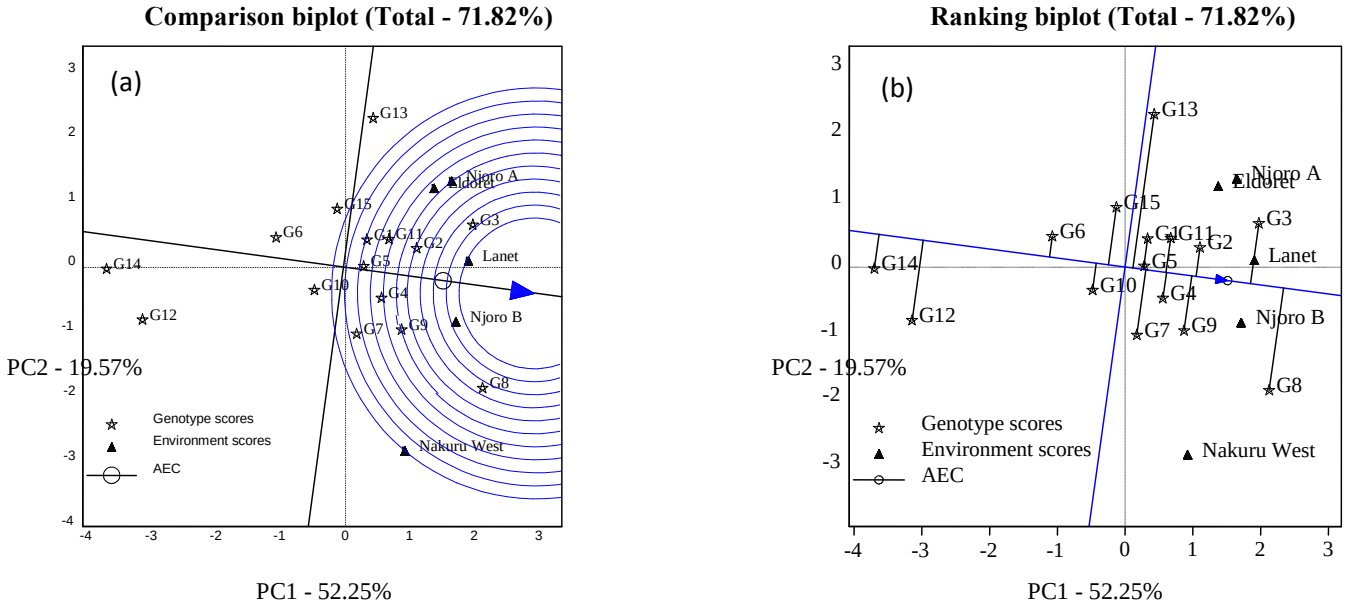

Figure 4.1. GGE biplots showing (a) genotype ranking (b) stability based on yield data. The Genotypes are G1-SBH 10/5/6; G2-SBH 1/12/9; G3-SBH 7/1/1; G4-Gazelle; G5-SBH 4/4/4; G6- SBH 10/2/3; G7-SBH 4/6/6; G8-Nyala; G9-EAI 3600; G10-SBH 6/6/6/2; G11-DPSB 8; G12-DPSB 19; G13- 931/5/34; G14-DPSB 3; G15-SBH 3/8/4/1.

4.2.2 Genotype adaptability and stability based on oil content

Analysis of variance revealed that the genotypes were significantly ($P < 0.01$) different in terms of oil content across the environments (Table 4.4). Results from ANOVA by AMMI had portioned the main effects of treatments into genotype, environment and genotype by environment interactions. The effects due to genotypes, environments and G × E interactions were significantly ($P < 0.01$) different among the components. The environment contributed 55.5% to the total sum of squares while the genotypes contributed 38.92% and the G × E interaction contributed only 5.6%.

The IPCA scores indicated there were low interactions between the genotypes and the environments. The IPCA scores (Table 4.5) ranged from 0.086 for SBH 3/8/4/1 to -0.749 for SBH 10/5/6. The first IPCA score was important and explained 50.3% of the variation while the second IPCA explained 32.8% of the variation. The best two genotypes in terms of their oil content per environment were 931/5/34 and SBH 7/1/1 for Njoro A and Lanet, 931/5/34 and Gazelle for Nakuru West and 931/5/34 and SBH 10/5/6 for Njoro B (Table 4.3). Genotype 931/5/34 was the best genotype in all environments. The mean oil content was highest at Nakuru west at 223 g kg^{-1} and least at Njoro which had a mean of at 179 g kg^{-1} in the late planted crop (Njoro B) (Table 4.3).

Stability based on oil content differed among the genotypes. All the genotypes had first IPCA scores of < 1. The highest IPCA 1 score of -0.75 was observed on genotype SBH/10/5/6 while the least score of 0.09 was observed for genotype SBH 3/8/4/1 (Table 4.5). Genotype 931/5/34 had the highest mean oil content of 218.8 g kg^{-1} while genotype DPSB 3 (165.9 g kg^{-1}) had the least mean oil content.

Table 4.4. AMMI analysis of oil and protein content of 15 soybean genotypes evaluated across five environments in 2011.

Source	Degrees of freedom	Mean square (oil content)	Mean square (protein content)
Treatments	74	13.11**	43.59**
Genotype	14	26.98**	26.31**
Environments	4	134.68**	649.34**
Block	10	0.81	6.88
Interactions	56	0.97**	4.65**
IPCA 1	17	1.60**	7.03**
IPCA 2	15	1.18**	6.66
Residuals	24	0.38	1.69
Error	140	0.39	3.02
Total	224	-	-

Table 4.5. Mean oil content and interaction scores of 15 soybean genotypes evaluated across five environments in 2011.

Genotype	Mean oil content g kg^{-1}	IPCA 1	IPCA 2
SBH 10/5/6	204.7	-0.74932	0.31025
SBH 6/6/6/2	192.1	-0.47153	-0.40684
DPSB 8	179.6	0.24843	0.67095
DPSB 19	170.1	0.35654	0.27518
931/5/34	218.8	0.19607	-0.91206
DPSB 3	165.9	0.41718	-0.91206
SBH 3/8/4/1	191.8	0.08556	-0.22194
SBH 1/12/9	196.3	0.48386	-0.55802
SBH 7/1/1	201.3	0.42027	0.26914
Gazelle	198.9	0.14682	-0.37258
SBH 4/4/4	202.6	-0.12200	0.14907
SBH 10/2/3	196.6	-0.66762	-0.01531
SBH 4/6/6	197.3	-0.63256	0.01009
Nyala	194.8	0.63476	0.24594
EAI 3600	200.2	-0.34646	0.24686

All the genotypes were stable for oil content as they had short vectors to the AEA axis (with arrow head) and all had absolute IPCA scores of < 1.0 (Fig. 4.2; Table 4.5). The GGE biplot analysis explained 94.71% (PC 1 89.68% and PC 2 5.08%) of the variation in stability for oil content among the genotypes [Fig. 4.2 (a)]. The most stable genotype was DPSB 3 with the shortest vector on AEA while SBH 931/5/34 was the least stable for its oil content among the genotypes studied. The order of stability in descending order was DPSB 3, DPSB 19, SBH 3/8/4/1, DPSB 8, SBH 7/1/1, SBH 4/4/4, Gazelle, SBH 6/6/6/2, EAI 3600, Nyala, SBH 4/6/6, SBH 10/2/3, SBH 1/12/9, SBH 10/5/6 and 931/5/34.

4.2.3 Genotype adaptability and stability based on protein content

The analysis of variance table indicated that genotype and environment interactions were significant ($P < 0.01$) denoting that genotypes responded differently across environments for protein content (Table 4.4). Genotypes accounted for 11.4% of the variation in protein content while environments accounted for 80.5%. The interaction accounted for 8.1% of the variation. The first and second principal component axis (PCA 1 and PCA 2) explained 64.6% and 17.2% of the variation, respectively denoting their importance [Fig.4.3 (a)]. Genotype DPSB 19 had the highest mean protein content of 402.8 g kg^{-1} while genotype 931/5/34 had the least with 352.1 g kg^{-1} (Table 4.6). Genotypes with protein content higher than the mean of 376.6 g kg^{-1} were the check EAI 3600, DPSB 19**,**

DPSB 3**,** DPSB 8, SBH 3/8/4/1, SBH 6/6/6/2, SBH 4/6/6 and SBH 10/2/3 (Table 4.6). There was low interaction between genotypes and the environment as indicated by low first IPCA scores. The most interactive genotype was SBH 7/1/1 with a score of 1.11 while the least interactive genotype was DPSB 3 with a score of 0.02.

The GGE biplot [Fig. 4.3 (a)] indicated that genotypes SBH 6/6/6/2, SBH 4/4/4 and SBH 7/1/1 were least stable among the genotypes tested while SBH 10/2/3, DPSB 3 and DPSB 19 were more stable in their protein content. Stable genotypes which had protein content above the mean of 376.6 g kg^{-1} were DPSB 19, SBH 10/2/3, SBH 6/6/6/2, SBH 4/6/6, DPSB 3 and DPSB 8 (Table 4.6).

4.2.4 Stability of important soybean yield components

Stability was highest on cultivar EAI 3600 for pods $plant^{-1}$ and least on DPSB 3 [Fig. 4.3 (a)]. The principal components explained 79.68% of the variation in stability among genotypes. The stability of genotypes for pods $plant^{-1}$ in descending order were EAI 3600, SBH 3/8/4/1, SBH 1/12/9, SBH 4/4/4, Nyala, SBH 10/5/6, SBH 4/6/6, DPSB 8, SBH 7/1/1, SBH 10/2/3, SBH 6/6/6/2, Gazelle, DPSB 19, 931/5/34 and DPSB 3.

Genotype EAI 3600 had highest stability based on 100-seed weight [Fig.4.3 (b)] while genotype DPSB 3 had least. The first principal component explained 80.63% of the variation while the second principal component explained only 12.09% of the variation in stability of genotypes based on seed weight. The stability in 100-seed weight in descending order was EAI 3600, 931/5/34, DPSB 19, SBH 7/1/1, SBH 4/4/4, SBH 10/5/6, SBH 10/2/3, SBH 4/6/6, Gazelle, Nyala, SBH 6/6/6/2, SBH 3/8/4/1, SBH 1/12/9, DPSB 8 and DPSB 3.

Genotype stability on seeds pod^{-1} [Fig.4.3 (c)] was highest in SBH 6/6/6/2 and least in DPSB 3. The first and second principal components accounted for 82.66% of the variation in stability of the genotypes based on number of seeds pod^{-1}. Genotype SBH 6/6/6/2 was highly stable for seeds pod^{-1} while DPSB 3 was the least stable for the trait. The stability for seeds pod^{-1} in descending order was SBH 6/6/6/2, 931/5/34, SBH 10/5/6, SBH 4/4/4, SBH 3/8/4/1, SBH 7/1/1, SBH 1/12/9, Nyala, DPSB 19, SBH 10/2/3, EAI 3600, SBH 4/6/6, Gazelle, DPSB 8 and DPSB 3.

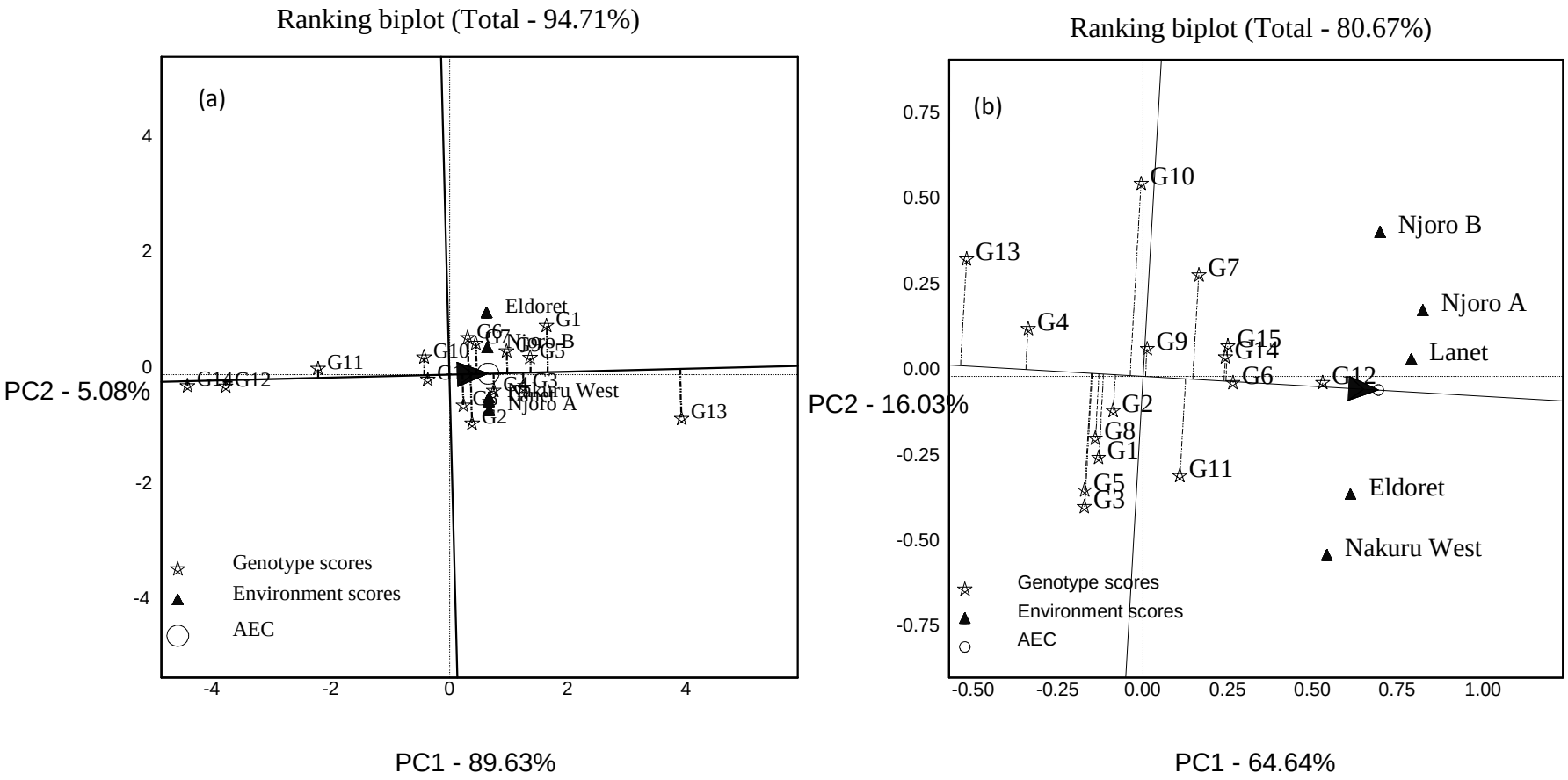

Figure 4.2. GGE biplots showing stability of soybean genotypes based on (a) oil content in g kg^{-1} (b) protein content in g kg^{-1}**.** The genotypes are G1-SBH 10/5/6; G2-SBH 1/12/9; G3-SBH 7/1/1; G4 Gazelle; G5-SBH 4/4/4; G6- SBH 10/2/3; G7-SBH 4/6/6; G8-Nyala; G9-EAI 3600; G10 SBH 6/6/6/2; G11-DPSB 8; G12-DPSB 19; G13 931/5/34; G14-DPSB 3; G15-SBH 3/8/4/1.

Table 4.6: Mean protein content and interaction scores of 15 soybean genotypes evaluated across 5 environments in 2011.

Genotype	Protein content in seed (g kg^{-1})	IPCA 1	IPCA 2
SBH 10/5/6	365.8	0.24702	0.80337
SBH 6/6/6/2	378.5	-0.74272	0.53584
DPSB 8	380.3	0.23320	-0.27976
DPSB 19	402.8	-0.93528	-0.75098
931/5/34	352.1	0.39008	1.09580
DPSB 3	391.7	0.02848	-1.05209
SBH 3/8/4/1	389.8	-0.74992	-0.45292
SBH 1/12/9	370.3	0.41640	0.51761
SBH 7/1/1	367.7	1.11370	-0.36843
Gazelle	360.9	0.44126	0.54953
SBH 4/4/4	368.5	0.90524	-0.46034
SBH 10/2/3	387.7	-0.82979	0.05189
SBH 4/6/6	384.1	-0.70330	0.48243
Nyala	372.0	0.55536	-0.72622
EAI 3600	377.6	-0.36974	0.05428

4.2.5 Broad sense heritability of the soybean genotypes

The heritability estimates ranged from 0.17-0.79 for days to flowering, maturity, plant height, pods $plant^{-1}$, seeds pod^{-1}, branches $plant^{-1}$, nodes $plant^{-1}$, seed yield, seed weight, oil content and protein content. Broad sense heritability estimates were low for protein content (0.17) and pods $plant^{-1}$ (0.24). The estimates were medium seed yield (0.49), oil content (0.50), number of branches $plant^{-1}$ (0.50, and (Table 4.7). High traits heritability were observed for number of nodes $plant^{-1}$ (0.76) flowering (0.76), harvest maturity (0.65), plant height (0.70), number of seeds pod^{-1} (0.72) and seed weight (0.79).

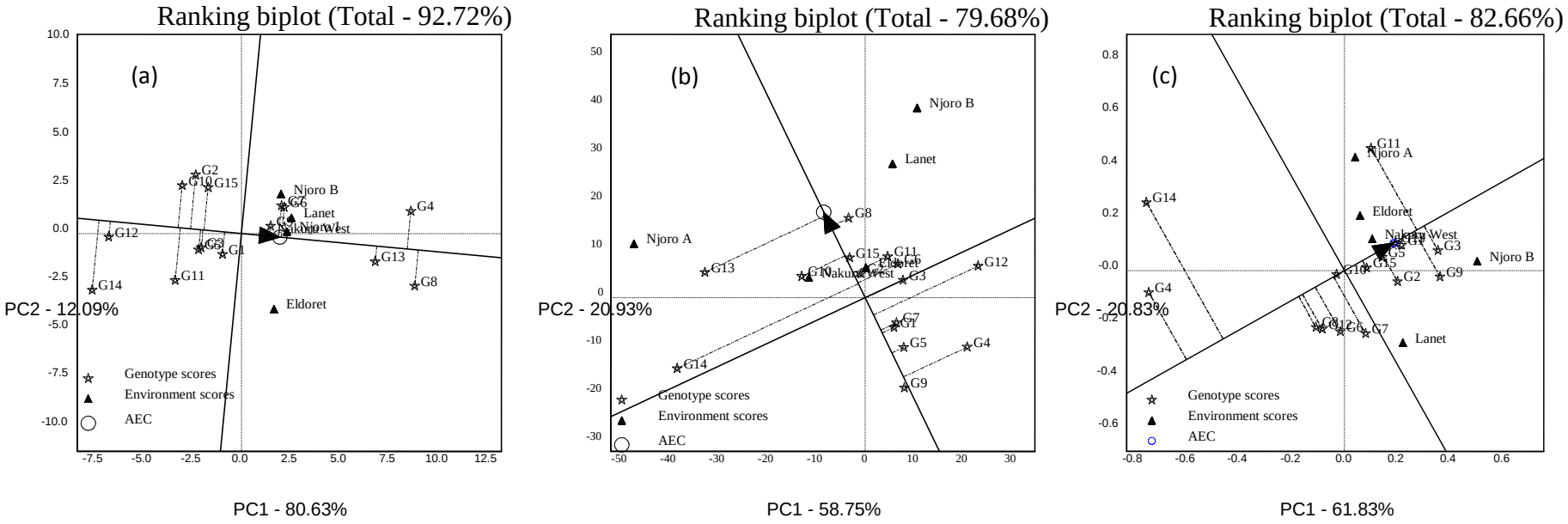

Figure 4.3. GGE biplots showing stability of soybean genotypes based on (a) pods plant^{-1} (b) 100-seed weight and (c) seeds pod^{-1}. Genotype codes are G1-SBH 10/5/6; G2-SBH 1/12/9; G3-SBH 7/1/1; G4-Gazelle; G5-SBH 4/4/4; G6-SBH 10/2/3; G7-SBH 4/6/6; G8-Nyala; G9-EAI 3600; G10-SBH 6/6/6/2; G11-DPSB 8; G12-DPSB 19; G13-931/5/34; G14-DPSB 3; G15-SBH 3/8/4/1.

Table 4.7. Variance components and heritability estimates of soybean genotype traits evaluated at Lanet, Nakuru West, Eldoret, Njoro A and B in 2011.

Traits		$\delta^2 e$	$\delta^2 g$	$\delta^2 ge$	H^2
50% flowering	(d)	50432.11	10816.44	95.66	0.76
Harvest maturity	(d)	468570.95	57082.19	464.41	0.65
Plant height	(cm)	290683.79	46306.81	1356.48	0.70
Pods plant^{-1}	(No.)	279184.56	5897.59	803.52	0.24
Seeds pod^{-1}	(No.)	19.49	3.49	0.29	0.72
Branches plant^{-1}	(No.)	1639.65	105.12	4.86	0.49
Nodes plant^{-1}	(No.)	4238.10	924.98	27.17	0.76
Seed yield	(Kg ha^{-1})	65406353.74	4297155.32	214073.34	0.49
Seed weight	(g)	4397.51	1089.62	18.41	0.79
Oil content	(g kg^{-1})	6060.80	407.94	3.29	0.50
Protein content	(g kg^{-1})	29223.16	411.56	16.96	0.17

$\delta^2 e$ - Experimental error, $\delta^2 g$ - Variance due to genotype, $\delta^2 ge$ - Variance due to genotype $\times$ environment interaction. H^2 - Broad sense heritability.

4.3 Discussion

4.3.1 Genotypes adaptability and stability for yield

The AMMI analysis of variance indicated significant differences due to genotypes for seed yield, oil and protein content denoting that there was diversity among the soybean genotypes studied. The mean squares for the environments were significant ($P < 0.01$) indicating that the selected environments were different from each other. The significant G × E interaction for seed yield, oil content and protein suggested that genotypes evaluated responded differently to different environments. The differences in environments were probably due to differences in edaphic and weather conditions. Further, soybean seed yield had been observed to be sensitive to environmental changes (Sudaric *et al.,* 2006).

When the GGE biplots are used to analyze stability of the genotypes, the line through the origin of the plot exhibits the average environment axis (AEA) while the perpendicular line to the AEA is the average ordinate environment axis (AOE) and this divides the genotypes into those with higher yield than the mean (on the right side of AOE) and those with lower yield than the mean on the left side of AOE. Projection of the genotypes on the AEA ranks the genotypes by yield where the increase is in the direction of the arrow (Mitrovic *et al.,* 2012). In this study, genotype and genotype plus environment (GGE) method demonstrated that genotypes SBH 7/1/1, Nyala, SBH 1/12/9, EAI 3600, Gazelle and DPSB 8 were the highest yielding genotypes while lowest yield were observed for DPSB 3

and DPSB 19. While evaluating soybean resistance to rust disease in Uganda, Tukamuhabwa *et al.* (2012) observed low yield on variety Maksoy 1N when grown at Ngeta while BSPS48A produced the highest grain yield at Nakabango. In addition, yield stability was also noted in wheat (Farshadfar *et al.*, 2012) and these differential performances of the soybean and wheat varieties showed G × E interaction.

Stability of the genotypes depends on the distances from the AEA. Genotypes near the AEA are considered stable (Hidayat *et al.*, 2011). This study showed that genotypes SBH 4/4/4, SBH 1/12/9, DPSB 8, SBH 10/5/6 and SBH 10/2/3 were stable for grain yield while cultivar Nyala and genotype 931/5/34 were less stable across the test environments. Among the genotypes that were stable, SBH 4/4/4, Gazelle, SBH 10/5/6 and SBH 1/12/9, SBH 10/5/6 and DPSB 8 produced grain yield above the mean grain yield across the test environments. Despite the fact that genotypes SBH 10/2/3, SBH 6/6/6/2 and DPSB 3 were stable for yield across the environments, grain yields were low and consequently could not be recommended for production across environments. Nassiuma and Wasike, (2002) evaluated soybean genotypes for yield stability in Kenya and reported that Gazelle, Nyala and EAI 3600 were stable for yield across the test environments. This contradicts the current findings where cultivar Nyala is revealed as unstable by both AMMI and GGE biplot analyses. However, the findings agree on the stability of EAI 3600 and genotype Gazelle which were observed as moderately stable. The differences in the results could have been due to differences in the set of environments used in the study. The study areas were two marginal areas (Gachoka and Thika) and two low altitude areas (Busia and Homabay) over a period of five years (1994-1998). This resulted in nineteen 19 environments as testing was done for four years in Busia.

In the stability ranking, both the AMMI and the GGE rankings were generally the same but not in all counts, for example, in both rankings, genotype Nyala was unstable but genotype DPSB 3 was regarded more stable in the GGE biplot than in the AMMI rankings as it had a high IPCA score.

4.3.2 Genotypes adaptability and stability for oil content

Genotypes SBH 4/4/4 and EAI 3600 were the most stable genotypes across environments for oil contents. The IPCA 1 scores were < 1.0 and the genotypes were all close to the AEA implying the genotypes had low significant differences in stability for oil content. However, genotype SBH 3/8/4/1 was the most stable for oil content across

environments though it had lower oil content than the mean of the trial. Tubic *et al.* (2011) while evaluating thirteen soybean varieties of different maturity groups also observed small differences in oil content stability. This observation could be due to the low G × E interaction. The variation in the oil content among the genotypes was due to environmental and genotypic effects. The implication is that environmental choice can be made on where to grow a specific genotype to get the desired oil content. G × E interactions observed in AMMI analysis could be attributed to weather and edaphic factors as observed by Tukamuhabwa *et al.* (2012). Njoro A and Njoro B were different because of amount of precipitation received and temperatures experienced during plant growth. There is a tendency for the oil content to be high in warmer environments [Lanet (1920 m.a.s.l.) and Nakuru west (2003 m.a.s.l.)] where genotype Nyala had high oil content compared to cool environments such as [Njoro (2185 m.a.s.l.) and Eldoret (2154 m.a.s.l.)] where the same genotype had a reduced oil content by about 2%. The temperature was moderated by the altitude of the respective environments. These results are in agreement with those of Ramana and Satyanarayana, (2006) who observed similar results while testing 16 soybean genotypes in India.

The negative correlation between oil and protein content as well as the negative correlation between yield and protein limits obtaining genotypes with high yield and protein contents (Marega *et al.,* 2001). This means that as the yield of a genotype increases the protein content reduces. Though this makes breeding for high yield and protein content difficult, it has been demonstrated that it's possible to obtain lines with high protein content and keep, simultaneously, the grain yield and the seed physiological quality (Li *et al.,* 1999; Mello *et al.,* 2004). The negative correlation between oil and protein was clearly demonstrated by the ranking of genotypes in Fig. 4.4 and 4.6. The phenomenon was exemplified by genotype 931/5/34 which had the highest oil content and the least protein content and DPSB 19 which had second lowest oil content and highest protein content. This implies that the breeder has to make a decision on which trait to prioritize, otherwise it's not easy to improve substantially, the oil and protein content simultaneously. AMMI and GGE biplot agree on the stability of all the genotypes based on oil content as they scored low (< 1.0) on this trait.

4.3.3 Genotype adaptability and stability for protein content

Protein and oil content are determined by genetic and environmental factors in soybean (Tubic *et al.,* 2011). Except for SBH 7/1/1 which had an interaction score slightly

>1.0, and thus the least stable among the genotypes, the genotypes were not significantly different in their stability for protein content. This could have been caused by the low G × E interactions (8.1%) observed in this experiment.

The AMMI analysis of variance (Table 4.8) revealed that environments contributed 80.5% of the variation for protein content in seed while genotypes and G × E interaction contributed 11.4% and 8.1%, respectively. This observation implies particular environments are better placed for production of soybean with higher protein content. Fehr (2003) analyzed protein content and found that genotype × environment interaction had no significant effects on soybean protein components. Genotype DPSB 19 was the best choice for protein production in all the environments. Soybean breeders' have expressed the need for genotypes with high protein and oil contents as well as high grain yield (Marega *et al.,* 2001).

4.3.4 Stability of important soybean yield components

In soybean, important yield components are pods plant^{-1}, seed size and seeds pod^{-1} (Khodadad, 2012). The genotypes under study varied in their stability in yield components. Each of the genotypes was unique on the stability of yield components and this might have contributed to yield stability of the genotypes. Genotype Gazelle was considered stable by GGE biplot analysis but there was no indication that the genotype had more than average stability in any of the important yield components. This implied that there are more factors that contribute to stability of genotypes than the contribution by important yield components. Yothasiri and Somawang, (2006) while evaluating 10 genotypes in 12 environments observed that all genotypes were above average in stability for 100-seed weight. However, stability in number of seeds pod^{-1} and number of pods plant^{-1} was below and above average among the genotypes.

4.3.5 Broad sense heritability of the soybean genotypes

Broad sense heritability was low for protein content, seed yield, number of branches plant^{-1}, pods plant^{-1} and medium for oil content. Heritability was high for days to 50% flowering, days to harvest maturity, plant height, and seeds pod^{-1}, number of nodes plant^{-1} and seed weight. Aditya *et al.,* (2011) in an experiment consisting of thirty one soybean genotypes got high heritability estimates for days to 50% flowering, plant height, pods per plant, number of primary branches, seed yield and seed weight. These results are consistent with the current findings for days to 50% flowering, plant height, and seed weight (Table

4.7). However, this was not so for pods plant^{-1}, number of primary branches and seed yield which registered low heritability estimates. Mukesh and Kamendra, (2009) in a study involving 20 elite soybean lines got high heritability estimates for plant height, number of pods plant^{-1}, number of primary branches and seed weight. There was low heritability in seeds pod^{-1}, number of nodes plant^{-1} and protein content. The results were not in agreement with the current results for seeds pod^{-1}, number of nodes plant^{-1} and number of branches (Table 4.7). Similar results were observed for protein content, 100-seed weight and plant height. The resultant disparity in the results may be due to the fact that heritability is a property not only of character but also of the population, environment and the circumstances to which the genotypes are subjected to as proposed by Falconer, (1960). The ultimate value of heritability depends upon the magnitude of all components of variance.

4. 4 Conclusion

The AMMI and GGE methods of stability analysis can identify highly performing and stable genotypes. The AMMI model revealed that the G × E interaction was an important source of variation in soybean yield and the GGE biplots were effective in visualizing the genotype performance. Identification of genotypes that are stable for yield is likely to include genotypes stable for oil and protein content. The oil and protein are least affected by G × E but are significantly affected by the environment. Genotypes EAI 3600 and SBH 4/6/6 were stable for yield and had high protein and oil content; yield above the mean and are good candidates for production and inclusion in a breeding programme. Genotypes SBH 4/4/4, SBH 7/1/1, SBH 1/12/9 and Gazelle may be recommended for inclusion in a breeding program where focus is high oil content. Heritability was low for seed yield. Selection for genotypes to include in a breeding program would thus be based on seed weight and days to flowering to cater for production of high yield and early maturity. Heritability for yield components was high for seeds per pod and seed weight and the traits could be used for selection of high yielding genotypes.

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CHAPTER FIVE

GENERAL DISCUSSION AND CONCLUSIONS

The availability of high yielding and stable varieties is among the constraints limiting production and adoption of soybean in Kenya. The study was carried out to determine the performance of fifteen soybean genotypes in five environments namely Njoro A and B, Lanet, Eldoret and Nakuru west which are all high altitude soybean growing areas. The objectives of the study was to i) estimate broad sense heritability of yield and its components ii) establish the stability of the genotypes for yield, oil and protein contents across the environments. Analysis of variance was used to assess the performance of the genotypes across the sites while additive main effects and multiplicative interactions (AMMI) and genotype plus genotype and environment (GGE) biplots were used to identify stable genotypes. Broad sense heritability estimates were determined by the variance component method.

Combined analysis revealed that there was significant ($P < 0.01$) variation in the main effects of genotype, environment and genotype × environment. This implied that there were genetic variations among the genotypes and that the genotypes responded differently across environments. There were variations of mean values of all the traits studied among the genotypes. Mean days to 50% flowering ranged from 74-100 with genotype DPSB 19 being the earliest and DPSB 3 being the latest. The genotypes contributed 59% to the total sum of squares while G × E interactions contributed 9% for days to flowering. The earliest and latest genotypes in maturity were also the earliest and latest to attain 50% flowering. There was a positive correlation between time to flowering and maturity.

The components that contribute to seed yield in soybean include the number of plants per unit area, seed size, seeds pod^{-1} and pod number plant^{-1} (Liu *et al.,* 2010). The mean yield was 1267.9 kg ha^{-1} with genotype Nyala produced the highest mean yield of 1600.9 kg ha^{-1} while genotype DPSB 3 had the least seed yield (661.7 kg ha^{-1}). The mean pods plant^{-1} was 39.3 but ranged from 32-47 for genotypes EAI 3600 and 931/5/34, respectively. There is considerable variation on seed size among the seeds produced by a soybean plant (Egli, 2012). Seed size produced has a direct effect on seed yield especially when the variation is caused by environmental conditions during seed filling stage (Egli, 2012). The current study has reported a mean 100-seed weight of 13.7 g with a range of 10.47-17.60 g for genotype DPSB 3 and Nyala, respectively. Genotype Nyala had the highest grain yield and highest

100-seed weight while genotype DPSB 3 had the least grain yield and least 100-seed weight. The trial mean number of seeds pod^{-1} was 2.3. Genotype Gazelle had the least number of seeds pod^{-1} (2.0) while highest number of seeds pod^{-1} was recorded on genotype EAI 3600 (2.4). Genetic and environmental factors control yield, protein and oil content of soybean (Wolf *et al.*, 1982, Maestri *et al.*, 1998, Bennet *et al*., 2003). Oil and protein contents varied among the genotypes and across the environments. Oil content ranged from 166.0 g kg^{-1} for DPSB 3 to 219.0 g kg^{-1} for 931/5/34. The mean protein content was 377.0 g kg^{-1}. Genotype 931/5/34 had the highest oil content (403.0 g kg^{-1}) while genotype DPSB 19 had the least (352.0 g kg^{-1}).

Performance of genotypes in the individual environments varied. There were significant ($P < 0.01$) differences among the genotypes for all traits studied except for protein content which was significant ($P < 0.05$) at Lanet. The site observed the highest mean seed weight at 2179 kg ha^{-1} for genotype Gazelle. At Eldoret and Nakuru West all the traits varied significantly except for number of seeds pod^{-1}. The best yielding genotype was Nyala with 1229 kg ha^{-1} while the least was 931/5/34 at Nakuru West while SBH 7/1/1 yielded highest at Eldoret (1492 kg ha^{-1}). Except for seeds pod^{-1} all the traits varied in Njoro A and B. The best yielding genotype in Njoro A was DPSB 8 at 1919.1 Kg ha^{-1} which was also late in maturity (208 days), tallest (110.9 cm) and had the highest number of seeds per pod (2.7). In the late planted crop (Njoro B), the best genotype in terms of yield was Nyala with 2397.6 kg ha^{-1} which also had 62.5 pods plant $^{-1}$. Significant variability among the genotypes for all the traits studied in the five environments allowed for selection of genotypes that performed well in each environment.

Heritability is an estimate of the genetic contributions to the phenotypic variance and in its broad sense encompasses additive, dominant and epistatic variance components (Gutierrez-Gonzalez *et al*., 2009). Heritability has value principally as a method for quantifying the notion of whether progress from selection for a plant character is relatively easy or difficult to make in a breeding programme (Hanson, 1963). Broad sense heritability in the current study ranged from 0.17 for protein content to 0.79 for 100-seed weight. The heritability estimates were high for days to harvest maturity, 100-seed weight, days to 50% flowering, plant height, number of seeds pod^{-1} and number of nodes plant^{-1}.

Determination of G × E interaction in plant breeding programmes and germplasm evaluation studies is desirable to find genotypes that show little interaction with the environment (Mebrahtu *et al.,* 2002). Use of stable genotypes for improved seed yield is a

vital objective for sustainable agriculture (Carpenter and Borad, 1997). Stability analysis in the current study was carried out using additive means and multiplicative interaction (AMMI) and genotype plus genotype and environment (GGE) bi-plots. AMMI revealed the most interactive genotypes as DPSB 3 with interaction score of -28.8 and Nyala with an interaction score of 17.23 implying they were unstable for seed yield while the least interactive genotype was DPSB 8 with an interactive score of 0.49 based on first IPCA suggesting it was the most stable among the genotypes. Low contribution of the G × E to the sum of squares (5.6%) and the low IPCA 1 scores, suggested that all the genotypes were generally stable for oil content in all environments tested. All the genotypes were stable for their protein content as they showed low PCA 1 scores. However, there were varying degrees of stability and the GGE biplot showed that genotypes SBH 6/6/6/2 and SBH 7/1/1 were the least stable among the genotypes tested while Gazelle, SBH 1/12/9, EAI 3600, SBH 10/2/3, 931/5/34 and DPSB 19 were more stable in their protein content.

5.1 Conclusion

Results from the combined analysis indicated that there were significant variations for all the traits studied. The variation in response of genotypes in different environments indicated the diversity of genotypes and that it would be possible to select genotypes for particular ecological zones. Farmers should thus grow the varieties that have been identified in the study suited to their environments. Heritability analysis indicated that yield, a quantitative character, was low but other traits such as 100-seed weight could be used as selection criteria for selection of high yielding genotypes in a breeding programme. The additive main effects and multiplicative interaction (AMMI) and genotype plus genotype and environment (GGE) methods of stability analysis can be effectively used for stability analysis. However, GGE biplots have the advantage of visual observation of the genotypes placement on the biplot. The disadvantage of the GGE biplots is that as the genotypes and environments increase or when their values are close; there is a tendency of overlaps that make identification of the environments and genotypes difficult to discern on the biplots as observed in figure 4.2(a) and 4.4(b).

5.2 Future Research

The study has resulted in the achievement of milestones as was limited to the area of the study. The study covered only the high altitude regions of the country but as soybean grows in low, medium and high altitude areas not exceeding 2200 m.a.s.l, further research

need be carried out to cover the low and medium altitude regions. Seed composition is important for it defines the end use quality of soybean products. Analysis of the seed composition and how it's affected by G × E is important to make decisions on what genotypes to grow where and with what specific end user qualities. Soybean is not only used for food but also for natural resource management, feed and forage. Analysis of biomass content within genotypes across environments and the effects of G × E on the same are important. Studies on bio-degradation and nutritional qualities are important to benefit natural resource management and animal nutrition respectively. As the number and spectrum of soybean consumers expands, there is need for studies on seed coat discoloration and seed cracking to improve on seed quality.

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APPENDICES

Appendix 1. Analysis of variance (ANOVA) tables for 50% flowering, days to harvest maturity, plant height, pods plant^{-1}, seeds pod^{-1}, branches plant^{-1}, nodes plant^{-1}, seed yield, 100-seed weight, oil content and protein content of fifteen soybean genotypes.

a) Analysis of variance table for days to 50% flowering.

Source	Degrees of freedom	Sum of squares	Mean squares	F. value	F. probability
Treatment	84	16269.573	193.685	39.48	<.0001
Error	140	686.888	4.906		
Total	224	16956.462			
Grand mean	84.048				
C.V.	2.635				

b) Analysis of variance table for days to harvest maturity.

Source	Degrees of freedom	Sum of squares	Mean squares	F. value	F. probability
Treatment	84	103153.306	1228.015	33.41	<.0001
Error	140	5145.688	36.754		
Total	224	108298.995			
Grand mean	163.115				
C.V.	3.716				

c) Analysis of variance for plant height.

Source	Degrees of freedom	Sum of squares	Mean squares	F. value	F. probability
Treatment	84	93113.906	1108.499	29.63	<.0001
Error	140	5237.985	37.414		
Total	224	98351.945			
Grand mean	70.17				
C.V.	8.71				

d) Analysis of variance for pods per plant.

Source	Degrees of freedom	Sum of squares	Mean squares	F. value	F. probability
Treatment	84	44860.614	534.054	10.90	<.0001
Error	140	6856.536	48.975		
Total	224	51717.150			
Grand mean	39.25				
C.V.	17.82				

e) Analysis of variance for seeds per pod.

Source	Degrees of freedom	Sum of squares	Mean squares	F. value	F. probability
Treatment	84	9.733	0.115	2.83	<.0001
Error	140	5.739	0.040		
Total	224	15.472			
Grand mean	2.30				
C.V.	8.786				

f) Analysis of variance for number of branches per plant.

source	Degrees of freedom	Sum of squares	Mean squares	F. value	F. probability
Treatment	84	335.035	3.988	8.37	<.0001
Error	140	66.702	0.476		
Total	224	401.737			
Grand mean	5.46				
C.V.	12.640				

g) Analysis of variance table for number of nodes per plant.

source	Degrees of freedom	Sum of squares	Mean squares	F. value	F. probability
Treatment	84	1714.884	20.415	16.46	<.0001
Error	140	173.601	1.240		
Total	224	1888.485			
Grand mean	13.42				
C.V.	8.298				

h) Analysis of variance for seed yield.

source	Degrees of freedom	Sum of squares	Mean squares	F. value	F. probability
Treatment	84	46542878.12	5554081.88	10.99	<.0001
Error	140	7060558.59	50432.56		
Total	224	53603436.71			
Grand mean	1267.76				
C.V.	17.714				

i) Analysis of variance for seed weight.

Source	Degrees of freedom	Sum of squares	Mean squares	F. value	F. probability
Treatment	84	1716.595	20.435	11.28	<.0001
Error	140	253.733	1.812		
Total	224	1970.328			
Grand mean	13.66				
C.V.	9.853				

j) Analysis of variance for soybean oil content.

Source	Degrees of freedom	Sum of squares	Mean squares	F. value	F. probability
Treatment	84	978.522	11.649	29.62	<.0001
Error	140	55.060	0.393		
Total	224	1033.582			
Grand mean	19.405				
C.V.	3.231				

k) Analysis of variance for soybean protein content.

Source	Degrees of freedom	Sum of squares	Mean squares	F. value	F. probability
Treatment	84	3294.588	39.221	12.99	<.0001
Error	140	422.789	3.019		
Grand mean	37.664				
C.V.	4.613				

Appendix 2. Rainfall data at Eldoret, Lanet and Njoro in 2011.

	Month	Jan.	Feb.	March	April	May	June	July	Aug.	Sept.	Oct.	Nov.	Dec.
Eldoret	Rainfall (mm)	5.2	36.5	73.3	44.7	126.7	190.8	170.9	284.1	85.3	83.0	164.4	41.3
	No. of days	1	3	8	6	14	14	16	20	8	8	19	4
Lanet	Rainfall (mm)	0	0	60	33.2	81.9	0	32.6	135.7	109.8	117.7	9.2	50.9
	No. of days	0	0	7	6	11	0	6	10	8	9	2	5
Njoro	Rainfall (mm)	3.9	9.5	130.5	28.9	120.5	177.7	158.6	124.9	145.4	102.1	165.3	104.6
	No. of days	1	3	14	11	13	18	19	18	19	14	17	12

Source: Eldoret University; KALRO-Lanet; KALRO-Njoro

Appendix 3. Soybean Production Statistics in 2011.

World Oilseed production		
Oil seed	(million tonnes)	%
Soybean	251.5	56
Rapeseed	60.8	13
Cotton seed	46.6	10
Peanut	35.5	8
Sunflower seed	38.9	9
Palm Kernel	13.4	3
Copra	5.8	1

World soybean production		
Country	(million tonnes)	%
United states	83.2	33
Brazil	72.0	29
Argentina	48.0	19
China	13.5	5
India	11.0	4
Paraguay	6.4	3
Canada	4.2	2
Other	13.1	5

Source: www.soystats.com 2012