

CHARACTERIZATION AND COMBINING ABILITY AMONG SELECTED SOYBEAN CULTIVARS

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the requirements for the award of Master of Science Degree in
Plant Breeding of Egerton University

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DECLARATION

This thesis is my original work and has not been presented for the award of a degree in any other university.

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DEDICATION

This thesis is dedicated to my late dad Mr. Peter Okwiri, and mum Mrs. Phyllis Okwiri in loving memory.

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ABSTRACT

Soybean [*Glycine max* (L.) Merrill] is one of the major sources of plant protein and oil in human and animal diets, which was introduced in Kenya in the 1970's. Soybean is currently being grown in many parts of the country particularly Western Kenya. However, information on genetic diversity, heterosis and combining ability for the introduced soybean genotypes, which would be useful in the development of a sound-breeding programme is lacking. Evaluation of genetic diversity and knowledge of heterosis and combining ability would be needed for successful germplasm exploitation. The objectives of this study were to (i) characterize twenty soybean genotypes based on morphological and agronomic variability (ii) estimate the combining ability and heterosis for agronomic characters among six soybean genotypes selected on the basis of genetic diversity. Twenty soybean genotypes, and six genotypes and their crosses were evaluated at the Egerton University, Njoro Kenya during 2001 and 2002 cropping seasons, respectively. The genotypes were significantly different for one or more of the characters evaluated. The similarity index suggested that there is considerable genetic diversity among the genotypes. Ward's cluster analysis grouped the genotypes into two major categories where similarities were revealed among eight short determinate genotypes forming the first category while twelve tall and determinate, semi-determinate or indeterminate genotypes were more divergent and formed the second category. Nine principal components accounted for 95% of the total variation. Characters, including number of nodes per plant, plant height, days to maturity, number

of seeds per pod, days to 50% flowering, 100-seed weight and leaf shape were the major sources of diversity among the soybean genotypes. Broad sense heritability estimates were generally greater for all characters (0.66 – 0.91) except days to seed emergence (0.38). Positive phenotypic correlations for days to 50% flowering, number of nodes per plant, plant height, number of pods per plant, number of seeds per pod and days to maturity with seed yield and a negative correlation between seed yield and bacterial blight resistance scores were generally greater. Better parent heterosis for seed yield was generally low in most of the crosses. General combining ability (GCA) effects were highly significant for days to 50% flowering, plant height, days to maturity and seed yield whereas, both general (GCA) and specific combining ability (SCA) effect were significant for 100-seed weight. The ratios of mean square, $2 \text{ GCA} / (2\text{GCA} + \text{SCA})$ were closer to unity, which indicated that additive gene effects were important than non-additive gene effects for all the traits measured in crosses. Bossier and EAI 3600 were identified as potential parents for a hybridization programme to develop improved lines for days to maturity and seed yield.

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TABLE OF CONTENTS

DECLARATION	II
DEDICATION	III
ACKNOWLEDGMENTS	IV
ABSTRACT	V
TABLE OF CONTENTS.....	VII
LIST OF TABLES	X
LIST OF FIGURES.....	XII
LIST OF APPENDICES	XIII
CHAPTER ONE	1
1.0 INTRODUCTION.....	1
1.1 Background Information.....	1
1.2 Statement of Problem	2
1.3 Objectives.....	2
1.4 Justification	3
CHAPTER TWO.....	4
2.0 LITERATURE REVIEW	4
2.1 Soybean Production in Kenya.....	4
2.2 Importance of Soybean Crop	5
2.3 Soybean Adaptability.....	6
2.4 Yield, Yield Components and Morphological Traits in Soybeans	7

2.5 Genetic Diversity	9
2.6 Heterosis in Soybean	11
2.7 Combining Ability in Soybean	13
2.8 Seed Protein Improvement in Soybean	14
2.9 Genetics of Soybean Resistance to Races of Bacterial Blight	15
CHAPTER THREE	17
3.0 MATERIALS AND METHODS	17
3.1 Experimental Site	17
3.2 Characterization of Soybean Genotypes	17
3.2.1 Planting and Data Collection	17
3.2.2 Statistical Analyses	25
3.2.2.1 Analysis of Variance (ANOVA)	25
3.2.2.2 Broad Sense Heritable (h^2_b)	26
3.2.2.3 Phenotypic Correlations (rp)	26
3.2.1.4 Principal Component Analysis	26
3.2.2.5 Cluster Analysis	27
3.3 Heterosis and Combining Ability	27
3.3.1 Statistical Analysis	28
3.3.1.1 Analysis of Variance (ANOVA)	28
3.3.1.2 Heterosis	29
3.3.1.3 Combining Ability	30
CHAPTER FOUR	31
4.0 RESULTS AND DISCUSSION	31
4.1 Characterization of Soybean Genotypes	31
4.1.1 Morphological Characters	31
4.1.1.1 Growth Habit	31
4.1.1.2 Hypocotyl Colour	34
4.1.1.3 Leaf Shape	34
4.1.1.4 Pubescence Colour	34
4.1.1.5 Flower Colour	35
4.1.1.6 Hilum Colour	35
4.1.2 Agronomic Characters	36
4.1.2.1 Days to Seed Emergence	36
4.1.2.2 Days to 50% Flowering	38
4.1.2.3 Bacterial Blight Resistance	38
4.1.2.4 Number of Primary Branches per Plant	39

4.1.2.5 Number of Main Stem Nodes per Plant	39
4.1.2.6 Plant Height.....	40
4.1.2.7 Lodging (%)	40
4.1.2.8 Number of Pods per Plant	41
4.1.2.9 Days to Maturity	41
4.1.2.10 Number of Seeds per Pod.....	42
4.1.2.11 Hundred seed weight.....	43
4.1.2.12 Seed Yield (kg ha ⁻¹).....	43
4.1.2.13 Protein Content (%).....	44
4.2 Broad Sense Heritability.....	45
4.3 Phenotypic Correlations.....	48
4.4 Principal Component Analysis.....	53
4.5 Cluster Analysis.....	55
4.6 Combining Ability.....	58
4.6.1 Performance of parents and crosses	58
4.6.1.1 Parents.....	58
4.6.1.2 F ₁ Crosses.....	61
4.6.2 Heterosis in F ₁	64
4.6.3 General and specific combining ability	66
CHAPTER FIVE	74
5.0 CONCLUSIONS AND RECOMMENDATIONS	74
5.1 Conclusions.....	74
5.2 Recommendation.....	75
REFERENCES.....	76
APPENDICES	89

LIST OF TABLES

Table 1. Name and source of 20 soybean genotypes.....	18
Table 2. Morphological and agronomic performance of 20 soybean genotypes grown at Egerton University, Njoro Kenya during the 2001 rainy season.	32
Table 3. Mean squares for thirteen agronomic characters in soybean grown at the Egerton University Njoro, Kenya during the year 2001.	37
Table 4. Broad sense heritability estimates for some characters in soybean grown at Egerton University, Njoro Kenya during the 2001 rainy season.	46
Table 5. Phenotypic correlation coefficients among 13 characters measured on 20 soybean genotypes.	49
Table 6. Principal component coefficients (e_i) of 19 characters in 20 soybean genotypes grown at Egerton University, Njoro Kenya.	54
Table 7. Combined analysis of variance for parents and F_1 crosses of five traits in a diallel cross of soybean grown at Egerton University, Njoro Kenya during the year 2002.....	59
Table 8. Mean performance of six soybean genotypes at Egerton University, Njoro Kenya.	60
Table 9. Mean performance of 15 soybean F_1 crosses at Egerton University, Njoro Kenya.	62
Table 10. F_1 Heterosis expressed as a percentage above the better parent for five soybean characters evaluated at Egerton University, Njoro Kenya.....	65
Table 11. Mean squares for general and specific combining ability of soybean F_1 progeny for five traits at Egerton University, Njoro Kenya.	68
Table 12. Estimates of general combining ability (GCA) effects of six soybean genotypes grown at Egerton University, Njoro Kenya.	69

Table 13. Estimates of specific combining ability (SCA) effects of six soybean
genotypes grown at Egerton University, Njoro Kenya..... 70

LIST OF FIGURES

- Figure 1. Resistance scores of soybean genotypes for bacterial blight (*Pseudomonas syringae* pv. *glycinea*) in natural field conditions observed at physiological maturity based on 0-9 scale. 24
- Figure 2. Dendrogram of the similarities among 20 soybean genotypes, grown at Egerton university, Njoro in Kenya during the 2001 rainy season using Ward's minimum variance method of cluster analysis..... 56

LIST OF APPENDICES

Appendix 1. Temperature data for the year 2001 and 2002 at Egerton University Njoro, Kenya.....	89
Appendix 2. Rainfall data for the year 2001and 2002 at Egerton University Njoro, Kenya.....	90
Appendix 3. Leaning angle and lodging area.....	91
Appendix 4. (a) Analysis of variance (ANOVA) tables for characterization of soybean genotypes.....	92
Appendix 4. (b) Analysis of variance (ANOVA) tables for combining ability among soybean genotypes.....	97

CHAPTER ONE

1.0 INTRODUCTION

1.1 Background Information

Soybean [*Glycine max* (L.) Merrill] is one of the major sources of plant protein and oil in human and animal diets in most parts of the world. On the average, soybean seed provides 40% protein and 21% oil. Soybean as a new industrial crop was introduced in Kenya by Food and Agricultural Organization of the United Nations (FAO) in 1970's. The current national demand is estimated at 150,000 metric tonnes per annum. However, the country's production of only 5000 metric tonnes per annum mostly from Western Kenya, falls far short of the demand (Vegetables Oil and Protein System Reports, 1997; Ephanto, 1997).

Preliminary research on current soybean germplasm adaptation was carried out by the German Technical Co-operation (GTZ) in collaboration with Kenya Agricultural Research Institute (KARI) and the Ministry of Agriculture from 1993 to 1998. This helped establish foundations for the development of soybean industry in Kenya. The project acquired and screened some germplasm obtained from local and foreign sources. Preliminary evaluation of these germplasm at various locations helped identify six promising cultivars namely Nyala, SCS-1, Sable, Bossier, Gazelle and EAI 3600 for general cultivation (KARI Report, 1998). Besides, earlier selection work by KARI had released some introductions for commercial production which include Hill, Blackhawk

and Perry 41 (KARI Report, 1998). Most of these soybean cultivars have low seed yield averaging 1000-2500 kg ha⁻¹, although the potential is up to 3000 kg ha⁻¹ (Judy and Whigham, 1976). They also have poor adaptability to dry areas of Kenya and are susceptible to common pests and diseases (KARI Report, 1999). Therefore there is need for increased soybean production in Kenya. This can be achieved through breeding high yielding and widely adapted cultivars. Effective breeding programme would require identification, characterization and description of superior germplasm. Information about characterization and combining ability among selected cultivars would be helpful in the development of a successful soybean breeding programme.

1.2 Statement of Problem

Several soybean germplasm have been introduced, evaluated and a few of them released for commercial production in Kenya but studies on genetic diversity for morphological and agronomic traits have not been carried out. Similarly, limited information on heterosis and combining ability is available for the soybean cultivars grown in Kenya.

1.3 Objectives

General Objective:

To provide agronomic and morphological descriptions among selected soybean genotypes in order determine the range of diversity represented within the genotypes and to estimate the combining ability and heterosis among selected genotypes for utilization in the development of improved cultivars.

Specific Objectives:

1. To characterize twenty soybean genotypes based on morphological and agronomic variability.
2. To estimate the combining ability and heterosis for agronomic characteristics among six soybean cultivars selected on the basis of genetic diversity.

1.4 Justification

Evaluation of genetic diversity is a prerequisite for successful germplasm exploitation through breeding. Characterization would therefore enable selection of most diverse genotypes to be used in crosses. Similarly, knowledge of heterosis patterns and combining ability of the soybean cultivars grown in Kenya would be useful in the development of a sound breeding and germplasm enhancement programme.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Soybean Production in Kenya

The majority of the Kenyan population lives in the rural areas. Most of them are low-income earners who practice subsistence agriculture. Besides, malnutrition cases are rampant. This is aggravated by the fact that the availability of animal protein has become a limitation to the majority of the people living in both urban and rural areas. Therefore, effective utilization of soybean can help reduce these problems (KARI Report, 1999).

Soybean has been grown in most maize growing areas in Kenya, i.e. Western, Nyanza and parts of the Rift Valley province. It has also been grown on limited acreage in Eastern and Central Provinces. Generally, the performance of the crop is poor resulting into low yields (KARI Report, 1999). To address the problem in the soybean sub-sector, the government is currently encouraging its production in the country. In the Rift Valley for example the land under the crop has increased from 46 ha in 1995 to 359 ha in 1997. This produced approximately 120 metric tons. The 1998 target was to bring 561 ha of land under soybean production. The estimated total production acreage in Kenya for 1998 was 6,400 ha while the one for 1999 was 10,800 ha (KARI Report, 1999). However, despite these efforts there still continues to be a growing imbalance between production and consumption growth rate in the country.

2.2 Importance of Soybean Crop

Plants are an important source of edible protein but seed protein lacks in one or more essential amino acids. Seed protein is considered to be lower in quality and require supplement if used in animal diets (Burton et al., 1982). Unlike other seed proteins, soybean is grown for its high quality protein content (40%) seeds apart from nitrogen fixation. Soybean protein is valuable because of its amino acid composition. It is high in lysine. In partially dehydrated form, soybean is a major component of most margarine and vegetable fats. The grains are consumed green, dry or sprouted, whole or split. Soy flour is a source of high quality protein and cholesterol free oil.

Raw soybeans which are not precooked, are blanched. Full fat flour or a mixture of the flour and maize meal is consumed. It is also used in baking products, beverages, meat substitutes and extenders. Soymilk is used to prepare cheese and other milk products. Soybean meal is used to manufacture animal feeds. Current research suggests that soybean help reduce blood cholesterol levels and lower the risk of osteoporosis. In a study of individuals consuming 40 g of soy-protein daily, an increase in bone density in the lumbar spine region in post-menopausal women was reported. Other forms in which soybean is consumed include, tofu or soy-card, meat analogs and whole bean cooked with maize (Daily Nation 10th September, 1998). Soybean is therefore an important food crop and a direct source of income.

2.3 Soybean Adaptability

Soybean in Kenya can be grown in widely diverse ecological conditions, i.e. in high, medium and low potential areas. Different varieties grow in different agroclimatic conditions. Selection of the right cultivar for a particular agro-ecological zone is important if economical yields are to be realized. Temperature requirements depend upon the cultivar. The optimum temperature range under which most cultivars can thrive well during the growth period is between 20-25°C. Generally, the crop grows well under fairly warm day and night temperatures. Seedlings are photoperiod sensitive, so cultivars suitable for one country may not be suitable for another. Day length may not be a problem in Kenya since all days are nearly of equal hours though soybean is essentially a short day crop (KARI Report, 1998). The optimum rainfall requirement is between 300–600 mm well distributed over the growing period. High moisture requirement is critical for germination. Soybeans are drought tolerant after germination. Moisture is also critical during flowering and pod formation stage. Soybean grows well in deep fertile and well-drained soils with high calcium content. Optimum pH of suitable soils ranges from 5.6–6.8. Heavy impermeable soils are unsuitable (KARI Report, 1998).

Soybeans have different maturity periods. In general, early maturing cultivars perform better than late maturing ones in areas of high temperatures and short spell rainfall. Late maturing cultivars on the other hand out yield the early maturing ones in high potential areas. Very early and very late maturing cultivars have low yields. However, these are

quantitative traits that are bound to change if a cultivar is shifted from one geographical area to another (KARI Report, 1997).

2.4 Yield, Yield Components and Morphological Traits in Soybeans

Previous research on soybeans in Kenya revealed inherent variability in many characteristics (KARI Report, 1998). In seed crops the most economically important part of the plant is the mature seed. Factors influencing seed development are finally reflected in the yield through seed size. Seed size is however determined by the rate of seed growth (Guldan and Brun, 1985). Soybean cultivars with seed size greater than 20 g 100-seeds⁻¹ are preferred for direct human consumption in some areas of the world. Preferred large seeded cultivars yield less than small seeded ones with seed size 12–19 g 100-seeds⁻¹ (Bahrenfus et al., 1978). Hartwig and Edwards (1970) reported that seed size had no effect on seed yield. Utilizing small seeded cultivar parents in a breeding programme may be a useful source of genes for improvement of yield in large seeded parents. However, it may be difficult to obtain segregants with seed size similar to large seeded parents (Weber, 1950). Although large seeds are preferred, small seeds may be of an advantage. Singh (1976) found that small seeded types tend to maintain viability during storage better than large seeded ones. Small seeds also require less moisture for germination. Hartwig and Edwards (1970) reported that large seeds were readily damaged by mechanical handling.

Studies have found that yield and/or the yield components of full season determinate and indeterminate soybean lines are affected by several factors (Board, 1987; Parvez et al., 1989). Akhter and Sneller (1996a) reported that increased plant height was associated with increased yield in determinate and indeterminate genotypes, particularly when height was correlated positively with the number of main stem nodes. However, there was no other partial correlation of yield with any other yield component that was significant. Seed yield was not affected by stem termination (Akhter and Sneller, 1996a).

Soybean plant morphology can be affected by use of qualitative genes. These alterations may be useful in deriving high yielding lines (Hartung et al., 1980). Subtle qualitatively inherited variation in soybean plant morphology could be exploited. Evaluation of the potential major genes that condition qualitative alterations in morphology and architecture could be used (Bernard and Weiss, 1973).

Pubescence density in soybean has been shown to affect plant vigour, insect injury and transpiration rates. Although dense pubescent types tend to yield slightly higher than normal pubescent types, yield advantage was not significant in any of the reports (Hartwig and Edwards, 1970; Singh et al., 1971; Ghorashy et al., 1971; Cooper, 1971).

Utility of narrow leaflet shapes in permitting greater light penetration into soybean canopy has been characterized (Hicks et al., 1969). However, yields were similar in narrow and ovate isolines (Hicks et al., 1969; Hartwig and Edwards, 1970). Leaflet

shape ranges from oval to lanceolate and is controlled genetically. Nearly, all commercial cultivars have broad leaflets (FAO, 1994). Broad leaflet lines yield more in most production environments probably because they intercept more light. However, a yield advantage for narrow leaflet lines has been demonstrated (Hartwig and Edwards, 1970). Narrow leaflets permit deeper light penetration. Solar radiation reaching the soil surface increase intensity of weed germination, which will compete with the crop for nutrient and solar radiation (FAO, 1994)

2.5 Genetic Diversity

Crop germplasm plays a very important role in the development of improved cultivars. Preserving genetic diversity is of paramount importance (Brown, 1989). Germplasm provides a repository of useful genes for the plant scientist. It also provides a source of new genes to solve future production problems. The investigations following the outbreak of the epidemic disease corn blight in the 1970's revealed that the genetic bases for many crops were narrow. Sneller (1994) estimated that 90 and 92 % of the parentage of elite public and proprietary soybean lines grown in the Northern and Southern regions of the United States, respectively, could be traced to 12 ancestors. The restricted genetic base could cause several problems for soybean breeders. It could lead to genetic vulnerability of the crop to disease or other stresses and it could limit gain from selection for metric traits such as yield due to lack of variation in crosses between lines derived from a narrow gene pool. In applied breeding it is commonly assumed that the cross of diverse rather than similar parents enhances breeding success.

Although genetic relations of breeding materials are never far from the mind of the breeder, quantification of diversity is elusive and therefore, measures of diversity are generally not used in the planning of the crosses. However, in Kenya soybean genotypes including recent introductions are expected to have some genetic diversity patterns, which have not been characterized. Germplasm studies often use cluster analysis for categorization (Basigalup et al., 1995). The clusters are determined from plant anatomical characteristics or geographical origins of particular populations or lines. Cluster analysis has been used to assess similarities among germplasm in many breeding programmes where genotypic and phenotypic repetitions of several characters were found among a set of populations, lines or accessions from which parents were selected for hybridization (Wilson et al., 1990; Veronesi and Falcinelli, 1988). It can be used as a method for the evaluation of genetic similarity in specific host-parasite interactions (Labeda and Jendrulek, 1987).

The intensive selection of useful genes among cultivated germplasm by modern breeding programmes has resulted in the decline of genetic diversity (Yingshan et al., 1999). However, studies have demonstrated the existence of genetic variability for morphological and agronomic characteristics among soybean genotypes (Xu et al., 1999). Kisha et al. (1997) have shown a positive association of genetic variation for seed yield and other agronomic traits in soybean populations and the genetic distance of parents. Thus, increasing the genetic diversity of soybean is an important objective. An ideal source of genetic diversity for a polygenic trait would be genetically diverse lines

with desirable phenotypes as they would be likely to have more desirable genes than lines with undesirable phenotypes, thus simplifying the breeding needed to use the diversity. The variance needs to be properly characterized so that the most diverse genotypes may be used as parents for hybridization and enhancement programme. To date, many soybean germplasm have been introduced in Kenya (KARI Report, 1998) but information on genetic diversity for morphological and agronomic traits is lacking. Therefore these germplasm could be a more readily usable genetic resource for the development of improved cultivars. Through exploitation of the available gene sources, some significant benefits can be brought to fruition.

2.6 Heterosis in Soybean

The attainment of maximum crop yields is an important objective of most breeding programmes. Interest in hybrid soybean has been stimulated with the finding of male-sterility gene, but no such viable system of producing hybrid soybean seed in quantity by utilization of male-sterility is available (Poehlman, 1987). In recent years yield increase has been obtained by plant breeders through heterosis (Poehlman, 1987).

It is important to validate the utility of diversity measures if they are to be applied in plant breeding. One way of validating genetic similarity measure is through prediction of heterosis (Gizlice et al., 1993; Cox and Murphy, 1990). Theoretically, the more distant the parents, the greater the number of genes they differ by, the greater the potential interaction of the genes in the form of dominance and epistasis, and thus the

greater the potential for heterosis (Falconer, 1989). The relationship between genetic distance and heterosis has been studied in both cross- and self-pollinated species. In maize, with genotypes from contrasting geographical regions, heterosis was positively associated with the genetic distance of parents (Moll et al., 1965; Prasad and Singh, 1986). The amount of heterosis among pearl millet landraces varied but large heterosis of certain crosses indicated that the parents were genetically more diverse than manifests of little or no heterosis (Ouendeba et al., 1995).

In soybean, there are a few reports indicating the existence of heterosis for important agronomic traits. Nelson and Bernard (1984) found high parent F_1 heterosis for yield as much as 19% but not for other phenotypic traits. They concluded that heterosis could not be predicted from parental characteristics. Gizlice et al., (1993) studied F_2 heterosis using five ancestors of southern US soybean cultivars and found that heterosis increased with phenotypic dissimilarity of parents. In a study conducted by Manjarrez-Sandoval et al. (1997), high parent F_2 heterosis was as high as 11% averaged over locations. This may justify the use of F_2 hybrids in soybean production. However, they concluded that extensive field-testing might be necessary to identify parental combinations required for commercial production.

Although there is no current use for heterosis in commercial soybean production, male sterility and cytoplasmic male-sterility systems have been developed for the production of hybrids (Carter and Burton, 1992; Gai et al., 1995). The commercial production of hybrids in other self-pollinated crops like rice (*Oryza sativa* L.) is now a reality

(Virmani, 1996). The discovery of male sterility, resulted in the widespread application of heterosis to rice production in China (Lijuan et al., 1999). In soybean, breeders incorporated early maturity and developed an extremely early maturing cultivar, which extended China's soybean production region (Wang and Gao, 1985).

2.7 Combining Ability in Soybean

Studies have been conducted for both general (GCA) and specific combining ability (SCA) in self- and cross-pollinated crops. Some inbred lines as well as pure lines have been found to combine well with each other to give high yielding progenies from crosses. Inbred- and pure-lines derived from genetically dissimilar populations combine best (Poehlman, 1987). Fonseca and Patterson (1968) studying wheat reported significant GCA effects for grain yield suggesting additive genetic variance. Results obtained by Li et al. (1995) from experiments carried out in sunflower found significant GCA for reduced cadmium level accumulation in F_1 . Ouendeba et al. (1993) reported positive GCA for grain yield, grain weight and negative GCA for downey mildew in crosses of pearl millet landrace populations indicating the predominance of additive gene effects. Significant positive GCA effects for grain yield and negative GCA effects for endosperm hardness of CYMMIT's quality protein maize germplasm was shown among crosses made in different populations (Vasal et al., 1993). F_1 and F_2 diallel analysis among dry bean genotypes exhibited large positive GCA effects for both grain yield and seed weight. Determinate parents tended to have positive GCA effects for the

architectural traits, whereas the opposite was true for the indeterminate types (Nienhuis and Singh, 1986).

There are limited reports about combining ability analyses in soybean. However, from a diallel set of crosses involving five soybean genotypes and 20 F₁ hybrids, estimates for GCA and SCA were significant for seed soluble protein and lipoxygenases, whereas only the estimate of GCA was significant for total seed protein (Zougari et al., 1999). In another diallel investigation on soybeans, positive GCA effects for total protein was observed, which indicated additive gene action (Chen, 1987). Cho and Scott (2000) reported significant GCA effects for soybean seed vigour and seed yield while significant GCA and SCA effects were found for seed weight hence both additive and non-additive gene effects were involved in conditioning seed weight. Parents that reveal high GCA estimates are good candidates in an improvement programme (Baker, 1978).

2.8 Seed Protein Improvement in Soybean

World soybean production will need to increase to meet the projected demand for high quality protein (Smith and Huyser, 1987). Breeding efforts have played a major role in increasing soybean production over the past 40 years (Burton, 1987), resulting in development of soybean cultivars that typically contain 415 g kg⁻¹ seed protein (Burton, 1991). Review papers (Burton, 1985; 1987; 1991) indicate that numerous researchers have attempted breeding for increased soybean seed protein concentration. However, a major drawback to the development of soybean cultivars with increased seed protein concentration is the negative genetic correlation between soybean seed yield and protein

in both determinate and indeterminate soybean (Burton, 1987). Nevertheless, Pantalone et al. (1996) found none significant correlation between soybean seed yield and protein implying that selection for favorable attributes can be obtained simultaneously. This is encouraging because the genetic variability of these two traits found in the population may enable breeders to select high yielding lines with high protein concentration (Pantalone et al., 1996). Improved protein content levels might be reached from parental lines in crosses, with the maintenance of a genetic background ensuring a sufficient yield level (Zougari et al., 1999).

There is considerable genetic variability among soybean germplasm for protein content. The environmental conditions however, influence the chemical composition of soybean seed but cultivars can be classified as high or low protein according to their use (FAO, 1994). Variation of seed protein content occurs across different agro-ecological zones (KARI Report, 1997). Studies have suggested that early seed may have different protein concentrations. Significant higher protein concentrations on seeds from the upper portion of plants was reported, compared to those from lower parts of the stem (Collins and Carter, 1956). Time of flowering was found to have a significant effect on the rate of protein accumulation in soybean seed (Gbikpki and Crookston, 1981).

2.9 Genetics of Soybean Resistance to Races of Bacterial Blight

A specific resistance gene (R-gene) in the plant is matched by a specific avirulence gene (*avr*-gene) in the pathogen. Only if both genes are present is the pathogen rapidly detected and contained. The genetics of this type of interaction, often referred to as

gene-for-gene resistance, were first described by Flor (1955) to account for varietal resistance to flax rust (*Melampsora lini*). Gene-for-gene resistance has since been described for interactions between plants and nematode, fungal, bacterial and viral pathogens (reviewed by Crute and Pink, 1996).

R genes in distantly related plant species occasionally share the same avirulence gene specificity. An example of two such functionally analogous R-genes is *RPMI* and *RpgI* from *Arabidopsis* and soybean, respectively. Both respond to *Pseudomonas syringae* strains expressing *avrB*, an avirulence gene isolated from *P. syringae* pv. *glycinea* (Innes et al., 1993; Bisgrove et al., 1994; Mukherjee et al., 1966; Staskawicz et al., 1987; Keen and Buzzell, 1991). The *Arabidopsis RPMI* gene is unusual in that it displays a dual specificity, also responding to *avrRpml* (Bisgrove et al., 1994), an avirulence gene isolated from *P. Syringae* pv. *maculicola* (Debener et al., 1991). However, it is not known whether functionally analogous R-genes result from the conservation of an ancestral gene through specification or whether convergent evolution is responsible.

Varietal resistance to bacterial blight (Causative agent, *P. syringae* pv. *glycinea*, *Psg*) in soybean was noted as early as 1919 (Coerper, 1919). A single, dominant gene conferring resistance to race 1 *psg* was identified by Mukherjee et al. (1966) and named *RpgI*. Subsequently, it was shown that the avirulence gene interacting with *RpgI* was *avrB* (Staskawicz et al., 1987; Keen and Buzzell, 1991). An allele or, tightly linked gene at the *RpgI* locus, specific for *avrRpml* was identified (Ashfield et al., 1995).

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Experimental Site

The field experiments were conducted at the Department of Agronomy Fields, Egerton University, Njoro. The Njoro location was selected because it is a representative of the soybean growing areas in Rift Valley Province. Njoro is located in Nakuru district and lies in LH₂₋₃ agro-ecological zone at an altitude of 2238 m above sea level. The site has a tropical climate (Jaetzold and Schmidt, 1982). The average maximum temperature in the year 2001 was 22.8°C while for the year 2002 (January–May) was 24.0°C. (Appendix 1). Rainfall in the year 2001 was 1133.2 mm and 453.4 mm in the year 2002 (January–May) (Appendix 2). The soils are classified as mollic andosols (Jaetzold and Schmidt, 1982). The soil is characterized by a pH of 5.7 and contains 55% sand, 23% silt, 22% clay and 2.1% organic carbon.

3.2 Characterization of Soybean Genotypes

3.2.1 Planting and Data Collection

Twenty genotypes were obtained from Kenya Agricultural Research Institute (KARI), National Plant Breeding Research Centre, Njoro, some of which were introduced by the German Technical Corporation (GTZ) soybean project (Table 1).

Table 1. Name and source of 20 soybean genotypes.

Name of genotype ^a	Source
Nyala	Zimbabwe
Blackhawk	USA
TGM-237-2	Nigeria
Hill	USA
EAI 3600	USA
813/5/11	Zimbabwe
847/6/11	Zimbabwe
914/5/39	Zimbabwe
928/5/5	Zimbabwe
931/5/34	Zimbabwe
941/5/7	Zimbabwe
932/5/11	Zimbabwe
932/5/38	Zimbabwe
SCS-1	Zimbabwe
Duicker	Zimbabwe
929/5/30	Zimbabwe
Gazelle	Zimbabwe
Bossier	USA
Sable	Zimbabwe
911/6/3	Zimbabwe

^a Obtained from KARI National Plant Breeding Research Centre, Njoro.

The twenty genotypes were planted in a randomized complete block design with three replications during the 2001 rainy season (April-November). They were grown in two-row plots, each 1.35m long with 10 plants. Distance between rows and between plants within rows was 0.45 m and 0.15 m, respectively. Each plot received a basal dose of 60 kg P_2O_5 ha⁻¹ and 23 kg N ha⁻¹ before planting (KARI Report, 1997). At thinning a second application of 20 kg N ha⁻¹ was applied as top dressing. Two seeds were sown per hole. The trial was hand planted and the plants were thinned to 1 plant per hill 20 days after emergence. Weeds were controlled by hand weeding. Insect pests and fungal pathogens were not controlled. Plants on the rows ends were not included for collection of data.

The International Plant Genetic Resources Institute (IPGRI) descriptor list for soybean was used for characterization. The following morphological and agronomic characters were recorded on six randomly selected plants in each replication:

1. Growth habit

The growth habit (stem type) was determined at maturity, when 95% of the pods turn brown (tan) (Fehr and Caviness, 1977).

Rating was:

3 = Determinate

5 = Semi-determinate

7 = Indeterminate

2. Hypocotyl colour

The hypocotyl colour was recorded at the time when the primary leaves were fully expanded as:

1 = green

2 = purple

3. Leaflet shape

Judged from the ratio of length/width (cm) of fully developed terminal leaflet on the middle part of the main stem. The measurement was done at flowering and the scores were:

3 = Narrow ($l/w = 2.2$ or more) = Lanceolate

5 = Intermediate ($l/w = 1.9 - 2.1$)

7 = Broad ($l/w = 1.8$ or less) = ovate.

4. Pubescence colour

Observed at flowering stage. The scores were:

1 = Grey

2 = Light brown

3 = Brown = tawny

5. Flower colour

Was recorded at flowering stage as:

3 = White

5 = Purple throat

7 = Purple

6. Hilum colour

Was rated as:

1 = Yellow

2 = Buff

3 = Brown

4 = Green

5 = Grey

6 = Imperfect black (black with buff outer ring).

7 = Black

8 = Others

7. Days to emergence

Days taken from planting to 50% of the plant emergence.

8. Days to flowering

Number of days taken from emergence to 50% of the plants with at least one open flower.

9. Lodging

Was rated from the leaning angle and the lodging area at physiological maturity. The angle was measured as the deviation from the upright position and the lodging area calculated as:

$$\left[\frac{\text{No. of lodged plants plot}^{-1}}{\text{Initial stand}} \times 100 \right]$$

The rating was:

- 0 = None
- 3 = Slight
- 5 = Moderate
- 7 = Severe
- 9 = Very severe

(Appendix 3 for details).

10. Number of primary branches per plant

Was counted at maturity per plant and the mean computed. A branch was defined as any appendage of the main stem with at least one node.

11. Number of nodes on the main stem

Was counted at maturity as the number of nodes on the main stem beginning with the cotyledonary node and ending with the node site of the last fully expanded trifoliate leaf.

12. Plant height (cm)

Was measured from the ground level to the tip of the main stem at maturity.

13. Number of pods per plant

All the pods per plant were counted at maturity and their mean computed.

14. Days to maturity

Was determined as the number of days from emergence to when 95% of the pods turned brown (tan).

15. Number of seeds per pod

Was calculated as a mean of the number of seeds from 50 randomly selected pods from six randomly selected plants plot⁻¹.

16. Hundred seed weight (g)

Dry weight of 100 seeds adjusted to 13% moisture content was recorded.

17. Seed yield (kg ha⁻¹)

Dry weight of threshed seeds per plot adjusted to 13% moisture content was recorded.

18. Total protein content (6.25 x N)

Total seed protein content (% dry wt. basis) was evaluated by Kjeldahl method as described by Okalebo et al. (1993).

19. Bacterial blight resistance

Visual ratings for resistance to bacterial blight at crop maturity were made under natural field conditions. The observations were made on the fully developed terminal leaflet from the middle part of the main stem. It was based on 0–9 scale (Sinclair, 1982) (Fig 1). Where:

0 = Immune

1-3 = Resistant

4-5 = Moderately susceptible

6-7 = Highly susceptible

8-9 = Extremely susceptible

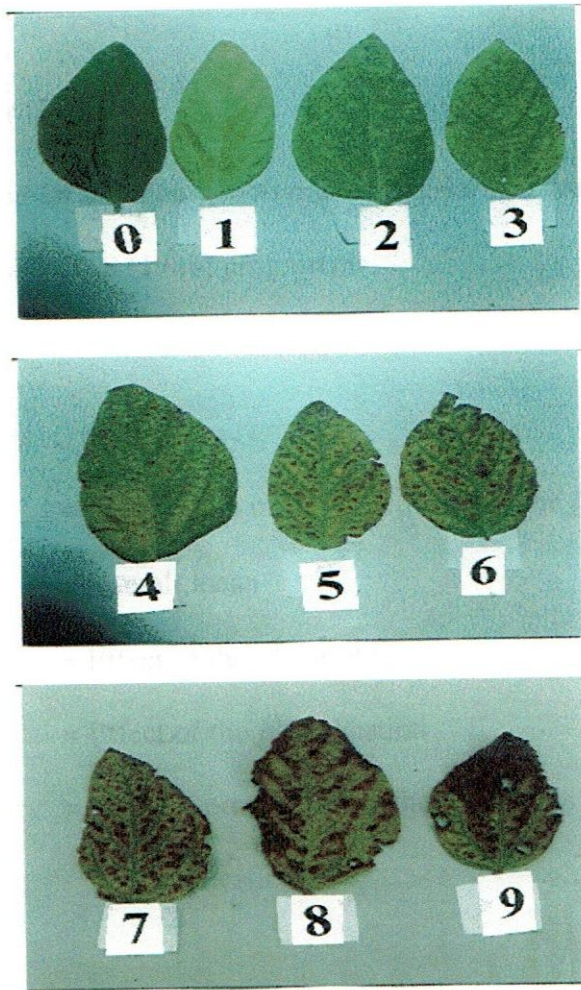


Figure 1. Resistance scores of soybean genotypes for bacterial blight (*Pseudomonas syringae* pv. *glycinea*) in natural field conditions observed at physiological maturity based on 0-9 scale; 0 = immune, 1-3 = resistant, 4-5 = moderately susceptible, 6-7 = highly susceptible, 8 - 9 = extremely susceptible.

3.2.2 Statistical Analyses

3.2.2.1 Analysis of Variance (ANOVA)

Analysis of variance of the 20 soybean genotypes was performed based on plot-mean values for all characters using SAS (1988) programme.

Statistical model:

$$Y_{ij} = \mu + g_i + b_j + e_{ij}$$

Where: Y_{ij} = Observation of the i^{th} genotype in the j^{th} replication
 μ = Overall mean
 g_i = Effect of the i^{th} variable
 b_j = Effect of the j^{th} replication
 e_{ij} = Random error effect of the i^{th} variable in the j^{th} replication

ANOVA Table.

Source of variation	d.f.	Expected mean square
Replication (r)	r - 1	$\sigma_e^2 + g\sigma_r^2$
Genotype (g)	g - 1	$\sigma_e^2 + r\sigma_g^2$
Error	(r - 1)(g - 1)	σ_e^2
Total	rg - 1	

Test for significance was done at 5% confidence level. Means were compared using Duncan's Multiple Range Test (DMRT) (Steel and Torrie, 1980).

3.2.2.2 Broad Sense Heritable (h^2_b)

Heritability on an entry-mean basis (Hanson, 1963; Nyquist, 1991) was calculated as follows:

$$h^2_b = \sigma_g^2 / \sigma_g^2 + \sigma_e^2$$

Where: σ_g^2 = Genetic variance

σ_e^2 = Experimental error

Values were derived from variance components estimated using expected mean squares (Dudley and Moll, 1969). Confidence intervals were calculated for heritability estimates with formulae of Knapp et al. (1985).

3.2.2.3 Phenotypic Correlations (rp)

The phenotypic correlations (rp) between characters x and y was calculated as follows:

$$rp = \frac{Cov(P_x, P_y)}{\sqrt{\sigma^2 P_x \sigma^2 P_y}}$$

Where, cov and σ^2 are the phenotypic covariance and variance, respectively for traits x and y (Falconer, 1989).

3.2.1.4 Principal Component Analysis

Variance among the soybean genotypes were further studied using the Principal Component Analysis (PCA) concerned with explaining the variance-covariance structure through a few linear combinations of the original variables (Kendall, 1980). This technique was used to assess similarities among the genotypes and to evaluate morphological and agronomic parameters contributing to the variations. Data were

standardized by character (Mean = 0, standard deviation = 1). Principal components were calculated from a matrix based on correlations between the characters. Specific procedures for PCA were executed with the microcomputer programme, SAS (1988).

3.2.2.5 Cluster Analysis

A hierarchical cluster analysis was run based on the genotype means of the variables according to Ward's minimum variance method as executed by the cluster procedures of SAS (SAS, 1988). Genotype means were standardized with a mean of zero and standard deviation of one. The most similar objects were first grouped and these initial groups were merged according to their similarities. As similarities decreased, all groups were fused into a single cluster. This method begun with the computation of variances among the genotype means and produced a dendrogram showing successive fusion of genotypes, which culminated at the stage where all genotypes belonged to one cluster.

3.3 Heterosis and Combining Ability

A diallel set of crosses excluding the reciprocals was made among six soybean cultivars: Bossier, Nyala, Blackhawk, EAI 3600, Hill, and TGM-237-2, selected on the basis of genetic diversity (Table 1). Crosses were made in the field during the rainy season (April–November) 2001. Synchronization of planting was done to ensure that all the cultivars flowered at the same time. Fifteen, F_1 hybrids were developed and a minimum of 15 hybrid seeds generated for each cross.

The 6 parents and their 15 hybrids were grown at the Egerton University, Department of Agronomy Field plots during the months of January–June the year 2002 in a randomized complete block design with three replications. The genotypes were grown in one-row plots with 5 plants each. Plot size was 0.6 m rows spaced 0.45 m apart. Plots received 60 kg ha⁻¹ P₂ O₅ and 23 kg ha⁻¹ N before planting. Seeds were sown by hand in hills 0.15 m apart. Rows that did not have 100% emergence were gapped soon after emergence to ensure maximum establishment. Seeds were inoculated with a strain of *Rhizobium japonicum* before planting. Weed management was manual and was near optimum. Fungal pathogens and insect pests were controlled through chemicals: furadan was used at planting to control soil pests and after emergence dimethoate and dithane M 45 were used to control insect pests and fungal pathogens, respectively. Data were recorded on days to 50% flowering, plant height at maturity, days to maturity, 100-seed weight and seed yield (Details under section 3.2).

3.3.1 Statistical Analysis

3.3.1.1 Analysis of Variance (ANOVA)

Analysis of variance was performed on the six parental lines and 15 F₁ hybrids for all characters (SAS, 1988).

Statistical model:

$$Y_{ij} = \mu + g_i + b_j + e_{ij}$$

Where Y_{ij} = Observation of the i^{th} variable in the j^{th} replication

μ = Overall mean

g_i = Effect of the i^{th} variable

b_j = Effect of the j^{th} replication

e_{ij} = Random error effect of the i^{th} variable in the j^{th} replication.

ANOVA Table

Source of variation	d.f.	Expected mean square
Replication (r)	$r - 1$	$\sigma_e^2 + g\sigma_r^2$
Genotype (g)	$g - 1$	$\sigma_e^2 + r\sigma_g^2$
Error (r x g)	$(r - 1)(g - 1)$	σ_e^2
Total	$rg - 1$	

Test for significance was done at 5% confidence level. Means were compared using Duncan's Multiple Range Test (DMRT) (Steel and Torrie, 1980).

3.3.1.2 Heterosis

Heterosis was expressed as the deviation (D_b) of cross mean (C_{ij}) from the better parent (P_b):

$$D_b = C_{ij} - P_b$$

Variance of the deviation was estimated as follows:

$$\text{Var}(D_b) = 2\text{MSE}$$

The replications were considered random effects and the genotypes (15 crosses and their 6 contrasting parents) as fixed effects. A "t" test was used to determine the significance of the better parent heterosis value.

3.3.1.3 Combining Ability

Plot-mean values in all replications were used for the diallel analysis. Griffing's method 4 (no reciprocal crosses, no parents), model 1 (fixed) (Griffing, 1956) was used to obtain estimates of combining ability among the soybean genotypes and their crosses. The model for combining ability was:

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + b_k + e_{ijk}$$

Where: Y_{ijk} = Mean values for the k^{th} plot of cross between the i^{th} and the j^{th} parents

μ = Overall mean.

g_i or g_j = GCA effect of the i^{th} or j^{th} parent.

s_{ij} = SCA effect of the cross between the i^{th} and the j^{th} parents.

b_k = Effect of the k^{th} replication.

e_{ijk} = Error effect peculiar to the ijk^{th} observation.

The model in Griffing's diallel was designed using the assumption that epistasis was not significant. The GCA and SCA mean square were tested against MSE. The GCA estimates were separated using DMRT with MSE (Steel and Torrie, 1980). The relative importance of GCA and SCA in determining progeny performance was assessed by estimating the ratios of mean square, $2GCA/(2GCA+SCA)$. The closer the ratio is to unity, the greater the predictability of progeny performance based on GCA alone. It confirms the predominance of additive gene effects over non-additive gene effects (Baker, 1978).

CHAPTER FOUR

4.0 RESULTS AND DISCUSSION

The main objectives of this study were to investigate the nature and degree of divergence among twenty selected soybean genotypes and to estimate the heterosis and combining ability in a 6 x 6 diallel cross. The results are given below.

4.1 Characterization of Soybean Genotypes

4.1.1 Morphological Characters

4.1.1.1 Growth Habit

Most of the genotypes were determinate and these were Nyala, Blackhawk, TGM-237-2, Hill, EAI 3600, 813/5/11, 847/6/11, 914/5/39, 928/5/5, 931/5/34, 941/5/7, 932/5/11, 932/5/38. Genotypes, SCS-1, Duicker and 929/5/30 were semi-determinate whereas Gazelle, Bossier, Sable and 911/6/3 were indeterminate (Table 2).

Similar results were obtained by Xu et al. (1999) where soybean accessions were found to be chiefly composed of determinate types while indeterminate and semi-determinate types held only a small proportion of the total accessions.

Table 2. Morphological and agronomic performance of 20 soybean genotypes grown at Egerton University, Njoro Kenya during the 2001 rainy season.

Genotype	Growth Habit ^b	Hypocotyl ^c colour	Leaf ^d shape	Pubescence ^e colour	flower ^f colour	Hilum ^g colour	Days to seed Emergence	Days to 50% Flowering	Bacterial blight resistance	Number of branches per plant
							(d)	(d)		
Nyala	I	2	3	1	7	3	9.33abc	81.00def	2.00ef	6.87j
Blackhawk	I	1	7	3	3	3	8.00d	82.00de	7.67a	9.53bcd
TGM-237-2	I	1	7	3	3	3	8.33cd	83.00de	7.33a	9.93abc
Hill	I	1	7	3	3	3	8.00d	82.67de	7.67a	9.07cde
EAI 3600	I	2	7	3	7	7	9.67ab	74.33gh	5.67b	10.67a
813/5/11	I	1	7	1	3	3	9.00abcd	80.00defg	5.33b	7.00j
847/6/11	I	2	7	1	7	1	9.00abcd	94.67c	3.33cde	8.00fghi
914/5/39	I	1	3	3	3	3	8.33cd	100.00abc	3.33cde	10.00abc
928/5/5	I	2	7	1	7	3	9.00abcd	83.67de	4.67bc	8.67defg
931/5/34	I	1	3	3	3	5	8.00d	96.67bc	3.00def	8.47efg
941/5/7	I	2	7	1	7	3	9.33abc	75.67fgh	7.33a	7.13ij
932/5/11	I	2	7	1	7	3	9.00abcd	101.70ab	4.33bcd	8.13efgh
932/5/38	I	2	3	1	7	7	8.67bcd	103.70a	2.67ef	9.47bcd
SCS-1	II	2	7	1	7	1	8.33cd	105.70a	2.00ef	10.27ab
Duicker	II	2	7	1	7	1	8.00d	84.67d	4.33bcd	9.53bcd
929/5/30	II	2	7	1	7	1	10.00a	84.33d	4.67bc	8.13efgh
Gazelle	III	2	7	1	7	1	9.00abcd	84.00d	2.00ef	8.73def
Bossier	III	2	7	3	7	7	8.00d	73.00h	2.00ef	7.73ghij
Sable	III	2	7	1	7	1	9.33abc	77.67efgh	3.00def	7.40hij
911/6/3	III	2	7	1	7	1	9.00abcd	84.33d	1.67f	8.67defg
Mean			7	1	7	1	8.77	86.63	4.20	8.71
S.e ^h							0.36	1.87	0.48	0.30

^a Within columns, means followed by the same letter are not significantly different at p=0.05 based on Duncan's Multiple Range Test.

^b I = Determinate, II = Semi determinate, III = Indeterminate.

^c 1 = Green, 2 = Purple.

^d 3 = Narrow, 7 = Broad

^e 1 = Gray, 3 = Tawny (Brown).

^f 3 = White, 7 = Purple

^g 1 = Yellow, 3 = Brown, 5 = Gray, 7 = Black

^h Standard error of genotype mean used in the Duncan's Multiple Range Test.

(Table 2 continued).

Genotype	Number of nodes per plant	Plant height (cm)	Lodging	Number of pods Per plant	Days to maturity (d)	Number of seeds per pod	Hundred seed weight (g)	Seed yield (Kg/ha ⁻¹)	Protein content (%)
Nyala	13.60defgh	62.83ij	3.00de	60.40def	164.7def	1.33gh	18.20ab	1212defg	39.07bcdef
Blackhawk	11.33h	51.27k	2.33de	47.90efgh	151.0gh	1.59cde	12.23e	835fg	37.30efgh
TGM 237-2	12.27fgh	54.80jk	5.00bcd	59.20def	151.7gh	1.49defg	12.40e	1031efg	40.93abcd
Hill	12.00gh	50.73k	4.33cd	56.70def	151.3gh	1.49defg	12.77e	787fg	38.13defgh
EAI 3600	11.83gh	50.27k	3.67de	48.90efg	150.3gh	1.49defg	15.27d	830fg	43.27a
813/5/11	14.53def	71.47hi	7.67ab	36.60gh	165.0def	1.38fgh	17.93ab	655g	33.50ij
847/6/11	14.87de	84.50efg	7.00abc	57.50def	178.0bc	1.41fgh	18.93a	1866abc	32.73ij
914/5/39	17.33bc	89.10bcde	5.00bcd	42.90fgh	188.0ab	1.44efg	18.83a	877fg	42.00abc
928/5/5	14.00defg	72.30hi	3.67de	45.10fgh	161.0fg	1.42fghg	17.20b	748fg	38.97bcdef
931/5/34	12.07fgh	53.47jk	1.00e	70.40cd	175.7cd	1.89a	17.63ab	2051ab	39.27bcde
941/5/7	13.93defg	62.53ij	2.33de	30.40h	146.3h	1.27h	14.70d	597g	40.33abcde
932/5/11	16.20cd	88.20cdef	5.00bcd	85.20abc	187.7ab	1.60cd	15.87cd	2084ab	42.30ab
932/5/38	16.27cd	80.13efgh	7.67ab	103.30af	192.3a	1.72bc	15.40d	2336a	38.77cdefg
SCS-1	19.67ab	85.23defg	3.67de	84.30bc	182.0abc	1.52def	15.67d	2441a	34.90hij
Duicker	20.06a	78.43fgh	4.33cd	73.50cd	159.7fg	1.47def	17.87ab	1612bcde	35.37hij
929/5/30	19.07ab	75.83gh	2.33de	75.80cd	172.7cde	1.53def	15.70d	1236cdefg	32.20j
Gazelle	18.13abc	97.03bc	7.67ab	55.90defg	182.7cabc	1.51def	17.93ab	1619bcde	35.80fghi
Bossier	19.67ab	98.73b	7.67ab	71.40cd	164.0ef	1.80ab	12.31e	1838abcd	41.27abcd
Sable	18.93ab	95.30bcd	8.33a	67.40cde	176.7bc	1.39fgh	18.30ab	1388cdef	35.73hij
911/6/3	20.60a	112.7a	5.00bcd	99.90ab	193.0a	1.48defg	17.00bc	2040ab	33.67ij
Mean	15.83	75.74	4.83	63.6	169.52	1.51	16.10	1404.0	37.78/
S.e ^h	0.77	2.22	0.83	6.09	3.6	0.05	0.42	199.6	2.91

^aWithin columns, means followed by the same letter are not significantly different at p=0.05 based on Duncan's Multiple Range Test.^h Standard error of genotype mean used in the Duncan's Multiple Range Test.

4.1.1.2 Hypocotyl Colour

Genotypes mainly had purple hypocotyls except Blackhawk, TGM-237-2, Hill, 813/5/11, 914/5/39 and 931/5/34 (Table 2). There is a pleiotropic effect of the gene (W_1) for purple flower colour in that the colour also shows up in hypocotyls of seedlings (Woodworth, 1923). Since, purple flowers are more prevalent among soybean accessions (Xu et al., 1999) it then follows that the same proportion of genotypes with purple hypocotyls occurs and this agreed with the findings in this study.

4.1.1.3 Leaf Shape

All the genotypes had ovate (broad) leaflets except, Nyala, 914/5/39, 931/5/34 and 932/5/38 which had lanceolate (narrow) leaflets (Table 2). Leaflet shape ranges from ovate to lanceolate and is genetically controlled. Nearly, all commercial cultivars have broad leaflets (FAO, 1994). Broad leaflet lines yield more in most production environments however, a yield advantage for narrow leaflet lines has been demonstrated (Hartwig and Edwards, 1970).

4.1.1.4 Pubescence Colour

Genotypes, Nyala, 813/5/11, 847/6/11, 928/5/5, 941/5/7, 932/5/11, 932/5/38, SCS-1, Duicker, 929/5/30, Gazelle, Sable and 911/6/3 had gray pubescence. On the other hand, Blackhawk, TGM-237-2, Hill, EAI 3600, 914/5/39, 931/5/34 and Bossier had tawny pubescence (Table 2). Xu et al. (1999) reported that Chinese soybeans had tawny pubescence types a little more than gray ones and a small proportion of the accessions

were glabrous. In this study, the proportion of genotypes with gray pubescence was greater than those with tawny pubescence however, no glabrous types were found.

4.1.1.5 Flower Colour

Most of the genotypes expressed purple flower colour except Blackhawk, TGM-237-2, Hill, 813/5/11, 914/5/39 and 931/5/34 that had white flowers (Table 2). Soybean accessions were found to have a little more purple than white flowers and a small proportion with mixed flowers (Xu et al., 1999). These results agree with results obtained from this study except there were no genotypes with mixed flower colours.

4.1.1.6 Hilum Colour

The genotypes expressed genetic variability for this trait. Nyala, Blackhawk, TGM-237-2, Hill, 813/5/11, 914/5/39, 928/5/5, 941/5/7 and 932/5/11 had brown hilum. EAI 3600, 932/5/38 and Bossier had seeds with black hilum. 847/6/11, SCS-1, Duicker, 929/5/30, Gazelle, Sable and 911/6/3 had yellow hilum. 931/5/34 was the only genotype with gray hilum.

The primary soybean hilum colours black, brown and yellow are genetically controlled and are prevalent among soybean accessions (Seo et al., 1993; Bhatt and Torrie, 1968; Williams, 1952). Gray hilum colour also occurs but is not so prevalent (Bhatt and Torrie, 1968; Williams, 1952).

4.1.2 Agronomic Characters

The analysis of variance indicated significant differences ($P = 0.01$) among the genotypes for all characters evaluated (Table 3). Three of the 13 characters measured had a coefficient of variability $< 10\%$. Lodging showed the largest coefficient of variability of 29.7% followed by seed yield 24.6% and number of pods per plant 16.6% (Table 3). High coefficient of variability for lodging might have resulted from sampling errors associated with a small population.

4.1.2.1 Days to Seed Emergence

Genetic variability for the number of days to seed emergence after planting was limited. Genotype, 929/5/30 notably took the highest number of days (10 d) to emerge whereas other genotypes emerged in about 8 to 9 days (Table 2).

Helms et al. (1996) showed that initial soil water content and temperature influence percent emergence of soybean. High temperature combined with low soil water content increased seed stress and reduced germination. However, these conditions are difficult to control in the field (Helms et al., 1996). It is therefore important for soybean producers to plant when there is adequate soil moisture for good stand establishment.

Table 3. Mean squares for thirteen agronomic characters in soybean grown at the Egerton University Njoro, Kenya during the year 2001.

Source of variation	d.f	Days to seed emergence (d)	Days to 50% flowering (d)	Bacterial blight resistance	Number of branches per Plant	Number of nodes per plant	Plant height (cm)	Lodging per plant	Number of pods per plant	Days to maturity (d)	Number of seeds per pod	Hundred seed weight	Seed yield (kg ha ⁻¹)	Protein content (%)
Replication(r)	2	0.22	33.02	2.45	0.13	0.32	73.87	6.07	35.9	73.72	0.001	0.06	7623	0.55
Genotype(g)	19	1.13**	302.59**	12.65**	3.51**	29.94**	1015.94**	14.30**	1168.5**	680.86**	0.07**	15.47**	1086732**	34.50**
Error	38	0.39	10.44	0.70	0.27	1.76	32.72	2.07	111.3	38.87	0.007	0.52	119491	15.96
C.V.		7.1	3.7	8.3	5.9	8.4	7.6	29.7	16.6	3.7	5.5	4.5	24.6	10.6

** Significant at p = 0.01.

4.1.2.2 Days to 50% Flowering

Considerable variability was found among the genotypes for this character. Four genotypes, Bossier (73 d), EAI 3600 (74 d), 941/5/7 (76 d) and Sable (78 d) were early flowering (Table 2). On the other hand the genotype, SCS-1 flowered after 106 days, which was the longest number of days to 50% flowering. However, it did differ significantly with 932/5/38 (104 d), 932/5/11 (102 d) and 914/5/39 (100 d) that were also late flowering. The remaining genotypes were clustered in the third group with a range of 80-90 days to flower.

Robinson and Wilcox (1998) reported significant differences among soybean isolines for days to flowering. Average flowering dates were nearly the same for determinate and indeterminate isolines. This demonstrated that growth habit had little effect on days to flowering (Robinson and Wilcox, 1998).

4.1.2.3 Bacterial Blight Resistance

The genotypes showed a wide variability for resistance to bacterial blight (*Pseudomonas syringe* pv. *glycinea*) under natural field conditions (Table 2). The short genotypes, Blackawk, TGM-237-2, Hill, EAI 3600, 813/5/11 and 941/5/7 were highly susceptible, except Nyala. On the other hand, the tall genotypes including 847/6/11, 914/5/39, 932/5/38, Gazelle, Bossier, Sable and SCS-1 showed high level of resistance to bacterial blight. Genotypes that showed moderate level of susceptibility were Duicker, 928/5/5, 929/5/30 and 932/5/11. These results suggested that the tall genotypes

could be exploited in selection programmes as sources of resistance to bacterial blight and could be used to improve the short susceptible genotypes with good traits. However, level of resistance of these genotypes should be evaluated and confirmed under artificial inoculation.

Varietal resistance to bacterial blight in soybean has been demonstrated (Coerper, 1919). A specific resistance gene in plant is matched by a specific avirulence gene in the pathogen. The genetics of this type of interaction often referred to as gene-for-gene resistance has been described (Flor, 1955). Genetically this could be due to epistasis.

4.1.2.4 Number of Primary Branches per Plant

The genotypes expressed variable branching characteristics. Though there was no clear pattern in branching characteristics, some genotypes were notable for high number of branches i.e. EAI-3600, SCS-1, 914/5/39 and TGM-237-2 while genotypes 813/5/11, 941/5/7, Sable, Nyala and Bossier had low number of branches (Table 2).

Quattara and Weaver (1995) found significant differences among soybean genotypes for main stem branches per plant. Determinate types had more main stem branches than the indeterminate ones. However, some indeterminate genotypes had more branches than their determinate counterparts (Quattara and Weaver, 1995).

4.1.2.5 Number of Main Stem Nodes per Plant

There was a clear trend for the number of main stem nodes. The indeterminate and semi-determinate genotypes such as Gazelle, Bossier, SCS-1, Duicker, Sable, 911/6/3,

929/5/30 and 931/5/4 were characterized by a high number of main stem nodes ranging from 18 to 20 nodes per plant (Table 2). On the other hand the determinate genotypes namely, Nyala, Blackhawk TGM-237-2, Hill, EAI 3600, 931/5/34, and 941/5/7) had a lower number of main stem nodes compared to the indeterminate and semi-determinate genotypes. These results indicate that on average, determinate lines had fewer main stem nodes than indeterminate lines and this difference between the two stem termination types was quite typical (May et al., 1990; Akhter and Sneller, 1996a).

4.1.2.6 Plant Height

The mean plant height for the indeterminate stem types was significantly higher than determinate types. The tallest genotype was 911/6/3 (112.7 cm), followed by Bossier (99 cm), Gazelle (97 cm), Sable (95 cm) and 914/5/39 (89 cm). The shortest genotypes were EAI 3600 (50 cm), Hill (51 cm), Blackhawk (51 cm), 931/5/34 (53 cm) and TGM-237-2 (55 cm) (Table 2). The trend is consistent with other observations reported earlier, where the determinate lines were significantly shorter than the indeterminate stem termination lines (May, et al., 1990; Akhter and Sneller, 1996a; Ablett et al., 1989; Foley et al., 1986; Quattara and Weaver, 1994).

4.1.2.7 Lodging (%)

The results show that the indeterminate genotypes namely, Gazelle, Bossier and Sable which were tall as well as tall determinate genotypes namely, 813/5/11, 847/6/11 and 932/5/38, had a higher lodging percentage vis a vis the short determinate types such as

Nyala, Blackhawk, EAI 3600, 931/5/34 and 941/5/7 which were relatively short (Table 2).

Mansur and Orf (1995) found variability among soybean genotypes for lodging resistance. Shorter determinate soybean lines lodged less than taller indeterminate lines. Short plant stature of determinate lines frequently results in less lodging than tall indeterminate lines (Ablett et al., 1989; Cooper, 1985; Foley et al., 1986; Robinson and Wilcox, 1998).

4.1.2.8 Number of Pods per Plant

Genetic variability was evident for this trait among the genotypes. Two genotypes, 932/5/38 and 911/6/3 were noted for high number of pods per plant with 103 and 100 pods, respectively (Table 2). Quattara and Weaver (1995) and Board et al. (1996) found significant differences among soybean cultivars for pods per plant. This is an important yield component that has a direct effect on yield. The existence of genetic variability for this trait among the genotypes is of great importance. The genotypes with high number of pods could be used as a valuable source of genes for the development of cultivars with improved yield potential.

4.1.2.9 Days to Maturity

Genetic variability was shown for maturity period. Genotypes 911/6/3 (193 d), 932/5/38 (192 d), 914/5/39 (188 d), 932/5/11 (188 d), Gazelle (183 d) and SCS-1 (182 d) were the late maturity group. The early maturing genotypes were 941/5/7 (146 d), EAI 3600

(150 d), Blackhawk (151 d), TGM-237-2 (151 d) and Hill (152 d) (Table 2). In general the determinate types were early maturing except genotypes 932/5/38 and 932/5/11, while the indeterminate and semi-determinate genotypes were medium to late maturing. However, there were a few exceptions, for example, Duicker (160 d) and Bossier (164 d) were earlier than other indeterminate and semi-determinate genotypes. On the other hand, 932/5/30 (192 d) was a very late maturing determinate genotype.

Significant difference for maturity date was demonstrated among soybean isolines. The average maturity date was virtually the same for determinate and indeterminate isolines (Robinson and Wilcox, 1998). Range of maturity was found to vary among soybean genotypes especially when the genotypes were moved from one location to the other (Cianzio, 1985).

4.1.2.10 Number of Seeds per Pod

Genotypes showed minimal variability for this character. Nonetheless, genotype 931/5/4 had the highest number of seeds per pods (1.89) followed by Bossier (1.80). The least number of seeds were observed in 941/5/7 (1.27) and Nyala (1.33), respectively. Most of the genotypes had an averaged of 1.5 seeds per pod (Table 2). Seeds per pod was reported to be significantly affected by cultivar differences. Similarly, the cultivars differed in terms of two-seeded and three-seeded pods (Board et al., 1996; Quattara and Weaver, 1995).

4.1.2.11 Hundred seed weight

Genetic variability was observed for hundred seed weight. Genotypes 847/6/11, 914/5/39, Sable, 813/5/11, 911/6/3, 928/5/5, Duicker, Gazelle and Nyala had comparably larger seed weights (17.2 - 18.9 g). EAI 3600, SCS-1, 929/5/30, 941/5/7, 932/5/11 and 932/5/38 had comparable medium seed weights (14.7 - 15.7 g), while Blackhawk, TGM-237-2 Bossier and Hill had smaller seed weights (12.2 - 12.8 g). These results are similar to those obtained by Mansur and Orf (1995).

Utilization of small seeded cultivar parents in a breeding programme may be a useful source of genes for yield improvement as well as other agronomic traits in large seeded cultivars, however it may be difficult to obtain segregants with seed size similar to large seeded parents (Weber, 1950). Small seeded types were found to maintain high viability during storage than large seeded ones (Singh, 1976).

4.1.2.12 Seed Yield (kg ha^{-1})

Little genetic variability was observed for seed yield. However, some genotypes were higher yielding while others had low seed yields. Genotypes, SCS-1 (2441 kg ha^{-1}), 932/5/38 (2336 kg ha^{-1}), 932/5/11 (2084 kg ha^{-1}), 931/5/4 (2051 kg ha^{-1}), 911/6/3 (2040 kg ha^{-1}), 847/6/11 (1886 kg ha^{-1}) and Bossier (1838 kg ha^{-1}) had high seed yields. Hill (787 kg ha^{-1}), EAI 3600 (830 kg ha^{-1}), 813/5/11 (655 kg ha^{-1}), 914/5/39 (877 kg ha^{-1}), 929/5/30 (1236 kg ha^{-1}), 928/5/5 (597 kg ha^{-1}), 941/5/7 (597 kg ha^{-1}), TGM-237-2 (1031 kg ha^{-1}), Blackhawk (835 kg ha^{-1}) and Nyala (1212 kg ha^{-1}) were low yielding

genotypes (Table 2). These findings agree with those reported by Board et al. (1996) where soybean seed yield was found to be affected by cultivar differences

Generally there was no clear trend in terms of productivity among the determinate, semi determinate and the indeterminate genotypes. Akhter and Sneller (1996a) and Robinson and Wilcox (1998) reported that seed yield was not affected by growth habit. These results also show that growth habit did not affect seed yield in that among the high yielding genotypes, Bossier (1838 kg ha⁻¹) and 911/6/3 (2040 kg ha⁻¹) were indeterminate, SCS-1 (2441 kg ha⁻¹) was semi-determinate, while 932/5/38 (2336 kg ha⁻¹), 932/5/11 (2084 kg ha⁻¹), 931/5/4 (2051 kg ha⁻¹) and 847/6/11 (1886 kg ha⁻¹) were determinate.

It has been shown that the late maturing cultivars outperform the early maturing cultivars in high potential areas (KARI Report, 1997). This was in agreement with the results obtained in this study in that the late maturing genotypes performed better than the early maturing ones. Therefore an extensive yield testing across different agro-ecological zones would ensure identification of productive cultivars for seed yield improvement. The existence of genetic variability for seed yield among these genotypes indicates that it would be possible to develop highly yielding lines.

4.1.2.13 Protein Content (%)

Limited variability was observed for seed protein content. Nevertheless, genotype EAI 3600 had the highest amount of seed protein of 43.4%, but it did not significantly differ

from the other genotypes, 932/5/11 (42%), 914/5/39 (42%), Bossier (41%), TGM-237-2 (41%), and 941/5/7 (40%). The genotypes that showed low seed protein content were 929/5/30 (32%), 847/6/11 (33%), 813/5/11 (34%), 911/6/3(34%), SCS-1 (35%) and Duicker (35%). These results are consistent with those obtained by Xu et al. (1999) and Pantalone et al. (1996).

There is considerable variability among soybean lines for protein content. However, the agro-climatic conditions influence the chemical composition of soybean seed (FAO, 1994). Variation of seed protein therefore, occurs across different agro-climatic conditions (KARI Report, 1997).

4.2 Broad Sense Heritability

High magnitude of broad sense heritability estimates for days to 50% flowering (0.90), bacterial blight resistance (0.85), number of branches per plant (0.80), number of nodes per plant (0.84) plant height (0.91), days to maturity (0.85) and 100-seed weight (0.90), were obtained. Significant medium heritability estimates for lodging (0.66), number of pods per plant (0.76), number of seeds per pod (0.75), seed yield (0.73) and seed protein (0.77) were also found (Table 4). However, a low heritability estimate for days to seed emergence (0.38) was non-significant.

Table 4. Broad sense heritability estimates for some characters in soybean grown at Egerton University, Njoro Kenya during the 2001 rainy season.

Trait	Heritability (h^2_b)
Days to seed emergence	0.38
Days to 50% flowering	0.90*
Bacterial blight resistance	0.85*
Number of branches per plant	0.80*
Number of nodes per plant	0.84*
Plant height	0.91*
Lodging	0.66*
Number of pods per plant	0.76*
Days to maturity	0.85*
Number of seeds per pod	0.75*
Hundred seed weight	0.90*
Seed yield	0.73*
Protein content	0.77*

* Estimate of heritability is significantly greater than other estimate obtained at the same location based on an examination of confidence intervals α level of 0.05.

High heritability estimates for lodging, seed protein content and seed weight were reported in soybean (Johnson et al., 1955; Burton, 1987; Pantalone, 1996; Mansur and Orf, 1995). Similarly, high heritability estimates were reported for plant height, number of main stem nodes, days to flowering and days to maturity (Akhter and Sneller, 1996b; Mansur and Orf, 1995). On the other hand, seed yield was shown to have low to medium heritability (Burton, 1987; Akhter and Sneller, 1996b). However, Mansur and Orf (1995) reported high broad sense heritability for soybean seed yield. The most probable reason for high heritability for seed yield was that seed yield was correlated with days to maturity, which is a highly heritable trait.

Estimates of variance and covariance components are subject to large standard errors making it difficult to derive meaningful heritability estimates (Nyquist, 1991). Nevertheless, the magnitude of the calculated heritability estimates of each trait compared with those of other traits provide an insight on the degree of genetic transmission from parent to offspring. Generally, large broad sense heritability (h^2_b), which is the ratio, σ_G^2 / σ_P^2 were obtained. The genetic component σ_G^2 can be partitioned into various components, $\sigma_G^2 = \sigma_A^2 + \sigma_D^2 + \sigma_I^2$ where, σ_A^2 is the genetic variance due to additive gene effects, σ_D^2 is the genetic variance due to dominance effects among alleles at a locus and σ_I^2 is the genetic variance arising from interaction between loci. The additive variance, σ_A^2 is the main determinant of the genetic properties and of the response to selection. The ratio, σ_A^2 / σ_P^2 is narrow sense heritability (h^2_n), which is the proportion of the variation that is due to additive gene effects (Mwandemele, 1993).

Hence, estimates of narrow sense heritability would be lower than broad sense heritability estimates.

Low broad sense heritability for days to seed emergence indicates that the trait is highly influenced by the environment. Helms et al. (1996) reported that soybean seed emergence was highly influenced by initial soil water content and temperature. It is however, common to find non-significant estimates for traits of the low heritability (Herridge and Rose, 1994; Pavetti et al., 1994; Pfeiffer and Egli, 1988; Pantalone et al., 1996).

An understanding of the heritability of agronomic traits is needed to assist breeders in selection programmes. Heritability estimates will be useful in quantifying expected gains from selection and developing appropriate breeding strategies (Hanson, 1963).

4.3 Phenotypic Correlations

Phenotypic correlations among 13 traits were based on plot mean values among the 20 genotypes (Table 5). Seed yield was positively correlated ($P=0.01$) with days to 50% flowering, number of nodes per plant, plant height, number of pods per plant, days to maturity and the number of seeds per pod, but negatively correlated with bacterial blight resistance scores. All characters were significantly correlated with days to maturity except days to seed emergence, number of seeds per pod, number of branches per plant and protein content. However, the correlation between days to maturity and bacterial blight resistance scores was negative.

Table 5. Phenotypic correlation coefficients^a among 13 characters measured on 20 soybean genotypes.

	DE	DF	BB	BR	NP	HT	LD	PP	DM	SP	HS	YL	PC
Days to seed emergence (DE)													
Days to 50% flowering (DF)	-0.19												
Bacterial blight resistance (BB)	-0.05	-0.34**											
Number of branches per plant (BR)	-0.26	0.30*	0.16										
Number of nodes per plant (NP)	0.08	0.15	-0.59**	-0.06									
Plant height (HT)	0.07	0.20	-0.69**	-0.17	0.86**								
Lodging (LD)	0.05	-0.03	-0.25	-0.08	0.36**	0.52**							
Number of pods per plant (PP)	-0.02	0.42**	-0.45**	0.08	0.50**	0.42**	0.18						
Days to maturity (DM)	0.06	0.69**	-0.73**	-0.01	0.58**	0.74**	0.33*	0.59**					
Number of seeds per pod (SP)	-0.33**	0.28*	-0.19	0.18	0.01	0.00	0.04	0.44**	0.24				
Hundred seed weight (HS)	0.28*	0.25	-0.49**	-0.21	0.29*	0.37**	0.18	0.02	0.50**	-0.28*			
Seed yield (YL)	-0.13	0.59**	-0.67**	0.05	0.47**	0.50**	0.14	0.73**	0.68**	0.52**	0.15		
Protein content (PC)	-0.01	-0.08	0.08	0.07	-0.02	0.01	-0.03	0.18	-0.06	0.24	-0.17	-0.11	

*, ** Significant at p=0.05 and 0.01, respectively.

^a Based on plot mean analysis at one location in Egerton University, Njoro during the year 2001 (n=20).

Significant negative correlation ($P=0.01$) for number of nodes per plants, plant height, number pods per plant, days to maturity, hundred seed weight, seed yield and days to 50% flowering with bacterial blight resistance scores was observed (Table 5). Hundred seed weight was positively correlated with days to seed emergence, number of nodes per plant, plant height, days to maturity, but negatively correlated with the number of seeds per pod and bacterial blight resistance scores. Significant correlation was observed for number of seeds per pod with days to 50% flowering and number of pods per plant but negatively correlated with days to seed emergence. Lodging was positively correlated with the number of nodes per plant, days to maturity and plant height. Protein content showed no correlation with any trait studied. Plant height was positively correlated with number of nodes per plant, lodging, number of pods per plant, days to maturity, hundred seed weight and seed yield but negatively correlated with bacterial blight resistance scores. Days to 50% flowering was the only character that was significantly correlated ($P=0.05$) with the number of branches per plant.

The yield components that showed the strongest association with seed yield were, number of pods per plant ($r = 0.73^{**}$) and number of seeds per pod ($r = 0.52^{**}$). The number of nodes per plant ($r = 0.47^{**}$), plant height ($r = 0.50^{**}$) and days to maturity ($r = 0.68^{**}$) also showed significant positive correlation with seed yield. Akhter and Sneller (1996a) and Board et al. (1996) also reported positive and significant correlation between number of main stem nodes, pods per plant and seeds per pod with seed yield. Seed yield was positively correlated with days to maturity (Mansur and Orf, 1995).

Increased plant height was also associated with increased yield in determinate and indeterminate genotypes, particularly when height was correlated positively with the number of main stem nodes (Akhter and Sneller, 1996a). All positive associations indicated above could be valuable aid in selection of superior cultivars. The bacterial blight incidence recorded negative and significant correlation with plant height ($r = -0.69^{**}$), days to maturity ($r = -0.73^{**}$) and seed yield ($r = -0.67^{**}$). This showed that tall and late maturing genotypes were resistant to bacterial blight, which resulted in relatively higher yields compared to the short, early maturing genotypes. These results also indicated that high level of bacterial blight susceptibility could have contributed to low yields. For example, genotypes Blackhawk, TGM-237-2, Hill, EAI 3600, 813/5/11 and 941/5/7 which were early maturing genotypes (Table 2) showed high susceptibility to bacterial blight and were characterized by low seed yields compared to the genotypes Gazelle, SCS-1, 911/6/3 and 932/5/38 which were tall late maturing genotypes and were highly resistant to bacterial blight. Significant negative relationship between tall wheat (*Triticum aestivum*) plants and resistance to Fusarium ear blight (*Fusarium culmorum*) was reported. The tall strawed lines showed less severe disease symptoms than short strawed lines following inoculation (Hilton et al., 1999). Comparison of areas under disease incidence and severity in naturally infected cultivars of peas (*Pisum sativum*) by bacterial blight (*Pseudomonas syringe* pv. *pisii*) indicated that yield loss was strongly correlated with disease severity (Roberts et al., 1995; Mansfield et al. 1997).

Burton (1987) reviewed that the major draw back to selection for increased soybean seed protein content is the inverse correlation between seed protein and yield. Non-significant correlation between seed protein content and seed yield was not consistent with trends reported in literature. However, Pantalone et al. (1996) reported non-significant correlations between seed protein concentration and seed yield in soybean. Non-significant correlation observed in this study might have resulted from sampling errors associated with the small population, which was limited to only 20 genotypes. Falconer (1989) noted that because of large standard errors associated with their estimates phenotypic correlations are seldom precise. Nevertheless non-significant correlations imply that selection for favourable attributes can be obtained simultaneously. High yielding and high protein lines could be selected from lines evaluated in this study. For example, genotype 932/5/11 (2084 kg ha^{-1}) was high yielding and had 42.3 % seed protein (Table 2). The yield for this genotype was similar to those of other productive genotypes SCS-1 (2441 kg ha^{-1}) and 932/5/38 (2336 kg ha^{-1}). The presence of genetic variability within soybean population would enable breeders to select high yielding lines with high seed protein concentration (Pantalone et al., 1996).

Significant positive correlations were recorded on lodging with plant height ($r = 0.52^{**}$), number of main stem nodes ($r = 0.36^{**}$) and days to maturity ($r = 0.33^{*}$) suggesting that plant height contributed highly to lodging. Mansur and Orf (1995) also reported significant positive correlation for lodging with plant height, days to maturity, and seed

yield. However, no correlation was found between lodging and seed yield in this study, which indicated that there was no seed yield loss associated with lodging.

4.4 Principal Component Analysis

This procedure grouped 19 variables into 19 components with eigenvalues lying between 0.001 and 6.56. By considering only the first nine components with eigenvalues greater than 0.39, more than 95% of the total variation could be explained (Table 6). Principal component 1 (PC 1) accounted for 35% of the total variation and it was associated with bacterial blight resistance, number of nodes per plant, plant height and days to maturity (Table 6). PC 2 accounted for 20% of the total variation and it consisted of number of seeds per pod. PC 3 explained 11% of the total variation and was mainly associated with leaf shape, days to flowering and 100-seed weight. PC 4 accounted for 9% of the total variation and consisted mostly of days to seed emergence, and hilum colour. PC 5 consisted of number of branches per plant and lodging and accounted for 7% of the total variation. PC 6 explained 5% of the total variation and was associated mainly with number of branches per plant and protein content. PC 7 accounted for 4% of the variation and was mainly associated with lodging. PC 8 accounted for 3% of the variation and was associated with number of branches per plant and protein content. PC 9 explained 2% of the variation and was also associated with days to seed emergence.

Table 6. Principal component coefficients (e_i) of 19 characters in 20 soybean genotypes grown at Egerton University, Njoro Kenya.

	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8	PC 9
Growth habit	0.26	-0.05	0.35	-0.27	-0.12	-0.10	-0.33	0.06	0.20
Hypocotyl colour	0.28	-0.17	0.17	0.04	0.15	-0.03	0.01	0.20	-0.24
Leaf shape	0.02	-0.27	0.41	-0.23	0.32	0.16	0.22	-0.15	0.02
Pubescence colour	-0.27	0.26	0.20	-0.07	-0.18	0.13	-0.33	0.06	0.00
Hilum colour	-0.13	0.25	0.19	0.42	-0.34	-0.06	0.20	0.29	0.03
Flower colour	0.28	-0.17	0.17	0.04	0.15	-0.03	0.01	0.20	-0.24
Days to seed emergence	0.11	-0.33	-0.06	0.41	-0.03	0.21	-0.05	-0.14	0.66
Days to 50% flowering	0.13	0.32	-0.37	-0.00	0.29	0.17	0.21	-0.11	-0.17
Bacterial blight resistance	-0.33	-0.13	0.10	-0.03	0.24	0.13	0.21	-0.23	0.05
Number of branches per plant	-0.10	0.25	0.04	-0.01	0.38	0.47	-0.08	0.64	0.22
Number of nodes per plant	-0.10	0.25	0.04	-0.01	0.38	0.47	-0.08	0.64	0.22
Plant height	0.33	-0.00	0.14	-0.21	0.03	0.07	-0.23	0.04	-0.09
Lodging	0.35	0.01	0.10	-0.19	-0.17	0.19	-0.04	-0.10	-0.12
Number of pods per plant	0.18	-0.01	0.15	-0.21	-0.45	0.27	-0.65	0.14	0.04
Days to maturity	0.26	0.27	0.10	0.08	0.26	-0.15	0.09	-0.11	0.35
Number of seeds per pod	0.31	0.21	-0.22	-0.05	-0.08	0.18	0.03	-0.17	0.26
Hundred seed weight	0.00	0.42	0.22	0.04	-0.04	-0.33	0.02	-0.10	0.20
Seed yield	0.20	-0.11	-0.46	-0.01	-0.19	0.11	-0.22	0.15	-0.02
Protein content	0.28	0.30	-0.03	0.05	0.18	-0.16	0.12	-0.09	-0.10
Percent variation	-0.00	0.22	0.22	0.33	-0.11	0.56	-0.22	0.43	-0.24
Eigenvalue	34.5	19.5	11.4	8.8	6.7	5.3	3.7	3.3	2.1
Cumulative percent of total Variation	6.56	3.70	2.16	1.58	1.27	1.01	0.70	0.62	0.39
	34.5	54.0	65.4	74.2	80.9	86.2	89.9	93.2	95.3

PC = Principle component.

4.5 Cluster Analysis

Results of the cluster analysis showed that 19 clusters were formed during the agglomeration process (Fig 2). However, all the 20 genotypes were pooled into two major categories of similarity. In the first major category the smallest variance was detected among Blackhawk, Hill and TGM-237-2 (cluster 17 and 16), and also between genotypes 928/5/5 and 941/5/7 (cluster 18). Genotypes 928/5/5 and 941/5/7 were joined by Nyala to form cluster 10. The genotypes 928/5/5, 941/5/7 and Nyala were joined to 813/5/11 to form cluster 8. Genotypes 928/5/5, 941/5/7, Nyala and 813/5/11 were joined to EAI 3600 to form cluster 6. In the second major category Gazelle and Sable were first joined (cluster 19) then followed by SCS-1 and Duicker (cluster 14). Gazelle and Sable were joined to 911/6/3 to form cluster 15. Cluster 15 was joined to genotypes 847/6/11 and 929/5/30 to form cluster 11 and 12. Minimum variance was also detected between 932/5/11 and 932/5/38 (cluster 13). Genotypes Blackhawk, Hill, TGM-237-2, 928/5/5, Nyala, 813/5/11, and EAI 3600 were clustered in the first major cluster while SCS-1, Duicker, Gazelle Sable, 911/6/3, 847/6/11, 929/5/30, 914/5/39, 931/5/34, 932/5/38 and Bossier formed the second cluster.

Results from the cluster analysis suggested that this method could be useful for determining the diversity among germplasm (Peters and Martinelli, 1989) or the similarity of an entry relative to other entries. It can be used to assign entries to their specific group of similarity.

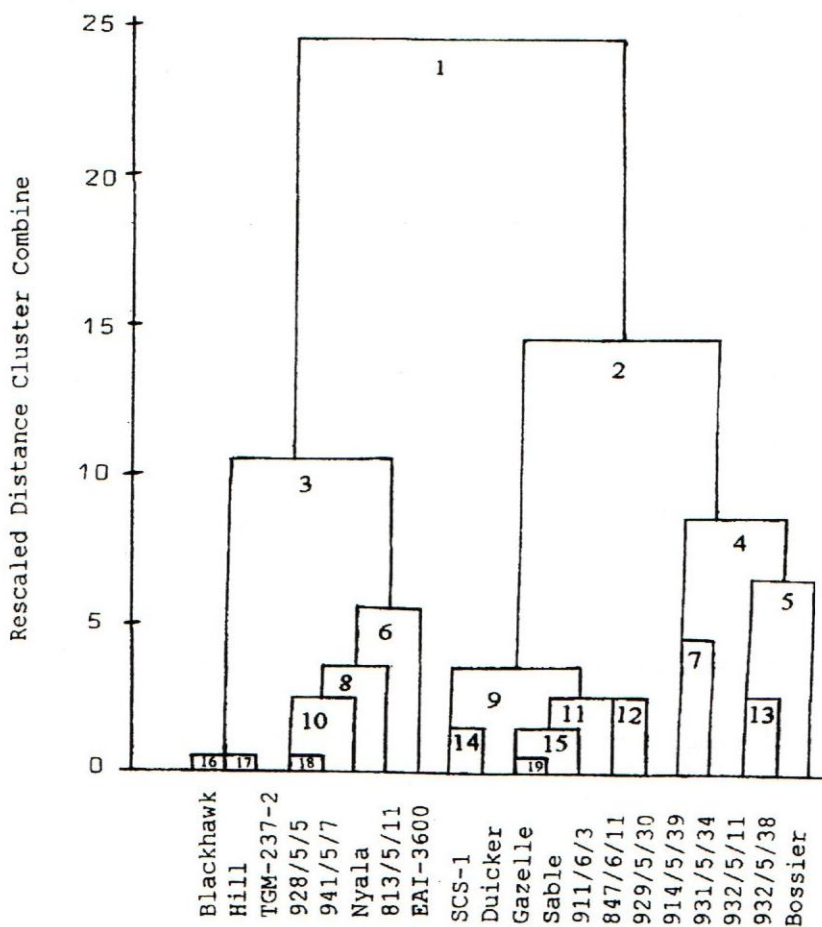


Figure 2. Dendrogram of the similarities among 20 soybean genotypes, grown at Egerton university, Njoro in Kenya during the 2001 rainy season using Ward's minimum variance method of cluster analysis.

In this study the first agglomerations (minimum variance) were formed among the short, determinate genotypes, which were characterized by early maturity and were susceptible to bacterial blight. Kilgore and Sneller (2000) reported that determinate soybean lines were shorter and early maturing than indeterminate lines. Lack of diversity among the first group of genotypes could probably be due to a common ancestry although there was no available information about the origin of the genotypes. Within this group of agglomeration the genotypes Blackhawk, Hill and TGM-237-2 shared high similarity and these are among the recommended cultivars. Gizlice et al. (1996) found that the breeding programmes influence patterns of diversity among soybean germplasm beyond that accounted for by maturity effects. The second group of similarity within the first agglomeration was revealed among genotypes 928/5/5 and 941/5/7, which were joined to Nyala to form one cluster. Similarly, genotype EAI 3600 was also pooled within the first agglomeration.

In the second agglomeration, proximity was demonstrated between Gazelle and Sable. This group was mainly composed of tall and late maturing genotypes, which expressed high resistance to bacterial blight. The second minimum variance was between SCS-I and Duicker. Bossier was also clustered within this group.

The clustering patterns obtained from different environments will be useful to select genetically diverse genotypes to be included in hybridization programmes to exploit greater heterosis (Singh, 1988). Sampling among cluster groups increase allelic diversity for selection followed by hybridization in breeding programmes (Spagnoletti-

Zeuli and Qualset, 1987). The results of clustering patterns agreed with principal component analysis and suggest that the most important characters contributing to the genetic diversity in these soybean cultivars are plant height, number of nodes per plant, bacterial blight resistance, days to maturity, number of seeds per pod, leaf shape, 100-seed weight and days to 50% flowering. Based on these the indeterminate cultivars Bossier and SCS-1 could be used in a crossing programme with determinate cultivars such as Hill, Blackhawk, and TGM-237-2 to combine important traits such as seed yield, resistance to bacterial blight, seed protein content, early maturity and plant height.

4.6 Combining Ability

4.6.1 Performance of parents and crosses

Combining ability analysis was carried out for five agronomic characters i.e. days to 50% flowering, plant height, days to maturity, seed yield and 100-seed weight in a 6 x 6 diallel cross excluding reciprocals. The combined analysis of variance indicated significant differences ($p=0.05$) among the parents and the crosses for all the five characters except days to 50% flowering among the parents (Table 7).

4.6.1.1 Parents

Bossier (61 d) was the earliest among the parents for days to 50% flowering, while TGM-237-2 (66 d) was the latest parent (Table 8). Significant differences were observed among the parents for plant height.

Table 7. Combined analysis of variance for parents and F₁ crosses of five traits in a diallel cross of soybean grown at Egerton University, Njoro Kenya during the year 2002.

Source of variation	d.f	Mean squares				
		Days to 50% Flowering (d)	Plant height (cm)	Days to maturity (d)	Seed yield (g plot ⁻¹)	100-seed weight (g)
Genotype (g)	20	11.82**	107.87**	22.30**	1120.64**	19.11**
Parent (p)	5	7.92	125.32**	29.02**	1353.23*	17.00**
Cross (c)	14	13.98**	106.73**	21.08**	892.84**	20.08**
Error (Genotype)	40	3.97	25.49	3.03	253.53	0.56
Error (Parent)	10	3.72	12.49	0.75	344.06	0.41
Error (Cross)	28	4.27	28.26	4.04	197.30	0.58

*, ** Significant at p=0.05 and 0.01, respectively.

Table 8. Mean performance of six soybean genotypes at Egerton University, Njoro Kenya.

Genotype	Days to 50% Flowering (d)	Plant height (cm)	Days to maturity (d)	Seed yield (g plot ⁻¹)	100-seed weight (g)
Bossier	61.33b	67.47a	137.00a	123.78a	12.84c
Nyala	63.00ab	50.37d	137.33a	100.04ab	18.54a
Blackhawk	65.33a	57.13bc	130.67c	66.70b	12.95c
EAI 3600	64.33ab	62.57ab	133.67b	120.96a	14.82b
Hill	64.67ab	51.93cd	130.33c	87.91ab	12.32c
TGM-237-2	65.67a	59.67b	131.67c	98.89ab	12.67c
Mean	64.06	58.19	133.44	99.79	14.02
Standard error ^b	1.11	2.04	0.50	10.71	0.37
C.V.	3.01	6.07	0.65	18.59	4.59

^a Within columns means not followed by the same letter are significantly different at $p=0.05$ based on Duncan's Multiple Range Test.

^b Standard error of a single parental mean used in the Duncan's Multiple Range Test.

Bossier (67 cm) was the tallest parent but was not significantly different from EAI 3600 (63 cm). TGM-237-2 (60 cm) and Blackhawk (57 cm) were not significantly different from EAI 3600 but were significantly different from Bossier. Nyala (50 cm) and Hill (52 cm) were the shortest parents.

Limited variability was shown for days to maturity. Bossier (137 d) and Nyala (137 d) were the latest maturing parents. However, Bossier was the earliest parent to flower. The earliest parents were Hill (130 d), Blackhawk (131 d) and TGM-237-2 (132 d) while EAI 3600 (134 d) was medium maturing. Most parents were similar in performance for seed yield. Bossier (124 g plot^{-1}), EAI 3600 (121 g plot^{-1}), Nyala (100 g plot^{-1}), TGM-237-2 (99 g plot^{-1}) and Hill (88 g plot^{-1}) were not significantly different. Blackhawk (67 g plot^{-1}) was the lowest yielding parent (Table 8).

Parents showed variability for 100-seed weight. Nyala (18.5 g) had the largest seed weight and was significantly different from EAI 3600 (14.8 g), which had medium seeds. On the other hand Bossier (12.8 g), Blackhawk (13.0 g), Hill (12.3 g), and TGM-237-2 (12.7 g) had significantly small seed weights (Table 8).

4.6.1.2 F₁ Crosses

Significant differences were observed among the F₁ crosses for days to 50% flowering. Bossier x Hill (59 d) was the earliest but was not significantly different Bossier x EAI 3600 (62 d), Blackhawk x Hill (63 d), Bossier x Nyala (61 d), and Bossier x Blackhawk (63 d) (Table 9). Crosses involving Bossier were generally early.

Table 9. Mean performance of 15 soybean F₁ crosses at Egerton University, Njoro Kenya.

Cross	Days to 50% Flowering (d)	Plant height (cm)	Days to maturity (d)	Seed yield (g plot ⁻¹)	100-seed weight (g)
Bossier x Nyala	60.67de	66.43ab	136.67a	139.07a	19.47a
Bossier x Blackhawk	63.00bcde	69.57a	133.67ab	130.31abc	12.95f
Bossier x EAI 3600	61.67cde	68.80a	136.67a	132.86ab	15.20de
Bossier x Hill	59.33e	65.87ab	136.00a	127.28abc	12.82f
Bossier x TGM-237-2	63.33bcd	63.10abc	136.67a	126.04abc	12.63f
Nyala x Blackhawk	65.33abc	54.10cd	136.00a	103.38cdef	18.29ab
Nyala x EAI 3600	67.67a	62.70bc	135.67ab	123.04abcd	19.09a
Nyala x Hill	65.67abc	51.27d	136.00a	103.84cdef	17.19bc
Nyala x TGM-237-2	63.33bcd	54.23cd	134.33ab	108.58bcde	17.28bc
Blackhawk x EAI 3600	65.00abc	57.47bcd	133.67abc	125.38abc	14.94de
Blackhawk x Hill	63.00bcde	53.67cd	130.00cd	78.53f	12.29f
Blackhawk x TGM-237-2	64.33abcd	56.40bcd	130.33cd	91.48ef	12.48f
EAI 3600 x Hill	66.33ab	61.97abc	132.00bcd	122.73abcd	14.26e
EAI 3600 x TGM-237-2	63.67bcd	57.10bcd	133.00abc	121.80abcd	15.95cd
Hill x TGM-237-2	64.33abcd	55.47cd	129.00d	97.65def	12.41f
Mean	63.78	59.87	134.11	115.45	15.15
Standard error ^b	1.19	3.07	1.16	8.12	0.44
C.V.	3.24	8.88	1.50	12.17	5.04

^a Within columns means not followed by the same letter are significantly different at $p=0.05$ based on Duncan's Multiple Range Test.

^b Standard error of a single cross mean used in the Duncan's Multiple Range Test.

The latest cross was Nyala x EAI 3600 (68 d), which was not significantly different from Nyala x Hill (66 d), Blackhawk x EAI 3600 (65 d), Blackhawk x TGM-237-2 (64 d), EAI 3600 x Hill (66 d) and Hill x TGM-237-2 (64 d) (Table 9).

The F_1 crosses were significantly different for plant height. The tallest was Bossier x Blackhawk (70 cm) however, it was not significantly different from Bossier x Nyala (66 cm), Bossier x EAI 3600 (69 cm), Bossier x Hill (66 cm) Bossier x TGM-237-2 (63 cm) and EAI 3600 x Hill (62 cm). The shortest was Nyala x Hill (51 cm), which was not significantly different from Nyala x Blackhawk (54 cm), Nyala x TGM-237-2 (54 cm), Blackhawk x EAI 3600 (57 cm) and Hill x TGM-237-2 (55 cm) (Table 9).

For days to maturity, there was limited variation among the crosses compared to the parents and most crosses were similar. Hill x TGM-237-2 was the earliest (129 d) and was not significantly different from Blackhawk x Hill (130 d), Blackhawk x TGM-237-2 (130 d), EAI 3600 (132 d) and EAI 3600 x TGM-237-2 (133 d). The other F_1 crosses were not significantly different (Table 9).

Significant differences were observed among the F_1 for seed yield. In general crosses involving EAI 3600 and Bossier were high yielding compared to crosses involving other parents. For example, Bossier x Nyala (139 g plot⁻¹), Bossier x EAI 3600 (133 g plot⁻¹) and Bossier x Blackhawk (130 g plot⁻¹), Bossier x Hill (127 g plot⁻¹), Bossier x TGM-237-2 (126 g plot⁻¹), Nyala x EAI 3600 (123 g plot⁻¹), Blackhawk x EAI 3600 (125 g plot⁻¹) and EAI 3600 x TGM-237-2 (122 g plot⁻¹) were high yielding but were not significantly different. Blackhawk x Hill (79 g plot⁻¹), Blackhawk x TGM-237-2 (91

g plot⁻¹), Hill x TGM-237-2 (98 g plot⁻¹), Nyala x Blackhawk (103 g plot⁻¹) and Nyala x Hill (104 g plot⁻¹) were low yielding.

The F₁ crosses were significantly different for 100-seed weight. Bossier x Nyala (19.5 g) and Nyala x EAI 3600 (19.1 g) had the largest seed weights. Bossier x EAI 3600 (15.2 g), Nyala x Hill (17.2 g), Nyala x TGM-237-2 (17.3 g), EAI 3600 x Hill (14.3 g) and EAI 3600 x TGM-237-2 (16.0 g) had medium seed weights. The remaining crosses had small seed weights i.e. Bossier x Blackhawk (13.0 g), Bossier x Hill (12.8 g), Bossier x TGM-237-2 (12.6 g), Blackhawk x Hill (12.3 g), Blackhawk x TGM-237-2 (12.5 g) and Hill x TGM-237-2 (12.4 g) (Table 9).

4.6.2 Heterosis in F₁

The heterosis percent over the better parent was calculated for all the five characters and are given in Table 10. The variance of the deviation was estimated as 2MSE and a “t” test was used to determine the significance of the better parent heterosis value.

The F₁ crosses were not different from their earliest parents for days to flowering except Nyala x EAI 3600 which was significantly ($p=0.01$) later than the early parent Nyala (Table 10). The F₁ crosses generally flowered later than their early parents. Percent better parent heterosis for plant height ranged from -4.3% (EAI 3600 x TGM-237-2) to 31.9% (Bossier x Nyala). Four of the crosses were significantly ($p=0.05$) taller than the shorter parents (Table 10).

Table 10. F_1 Heterosis^a expressed as a percentage above the better parent for five soybean characters evaluated at Egerton University, Njoro Kenya.

Cross	Days to ^b 50% Flowering (d)	Plant ^b height (cm)	Days to ^b maturity (d)	Seed yield (g plot ⁻¹)	100-seed weight (g)
Bossier x Nyala	-1.1	31.9**	-0.2	12.4	5.0
Bossier x Blackhawk	2.7	21.8	3.8**	5.3	0.0
Bossier x EAI 3600	0.6	10.0	2.2*	7.3	2.6
Bossier x Hill	-3.3	26.8**	4.3**	2.8	-0.2
Bossier x TGM-237-2	3.3	5.7	3.8**	1.8	-1.6
Nyala x Blackhawk	3.7	7.4	4.1**	3.0	-1.4
Nyala x EAI 3600	7.4**	24.5**	1.5	1.7	3.0
Nyala x Hill	4.2	1.8	4.3**	3.4	-7.3*
Nyala x TGM-237-2	0.5	7.7	2.0	8.1	-6.8*
Blackhawk x EAI 3600	1.0	0.6	2.3	3.6	0.8
Blackhawk x Hill	-2.6	3.4	-0.3	-10.6	5.1
Blackhawk x TGM-237-2	-1.5	-1.3	-0.3	-7.5	-3.6
EAI 3600 x. Hill	3.1	19.3*	1.3	1.5	-3.8
EAI 3600 x TGM-237-2	-1.0	-4.3	1.0	0.7	7.6*
Hill x TGM-237-2	-0.5	6.8	-1.0	-1.2	-2.6

*, ** Significant at $p=0.05$ and 0.01 , respectively.

^a Percent heterosis above the better parent calculated as $F_1 - P_b \times 100 / P_b$

^b Earlier parent for days to flowering, earlier parent for days to maturity and shorter parent for plant height were considered as better parent and were used for heterosis computation.

The F_1 heterosis was significant ($p=0.05$) for days to maturity among six crosses but the F_1 crosses generally tended to mature late than their early parents. For seed yield, better parent heterosis ranged from -10.6% (Blackhawk x Hill) to 12.4% (Bossier x Nyala) but heterosis was not significant in any of the crosses in this study. The range of better parent heterosis found in this study agreed with previous reports in soybean (Gizlice et al., 1993; Manjarrez-Sandoval et al., 1997). The better parent heterosis for 100-seed weight ranged from -7.3% (Nyala X Hill) to 7.6% (EAI 3600 X TGM-237-2). Similar range of better parent heterosis for 100-seed weight were reported by Manjarrez-Sandoval et al. (1997). Only few crosses showed significant heterosis in one or more of the characters studied. However, there was no significant better parent heterosis for seed yield, though the amount of heterosis varied from cross to cross. The significance of better parent heterosis values among crosses for different traits is an indication of the usefulness of the genotypes. The large heterosis of certain crosses indicates that the parental genotypes are genetically more diverse than those genotypes that manifest little or no heterosis (Mungoma and Pollak, 1988). Selection within the genotypes with the highest heterosis for a given trait would ensure a rapid progress in the development of improved lines or cultivars (Baker, 1978).

4.6.3 General and specific combining ability

Since parents were excluded from this analysis based on Griffing's method 4 (Griffing, 1956), unbiased estimates of GCA and SCA were obtained (Singh et al., 1992). Mean squares from the analysis of variance for general combining ability (GCA) and specific

combining ability (SCA) are shown in Table 11. GCA source of variation was significant ($p=0.01$) for all characters i.e. days to 50% flowering, plant height, days to maturity and seed yield while SCA was only significant ($p=0.05$) for 100-seed weight. The GCA effects of six genotypes are presented in Table 12, while the SCA effects are presented in Table 13. The parent Bossier had consistently the highest positive GCA for plant height, days to maturity, seed yield and the highest negative GCA for days to flowering. Large and positive GCA effects for seed yield was also observed with EAI 3600 (Table 12). Blackhawk, Hill, TGM-237-2 and EAI 3600 had high GCA effects for days to maturity. For 100-seed weight, Nyala had the largest positive GCA effects while the remaining genotypes except EAI 3600 had negative GCA effects (Table 12). The best performing progenies may be produced by crossing two parents showing the highest general combining ability, for example Bossier and EAI 3600 had the highest GCA estimates for seed yield. Their cross is expected to produce a population with improved seed yield. Genotypes that reveal high GCA estimates are good candidates to be used as parents in an improvement programme (Baker, 1978). Bitzer et al. (1971) found that wheat cultivar with the highest GCA effects for seed yield was the best combiner for seed yield.

Table 11. Mean squares for general and specific combining ability of soybean F₁ progeny for five traits at Egerton University, Njoro Kenya.

Source of variation ^a	d.f	Mean squares				
		Days to 50% flowering (d)	Plant height (cm)	Days to maturity (d)	Seed yield (g plot ⁻¹)	100-seed weight (g)
GCA	5	8.29**	86.35**	16.13**	649.6**	17.87**
SCA	9	2.65	7.37	1.97	102.07	0.48*
Error	28	1.42	9.42	1.35	65.77	0.19

*,** Significant at p=0.05 and 0.01, respectively.

^a GCA: general combining ability; SCA: specific combining ability.

Table 12. Estimates of general combining ability (GCA) effects of six soybean genotypes grown at Egerton University, Njoro Kenya.

Parent	General combining ability effects				
	Days to Flowering (d)	Plant height (cm)	Days to maturity (d)	Seed yield (g plot ⁻¹)	100-seed weight (g)
Bossier	-2.72a	8.60a	2.78b	19.56a	-0.67c
Nyala	0.94b	-2.66c	2.03b	0.15b	3.89a
Blackhawk	0.44b	-2.05c	-1.22a	-12.31c	-1.20cd
EAI 3600	1.36b	2.16b	0.11a	12.12a	0.92b
Hill	-0.06b	-2.79c	-1.89a	-11.83c	-1.70d
TGM-237-2	0.03b	-3.27c	-1.81a	-7.94bc	-1.25d
Standard error ^b	0.55	1.40	0.53	3.70	0.58

^a Within columns means not followed by the same letter are significantly different at $p=0.05$ based on Duncan's Multiple Range Test.

^b Standard error of a single cross mean used in the Duncan's Multiple Range Test.

Table 13. Estimates of specific combining ability (SCA) effects of six soybean genotypes grown at Egerton University, Njoro Kenya.

Cross	Days to 50% Flowering (d)	Plant height (cm)	Days to maturity (d)	Seed yield (g plot ⁻¹)	100-seed weight (g)
Bossier x Nyala	-1.33	0.62	-2.25	3.91	1.10
Bossier x Blackhawk	1.50	3.14	0.00	7.59	-0.33
Bossier x EAI 3600	-0.75	-1.84	-0.33	-14.29	-0.20
Bossier x Hill	-1.65	0.18	1.00	4.08	0.03
Bossier x TGM-237-2	2.25	-2.10	1.58	-1.04	-0.60
Nyala x Blackhawk	0.17	-1.07	1.08	0.08	0.45
Nyala x EAI 3600	1.58	3.32	-0.58	-4.70	-0.88
Nyala x Hill	1.00	-3.16	1.75	0.05	-0.15
Nyala x TGM-237-2	-1.42	0.29	1.00	0.91	-0.52
Blackhawk x EAI 3600	-1.58	-2.53	0.67	10.11	0.07
Blackhawk x Hill	-1.17	-1.38	-1.00	-12.80	0.03
Blackhawk x TGM-237-2	0.08	1.84	-0.75	-3.73	-0.22
EAI 3600 x Hill	1.25	2.71	-0.33	6.97	-0.12
EAI 3600 x TGM-237-2	-1.50	-1.67	0.83	2.16	1.13
Hill x TGM-237-2	0.58	1.65	-1.42	1.95	0.21

Short plant height is a useful trait when dealing with lodging. Nyala, Blackhawk, Hill and TGM-237-2 had negative GCA estimates for plant height suggesting that they could be used to breed for reduced plant height and to reduce losses due to lodging. However, no yield losses associated with lodging were observed in this study because there was no correlation between these two traits. For days to maturity, high GCA was observed in Blackhawk, Hill, TGM-237-2 and EAI 3600 for earliness. These parents could be used for contribution of early maturity genes.

Positive GCA effects were found for 100-seed weight in parents with large and medium seeds such as Nyala and EAI 3600, but all small seeded parents showed negative GCA effects for 100-seed weight. Cho and Scott (2000) observed similar results. These results indicated that genes associated with large seeded parents combine positively in these crosses because it was easier to fix these genes due to additive nature. Small seeded parents may have negative effects on seed weight improvement but they may be used to improve seed yield because for example in this study, one parent Bossier which had small seeds had a high positive GCA effect for seed yield (Table 12). Since both GCA and SCA mean squares were significant for 100-seed weight, and GCA were positive for large and negative for small seeded parents, it is plausible that additive x additive variability might have contributed to seed weight by small seeded parents. According to Bhullar et al. (1979), additive x additive gene action could cause significant contribution of SCA variances to a population.

In a diallel cross performance of each progeny is broken into GCA (main effects) and SCA (interactions). When SCA mean square was not significant, the performance of a single-cross progeny could be adequately predicted on the basis of GCA alone. Significant GCA is caused mainly by additive gene effects, even though non-additive gene effects may also be involved. The best performing progeny may be produced by crossing the two parents having the highest GCA (Baker 1978). Large positive GCA values indicated effective transmission of genes of traits from parents to their offspring (Bdliya and Burris, 1988).

The ratios of mean square, $2 \text{ GCA} / (2 \text{ GCA} + \text{SCA})$ for days to 50% flowering, plant height, days to maturity, seed yield and 100-seed weight were 0.86, 0.96, 0.96, 0.93 and 0.99, respectively. Griffing (1956) has shown that the total genetic variance among a single cross progeny is equal to twice the GCA component of the variance ($2\sigma_G^2$) plus SCA component of the variance (σ_S^2). Based on this relationship, the relative importance of GCA and SCA in determining progeny performance should be assessed by estimating the mean squares and expressing them in the ratio $2 \text{ GCA} / (2 \text{ GCA} + \text{SCA})$. The closer this ratio is to unity the greater the predictability of progeny performance based on GCA alone (Baker, 1978). The ratios of mean square, $2 \text{ GCA} / (2 \text{ GCA} + \text{SCA})$ in this study were close to 1 for all the five traits measured and this therefore confirmed the predominance of additive effects over non-additive effects. This suggest that selection may be effective in F_2 and later generations for the traits studied. Li and Rutger (1980) reported similar findings for seedling vigour in rice (*Oryza sativa*

L.). It is encouraging that additive gene effects were prevalent for these traits because it would be difficult to exploit non-additive effects since hybrids are not used in soybean. Singh et al. (1992) gave examples to suggest that when SCA effects are predominant in self-pollinated crops the major portioning of the variability then, is due to additive x additive effects. Therefore selection should be delayed to later generations. Bhullar et al. (1979) pointed out that this could also be due to divergence among progenies in the same parental array.

CHAPTER FIVE

5.0 CONCLUSIONS AND RECOMMENDATIONS

5.1 Conclusions

Significant differences were found among twenty soybean genotypes, which were characterized based on morphological and agronomic characters including, growth habit, hypocotyl colour, leaf shape, pubescence colour, flower colour, hilum colour, days to seed emergence, days to 50% flowering, bacterial blight resistance, number of branches per plant, number of nodes per plant, plant height, lodging, pods per plant, days to maturity, number of seeds per pod, 100-seed weight, seed yield and seed protein content.

Cluster analysis based on the above characters revealed a significant amount of genetic diversity among the soybean genotypes. The genotypes were clustered into two major groups of similarities. The first group was mainly composed of eight short and determinate genotypes, which were early to medium maturing but susceptible to bacterial blight. The second group was more divergent and was mainly composed of twelve tall and determinate, semi-determinate or indeterminate genotypes, medium to late maturing but resistant to bacterial blight. Similarly, the first three principal components which accounted for 65% of the total variation agreed with cluster analysis groups and were associated with bacterial blight resistance, number of nodes per plant,

plant height, days to maturity, number of seeds per pod, leaf shape, 100-seed weight and days to 50% flowering.

High positive correlations were found for days to 50% flowering, number of nodes per plant, plant height, number of pods per plant, days to maturity and number of seeds per pod with seed yield while a negative correlation was found between seed yield and bacterial blight resistance scores.

General combining ability (GCA) effects were highly significant for days to 50% flowering, plant height, days to maturity, and seed yield where as both GCA and specific combining ability (SCA) effects were significant for 100-seed weight. However, the ratio of mean square, $2 \text{ GCA} / (2 \text{ GCA} + \text{SCA})$ were closer unity for all the five traits measured which confirmed the predominance of additive gene effects over the non-additive gene effects. Similarly, high broad sense heritability estimates of 0.73 to 0.91 were obtained for these five traits.

5.2 Recommendation

Seed yield and days to maturity could be improved through hybridization and selection. Since, early maturity was found to contribute low seed yield in this region, the cross between Bossier and EAI 3600 would be appropriate for the breeding of high yielding and medium maturing cultivars. This is because both parents had high GCA for seed yield while EAI 3600 had high GCA for earliness suggesting that selection in F_2 and later generations could be effective.

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APPENDICES

Appendix 1. Temperature data for the year 2001 and 2002 at Egerton University Njoro, Kenya.

Month and year	Max (°C)	Min (°C)	Mean (°C)
January 2001	23.0	11.6	17.3
February "	24.8	10.0	17.4
March "	24.8	10.3	17.2
April "	22.5	11.3	16.9
May "	23.0	11.0	17.0
June "	21.6	9.7	15.7
July "	21.5	9.4	15.5
August "	21.9	9.6	15.8
September "	23.2	9.9	16.6
October "	23.6	10.6	17.1
November "	21.2	11.0	16.1
December "	22.7	9.6	16.2
January 2002	23.8	10.2	17.0
February "	25.6	9.3	17.5
March "	24.1	10.6	17.4
April "	23.8	11.2	17.5
May "	22.7	11.0	16.9

Source: Department of Water and Environmental Engineering, Egerton University, weather station.

Appendix 2. Rainfall data for the year 2001 and 2002 at Egerton University Njoro,
Kenya

Month and year	Rainfall (mm)
January 2001	93.5
February "	63.6
March "	121.0
April "	119.7
May "	46.8
June "	117.1
July "	104.4
August "	116.1
September "	80.3
October "	153.5
November "	98.8
December "	18.4
January 2002	39.4
February "	28.4
March "	127.4
April "	60.6
May "	197.6

Source: Department of Water and Environmental Engineering, Egerton University, weather station.

Appendix 3. Leaning angle and lodging area.

Leaning angle						
		0-9 ⁰	10-19 ⁰	20-29 ⁰	40-49 ⁰	60 ⁰ >
Lodging Area	0-19%	1	1	1	1	1
	20-39%	1	1	3	3	5
	40-59%	1	3	3	5	7
	60-79%	1	3	5	7	9
	80% >	3	3	5	7	9

Source: International Plant Genetic Resources Institute (IPGRI, 1994), descriptions for soybean. FAO, Rome.

Appendix 4. (a) Analysis of variance (ANOVA) tables for characterization of soybean genotypes.

Analysis of variance table for days to seed emergence

Source of variation	d.f.	s.s.	m.s.	F value	F pr.
Rep	2	0.4333	0.2167	0.55	
Trmt	19	21.4000	1.1263	2.87	0.003
Error	38	14.9000	0.3921		
Total	59	36.7333			

Grand mean 8.767
s.e. 0.3615
c.v. 7.1

Analysis of variance table for days to 50% flowering

Source of variation	d.f.	s.s.	m.s.	F value	F pr.
Rep	2	66.03	33.02	3.16	
Trmt	19	5749.27	302.59	28.99	<.001
Error	38	396.63	10.44		
Total	59	6211.93			

Grand mean 86.63
s.e. 1.87
c.v. 3.7

Analysis of variance table for bacterial blight resistance

Source of variation	d.f.	s.s.	m.s.	F value	F pr.
Rep	2	4.9000	2.4500	3.52	
Trmt	19	240.2667	12.6456	18.18	<.001
Error	38	26.4333	0.6956		
Total	59	271.6000			

Grand mean 4.20
s.e. 0.482
c.v. 8.3

Appendix 4. (a) Analysis of variance (ANOVA) tables for characterization of soybean genotypes.

Analysis of variance table for days to seed emergence

Source of variation	d.f.	s.s.	m.s.	F value	F pr.
Rep	2	0.4333	0.2167	0.55	
Trmt	19	21.4000	1.1263	2.87	0.003
Error	38	14.9000	0.3921		
Total	59	36.7333			

Grand mean 8.767
s.e. 0.3615
c.v. 7.1

Analysis of variance table for days to 50% flowering

Source of variation	d.f.	s.s.	m.s.	F value	F pr.
Rep	2	66.03	33.02	3.16	
Trmt	19	5749.27	302.59	28.99	<.001
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