ASSESSMENT OF DIVERSITY AMONG COWPEA ACCESSIONS FROM SEMI-ARID AREAS OF KENYA

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Assessment of Diversity among Cowpea Accessions from Semi-Arid Areas of Kenya

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DECLARATION

This thesis is my original work and has not been presented for a degree in any other University

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DEDICATION

I dedicate this work to my late parents Christine Munyao and Charles Mwita, and my dear husband James Joshua.

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ABSTRACT

Cowpea is an important legume crop adapted and widely grown in marginal areas. The crop is grown mainly from landraces and only a handful of improved varieties have been developed. Although breeding and identification of superior lines is dependent upon existence of crop diversity, there is limited information on diversity among the Kenyan cowpea. The objective of this study was to determine variation among cowpea accessions from semi-arid areas of Kenya at morphological and molecular levels. One hundred and ten cowpea accessions obtained mainly from semi arid region of Kenya were planted in a Randomized Complete Block Design with three replicates. Quantitative and qualitative morphological data were collected over the growing period and on harvested seed. For molecular characterization, DNA was extracted from leaves obtained from two week old seedlings grown in pots. Variation among the genotypes was determined through amplifying the DNA using twenty pairs of selected SSR markers. Even distribution of accessions across traits of the characters was recorded for immature pod color, leaf color, seed shape and testa texture, whereas uneven distribution was recorded for terminal leaflet shape, raceme position, pod attachment, pod curvature, mature pod color, flower color and eye color. ANOVA revealed significant differences ($p=0.05$) among accessions for number of days to 50% emergence, pod length, number of pods per plant and number of seeds per pod. The first five principal components accounted for 19.8, 18, 15.9, 12.4 and 11.22 of the total variation respectively amounting to 77%. Correlation analysis revealed significant ($p=0.05$) relationship for 50% emergence to 50% flowering ($r= -0.2131$), 50 % emergence to number of pods per plant ($r= -0.5258$), emergence to terminal leaflet length ($r= -0.1881$) and emergence to terminal leaflet width ($r= 0.2042$); terminal leaflet length to terminal leaflet width ($r= 0.5230$) and pod length to number of pods per plant ($r= 0.5470$). Based on morphological characteristics, the accessions were grouped into two main clusters, with one cluster having 103 accessions that included all registered varieties while the other cluster had seven accessions. Molecular characterization of one hundred and ten accessions (110) was done using eight pairs of the SSR markers that were polymorphic. Analysis of the molecular variance showed that close to 100% of the variation was within accessions. Heterozygosity ranged from 0 to 0.5 with a mean value of 0.19. The molecular data subjected to cluster analysis grouped the accessions into three groups. Therefore, cowpeas grown in semi rid areas of Kenya are variable and closely related to the registered cowpea varieties evaluated. The set of accessions could be used for identification of preferred lines for this region. The morphological data gave significant variation among the characteristics while molecular characterization showed no significant variations among the populations.

CHAPTER ONE

INTRODUCTION

1.1 Background of the study

Cowpea (*Vigna unguiculata*), is a valuable food legume extensively grown in the tropics and subtropics of Africa (Lesley, 2005). The area under cowpea production is estimated to be 14.5 million ha worldwide with an annual production of 6.5 million metric tonnes (Njonjo, 2018).

In eastern Africa, cowpea is widely grown especially in Tanzania and Kenya. In Kenya, cowpea is the third most important food legume after common bean and pigeon peas (Njonjo, 2018). In 2012, there was an estimated area of 214,492 ha under cowpea production in Kenya, out of which 187,910 ha were from eastern province (Njonjo, 2018, MoALF, 2015). It is mainly grown as an intercrop with maize, sorghum or cassava (Asiwe, 2009).

Cowpea is cultivated mainly for its green leaves which are used as vegetables, immature pods used as filler or for mature grains (Bewley et al., 2006). This crop is highly palatable and nutritious as it contains several minerals including iron, calcium, phosphorus and zinc, and it is also free from anti-nutritive factors (Njonjo, 2018).

Cowpea is an important food security legume grown in the Arid and Semi Arid Lands (ASALS) of Kenya especially semiarid lands of eastern Kenya (Gachimbi et al., 2007). This crop has a deep root system and matures early hence its adaptability to unfavorable conditions. It is rich in nutrients and hence is good for reducing food and nutrition insecurity (Joshua *et al.*, 2019). Apart from being very nutritive, cowpea can be a source of income for household needs as well as enabling farmers to pay for inputs, labor and

maintenance of other later maturing crops, through the sale of its leaves and grains (Bennett & Jennings, 2013).

Farmers in Kenya experience low cowpea grain yields due to various constraints ranging from damage by pests and diseases to lack of high yielding varieties (Sariah, 2010). About 90% of the seed sown in the ASALS are informally produced by Non-Governmental Organizations (NGOs), farmers, farmer groups or community based organizations (Muthoni & Nyamongo, 2018). Most farmers often get seeds of variable quality from their own saved seed, social networks (friends and neighbors) or from local traders hence recycling seeds.

Improved cowpea varieties are at different levels of adoption among farmers. Certified seeds are quite expensive and inaccessible compared to local varieties that are sold at a fraction of the price of the certified seeds (Sperling *et al.,* 2004; Rubyogo *et al.,* 2007; Njonjo, 2018). The farmers also prefer the local varieties as they are more palatable compared to the improved varieties. In an effort to improve farmers' access to improved seed, governmental organs and NGOs carry out community based seed interventions such as seed and cultural fairs, community based bulking, seed recovery and bulking banks (Setimela *et al.,* 2004). The Kenyan government has been distributing large quantities of seeds to farmers in the Arid and Semi Arid areas since 1992 especially during emergency situations (Nagarajan, *et al.,* 2008) following drought. Cowpea is mostly grown by small scale farmers in developing countries and has received low attention from researchers (Adebowale, 2011; Timko and Singh 2008) hence attracting less donor support. Information on cowpea use and cultivation is scarce making it difficult to determine the extent to which farmers use traditional varieties, the adoption of improved and registered varieties.

Landraces have played a big role in the introduction of improved varieties as they have rich and complex ancestry with great variations in response to many stresses as well as

vast resources for improved varieties (Litchfouse *et al.,* 2011). A large number of cowpea varieties evolving from local landraces have been commercialized (Pratap & Kumar, 2011). However, landraces have rarely been used in hybridization to understand their breeding value in the improvement of grain yield and other traits in cowpea. Although cowpea is reported to have high protein value, high variability, high adaptability and drought tolerance capacity (Ashraf *et al.,* 2012), little research has been done on their landraces hence loss of superior genes that would be useful for genetic manipulation and improvement of the crop.

1.2 Problem Statement

Cowpea farmers in semi arid parts of Kenya face the challenge of low yields. One of the reasons for low yields is inadequate access to improved varieties. Although there are several improved varieties registered in Kenya (KEPHIS), their adoption is not known (Setimela *et al.,* 2004). Farmers still grow their own seed and other mixed lines whose overall yields are low (Stoilova & Pereira, 2013). A wide range of accessions have been collected from marginal areas of the country. The accessions have the potential to be used as germplasm for breeding, selection and identification of improved and adaptable accessions for the region. Whereas genetic advance in a crop is dependent on the existence of heritable variation in the available germplasm, only a few studies have been conducted to document the extent of this variation and hence this study was conducted. The objective of the study was to determine variation among cowpea accessions from semi-arid areas of Kenya using both morphological and molecular markers.

1.3 Justification

Cowpea breeding and identification of superior lines is dependent upon existence of known crop diversity. However, there is limited information on diversity among the Kenyan cowpea populations. Development of improved varieties exhibiting early

maturity, good grain quality, resistance to diseases and pests can significantly lead to increased yields (Lesley 2005). Farmers can benefit a lot from improving the local varieties thus increasing their productivity and reducing poverty. Improvement programmes introduced can provide information on the genetic diversity within the accessions.

Genetic characterization is invaluable to gene banks as it makes sampling and use of available genetic resources easy. In addition, breeders are able to select crops with superior characteristics from the genetic variations of the various parental lines. Genetic variation is the raw materials for plant improvement (Doumbia, 2011).

1.4 General objective

To determine variation among cowpea accessions from semi-arid areas of Kenya

1.4.1 Specific objectives

i. To evaluate the diversity among cowpea accessions based on morphological traits
ii. To determine diversity among cowpea accessions using SSR markers

1.5 Hypotheses

i. There are no morphological differences among cowpea accessions grown in Kenya
ii. Cowpea accessions grown in Kenya are not genetically different

CHAPTER TWO

LITERATURE REVIEW

2.1 Crop botany

Cowpea (*Vigna unguiculata*) is a dicotyledonous crop that belongs to the genus V*igna* and family leguminosae. It is a diploid plant with 2*n* = 22 chromosomes (Timko & Singh, 2008) and a genome size estimated to cover 620 million base pairs (Timko *et al,* 2008). The name cowpea was probably coined from the fact that it is a source of hay for cows in the southern United States of America and other parts of the world. Cowpea is referred to by different local names around the world. For example, in West Africa, it is known by the names "niebe", "wake", and "ewa" while in Brazil it is "caupi". Other names include "southern peas", "black eyed peas", "Field Peas", "pink eyes" and "crowders" (Timko *et al.,* 2008) in the southern United States. In Kenya, cowpea is referred to by different local names among the Kenyan communities. For example, cowpea is known as Kunde (Swahili), Mathoroko (Kikuyu), Nthooko (Kikamba) and Egesare (Kisii) (Savala *et al.,* 2003).

The exact origin of cowpea is unknown, although, Africa and Asia are discussed as the domestication areas of this crop (Sariah, 2010). Southern Africa has the highest genetic diversity of cowpea with the most primitive forms of wild cowpea and it is the most probable center of cowpea domestication (Acquaah, 2012). The origin and domestication of cowpea has been determined over time based on morphological and cytological evidence as well as information on its geographical distribution and cultural practices (Acquaah, 2012). Cultivated cowpea evolved overtime through domestication and selection from annual wild cowpea, a process during which, seed dormancy and pod dehiscence was lost (Anderson & Vicente, 2010).

2.2 Morphology

Cowpea accessions have high morphological variation. Cowpea accessions are divided according to their uses: for grain, forage or dual purpose. Cowpea plant is an herbaceous, prostate, climbing or sub erect annual plant growing 15-80 cm high (Omoigui et al., 2018). Leaves are alternating trifoliate with a petiole of 5-25 cm long. The first pair is simple and opposite. The lateral leaflet is opposite and asymmetrical and the central one is symmetrical and ovate. Leaves vary in sizes (6-16*4-11cm) and shape from linear, lanceolate to ovate. The color of the leaves can be pale green to dark green. The stems are striate, smooth or slightly hairy some with a purple tinge (Oluwakemi et al., 2021).

The flowers may range from white, yellow, pink, pale blue or purple. The flowers are arranged in racemose or intermediate inflorescence at the distal ends of 5-60cm long peduncles. The flowers are in alternate pairs with two flowers per inflorescence. Flowers are distinct, self pollinating and are produced on short pedicels. Flowers open early in the morning and close at midday. After the flowers open once, they wilt and collapse (Doumbia et al., 2013). The resulting fruits which are pods vary in sizes, shapes, colors and texture. The pods are cylindrical and may be curved or straight growing as long as 22 cm with 8-20 seeds per pod. A mature cowpea seed weight ranges from 8 to 32 mg (Doumbia et al., 2011). The seeds have different sizes and shapes with the common ones being kidney shaped, ovoid, crowder, globose or rhomboid. The seed shape correlates with that of the pod (Oluwakemi et al., 2021). The seed coat can be smooth or wrinkled with various colors including white, green, brown, black, cream, gray, purple, red, speckled, blotched, eyed or dotted.

This crop has a determinate or indeterminate growth habit. Most cowpea genotypes have the indeterminate growth habit. Cowpea has well developed rooting system and thick stems and branches, some of the qualities which make it adapted to harsh conditions.

The early flowering cowpea varieties can mature as early as in 55 days providing the farmers with the first source of food after the "hunger period" (Hall *et al.,* 2003). On the other hand, late maturing varieties can take as long as 150 days depending on photoperiod. Flowers are produced on racemes on 15 to 40 mm peduncles arising from the leaf axils (Timko *et al.,* 2008). Cowpea plant commonly bears two or three pods per peduncle and sometimes more than three pods are produced if the conditions are favorable. Cowpea emergence is epigeal like in common beans where the cotyledons emerge above the ground during germination. Cowpea is a self pollinating crop but some out crossing has been recorded of as high as 5% (Timko et al., 2007).

2.3 Uses of cowpea

Cowpea is a very important crop. It is a source of food for human, feed for animals and also as an income generating commodity for farmers and traders (Singh, 2002). Cowpea crop is useful at all its stages of growth. This crop has the ability to restore soil fertility through biological Nitrogen Fixation hence it is very useful in farming systems when rotated with other crops. The early maturing varieties give current harvest earlier than other crops and serves to shorten the hunger period as often occurs in before harvesting the current season's crop in many farming communities in Africa (Muniu, 2017).

The dry cowpea grains are important for human consumption. The seeds are cooked and eaten solely or as a side dish mixed with vegetables, spices and oil to make a thick soup which accompanies the staple foods such as cassava, yam or plantains (Silva et al, 2019). The dry seeds can also be canned for export. In West Africa, the seeds are decorticated and ground into flour for making cakes. The fresh or dried leaves are also used as vegetables in many parts of Asia and Africa (Grubben & Denton, 2004). In addition, fresh peas and green immature pods can also be used as vegetables. Cowpea leaves are either boiled or fried for eating with porridge (Timko & Singh, 2008). In addition, the leaves can also be sundried or boiled; sundried for preservation to be used

in the dry season. The immature seedless pods can be cooked as vegetables or even canned for export (Madamba et al., 2006). . The cowpea plant as a whole can be used in feeding livestock especially in the dry season. As fodder, it can be grazed directly or cut and mixed with dry cereals for feeding animals (Timko et al., 2007). In United States of America, cowpea is used as green manure and cover crop (Muniu, 2017). In Nigeria, some cowpea cultivars are grown for extracting fibre that can be used for making fishing gear or for paper processing (Zia-ul-haq et al., 2010). Its ability to survive under drought conditions, mature early and fix nitrogen in the soil makes cowpea crop to grow well in tropical soils which have low moisture and low soil fertility. Other uses include medicinal value where leaves and seeds are applied as poultice to treat swellings and skin infections (Grubben, 2004); leaves are also chewed as a remedy for toothaches.

2.4 Production systems

Dry grain production of cowpea is estimated to be about 6.5 million metric tons annually under 14.5 million acres worldwide (Njonjo, 2018). However, the amount of leaves and pods produced is not reflected in any statistical data but it is estimated to be large. Over 70% of worldwide cowpea production takes place in west and central Africa (Timko et al., 2008). This crop is usually grown as an intercrop with pearl millet, maize, cassava or sorghum and sometimes as sole crop (Timko & Singh, 2008). Cowpea can fix up to 150kg N/ha under favourable conditions (Woomer *et al.*, 2004; Olal, 2015). Cowpea productivity in Kenya ranges between 200-500 kg/ha for small scale farmers (Olal, 2015)

2.5 Landraces

Landraces result from a long time of natural and artificial selection by farmers to select better adapted varieties for the local environments (Casanas *et al.*, 2017). Although cowpea is reported to have high protein value, high variability, high adaptability and

drought tolerant capacity (Ashraf *et al.*, 2012), little research has been done on their landraces hence loss of superior genes that would be useful in genetic manipulation.

Landraces have played a big role in the introduction of improved varieties as they have rich and complex ancestry with great variations in response to many stresses as well as vast resources for improved varieties (Litchfouse et al., 2011). A large number of cowpea varieties evolved from local landraces have been commercialized (Pratap & Kumar, 2011). However, landraces have rarely been used in hybridization to understand their breeding value in the improvement of grain yield and other traits in cowpea.

2.6 Released cowpea varieties in Kenya

The list of released cowpea varieties in Kenya is shown on Table 1. These varieties are grown either for their leaves, seeds or both (dual purpose).

Table 2.1: Improved cowpea varieties in Kenya

	Variety	Year released	Owner(s)	Maturity (days)	Target areas of production (Masl)	Grain yield (t/ha)	Special characteristics
1.	**KVU HB 48 E 10**	1987	KARI	85-95	0-1200	1.2-1.4	Tolerant to viral diseases; grown for vegetable use
2.	**KVU 27-1**	1989	KARI	70-90	600-1200	1.5-1.8	Dual purpose; dark red seeds;
3.	**ICV 11**	1992	ICIPE	75	1-1500	2.2	Pest tolerant;
4.	**MTW 610**	1998	IITA	60	1-1500	2.5	Large seeds
5.	**MTW 63**	1998	IITA	60	1-1500	2.5	Pest tolerant;
6.	**Kunde 1**	ND	Western Seed Co.	75-90	Below 2000	1.2-2.5	Dual purpose;
7.	**Machakos 66 (M66)**	1998	KARI	85-95	1200-1500	1.5-1.8	Dual purpose; creamy brown seeds and deep green midribs; tolerant to cowpea yellow mosaic virus and scab
8.	**Katumani 80 (K80)**	2000	KARI	75-85	0-1500	1.8-2.0	Dual purpose; creamy brown seeds; resistant to aphids
9.	**KVU-419 (Kunde 419)**	2000	KARI	65-72	0-1200	1.2-1.5	Drought tolerant, extra early maturity
10.	**KCP 022**	2000	KARI	60-75	0-1200	1.2-2.5	Super early maturity drought tolerant
11.	**Kunde Mboga**	2014	Simlaw seeds Co.	120-140	Low and mild altitude	Seed yield 1.6-2.2	Vegetable use.
12.	**Simlaw Kunde**	2014	Simlaw seeds Co.	75-90	Low and mild altitude	1.8-2.6	Drought resistant. Large seeds Drought tolerant High yielding

	Variety	Year released	Owner(s)	Maturity (days)	Target areas of production (Masl)	Grain yield (t/ha)	Special characteristics
13.	**1002/1005/3 (Kunde Faulu)**	2017	KALRO	70-80	Low-high altitudes(5-2000 msl) coast, eastern central and western	1.5-2.13	Large seeds Early maturity Alectra tolerant Dual purpose
14.	**1005/1002/1 (Kunde Tamu)**	2017	KALRO	70-80	Low-high altitudes 5-2000 msl	1.5-2.0	Early maturity *Alectra vogelii* tolerant Dual purpose
15.	**1005/1003/3 (KAT Kunde)**	2017	KALRO	80-90	Low-high altitudes ranging from 5-2000 msl	1.4-2.0	*Alectra vogelii* tolerant Dual purpose
16.	**1005/1002/1/1/1 (Kunde Soko)**	2017	KALRO	80-90	(Coastal eastern and western)	1.4-1.9	Large seeds *Alectra vogelii* tolerant Dual purpose
17.	**1005/1004/3 (Kunde Tumaini)**	2019	KALRO	80-90	Altitudes 600-1500 msl AEZ: LM 4-5, LM 3-4	1.5-2	Drought tolerant Tolerant to *Alectra vogelii* parasitic weed Dual purpose White grain with brown eyes

2.7 Environmental requirements for cultivation of cowpea

Cowpea thrives well under a wide range of environmental conditions. In Kenya, cowpea does well in arid and semi arid areas but is also recommended for medium and higher altitudes between 1200-1500 metres above sea level (Karanja, 2016). This crop can survive high temperatures and drought conditions but is easily affected by frost. It requires a temperature range of 15ºC-30ºC (Karanja, 2016) but does best at 36.1ºC (Muniu, 2017). Cowpea germinates rapidly under warm temperatures while the cold temperatures slow germination. Cowpea can grow well in well drained soils including sandy, clay or loamy soils but does not tolerate waterlogging (Karanja, 2016). The soils should have a PH range of 5.5-6.5 (Nkouannessi 2005; Olal, 2015).

2.8 Cowpea characterization

In many areas, cowpea yields are low because the environments where they are produced have various abiotic and biotic stresses (Makari, 2022). The yields may also vary due to differences in the growth and development of each plant. Knowledge of the extent, distribution and nature of the variation would help in the development of cowpea genotypes with high yield potential and improved adaptation to environmental stresses (Sheidu, 2023)

In the past, genetic diversity in plants was evaluated by studying the differences between quantitative characters and qualitative traits (Kameswara, 2004). It has been important in classifying cultivars and in the study of taxonomic status (Doumbia, 2011).

Morphological characterization is still the first step in the studies of genetic relationships in many breeding programmes. However, evaluation of genetic relationships among germplasm is lengthy and expensive (Doumbia, 2011). Morphological characters are

believed to be controlled by complex genes that are subject to environmental modification and interactions including epistatic interactions (Doumbia 2011).

Most of the best cultivated and breeding materials have limited number of observable morphological markers; most of which have deleterious effects on agronomic performance (Doumbia, 2011). Therefore, morphological characterization cannot adequately describe cultivars without many replications over a long time (Malek *et al,* 2014). Comparisons can only be made for morphological characteristics taken from the same location at the same time.

Determination of genetic diversity in cowpea genotypes is very important in the development of superior cultivars. Traditionally, the estimation of genetic diversity made use of morphological markers. However, the limited number of morphological markers, their poorly known genetic control and environmental influence on phenotypic expression at different stages of growth has limited their reliability over time (Sariah, 2010). Development of molecular markers such as restriction fragment length polymorphism (RFLP) (Lambrides *et al.,* 2000), random amplified polymorphic DNAs (RAPDs) (Betal *et al.,* 2004), amplified fragment length polymorphism (AFLP) (Zong *et al,* 2003) and microsatellites (Li *et al.,* 2001; Wang et al 2004) have greatly improved the analysis of plant genomes and the genetic structure and variations among cowpea accessions (Sariah, 2010). In the past RAPDs have been used to study genetic diversity between cowpea cultivars (Ba et al., 2004). Studies using SSR markers to characterize diversity among cowpea accessions collected from different agroecological zones have been carried out in Kenya, (Kuruma, *et al,* 2008, Wamalwa *et al.,* 2016). Studies show that simple sequence repeats (SSR) markers which are single locus with multiple alleles are better than other markers and are effective in differentiating genotypes (Doumbia, 2011). They are highly polymorphic, codominant and easily reproducible (Asare *et al.,* 2010; Mafakheri et al., 2017). SSRs have been widely used in genotyping, seed purity

checks and protection of varieties (Asare et al., 2010). They have also been used for pedigree analysis and genetic mapping of simple and quantitative characteristics (Asare *et al.,* 2010).

CHAPTER THREE

MATERIALS AND METHODS

3.1 Experimental site

The experiments were conducted in the laboratory and experimental farm of Jomo Kenyatta University of Agriculture and Technology in Juja. Juja is located in central Kenya at 1 º 11′ 0″ south, 37 º 7' 0" East. This area has semi-arid conditions under AEZ IV (Jaetzold and Schmidt 1983) with two distinct rain seasons. The long rains fall from March to May while the short rains fall between October and December; with an average annual rainfall of 989 mm. The daily temperature ranges from 10-30ºC depending on the season. The area has rich black cotton soils.

3.2 Plant materials

One hundred and ten accessions, (Appendix I) were used for this study. Collections from farmers in semi arid region of Kenya comprising of 82 accessions were procured from the National Gene Bank of Kenya; Muguga Kenya. These comprised of accessions from Machakos (74), Makueni (3) and Kitui (5). Twenty-three landraces from Machakos (14) and Baringo (9) were collected directly from farmers and five commercial lines (K80, M66, Kenkunde, KAR 1 and KVU-27-1) were obtained from registered seed companies.

3.3 Field Experimental Design

The trial was laid down in a Randomized Complete Block Design (RCBD) with three replications. Blocking of the replicates was based on the gradient of the field. Each replicate measured 12m by 24m comprising of 110 plots. Cowpea seed was sown in three lines per plot at inter- and intra-row spacing of 0.6m and 0.3m respectively. Two

cowpea seeds were planted per hole and later thinned to a single plant per hole after two weeks from date of germination. Irrigation was done immediately after planting and whenever it became necessary. Weeding was done manually three weeks from date of planting followed by rouging of weeds whenever they emerged.

3.4 Data collection

Qualitative and quantitative agronomic data was collected and recorded from five plants in the middle row of each plot as described by IBPGR (1983). Data collected at emergence was the number of days it took for 50% of the plants to emerge. Data for vegetative stage of development recorded at six weeks; growth habit, growth pattern, twining tendency, pigmentation, terminal leaflet shape, leaf color, terminal leaflet length, terminal leaflet width and number of main branches. At flowering stage of development, data recorded included raceme position, pod attachment, immature pod pigmentation, pod curvature, flower color, pod length, number of seeds per pod and pods per plant. At harvesting, data was obtained for mature pod color, seed shape, texture of testa, seed color, eye color and 100 seed weight.

3.5 Molecular characterization of cowpea

This experiment was carried out at the Cassava Diagnostics Laboratory in Jomo Kenyatta University of Agriculture and Technology in Juja Kenya.

One hundred and ten accessions; (Appendix 1) were planted in pots filled with sand in the green house. The leaf samples of all the accessions were obtained from each genotype two weeks after planting. The leaf samples (0.4g) were freeze dried and then stored at -70^{o} C until used for DNA extraction.

About 0.1g of young leaf tissue of each accession was taken and DNA extracted according to the CTAB DNA extraction protocol (Doyle & Doyle, 1990). Briefly, each 0.1g of leaf sample was ground in a mortar with a pestle with the aid of acid washed sand to break the cell walls and membranes. 1500µl CTAB buffer was added and the slurry was transferred to a 2,000µl Eppendorf tube. The solution was mixed thoroughly to suspend the cellular material and incubated for 30 minutes at 65ºC in a water bath. The slurry was then centrifuged at 13,000 rpm for ten minutes. 750µl of the supernatant was transferred to a fresh Eppendorf tube and mixed with an equal amount of chloroform: Isoamyl alcohol; 24:1 v:v and the solution vortexed for three minutes. The solution was span in a centrifuge at 13,000 rpm for 10 minutes. The aqueous layer was transferred (400µl) into a fresh tube Eppendorf tube using a pipette. An equal volume of ice cold isopropanol was added and the tubes incubated in a freezer for 10 minutes at -20 ºC and then centrifuged at 13,000 rpm for ten minutes. The supernatant was decanted carefully leaving DNA pellet at the bottom of the tube. The pelleted DNA was washed with 500µl 70% ethanol and centrifuged at 13,000rpm for 5minutes. DNA was dried at room temperature for 20 minutes or until the ethanol evaporated and then dissolved in 50 µL of deionized water. The DNA samples were then stored at -20°C until used.

The quality of the extracted DNA samples was tested on 1% Agarose. 1g of agarose was weighed and mixed with 100 mL Tris/Borate/EDTA (TBE) buffer. This solution was poured in a flask and heated in a microwave for three minutes or until the agarose was fully dissolved. The solution was allowed to cool and 2µl of Ethidium Bromide added. About 5µl of the extracted DNA sample were mixed with 2µl dye loaded on to the gel and run for 30 minutes.

Molecular characterization of one hundred and ten accessions (110) was done using 20 primer pairs of Simple Sequence Repeat (SSR) markers to analyze the variations and relatedness among the genotypes. Initially, 20 pairs of SSR markers (Table 1) were

screened for polymorphisms using mixed DNA samples. These primers were similarly used by Li *et al.* (2001), Asare et al. (2010) and Doumbia et al. (2013). PCR amplification was carried out in 0.2-mL PCR tube with final volume of 12.5µL, comprising of a master mix containing 2.5µ 10 ×PCR buffer, 0.25µM of each primer, 0.5 U Taq DNA polymerase. For each of these 2 µL sample DNA template DNA was added. The tubes were placed in a Gene-Amp PCR system 2720 (Applied Bio systems, USA) with an initial DNA denaturation at 94 °C for 5 minutes followed by 35 cycles of 30 seconds at 94 °C, 30 seconds at 45 °C to 65 °C for annealing temperature depending on the primer pair, 1 minute at 72 °C and a final incubation at 72 °C for 10 minutes (Table 4). The PCR products were then analyzed on 2% agarose gels using 0.5 ×TBE buffer stained with 2mg/mL ethidium bromide to establish polymorphism. The gel associated with each marker was photographed under a UV trans illuminator. The amplified bands were scored for each accession as present (1) or absent (0).

Table 3.1: SSR Markers used in the study

Name	Primer sequence	No bases	Source
SSR-6265F	5'-CAG AAG CGG TGA AAA TTG AAC -3'	21	Doumbia/Asare
SSR-6265R	5'- GCA TGT TGC GAC AAT GG-3'	17	
SSR-6258F	5'- GGT TTC CTA GTT GGG AAG GAA-3'	21	Doumbia/Asare
SSR-6258R	5'-ATT ATG CCA TGG AGG GTT CA-3'	20	
SSR-6243F	5'-GTA GGG AGT TGG CCA CGA TA-3'	20	Doumbia/Asare
SSR-6243R	5'-CAA CCG ATG AAA AAG TGG ACA-3'	21	
SSR-6218F	5'-GTG GAA GGA ATG GGT CCA G-3'	19	Doumbia/Asare
SSR-6218R	5'-AGG AAA TTT GCA TTC CCT TGT-3'	21	
SSR-6217F	5'-GGG AGT GCT CCG GAA AGT-3'	18	Doumbia/Asare
SSR-6217R	5'-TTC CCT ATG AAC TGG GAG ATC-3'	21	
SSR-6353F	5'-TCA TGG GTT AAA TTT GCT TCA A-3'	22	Doumbia/Asare
SSR-6353R	5'-AAA CCA TGT GGT TGT TGC AC-3'	20	
SSR-6352F	5'-GTT GTG AGC TTC CCC AGA TG-3'	20	Doumbia/Asare
SSR-6352R	5'-ATT TTT GAA CCC ACC ACC AG-3'	20	
SSR-6336F	5'-TGA AAA CAA CGA TAT GCA GAA-3'	21	Doumbia/Asare
SSR-6336R	5'-TCA GTC TTA GAA TTG AGT TTT C-3'	22	
SSR-6323F	5'-CAA AGG GTC ATC AGG ATT GG-3'	20	Doumbia/Asare
SSR-6323R	5'-TTT AAG CAG CCA AGC AGT TGT-3'	21	
SSR-6451F	5'-AAA GAG ATA CAC ATG CCT AAC-3'	21	Doumbia/Asare
SSR-6451R	5'-GAC CAA CAG CGA CTT TGA GC-3'	20	
SSR-6277F	5'-CAC CCC CGT ACA CAC ACA-3'	18	Doumbia/Asare
SSR-6277R	5'-CAC TTA AAT TTC CAC CAG GCA T-3'	22	
SSR-6436F	5'-CAG AAT CCT TGT GAA CCT G-3'	21	Doumbia/Asare
SSR-6436R	5'-TTT CGC AAT ATG CCC TTT TC-3'	21	
SSR-6375F	5'-GCT CGG ATA TGG TCC TGA AA-3'	20	Doumbia/Asare
SSR-6375R	5'-TCA GTG TCA GCA CCA TCC C-3'	19	
SSR-6371F	5'-TGC TCA TCG TGC TTT GTC TT-3'	21	Doumbia/Asare
SSR-6371R	5'-CAC TTC AGA CTT AGA GCG AAG-3'	21	
SSR-6370F	5'-CAA CTT CAC AGC CCT CAA-3'	18	Doumbia/Asare
SSR-6370R	5'-TTG AAG GTA TGG CCT TTT GTT T-3'	22	
SSR-6356F	5'-TGC AAT ATG GAC CAG AAG AAA-3'	21	Doumbia/Asare
SSR-6356R	5'-ATG CCC CAA CAA CAA CAT TT-3'	20	
SSR-6613F	5'-CTA TTG GAA TCT TGC CGT TG-3'	20	Doumbia/Asare
SSR-6613R	5'-CTT TAC CTT TAT GCA AAC CAA T-3'	22	
SSR-6608F	5'-CTA AAT TAT AAT ATT CGT CGG T-3'	21	Doumbia/Asare
SSR-6608R	5'-GGT TAA GGA AAA GAG GGT AGG-3'	21	
SSR-6603F	5'-GAG AAC TTC ACG CAC AAT AG-3'	20	Doumbia/Asare
SSR-6603R	5'-CGC GGT AGC ATG ATT GAA TTT-3'	21	
SSR-6587F	5'-GAT ATA GAA TAG CAT ATT TAA C-3'	22	Doumbia/Asare
SSR-6587R	5'-GTT GAA AGT TTG ATA GTA AAG-3'	21	

Asare et al (2010) and Doumbia, (2011)

Table 3.2: PCR amplification conditions used in the study

Stages	Temperature	Time (s)	Number of cycles
Initial Denaturation	94	300	1
Denaturation	94	30	
Annealing	55	45	35
Extension	72	60	
Final Extension	72	600	1
End	4	∞	

3.6 Data Analysis

The field data was recorded in data sheets and thereafter entered, organized and managed in an excel sheet. These data were analyzed using GENSTAT program version 14. Qualitative data was used to assess the distribution of accessions in different traits of the respective characteristics expressed as a percentage of the total number of accessions; number of accessions possessing a certain attribute of character divided by the total number of accessions multiplied by 100. Quantitative data was subjected to ANOVA to determine the variation in the respective traits. The contribution of the respective characters to the variation of the different traits was assessed using Principal Component Analysis. The accessions were classified into groups using cluster analysis while correlation among traits was determined using Pearson correlation analysis. Unweighted ranking of the characters positively associated with yield and productivity was done by ranking five traits; pod length, number of pods per plant, number of seeds per plant and number of branches per plant, individually and summing up the ranks for each accession. The sum of ranks was used to estimate the accessions potential providing ranking of greatest performance and least performance.

For the molecular data, the bands that were not polymorphic with at least one of the samples were not scored. The polymorphic bands were scored as present or absent (1/0). This was then used as raw data to generate a matrix which was subjected to Principal Component Analysis and analysis of molecular variance (AMOVA).

CHAPTER FOUR

RESULTS

4.1 Variation in the Cowpea Accessions for Qualitative Characters

Variation among the accessions based on each character (Appendix II) was evaluated by determining the distribution of these accessions in the respective traits. The accessions could be evenly distributed across the traits for a character or skewed in favor of one of the traits within a character. The distribution of accessions among the traits of 15 qualitative morphological characters is presented in Table 4.1. Distribution of accessions among the traits were evenly distributed for immature pod color, leaf color, seed shape and twining tendency and skewed for terminal leaflet shape, raceme position, pod attachment, pod curvature, mature pod color, flower color, testa texture and eye color.

The accessions could be placed into three groups based on growth habit: acute erect, semi erect and intermediate. Over half of the accessions (73%) were semi erect, acute erect (23%) and 5% intermediate. Two classes of growth pattern were observed; determinate (27%) and indeterminate (73%). It was also recorded that the accessions had three distinct groups based on the raceme position; above canopy (24%), upper canopy (56%) and throughout the plant (20%). Based on pod color, both mature and immature pods showed a wide range of variation. There were accessions that had no pigmentation (green) on immature pods to those with uniform pigmentation; 31% of the accessions did not have pigmented pods, 34% of the lines had pigmented valves and green sutures, splashes of pigment were observed in 28% of the accessions and 6% of the lines had pigmented tips. Only 1% of the accessions had uniformly pigmented immature pods. The mature dried pods also showed uneven distribution of accessions; straw (65%), dark brown (34%), dark purple (1%). The accessions also showed uneven distribution for

flower color and terminal leaflet shape. The observed flower colors included; white (1%), white-purple (4%), purple (95%) and terminal leaflet shape: Globose (99%) and hastate (1%). 88% of the lines under study produced slightly curved pods while the remaining 12% had straight pods.

Twining tendency of the accessions showed even distribution with 6% of the accessions with no twining, 39%, 42% and 13% of the accessions were observed to show slight, intermediate and pronounced twining respectively.

Table 4.1: Distribution of accessions among respective categories of the evaluated morphological characters

Crop Characteristic	Distribution of the accessions in respective traits (%)	
1. Growth Habit	Acute erect	22.7
	Semi erect	72.7
	Intermediate	4.5
2. Growth pattern	Determinate	27
	Indeterminate	73
3. Twinning tendency	None	6
	slight	39
	Intermediate	42
	Pronounced	13
4. Pigmentation	None	43.6
	very slight	36.3
	Moderate	4.5
	Intermediate	10.9
	Extensive	4.5
5. Terminal leaflet shape	Globose	99
	Hastate	1
6. Raceme position	Above canopy	24
	upper canopy	56
	Throughout	20
7. Pod attachment	Pedant	81
	30-90º	16
	Erect	3
8. Immature pod color	None	31
	pigmented valves green sutures	34
	splashes of pigment	28
	uniformly pigmented	1
	pigmented tip	6
9. Pod curvature	Straight	12
	Slightly curved	88
10. Mature pod color	Straw	64.5
	Dark brown	33.6
	Black/dark purple	1.8
11. Flower color	White	1
	white purple	4
	purple	95
12. Leaf color	Pale green	1
	intermediate green	54.5
	Dark green	44.5
13. Seed shape	Kidney	2
	ovoid	47
	Globose	1
	Rhomboid	50
14. Eye color	Absent	81
	Brown splashes	2
	Tan brown	3
	Blue to black	4
	speckled	10
15. Testa texture	Smooth	89
	Smooth to rough	7
	Rough to wrinkled	4
16. Seed coat colour	White	4
	Cream	13
	Brown	23
	Red	44
	Purple	0
	Black	10
	Other	6

Eighty accessions had semi erect growth habit, 25 had acute erect growth habit and 5 accessions portrayed intermediate type of growth habit. Eighty accessions had indeterminate growth pattern while the remaining 30 accessions were determinate. Fourty three genotypes had slight twining tendency; 46 accessions showed intermediate twining tendency while 14 accessions had pronounced twining tendency. GBK 003650, GBK 003651, GBK 003674, GBK 003713, GBK 003726, GBK 003780 and GBK 003796 did not show any twining tendency.

GBK 003713, GBK 003816, KOL 6, KOL 8 and MBL were pigmented moderately at the base and tips of petioles; MAR. 5, Kenkunde and GBK 034722 showed extensive pigmentation; GBK 003657, GBK 003658, GBK 003663, GBK 003670 B, GBK 003687 B, GBK 003696, GBK 003699, GBK 003701, GBK 003709, KIP 1, KIP 2 and LAM 4 had intermediate pigmentation. 40 accessions had very slight pigmentation while the remaining 48 accessions showed no pigmentation. All accesssions had globose shaped terminal leaflets except GBK 003804 that had hastate shaped terminal leaflets. Sixty two accessions had raceme on the upper canopy. Twenty six had their racemes mostly above the canopy while 22 genotypes had raceme spread throughout the canopy. Eighty nine genotypes had their pod attachment to penducle to be pendant. Eighteen accessions had their pods to peduncle attachment between 30 and 90 down from erect. GBK 003685 and KOL 2 had erect pod to peduncle attachment. Pigmented valves and green sutures were found on immature pods of 37 accessions. Thirty one accessions had splashes of pigment on their pods. Seven accessions showed pigmented tip on their immature pods. No pigmentation was found on 34 accessions and only GBK 003705 from Machakos showed uniformly pigmented immature pods. Ninety seven accessions had slightly curved pods while thirteen accessions had straight pods. Three pod colours were obtained at maturity. Seventy one varieties were straw (65%) coloured pods, 37 accessions dark brown podcolor at maturity and 2 accesions showed black to dark purple color. Three flower colours were observed in this study. A hundred and five accessions showed purple coloured flowers. Only GBK 003650 produced white flowers while GBK 003675 A, GBK 003727, GBK 003916 and GBK 046540 had purple-white flowers. Fourty nine cowpea accessions had dark green leaf color, 60

had intermediate green leaves and only GBK 003985 had pale green leaves. Fifty five genotypes had rhomboid shaped seeds. Only GBK 003651 had globose shaped seeds. Two accessions had kidney shaped seeds and they were GBK 003717A and GBK 046540. The seeds of 52 accessions had ovoid shape. Eighty nine accesions had no (0) eye colour; Eleven accessions had speckled (7) eye colour; four accessions had brown splashes; three had tan brown eye colour. The testa texture of 98 accessions were smooth while 8 were smooth to rough. Four genotypes had rough to wrinkled testa texture.

4.2 Variation among accessions for Quantitative Characters

The means and ranges among accessions for respective quantitative characteristics are presented in Table 4.2. The accessions were significantly different for number of days to 50% emergence, pod length, number of pods per plant and number of seeds per pod. There were no significant differences among the accessions for one hundred seed weight, number of branches per plant, number of days to 50% flowering, terminal leaflet length and terminal leaflet width (Table 4.2).

From the day of planting, the accessions germinated between 4 to 8 days with an average of 6.06 days. Seven accessions germinated after 4 days, 45 accessions emerged after 5 days, 35 genotypes after 6 days and the remaining accessions emerged after 8 days.

The accessions attained 50% flowering between 65 and 75 days after emergence with a mean of 70 days. KOL 5 and M66 were the earliest genotypes to flower at 65 days. On the other hand, KOL 2, GBK 046540, GBK 003717A, GBK 003676, GBK 003675 and GBK 003652 were late flowering genotypes flowered at 75 days.

Terminal leaflet length for the accessions ranged between 3.4cm and 5.8 cm with an average of 4.39 cm. GBK 003663 and K80 had the shortest and longest terminal leaflets respectively.

The terminal leaflet width ranged from 1.8 to .1 cm with an average of 2.8cm. GBK 003701 and GBK 003674 had the shortest and longest width across the leaf of the accessions.

The average number of branches counted per plant was 4.38 with a range of 3.4 to 5.2. Most accessions had 4 branches per plant.

The number of pods per plant was observed to range between 6.67 and 30 pods per plant with an average of 21.95 pods per plant. GBK 003698 had the highest number of pods per plant while GBK 003713 had least number of pods per plant.

The length of pods of the accessions was observed to range from 9.01 cm to 13.96 cm with a mean length of 11.56 cm. GBK 003650, GBK 003651, GBK 003660, GBK 003663, GBK 003675 A, GBK 003682, GBK 003685, GBK 003689, GBK 003693, GBK 003694, GBK 003697 and GBK 003701 were some of the accessions that gave long pods on average.

The number of seeds per pod averaged at 8.36 with a range of 5.07 to 11.07 cm. GBK 003682, GBK 003693, GBK 003694, GBK 003697, GBK 003701, GBK 003876, GBK 027089, K80, M66, and MAR.2 are some of the accessions that were observed to give high number of seeds per pod.

Table 4.2: Variation in quantitative morphological traits among cowpea accessions

Trait	*P*	Mean	Range	SD	CV (%)
Emergence -50% (days)	‹*0.001*	6.06±1.24	4.3-8.3	0.966	20.4
Flowering- 50% (days)	0.28	70.87±3.27	65-75.7	1.952	4.6
Terminal leaflet length (cm)	0.487	4.39±0.83	3.4-5.8	0.486	19
Terminal leaflet width(cm)	0.42	2.81±0.72	1.8-4.11	0.428	25.6
No. of branches per plant	0.155	4.38±0.69	3.4-5.2	0.42	15.7
No. of pods per plant	‹*0.001*	21.95±5.31	6.67-30	4.54	24.2
Pod length(cm)	0.006	11.56±1.51	9.01-13.96	1.051	13.1
No. of seeds per pod	0.005	8.36±1.92	5.07-11.07	1.34	22.9
100Seed Weight (g)	0.398	8.8±2.05	5.9-11.4	1.21	23.2

The average 100 seed weight was 8.8 g with a range between 5.9g and 11.4g. Some of the accessions with large seeds included GBK 003654, GBK 003666, GBK 3676 B, GBK 003687, GBK 003701 and GBK 003723.

Ranking based on pod length, number of pods per plant, number of seeds per plant and number of branches per plant, was used to identify accessions with high and low potential yields. The accessions that showed high potential (top 20) and least potential (bottom 20) in productivity based on overall unweighted ranking among characters positively associated with productivity are presented in Table 4.3. These results indicate that the top 5% of the lines that showed high productivity potential are GBK 003662, GBK 003663, GBK 003676, GBK 003723, GBK 003650 and GBK 003642 which superseded the registered varieties. K80 was ranked number 20 whereas Kenkunde and M66 were ranked 91 and 104 respectively. The overall ranking for all accessions is presented in Appendix 2.

Table 4.3: Mean values of 20 highest and 20 lowest accessions based on quantitative traits

ACC	PL	SPP	100SW	PPP	BP	Ranks
High Rank						
GBK 003662	11.8	10.9	8.7	26.3	4.7	1
GBK 003663	12.6	10.2	6.7	27.0	4.1	2
GBK 003676	10.5	8.1	8.7	26.7	4.3	3
GBK 003723	11.9	8.6	11.2	23.0	4.2	4
GBK 003650	12.9	9.6	9.5	26.7	5.1	5
GBK 003642	9.9	6.2	9.3	10.7	4.3	6
GBK 003669	11.4	10.8	9.8	22.0	4.7	7
GBK 003668 D	13.0	9.5	8.3	25.3	4.3	8
GBK 003780	12.9	9.1	7.1	19.7	5.1	9
GBK 003709	10.3	7.8	6.2	7.0	4.9	10
GBK 003685	12.0	8.5	8.3	26.0	3.9	11
KAB 1	11.9	9.3	10.8	22.3	4.8	12
GBK 003985	12.6	9.5	10.2	23.0	5.2	13
GBK 003796	11.5	6.3	9.1	23.3	4.1	14
GBK 003645	11.5	6.5	8.9	27.0	4.1	15
GBK 003676	11.7	9.6	9.3	20.7	4.2	16
GBK 003676 B	11.0	7.0	11.4	20.7	4.4	17
GBK 003687	11.6	6.3	6.9	25.0	4.0	18
GBK 003654	9.5	5.1	10.0	19.7	4.8	19
K80	13.0	10.9	8.4	28.3	4.5	20
Low Rank						
Kenkunde	12.7	8.2	8.9	21.3	4.1	91
GBK 003698	12.3	9.3	9.2	30.0	4.5	92
GBK 003694	12.5	10.3	8.5	21.3	3.9	93
GBK 003711	11.0	9.2	9.7	22.7	3.8	94
KOL 8	12.0	8.0	8.0	19.0	4.3	95
KOL 2	11.3	8.6	8.3	18.3	4.5	96
KAT 1	11.9	9.4	8.1	21.7	4.2	97
MBL	10.6	7.8	11.4	18.7	3.9	98
MAC 1	12.3	7.1	9.4	24.3	4.3	99
GBK 003682	13.2	10.2	10.0	25.3	4.5	100
GBK 003687 B	10.1	8.5	10.0	24.7	4.7	101
MAR.5	12.6	6.7	10.1	10	4.9	102
MAR.3	11.2	7.0	7.8	7.0	4.6	103
M66	13.1	10.4	9.7	19.7	4.1	104
MAC 3	11.9	8.5	9.6	18.0	4.3	105
K0L9 C	10.1	7.5	11.4	25.3	4.7	106
GBK 005173 B	10.4	7.7	6.9	26.7	4.5	107
KIP 2	11.3	6.9	9.3	24.7	4.3	108
GBK 027089	11.2	10.9	7.8	19.3	5.1	109
GBK 034722	11.1	7.8	8.7	23.0	4.9	110

Ranking of accessions based un-weighted indices of five traits; pod length, number of pods per plant, number of seeds per plant and number of branches per plant

ACC=accession number PL=Pod length SPP=Number of seeds per pod 100SW=a hundred seed weight PPP= number of pods per plant BP=Number of main branches per plant

Pair wise correlation values among the quantitative traits are presented in Table 4.4. Significant positive correlation among the traits was found for number of days to 50% emergence and terminal leaflet length (r= 0.188), number of days to 50% emergence and terminal leaflet width (r=0.204), terminal leaflet length and terminal leaflet width(r=0.523), and pod length and number of seeds per pod (r=0.547). Significant negative correlation was recorded for number of days to 50% emergence and number of days to 50% flowering (r=-0.21) and number of days to 50% emergence and number of pods per plant were (r=-0.53).

Table 4.4: Pearson's correlation among quantitative traits recorded on cowpea

Character	E (50%)	BP	TLL	TLW	F (50%)	PPP	PL	SPP	100SW
E (50%)	1								
BP	-0.0273	1							
TLL	**0.1881***	-0.0242	1						
TLW	**0.2042***	0.0880	**0.5230****	1					
F (50%)	**-0.2131***	0.0510	-0.0787	0.0890	1				
PPP	**-0.5258****	-0.1200	-0.0611	0.0742	0.1376	1			
PL	0.0510	-0.1324	-0.0221	-0.0328	-0.1147	0.0986	1		
SPP	0.0749	0.0789	-0.0091	0.0560	-0.0295	0.1742	**0.5470****	1	
100SW	0.0085	0.0392	0.0424	0.0140	0.0782	0.1053	0.0411	0.0429	1

PL=Pod length
SPP=Number of seeds per pod
100SW=a hundred seed weight
PPP= number of pods per plant
BP=Number of main branches per plant
E (50%)= 50% emergence

F (50%)=50% flowering
TLL= Terminal leaflet length
TLW=Terminal leaflet width
*-significant
**-highly significant

The quantitative characters evaluated were reduced to five major principal components that accounted for 19.8, 18.0, 15.91, 12.4 and 11.2 respectively accounting for 77% of the total variation (Table 4.5). PC1 was attributed mainly to number of days to 50%, emergence, number of pods per plant, terminal leaflet length and terminal leaflet width. PC 2 was attributed to pod length and seeds per pod. PC 3 was associated with number of days to 50% emergence, number of days to 50% flowering, number of pods per plant, terminal leaflet length and terminal leaflet width (Table 4.5).

Table 4.5: Eigen vectors and values for five Principal Components

	PC 1	**PC 2**	**PC 3**	**PC 4**	**PC 5**
Eigen value	1.782	1.620	1.431	1.116	1.010
% variance	19.80	18.00	15.91	12.40	11.22
Cumulative Variance	19.80	37.80	53.71	66.11	77.33
Vector Loadings					
% 100Seed Weight	0.05686	0.05984	0.01451	0.54445	0.73494
No. of Branches/Plant	-0.07734	-0.10131	0.07847	-0.65861	0.60621
Emergence (50%)	-0.57700	0.09694	-0.29519	0.00341	0.02544
Flowering (50%)	0.21671	-0.14965	0.38164	-0.37066	-0.12195
Pod Length	0.07599	0.65918	-0.17454	-0.08388	-0.16279
No. of Pods/Plant	0.46836	0.21126	0.44474	0.20598	0.00878
No. of Seeds/Pod	0.06598	0.66252	-0.03755	-0.24503	0.16710
Terminal Leaflet Length	-0.46927	0.11945	0.44362	0.15119	-0.13919
Terminal Leaflet Width	-0.40149	0.14837	0.57826	0.00644	0.05451

The quantitative data for nine characters evaluated were subjected to multivariate cluster analysis generating a dendrogram classifying the accessions in groups based on similarity. Figure 1 shows the relationship among the 110 accessions that were evaluated

based on quantitative characters. The accessions are initially divided into two major clusters (1 and 2), 61% at similarity level. Cluster 1 is subdivided into two sub-clusters A and B. Sub-cluster A had five accessions while sub-cluster B had two accessions. Cluster 1 is comprised of seven accessions (Appendix 1, Table 4.6) obtained from Machakos except one, KIP2, from Baringo. Cluster 2 had 82 accessions obtained from Machakos.

Cluster 2 also had two sub-clusters C and D which are divided further into four groups; I, II, III and IV respectively. Sub-cluster C group I had 84 accessions while sub cluster C group II had 3 accessions. Sub-cluster D group III and sub-cluster D group IV each had 8 accessions. The commercial varieties were observed to have been grouped in one cluster; Cluster 2 sub-cluster C group I. Collections from the National Gene Bank of Kenya procured from Machakos were found in all clusters with majority in Cluster 2, sub-cluster C; I (Figure 1)

Collections obtained directly from farmers in Kola in Machakos were also observed to be evenly distributed across all clusters with Cluster 1 A having one accession, cluster C I has four accessions, cluster D III has one accession and cluster D IV having two accessions. Accessions from Makueni were distributed into two groups; cluster 2 C I had two accessions and cluster 2 D IV had one accession. Accessions from Kitui were grouped into one cluster; Cluster 2 C I except for one accession that was grouped in Cluster 2 D IV (Figure 4.1). Accessions that were sourced from the central Rift Valley; Baringo county were spread out throughout the clusters; cluster 1 A (1), cluster 2 C I (6) and 2 C II (2).

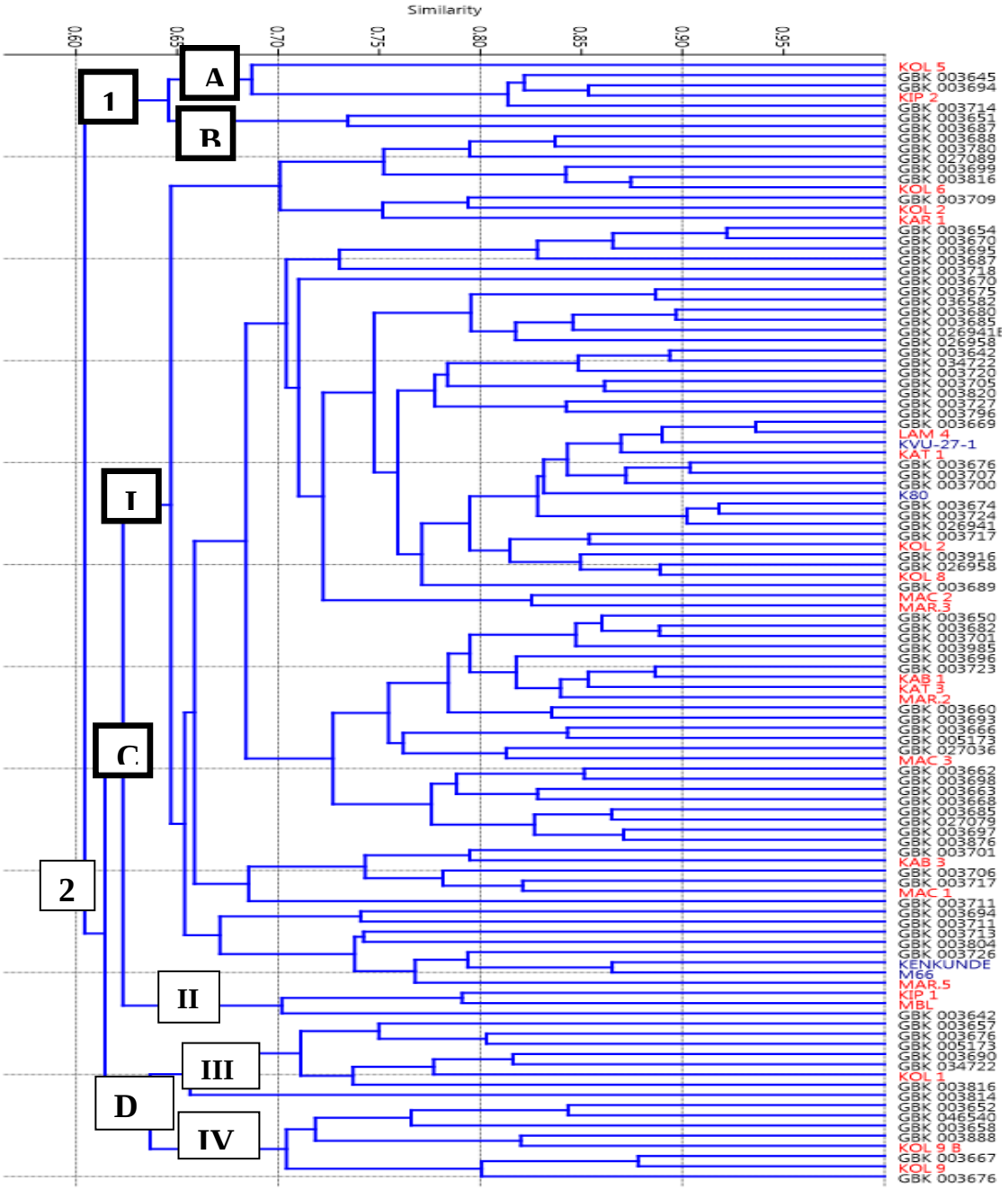

Figure 4.1: Relationships among cowpea collections from Semi-Arid Areas of Kenya and commercial lines

Table 4.6: Distribution of accessions within clusters based on similarity among quantitative traits

Cluster	Similarity of coefficient	No. of accessions	Name of accessions
Cluster 1	0.61		
A	0.64	5	KOL 5, GBK 003645, GBK 003694, KIP 2, GBK 003714
B	0.64	2	GBK 003651, GBK 003687
Cluster 2	0.61		
C I	0.64	84	GBK 003688, GBK 003780, GBK 027089, GBK 003699, GBK 003816, KOL 6, GBK 003709, KOL 2, KAR 1, GBK 003654, GBK 003670, GBK 003695, GBK 003687, GBK 003718, GBK 003670, GBK 003675, GBK 036582, GBK 003680, GBK 003685, GBK 026941 B, GBK 026958, GBK 003642, GBK 034722, GBK 003720, GBK 003705, GBK 003820, GBK 003727, GBK 003796, GBK 003669, LAM4,KVU-27-1, KAT 1, GBK 003676, GBK 003707, GBK 003700, K80, GBK 003674, GBK 003724, GBK 026941, GBK 003717, KOL 2, GBK 003916, GBK 026958,KOL 8, GBK 003689, MAC 2, MAR.3, GBK 003650, GBK 003682, GBK 003701, GBK 003985, GBK 003696, GBK 003723, KAB 1, KAT 3, MAR.2, GBK 003660, GBK 003693, GBK 003666, GBK 005173, GBK 027036, MAC 3, GBK 003662, GBK 003698, GBK 003663, GBK 003668, GBK 003685, GBK 027079, GBK 003697, GBK 003876, GBK 003701, KAB 3, GBK 003706, GBK 003717, MAC 1, GBK 003711,GBK 00394, GBK 003711, GBK 003713, GBK 003804, GBK 003726, KENKUNDE, M66, MAR.5
C II	0.70	3	KIP 1, MBL,GBK 003642
DIII	0.67	8	GBK 003657, GBK 003676, GBK 005173, GBK 003690, GBK 034722, KOL 1, GBK 003816, GBK 003814
DIV	0.71	8	GBK 003642, GBK 046540, GBK 003658, GBK 003888, KOL 9B, GBK 003667, KOL 9, GBK 003676

4.3 Molecular characterization based on SSR markers

Twenty primer pairs (forward and reverse) were used in genetic characterization of 110 cowpea accessions from semi arid region of Kenya. Seven of the SSR primer pairs did not amplify any fragment and five more generated monomorphic allelic amplifications across all the tested accessions; all these were excluded in the analysis as they did not

show any variations between the genotypes. Figure 4.2 shows the monomorphic bands while Figure 4.3 and Figure 4.4 show polymorphic bands.

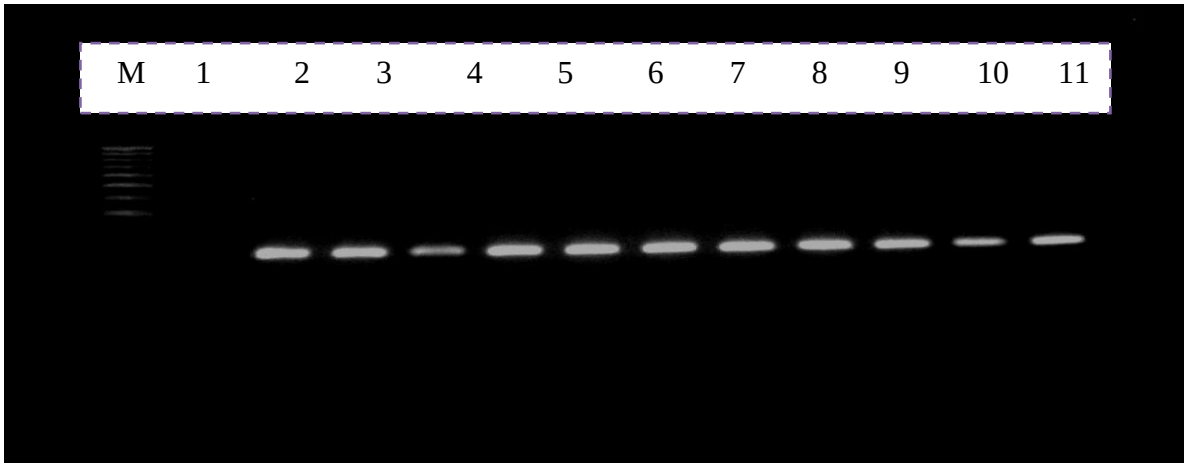

Figure 4.2: Monomorphic band on Agarose gel for primer SSR 6356

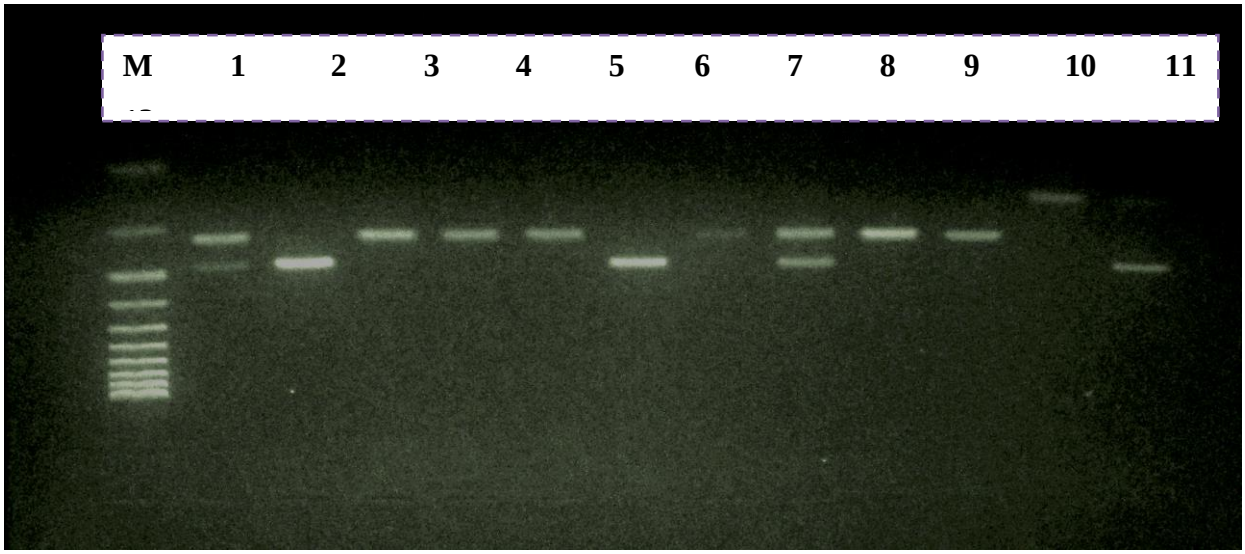

Figure 4.3: Polymorphic bands on Agarose gel for primer SSR 6608

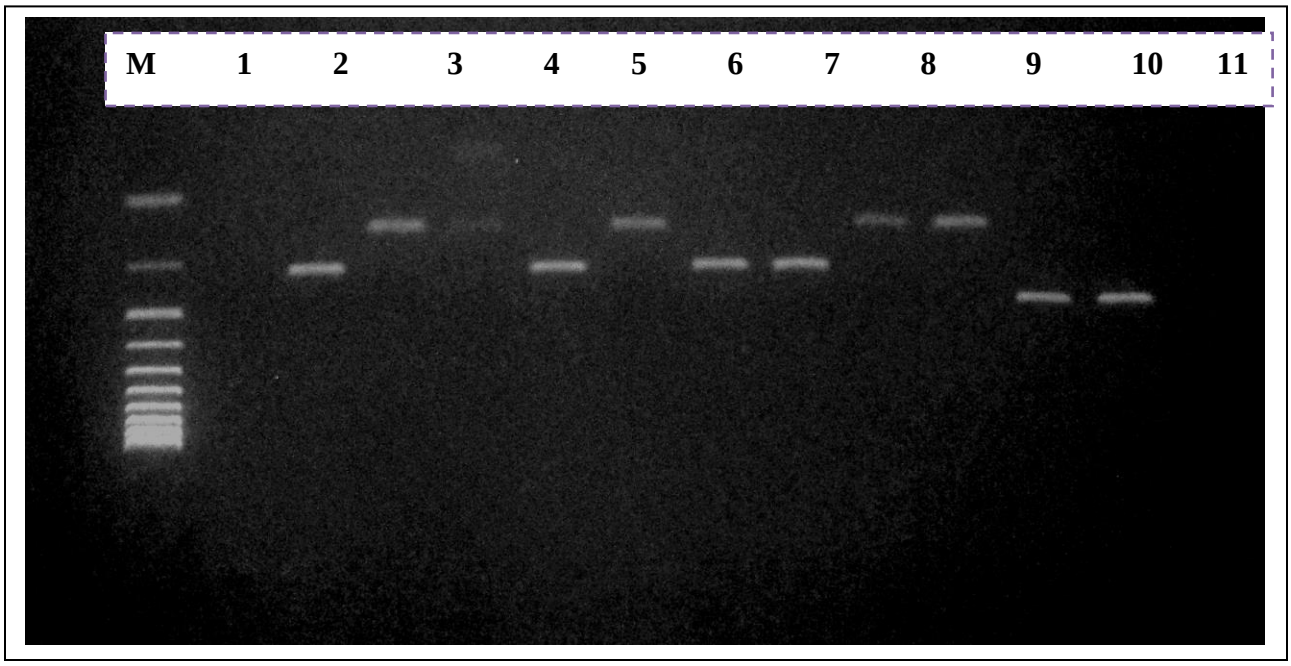

Figure 4.4: Polymorphic band on Agarose gel for PCR products for SSR 6243

Key:

1.GBK 003642	7.GBK 003652
2.GBK 003642 A	8.GBK 003654
3.GBK 003645	9.GBK 003657
4.GBK 003650	10.GBK 003658
5.GBK 003651	11.GBK 003660
6.GBK 003642	12.GBK 003662

Out of the twenty primers screened, seven pairs of primers were monomorphic, five did not amplify and eight were polymorphic as shown on Table 4.7.

Table 4.7: Amplification status of the SSR markers

Primer Set	Name	Primer sequence	Status
1	SSR-6265F	5'-CAG AAG CGG TGA AAA TTG AAC -3'	Polymorphic
	SSR-6265R	5'- GCA TGT TGC GAC AAT GG-3'	
2	SSR-6258F	5'- GGT TTC CTA GTT GGG AAG GAA-3'	Did not amplify
	SSR-6258R	5'-ATT ATG CCA TGG AGG GTT CA-3'	
3	SSR-6243F	5'-GTA GGG AGT TGG CCA CGA TA-3'	Polymorphic
	SSR-6243R	5'-CAA CCG ATG AAA AAG TGG ACA-3'	
4	SSR-6218F	5'-GTG GAA GGA ATG GGT CCA G-3'	Monomorphic
	SSR-6218R	5'-AGG AAA TTT GCA TTC CCT TGT-3'	
5	SSR-6217F	5'-GGG AGT GCT CCG GAA AGT-3'	Polymorphic
	SSR-6217R	5'-TTC CCT ATG AAC TGG GAG ATC-3'	
6	SSR-6353F	5'-TCA TGG GTT AAA TTT GCT TCA A-3'	Monomorphic
	SSR-6353R	5'-AAA CCA TGT GGT TGT TGC AC-3'	
7	SSR-6352F	5'-GTT GTG AGC TTC CCC AGA TG-3'	Polymorphic
	SSR-6352R	5'-ATT TTT GAA CCC ACC ACC AG-3'	
8	SSR-6336F	5'-TGA AAA CAA CGA TAT GCA GAA-3'	Monomorphic
	SSR-6336R	5'-TCA GTC TTA GAA TTG AGT TTT C-3'	
9	SSR-6323F	5'-CAA AGG GTC ATC AGG ATT GG-3'	Monomorphic
	SSR-6323R	5'-TTT AAG CAG CCA AGC AGT TGT-3'	
10	SSR-6451F	5'-AAA GAG ATA CAC ATG CCT AAC-3'	Polymorphic
	SSR-6451R	5'-GAC CAA CAG CGA CTT TGA GC-3'	
11	SSR-6277F	5'-CAC CCC CGT ACA CAC ACA-3'	Did not amplify
	SSR-6277R	5'-CAC TTA AAT TTC CAC CAG GCA T-3'	
12	SSR-6436F	5'-CAG AAT CCT TGT GAA CCT G-3'	Polymorphic
	SSR-6436R	5'-TTT CGC AAT ATG CCC TTT TC-3'	
13	SSR-6375F	5'-GCT CGG ATA TGG TCC TGA AA-3'	Polymorphic
	SSR-6375R	5'-TCA GTG TCA GCA CCA TCC C-3'	
14	SSR-6371F	5'-TGC TCA TCG TGC TTT GTC TT-3'	Did not amplify
	SSR-6371R	5'-CAC TTC AGA CTT AGA GCG AAG-3'	
15	SSR-6370F	5'-CAA CTT CAC AGC CCT CAA-3'	Did not amplify
	SSR-6370R	5'-TTG AAG GTA TGG CCT TTT GTT T-3'	
16	SSR-6356F	5'-TGC AAT ATG GAC CAG AAG AAA-3'	Monomorphic
	SSR-6356R	5'-ATG CCC CAA CAA CAA CAT TT-3'	
17	SSR-6613F	5'-CTA TTG GAA TCT TGC CGT TG-3'	Monomorphic
	SSR-6613R	5'-CTT TAC CTT TAT GCA AAC CAA T-3'	
18	SSR-6608F	5'-CTA AAT TAT AAT ATT CGT CGG T-3'	Polymorphic
	SSR-6608R	5'-GGT TAA GGA AAA GAG GGT AGG-3'	
19	SSR-6603F	5'-GAG AAC TTC ACG CAC AAT AG-3'	Monomorphic
	SSR-6603R	5'-CGC GGT AGC ATG ATT GAA TTT-3'	
20	SSR-6581F	5'-GAT ATA GAA TAG CAT ATT TAA C-3'	Did not amplify
	SSR-6581R	5'-GTT GAA AGT TTG ATA GTA AAG-3'	

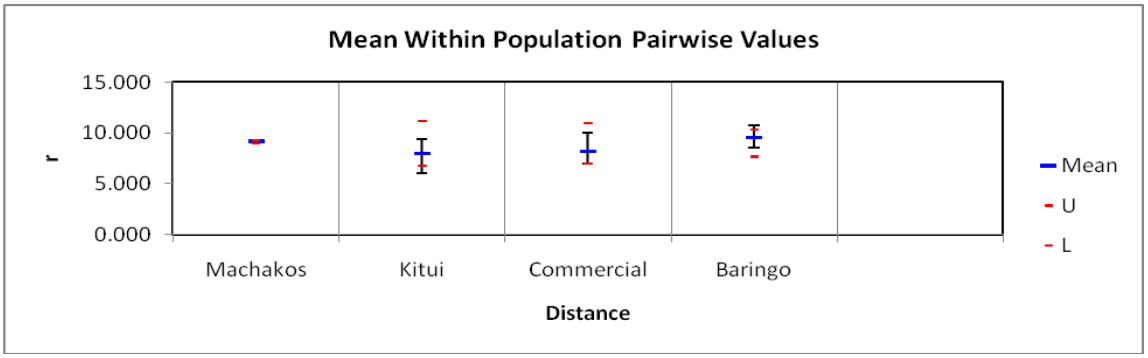

Figure 4.5: Shows the pair wise values means within the populations

There were five populations based on the sources of accessions. Evaluation was carried out to determine variation among these different classes of the materials. Analysis of molecular variance (AMOVA) was done to determine the total genetic variation among and within the populations as shown in Table 4.8 and Appendix 7. It was established that there is no variation among the populations. All the variation (100%) was accounted for within the population (among the genotypes). The genetic distance among the accessions ranged from 0.006 to 0.105

Table 4.8: Allelic Molecular Variance of the cowpea accessions

Source of variation	Df	SS	MS	Est. Var.	Genetic variation (%)
Among Pops	4	6.079	1.520	0.005	0%
Within Pops	102	150.483	1.475	1.475	100%
Total	106	156.561		1.480	100%

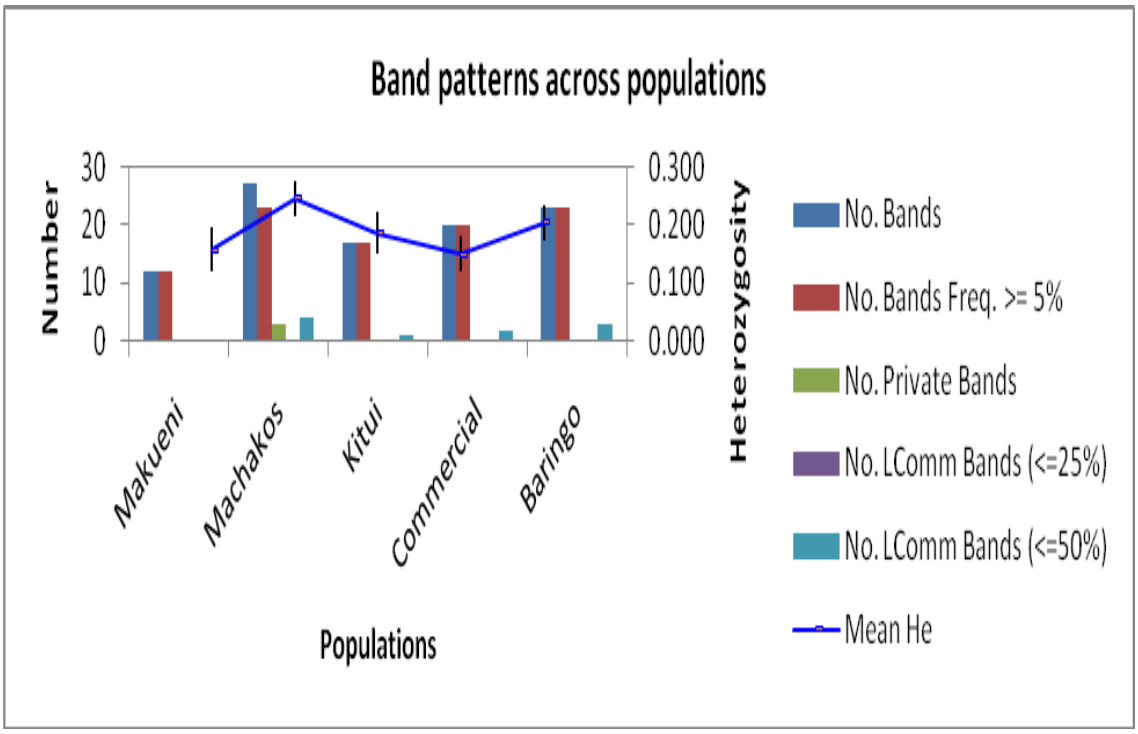

Figure 4.6: Variation of band patterns across populations

Table 4.9: Pairwise population matrix of Nei Genetic distance and Nei Genetic Identity among cowpea populations

	Makueni	**Machakos**	**Kitui**	**Commercial**	**Baringo**
Makueni	-	0.955	0.918	0.901	0.931
Machakos	0.079	-	0.991	0.927	0.994
Kitui	0.130	0.023	-	0.963	1.003
Commercial	0.147	0.087	0.061	-	0.964
Baringo	0.111	0.015	0.018	0.054	-

The genetic variation observed among the different populations was low with the least distance genetic distance of 0.015 observed between Baringo and Machakos while the greatest genetic distance of 0.147 observed between Commercial seeds and Makueni. The lowest genetic distance among semi arid regions was observed between Kitui and Machakos with genetic distance of 0.023 while the highest genetic distance was observed between Kitui and Makueni with genetic distance of 0.130 (Table 4.9).

An average of 1.86 alleles was produced by Machakos population compared to 0.79 generated by Makueni population. uHe values are higher in all regions compared to he He values. Machakos population recorded the highest He (0.246) and uHe (0.247) values respectively while Commercial seeds recorded the lowest He (0.15) and uHe (0.167) respectively.

Table 4.10: Estimated genetic diversity of accessions within populations

Population	N	Na	Ne	I	He	uHe	P%
Makueni	2.000	0.793	1.268	0.229	0.157	0.209	37.93
Machakos	86.000	1.862	1.387	0.384	0.246	0.247	93.1
Kitui	5.000	1.103	1.316	0.278	0.185	0.206	51.72
Commercial	5.000	1.207	1.227	0.237	0.150	0.167	51.72
Baringo	9.000	1.517	1.315	0.323	0.205	0.217	72.41
Total	107						
Mean					0.189	0.209	61.38
					0.015	0.017	

N= Number of individuals

Na = No. of Different Alleles
Ne = No. of Effective Alleles = 1 / (p^2 + q^2)
I = Shannon's Information Index = -1* (p * Ln (p) + q * Ln(q))
He = Expected Heterozygosity = 2 * p * q
uHe = Unbiased Expected Heterozygosity = (2N / (2N-1)) * He

Where for Diploid Binary data and assuming Hardy-Weinberg Equilibrium, q = (1 - Band Freq.)^0.5 and p = 1 - q.

P%= percentage of polymorphic loci

The molecular data generated from the informative SSR markers clustered the 107 accessions into three main clusters; I, II and III (Fig 6). Cluster I had the highest number of accessions (54), Cluster II had 44 accessions while cluster II had the least number of accessions (9). It was observed that the accessions did not cluster based on their place of origin rather they were distributed across the clusters.

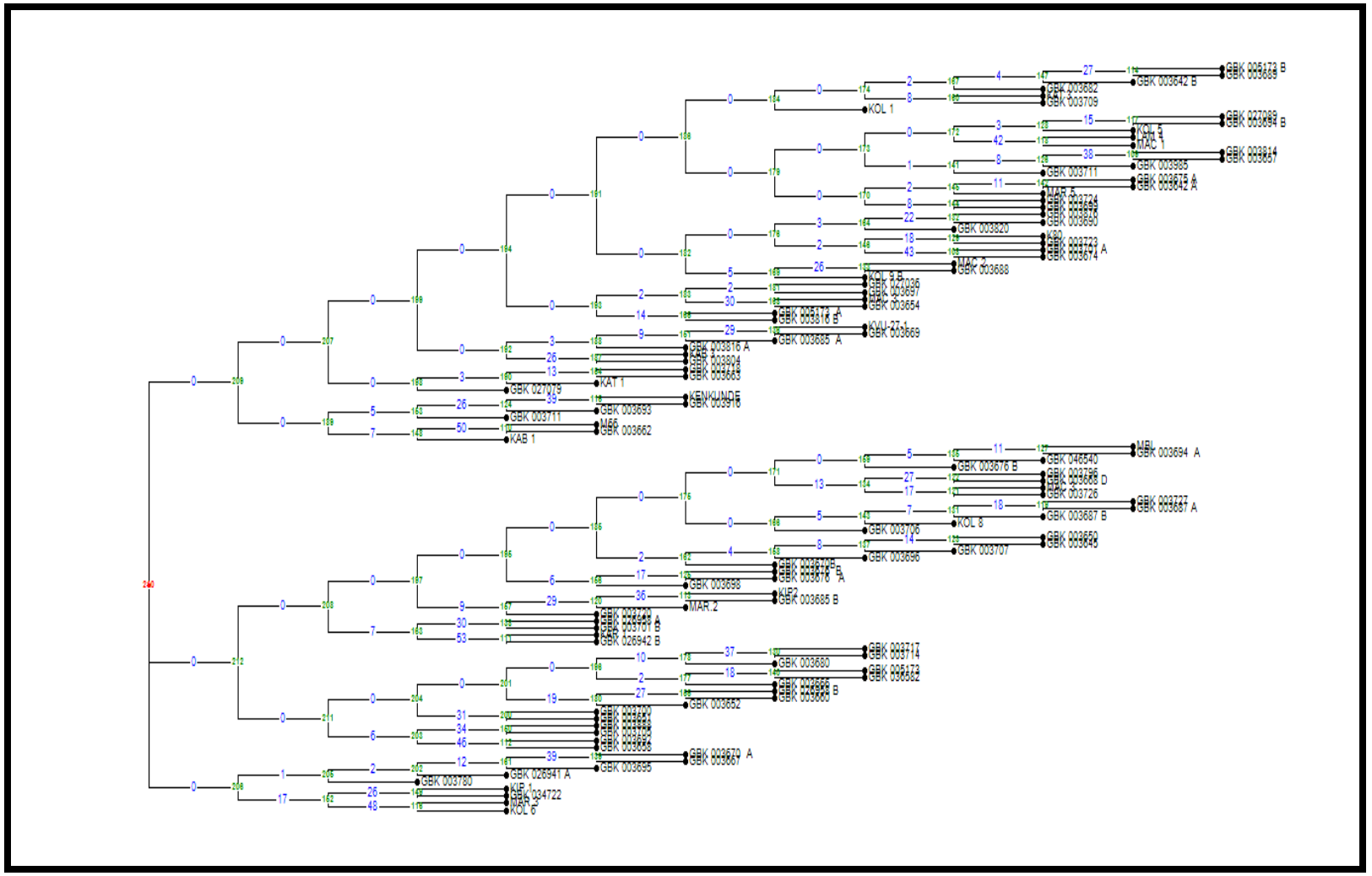

Figure 4.7: Clustering of cowpea accessions based on variation in SSR markers

CHAPTER FIVE

DISCUSSION

5.1 Discussion

Genetic diversity is an important aspect in plant breeding programmes. It informs on whether progress can be made in selection for desirable attributes from a population. It also provides an indication of richness and distribution of the alleles available in the population. The accessions in this study comprised of landraces originally collected from the semi arid region of the country and conserved in the National Gene Bank of Kenya, collections from farmers' fields in semi arid region and commercial lines listed by the Registrar of plant varieties (KEPHIS). Skewed or uneven distribution of accessions among the qualitative characters was recorded for terminal leaflet shape, raceme position, pod attachment, pod curvature, mature pod colour, flower colour and eye colour. The low occurrence of accessions in some categories of the respective traits of the characters indicated that some of the alleles were rare in the population or were recessive. Even distribution of accessions in traits was observed for immature pod colour, leaf colour, seed shape and testa texture. Such even distribution of the accessions among the various categories of traits could be attributed to non-selective pressure among such characters.

In this study, 95% of the accessions produced purple flowers which corroborated with Doumbia et al. (2013), who similarly established that most accessions produced purple flowers, followed by white flowers and the least were white-purple flowered accessions. In a similar study, Cobbinah et al. (2011) also found that majority of accessions gave purple flowers. Unlike Cobbinah et al. (2011) and Doumbia *et al.,* (2013), this study showed that the accessions with white flowers were less than the white-purple flowered accessions. This could be attributed to ecological and climatic conditions or the farmers' preferences that may not favor accessions with white flowers. In another study, Gibbon

and Pain (1985) showed that there were additional flower colours of cowpea such as pale-blue, yellow and pink though they were not observed in this study (Doumbia et al, 2014). Sangwan and Lodhi (1998) indicated that purple flower colour is dominant over white which has a monogenic recessive nature of inheritance.

Five classes of immature pod pigmentation (IBPGR, 1983) were found in this study. This compared favorably with Nkouannessi (2005) who reported four classes and Doumbia (2011) who had six groups of immature pod pigments.

Raceme position plays a very important role in the harvesting of mature pods. When racemes are on the same level as the canopy or within the canopy, harvesting becomes difficult as most pods are hidden. Pandey and Ngarm (1985) and Bennett-Lartey and Ofori (1999) indicated that accessions which bear racemes above the canopy are easier and cheaper to harvest compared to racemes borne throughout the canopy. Above canopy raceme accessions encourage use of mechanical harvesting while those borne within or throughout the canopy require uprooting of the whole plant (Cobbinah *et al.*, 2011). Cobbinah et al. (2011), observed that 59.7% of the accessions had above canopy racemes, 29.8% had the same level as the plant racemes and 10.4% had racemes within the canopy. In contrast, this study showed that 56% of the accessions produced upper canopy racemes, 24% of the accessions had a raceme position above canopy and 20% had raceme throughout the canopy. Grain cowpea farmers in the marginal areas prefer cowpea which has raceme position above the canopy.

Nkoiannessi (2005), showed that seed testa texture ranged from rough to wrinkled. On the other hand, Adebowale et al., (2011) reported accessions with smooth to rough seed texture. This study showed that 89% of the accessions had smooth textured seeds, 7% smooth to rough textured seeds and 4% rough to wrinkled textured seeds. Smooth seed coat texture is preferred in Eastern Africa, unlike in West Africa where preference for

rough seed coat allows for easy removal of the seed coat that is important for indigenous food preparations (Singh & Ishiyaku, 2000).

Commercial lines; K80, Kenkunde, M66, Kvu-27-1 and KAR 1 were classified together in group two by cluster analysis. This could be attributed to breeding and selection of these varieties for the region where they have been supplied as government interventions following drought as a mitigation measure (Recha *et al.,* 2012). Accessions obtained from farmers in Kola of Machakos County were evenly distributed in all clusters of the accessions. The even distribution of accessions across groups was also observed for materials procured from farmers in Baringo and those from Machakos counties. The even distribution is an indication of sharing and exchange of seed among the farmers. Therefore, there is no clear pattern in distribution of the accessions associated with areas of origin. The farmers also seem to have similar preferences in the attributes of the cowpea.

Based on variation in SSR markers, the results indicated a low level of genetic diversity among the cowpea genotypes as noted from principal coordinates analysis which did not cluster the accessions in any specific groupings. Asare et al. (2010), used 25 pairs of SSR markers. Of these, 20 pairs of SSR markers gave reproducible polymorphism. These primer combinations gave a total of 74 alleles at 20 loci with 3.8 alleles per locus on average. According to Ogunkanmi et al. (2014), 12 SSR markers generated 37 alleles with the number of alleles per locus ranging from 2 to 5 and an average of 2.92 alleles per locus. Ali et al. (2015) studied the genetic diversity and phylogenetic relationships among 252 cowpea accessions collected in six geographical regions of Sudan using 18 pairs of SSR markers. Sixteen primers gave reproducible polymorphism and a total of 129 alleles were detected with an average of 8.1 alleles per locus. In this study, a total of eight markers generated a total of 29 alleles with the number of alleles per locus ranging from 2 to 5 and an average of 3.63 alleles per locus.

Asare et al. (2010) reported low genetic variability among Ghanaian cultivated genotypes. Doumbia (2011), reported low level of similarity between and within the accessions. Kuruma et al. (2008) reported similar results as the current study; low level of genetic diversity among cowpea genotypes. The high similarity among the accessions indicates high levels of geneflow among the populations (Doumbia, 2011). Ali *et al,* (2015) found out that there was low genetic diversity among Sudanese cowpea population with more variations within individuals.

CHAPTER SIX

CONCLUSION AND RECOMMENDATIONS

6.1 Conclusion

The accessions used in the trial were variable in the characters that they were evaluated in. Accessions similarly were evenly distributed across the traits of the various characteristics; an indication of a wide range of alleles in the accessions used in the study. The study showed that there was a high level of variation among the cowpea accessions with respect to qualitative and quantitative traits. In terms of a performance index derived from yield associated attributes; GBK 003662, GBK 003663, GBK 003676, GBK 003723, GBK 003650 and GBK 003642 were among the top 5% accessions in the trial. The study showed that there was a high level of similarity among the cowpea accessions with respect to SSR markers. The SSR markers used in this study showed no variation among the cowpea accessions.

6.2 Recommendations

All the variations were found within the individual accessions. Accessions GBK 003662, GBK 003663, GBK 003676, GBK 003723, GBK 003650 and GBK 003642 were among the top 5% high yielding accessions in the trial. These superior accessions could be adopted widely for cultivation by farmers. Future studies should explore using more SSR primers in order to detect the variation among accessions in this species. Moreover, a larger sample of cowpea accessions should be included in studies.

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APPENDICES

Appendix I: Cowpea accessions used in the study and their collection area

Accession	Source County	Area/locality	Latitude	Longitude
GBK-003642 A	Machakos	KDFS	0º35 S	37º15 E
GBK-003642 B	Machakos	KDFS	0º35 S	37º15 E
GBK-003645	Machakos	KDFS	0º35 S	37º15 E
GBK-003650	Machakos	KDFS	0º35 S	37º15 E
GBK-003651	Machakos	KDFS	0º35 S	37º15 E
GBK-003652	Machakos	KDFS	0º35 S	37º15 E
GBK-003654	Machakos	KDFS	0º35 S	37º15 E
GBK-003657	Machakos	KDFS	0º35 S	37º15 E
GBK-003658	Machakos	KDFS	0º35 S	37º15 E
GBK-003660	Machakos	KDFS	0º35 S	37º15 E
GBK-003662	Machakos	KDFS	0º35 S	37º15 E
GBK-003663	Machakos	KDFS	0º35 S	37º15 E
GBK-003666	Machakos	KDFS	0º35 S	37º15 E
GBK-003667	Machakos	KDFS	0º35 S	37º15 E
GBK-003668 D	Machakos	KDFS	0º35 S	37º15 E
GBK-003669	Machakos	KDFS	0º35 S	37º15 E
GBK-003670 A	Machakos	KDFS	0º35 S	37º15 E
GBK-003670 B	Machakos	KDFS	0º35 S	37º15 E
GBK-003674	Machakos	KDFS	0º35 S	37º15 E
GBK-003675	Machakos	KDFS	0º35 S	37º15 E
GBK-003676 A	Machakos	KDFS	0º35 S	37º15 E

Accession	Source County	Area/locality	Latitude	Longitude
GBK-003676 B	Machakos	KDFS	0º35 S	37º15 E
GBK-003680	Machakos	KDFS	0º35 S	37º15 E
GBK-003682	Machakos	KDFS	0º35 S	37º15 E
GBK-003685 A	Machakos	KDFS	0º35 S	37º15 E
GBK-003685 B	Machakos	KDFS	0º35 S	37º15 E
GBK-003687 A	Machakos	KDFS	0º35 S	37º15 E
GBK-003687 B	Machakos	KDFS	0º35 S	37º15 E
GBK-003688	Machakos	KDFS	0º35 S	37º15 E
GBK-003689	Machakos	KDFS	0º35 S	37º15 E
GBK-003690	Machakos	KDFS	0º35 S	37º15 E
GBK-003693	Machakos	KDFS	0º35 S	37º15 E
GBK-003694 A	Machakos	KDFS	0º35 S	37º15 E
GBK-003694 B	Machakos	KDFS	0º35 S	37º15 E
GBK-003695	Machakos	KDFS	0º35 S	37º15 E
GBK-003696	Machakos	KDFS	0º35 S	37º15 E
GBK-003697	Machakos	KDFS	0º35 S	37º15 E
GBK-003698	Machakos	KDFS	0º35 S	37º15 E
GBK-003699	Machakos	KDFS	0º35 S	37º15 E
GBK-003700	Machakos	KDFS	0º35 S	37º15 E
GBK-003701 A	Machakos	KDFS	0º35 S	37º15 E
GBK-003701 B	Machakos	KDFS	0º35 S	37º15 E
GBK-003705	Machakos	KDFS	0º35 S	37º15 E
GBK-003706	Machakos	KDFS	0º35 S	37º15 E
GBK-003707	Machakos	KDFS	0º35 S	37º15 E

Accession	Source County	Area/locality	Latitude	Longitude
GBK-003709	Machakos	KDFS	0º35 S	37º15 E
GBK-003711 A	Machakos	KDFS	0º35 S	37º15 E
GBK-003711 B	Machakos	KDFS	0º35 S	37º15 E
GBK-003713	Machakos	KDFS	0º35 S	37º15 E
GBK-003714	Machakos	KDFS	0º35 S	37º15 E
GBK-003717 A	Machakos	KDFS	0º35 S	37º15 E
GBK-003717 B	Machakos	KDFS	0º35 S	37º15 E
GBK-003718	Machakos	KDFS	0º35 S	37º15 E
GBK-003720	Machakos	KDFS	0º35 S	37º15 E
GBK-003723	Machakos	KDFS	0º35 S	37º15 E
GBK-003724	Machakos	KDFS	0º35 S	37º15 E
GBK-003726	Machakos	KDFS	0º35 S	37º15 E
GBK-003727	Machakos	KDFS	0º35 S	37º15 E
GBK-003780	Machakos	KDFS	0º35 S	37º15 E
GBK-003796	Machakos	KDFS	0º35 S	37º15 E
GBK-003804	Machakos	KDFS	0º35 S	37º15 E
GBK-003814	Machakos	KDFS	0º35 S	37º15 E
GBK-003816 A	Machakos	KDFS	0º35 S	37º15 E
GBK-003816 B	Machakos	KDFS	0º35 S	37º15 E
GBK-003820	Machakos	KDFS	0º35 S	37º15 E
GBK-003876	Machakos	KDFS	0º35 S	37º15 E
GBK-003888	Machakos	KDFS	0º35 S	37º15 E
GBK-003916	Machakos	KDFS	0º35 S	37º15 E
GBK-003985	Machakos	KDFS	0º35 S	37º15 E

Accession	Source County	Area/locality	Latitude	Longitude
GBK-005173 A	Machakos	KDFS	0º35 ́S	37º15 ́E
GBK-005173 B	Machakos	KDFS	0º35 ́S	37º15 ́E
GBK-027036	Machakos	Ndalani Loc. (Ndalani Maktano)	1º45’8’S	37º19’5 ́E
GBK-027079	Machakos	Ndalani Loc. (Ndalani Maktano)	2º37’25 ́S	37º15 ́E
GBK-027089	Machakos	Mukuyuni, Kibwezi	2º23’38 ́S	37º15 ́E
GBK-026941 A	Kitui	Kanyangi Loc. Wangata	1º36’12 ́S	37º54’35 ́E
GBK-026941 B	Kitui	Kanyangi Loc. Wangata	1º36’12 ́S	37º54’35 ́E
GBK-026958 A	Kitui	Mutha Loc.	1º48’30 ́S	38º25’0 ́E
GBK-026958 B	Kitui	Mutha Loc.	1º48’30 ́S	38º25’0 ́E
GBK-046540	Kitui	Maliku – Kitui	1º34.986 ́S	37º54.946 ́E
GBK-034722 A	Makueni	Sakai; 13km Kilata Tawa Road	1º39 ́S	37º35 ́E
GBK-034722 B	Makueni	Sakai; 13km Kilata Tawa Road	1º39 ́S	37º35 ́E
GBK-036582	Makueni	Sakai; 13km Kilata Tawa	1º39 ́S	37º35 ́E

Accession	Source County	Area/locality	Latitude	Longitude
		Road		
K80	Commercial	Commercial		
KENKUNDE	Commercial	Commercial		
KVU-27-1	Commercial	Commercial		
M66	Commercial	Commercial		
KAR 1	Commercial	KALRO		
KAT 1	Machakos	Katumani		
KAT 3	Machakos	Katumani		
KOL 1	Machakos	Kola		
KOL 2 A	Machakos	Kola		
KOL 2 B	Machakos	Kola		
KOL 5	Machakos	Kola		
KOL 6	Machakos	Kola		
KOL 8	Machakos	Kola		
KOL 9 A	Machakos	Kola		
KOL 9 B	Machakos	Kola		
KOL 9 C	Machakos	Kola		
MAC 1	Machakos	Machakos		
MAC 2	Machakos	Machakos		
MAC 3	Machakos	Machakos		
MAR.2	Baringo	Margat		
MAR.3	Baringo	Margat		
MAR.5	Baringo	Margat		
MBL	Baringo	Mbili mbili		
LAM 4	Baringo	Lambwe		

Accession	Source County	Area/locality	Latitude	Longitude
KIP 1	Baringo	Kipsarum		
KIP 2	Baringo	Kipsarum		
KAB 1	Baringo	Kabartonjo		
KAB 3	Baringo	Kabartonjo		

GBK=Gene Bank of Kenya; KDFS=Katumani Dryland Farming Station; A, B, D=Selections within the accession

Appendix II: Data scoring of the traits evaluated during the trial

TRAITS	Acronym	SCORING
Growth habit	GH	1. Acute erect 2. Erect 3. Semi erect 4. Intermediate 5. Semi prostate 6. Prostate 7. Climbing
Growth pattern	GP	1. Determinate 2. Indeterminate
Twinning tendency	TT	0 None 3 Slight 5 Intermediate 7 Pronounced
Pigmentation	P	0 None 1 Very slight 3 Moderate at the base and tips of petioles 5 Intermediate 7 Extensive 9 Solid
Terminal leaflet shape	TLS	1 Globose 2 Sub-globose 3 Sub-hastate 4 Hastate
Raceme position	RP	1 Mostly above canopy 2 In upper canopy 3 Throughout canopy
Pod attachment	PA	3 Pedant 5 30-90 down from erect 7 Erect
Immature pod color		0 None 1 Pigmented tip 2 Pigmented sutures 3 Pigmented valves, green sutures 4 Splashes of pigment 5 Uniformly pigmented 6 Other
Pod curvature	PC	0 Straight 3 Slightly curved 5 Curved 7 Coiled
Mature pod color	MPC	1 Pale tan/ straw 2 Dark tan 3 Dark brown 4 Black or dark purple 5 Other
Flower color	FC	1 Purple 2 white-purple 3 White
Leaf color	LC	3 Pale green 5 Intermediate green 7 Dark green
Seed shape	SS	1 Kidney 2 Ovoid 3 Crowder 4 Globose 5Rhomboid
Eye color	EC	0 Absent 1 Brown splash/gray 2 Tan brown 3 Red 4 Green 5 Blue to black 6 Blue to black spots/mottle 7 Speckled 8 Mottled 9 Mottled and speckled 10 Other
Seed coat color	SCC	1 White 2 Cream 3 Brown 4 Red 5 Purple 6 Black 99

TRAITS	Acronym	SCORING
		Other
Testa texture	Tt	1 Smooth 3 Smooth to rough 5 Rough 7 Rough to wrinkled 9 Wrinkled
Days to 50% emergence	E (50%)	From planting to the time when 50% of the seeds have germinated
Days to 50% flowering	F (50%)	From planting date to when 50% of the plants have produced flowers
Terminal leaflet length	TLL	Mean length of 10 terminal leaflets from 10 randomly selected plants
Terminal leaflet width	TLW	Mean width of 10 terminal leaflets measured on the broadest part of 10 randomly selected plants
Pod length	PL	Mean length of 10 mature pods from 10 randomly selected plants
Seeds per pod	SPP	Mean number of the randomly selected pods
100Seed Weight	100SW	Mean weight of 100 seeds with moisture content of 12%
Number of pods per plant	PPP	Mean number of mature pods from 10 randomly selected plants
Number of main branches per plant	BP	At 8 weeks after planting. Mean of 10 randomly selected plants

Adapted from IBPGRI (1983)

Appendix III: Ranking based on characteristics associated with performance of cowpea genotypes

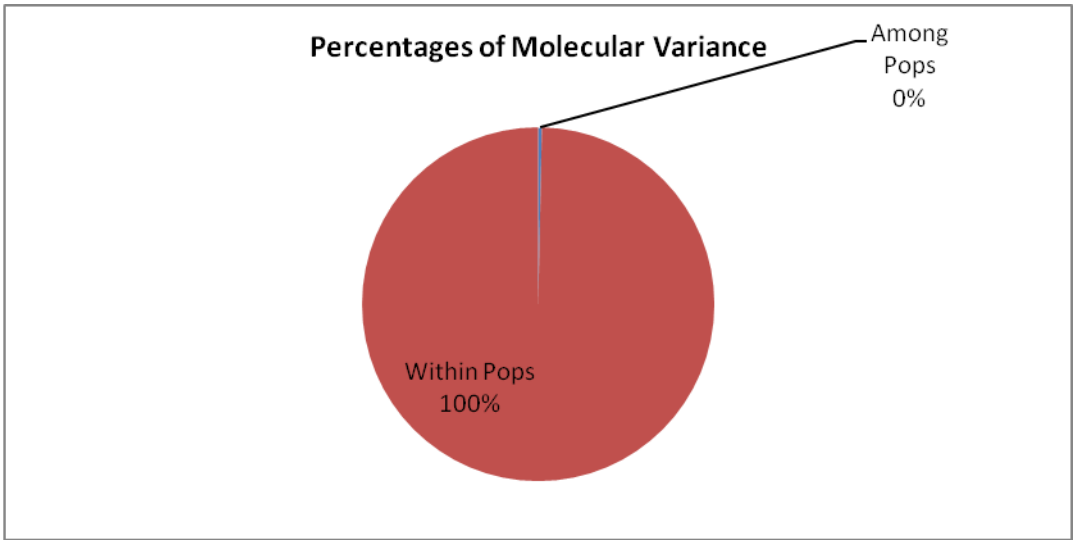
ACC	PL	SPP	100SW	PPP	BP	Selection Index	Ranks
GBK 003662	98	110	106	101	71	486	1
GBK 003663	103	91	77	98	103.5	472.5	2
GBK 003676	108	99	90	88.5	62.5	448	3
GBK 003723	89	88	100	55	109.5	441.5	4
GBK 003650	104	106.5	41	107	71	429.5	5
GBK 003642	79	82.5	70	110	71	412.5	6
GBK 003669	110	106.5	64	95.5	28	404	7
GBK 003668 D	65	108	52	95.5	80.5	401	8
GBK 003780	70	81	103.5	51.5	90	396	9
GBK 003709	54.5	86.5	101.5	66.5	71	380	10
GBK 003685	93.5	96	75	83.5	28	376	11
KAB 1	97	97.5	53.5	24.5	103.5	376	12
GBK 003985	87	46.5	101.5	40.5	96	371.5	13
GBK 003796	48	105	88.5	49	80.5	371	14
GBK 003645	90.5	85	80.5	108	5	369	15
GBK 003676	105	89	35	88.5	45	362.5	16
GBK 003676 B	71	104	31	88.5	62.5	357	17
GBK 003687	51	54	105	83.5	62.5	356	18
GBK 003654	50	72	66	103.5	62.5	354	19
K80	106	102.5	83	28	33.5	353	20
GBK 003696	46	71	68	75	85.5	345.5	21
GBK 003718	75	102.5	85	60	19	341.5	22
GBK 003720	68	67	107	55	38.5	335.5	23
GBK 003675 A	66.5	75.5	78.5	91	19	330.5	24
GBK 003660	88	100	6	101	33.5	328.5	25
GBK 003690 A	13	59	92	79	85.5	328.5	26
KOL 6	90.5	51	83	12.5	90	327	27
GBK 026958 A	92	91	55.5	35.5	52	326	28
GBK 027036	83.5	74	29.5	35.5	103.5	326	29
GBK 003680	15	31	110	88.5	80.5	325	30
KOL 2	72	82.5	92	15	62.5	324	31
GBK 046540	102	75.5	10	28	107.5	323	32
GBK 003685	76	54	63	83.5	45	321.5	33

ACC	PL	SPP	100SW	PPP	BP	Selection Index	Ranks
GBK 003705	109	97.5	18.5	66.5	28	319.5	34
GBK 003670 B	59	64.5	98.5	93	3	318	35
GBK 003689	82	78.5	69	79	8.5	317	36
GBK 003674	5	68	47	93	103.5	316.5	37
GBK 003814	49	94	53.5	49	71	316.5	38
MAC 2	85	93	25	6	103.5	312.5	39
GBK 003642 A	41	10.5	60.5	109	85.5	306.5	40
GBK 003697	81	26.5	76	75	45	303.5	41
KIP 1	40	52	103.5	18	90	303.5	42
GBK 003694 B	47	73	15	75	90	300	43
GBK 026941B	62	91	72	35.5	38.5	299	44
GBK 003701	56	28	72	66.5	76	298.5	45
KAR 1	37	109	21.5	24.5	103.5	295.5	46
GBK 003820	101	70	17	44.5	62.5	295	47
MAR.2	86	13.5	94	4	96	293.5	48
GBK 003816	83.5	101	45	44.5	19	293	49
GBK 003652	64	95	12	105.5	13.5	290	50
GBK 003701	1	22	98.5	66.5	100	288	51
GBK 003707	77	44	95.5	66.5	1	284	52
GBK 003916	10.5	54	83	40.5	96	284	53
GBK 003888	93.5	50	62	44.5	33.5	283.5	54
KOL 5	69	61	80.5	15	52	277.5	55
GBK 003670	73	57	35	93	19	277	56
GBK 003688	45	32	20	83.5	96	276.5	57
GBK 003876	95	64.5	26	44.5	45	275	58
KVU-27-1	96	42.5	48	10	76	272.5	59
GBK 003724	33	37	50.5	55	96	271.5	60
GBK 034722	60.5	64.5	5	30.5	109.5	270	61
GBK 003816	66.5	84	28	47	38.5	264	62
GBK 003699	28	61	21.5	71	80.5	262	63
GBK 003693	43.5	19	74	79	45	260.5	64
GBK 003666	19.5	46.5	50.5	98	45	259.5	65
GBK 003706	60.5	40	46	66.5	45	258	66
GBK 003726	31	78.5	86	53	8.5	257	67
GBK 003700	25	46.5	60.5	71	52	255	68
GBK 003658	52	9	59	101	33.5	254.5	69
GBK 026958	32	21	108.5	35.5	56	253	70

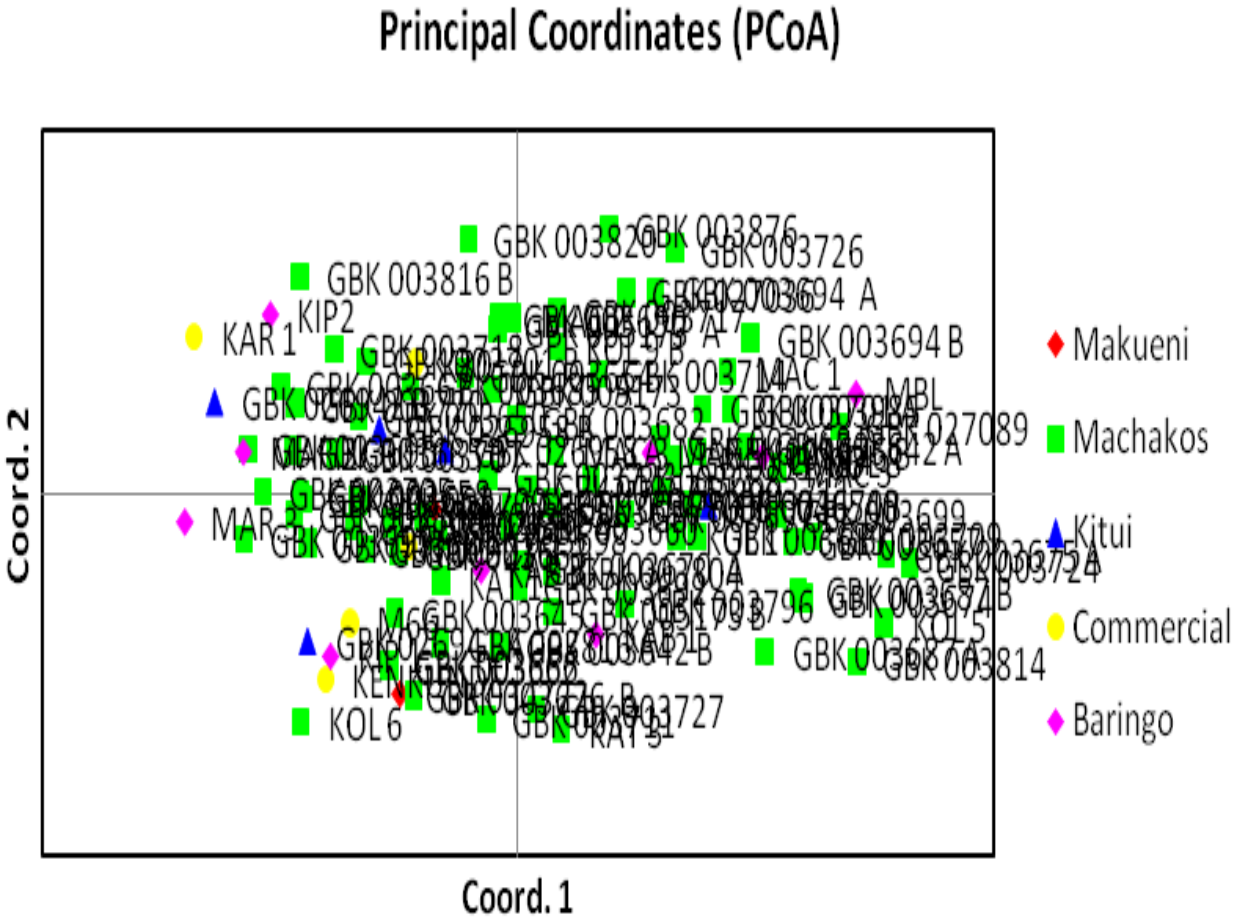
ACC	PL	SPP	100SW	PPP	BP	Selection Index	Ranks
GBK 003717 A	38.5	78.5	41	60	33.5	251.5	71
GBK 003657	14	10.5	41	103.5	80.5	249.5	72
LAM 4	107	46.5	55.5	9	28	246	73
GBK 003717 B	63	29	78.5	60	13.5	244	74
GBK 003651	58	26.5	38.5	105.5	13.5	242	75
KOL 9 B	99	69	43	11	19	241	76
GBK 003714	34	78.5	4	60	56	232.5	77
GBK 003667	17	34.5	8	98	71	228.5	78
GBK 003804	18	34.5	29.5	49	96	227	79
GBK 005173	80	49	16	40.5	38.5	224	80
GBK 003695	12	17	95.5	75	23.5	223	81
KOL 1	42	64.5	35	18	62.5	222	82
GBK 003711	2	15	88.5	60	52	217.5	83
GBK 036582	6	1	92	28	90	217	84
GBK 003713	54.5	6	67	60	28	215.5	85
GBK 003727	9	7	35	51.5	107.5	210	86
KAT 3	74	41	27	22	45	209	87
GBK 026941	10.5	2	97	35.5	62.5	207.5	88
KAB 3	26	61	7	24.5	85.5	204	89
GBK 027079	78	17	65	35.5	6	201.5	90
KENKUNDE	22	36	108.5	20.5	13.5	200.5	91
GBK 003698	19.5	24.5	14	71	71	200	92
GBK 003694	100	12	3	75	2	192	93
GBK 003711	24	24.5	57.5	60	23.5	189.5	94
KOL 8	29	86.5	49	12.5	8.5	185.5	95
KOL 2	23	33	32	15	80.5	183.5	96
KAT 1	43.5	39	13	24.5	62.5	182.5	97
MBL	53	57	57.5	1	13.5	182	98
MAC 1	30	57	23	7	62.5	179.5	99
GBK 003682	57	5	9	83.5	23.5	178	100
GBK 003687 B	21	17	44	83.5	8.5	174	101
MAR.5	36	23	24	2.5	76	161.5	102
MAR.3	16	38	2	2.5	96	154.5	103
M66	3	42.5	87	8	4	144.5	104
MAC 3	8	4	72	5	52	141	105
KOL 9 C	4	30	38.5	20.5	45	138	106
GBK 005173 B	7	20	35	40.5	33.5	136	107

ACC	PL	SPP	100SW	PPP	BP	Selection Index	Ranks
KIP 2	38.5	13.5	1	18	56	127	108
GBK 027089	27	3	18.5	32	23.5	104	109
GBK 034722	35	8	11	30.5	13.5	98	110

Appendix IV: Analysis of Molecular Variance



Appendix V: Principal coordinates



Appendix VI: Principal component analysis of cowpea genotypes

Axis No.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
EigenValue	5.61	3.95	3.88	3.42	3.13	2.71	2.64	2.24	2.16	2.07	1.87	1.68	1.51	1.35	1.19	1.01
GBK 034722	0.12	0.44	-0.16	-0.01	0.03	-0.07	0.15	-0.17	-0.07	-0.03	0.02	-0.01	-0.11	0.05	0.03	0.02
GBK 036582	0.17	-0.11	0.29	0.00	-0.30	0.15	-0.16	0.02	0.30	-0.27	0.05	-0.07	-0.02	-0.08	0.10	-0.02
GBK 003642 A	-0.25	-0.20	-0.29	0.00	0.02	-0.05	-0.17	0.07	-0.01	-0.13	-0.07	-0.15	-0.26	0.04	-0.09	0.14
GBK 003642 B	0.08	0.19	-0.10	-0.35	-0.32	-0.27	-0.20	0.14	0.08	-0.10	-0.02	0.14	0.06	-0.06	-0.13	0.11
GBK 003645	0.24	-0.02	0.07	0.19	-0.45	0.02	-0.20	-0.13	-0.17	0.16	0.02	0.25	-0.05	0.02	-0.09	-0.06
GBK 003650	0.19	-0.17	0.35	0.05	-0.29	-0.03	-0.19	0.00	0.33	0.07	0.16	0.00	-0.10	0.21	0.14	0.02
GBK 003651	0.32	-0.12	-0.09	0.12	0.11	-0.15	-0.09	0.02	-0.09	-0.20	0.07	0.08	0.10	0.03	-0.01	0.05
GBK 003652	0.17	-0.11	-0.07	0.13	0.01	-0.15	-0.15	0.22	0.14	-0.28	0.14	0.00	0.08	0.14	0.12	-0.06
GBK 003654	0.01	-0.15	-0.26	-0.31	-0.19	0.03	0.06	0.18	-0.09	0.05	0.13	0.00	0.18	0.03	0.04	-0.05
GBK 003657	-0.38	0.06	-0.26	0.31	-0.18	-0.18	-0.08	-0.29	0.06	0.12	0.10	-0.05	0.06	0.01	0.04	-0.05
GBK 003658	0.24	0.05	-0.09	-0.01	0.35	0.15	-0.02	-0.03	0.25	-0.04	0.05	0.19	0.07	-0.03	-0.20	-0.10
GBK 003660	0.04	0.08	0.17	-0.11	0.18	0.25	-0.04	0.33	-0.13	-0.09	0.06	-0.01	0.04	-0.10	0.12	-0.07
GBK 003662	0.24	0.09	-0.17	0.26	-0.18	0.08	0.03	0.00	0.19	-0.30	-0.12	-0.07	0.08	0.08	-0.10	0.07
GBK 003663	0.10	0.26	-0.02	-0.16	0.14	0.17	0.21	0.12	-0.12	0.21	-0.06	-0.15	-0.05	0.00	-0.06	-0.05
GBK 003666	0.24	0.15	0.07	0.15	-0.29	0.15	0.13	0.14	-0.15	-0.04	-0.19	0.26	-0.09	-0.14	-0.14	-0.02
GBK 003667	0.27	-0.23	-0.10	0.01	-0.08	0.03	-0.15	-0.13	-0.12	0.00	-0.11	-0.17	0.04	-0.01	0.12	0.01
GBK 003668 D	-0.14	-0.16	0.18	0.34	0.16	0.20	0.07	0.04	0.14	-0.10	-0.08	-0.10	0.19	0.14	-0.08	0.13
GBK 003669	0.23	0.14	-0.07	0.05	0.18	-0.02	0.14	-0.19	0.13	-0.26	0.08	0.07	-0.05	0.08	0.05	0.17
GBK 003670 A	0.06	0.01	-0.06	0.17	0.00	0.31	-0.15	-0.18	-0.09	0.03	-0.08	-0.16	-0.04	-0.20	0.03	-0.04

Axis No.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
GBK 003670B	-0.17	-0.08	-0.04	0.09	0.04	0.15	-0.18	-0.40	0.04	0.04	-0.21	0.11	0.06	-0.06	0.19	0.14
GBK 003674	-0.30	0.20	0.40	0.04	-0.19	-0.05	0.10	0.18	0.23	-0.20	-0.13	-0.01	-0.05	-0.18	-0.14	-0.20
GBK 003675 A	-0.43	0.05	-0.14	0.19	-0.02	0.17	0.10	0.22	0.06	-0.09	-0.08	-0.22	-0.18	-0.05	0.00	-0.04
GBK 003676 A	-0.03	0.01	0.12	0.12	-0.01	0.10	-0.19	0.23	-0.13	0.41	-0.15	0.04	0.12	-0.10	-0.12	0.12
GBK 003676 B	0.20	0.22	-0.06	-0.01	-0.11	0.03	-0.26	0.25	0.01	0.29	0.19	0.18	-0.07	0.16	0.03	0.08
GBK 003676 B	-0.19	-0.15	0.02	0.19	-0.01	-0.08	0.04	0.08	0.00	0.16	-0.21	-0.17	0.18	0.22	-0.11	0.05
GBK 003680	0.21	-0.12	-0.17	0.21	-0.06	-0.12	0.15	0.22	0.04	-0.07	-0.21	0.00	0.23	0.08	0.04	-0.18
GBK 003682	-0.05	-0.02	-0.13	-0.43	-0.11	-0.09	-0.21	-0.07	-0.03	-0.01	-0.01	-0.17	0.08	0.02	0.14	-0.02
GBK 003685 A	0.08	-0.10	-0.09	-0.11	-0.07	0.23	0.36	-0.15	-0.03	0.02	-0.02	-0.26	-0.09	0.09	-0.01	0.09
GBK 003685 B	0.33	-0.14	0.33	-0.05	-0.15	0.19	0.22	-0.07	0.15	0.01	-0.02	0.05	-0.09	-0.13	0.04	0.10
GBK 003687 A	-0.25	0.20	0.19	0.01	-0.29	-0.16	-0.30	0.01	-0.05	0.09	-0.10	0.02	-0.17	0.02	-0.09	0.18
GBK 003687 B	-0.31	0.12	-0.06	0.15	0.07	-0.21	-0.20	-0.19	-0.19	0.16	-0.15	0.01	-0.08	0.00	0.02	0.06
GBK 003688	-0.16	0.24	0.31	-0.12	0.21	-0.04	0.12	-0.01	-0.21	0.08	0.07	-0.02	0.22	-0.08	-0.02	0.08
GBK 003689	-0.18	-0.06	-0.32	0.08	-0.21	0.20	-0.01	-0.07	0.24	-0.23	0.14	-0.20	0.04	0.07	-0.10	0.00
GBK 003690	-0.04	-0.21	-0.13	0.08	0.26	-0.24	0.31	0.04	0.08	0.10	0.14	0.14	-0.13	-0.11	-0.12	0.12
GBK 003692	0.05	0.02	-0.35	0.05	0.20	0.16	-0.16	-0.01	0.11	-0.02	-0.13	0.20	0.10	-0.16	-0.09	0.07
GBK 003693	0.32	0.08	0.01	0.30	0.15	-0.23	0.05	0.08	0.11	0.04	0.25	-0.07	-0.07	-0.02	0.05	-0.09
GBK 003694 A	-0.15	-0.39	0.29	-0.01	-0.14	0.00	0.03	-0.12	-0.10	0.16	0.00	0.09	0.06	0.05	-0.28	-0.03
GBK 003694 B	-0.35	-0.20	-0.03	0.16	-0.03	-0.25	0.13	-0.20	0.14	0.07	0.07	0.15	0.26	0.01	0.11	-0.04
GBK 003695	0.31	-0.12	-0.29	-0.09	-0.06	0.03	-0.17	-0.05	-0.04	0.07	0.04	0.02	0.23	-0.05	0.03	-0.03
GBK 003696	-0.02	0.07	0.22	0.32	0.24	0.21	-0.22	-0.10	-0.14	-0.02	0.02	0.01	0.02	0.00	-0.08	0.07
GBK 003697	-0.18	0.15	0.10	0.01	-0.08	0.20	0.05	0.18	-0.30	-0.01	-0.02	-0.07	-0.02	0.18	0.07	0.05

Axis No.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
GBK 003698	0.15	-0.01	0.20	0.24	0.13	-0.06	-0.23	0.00	-0.27	0.02	0.07	-0.03	0.03	0.10	0.05	0.00
GBK 003699	-0.30	0.05	0.12	0.08	0.22	0.10	-0.01	0.11	-0.02	-0.16	-0.09	0.13	-0.15	-0.24	0.25	0.02
GBK 003700	0.25	-0.13	-0.20	0.10	-0.02	-0.06	0.11	0.16	-0.16	-0.03	-0.14	0.07	0.14	0.03	0.05	0.09
GBK 003701 A	-0.29	0.05	0.25	-0.24	0.08	-0.06	0.05	0.22	0.32	-0.08	-0.01	-0.10	0.14	-0.20	-0.10	0.12
GBK 003701 B	0.21	-0.27	0.04	-0.11	0.28	0.02	-0.12	-0.13	0.19	0.23	0.16	-0.10	-0.02	-0.16	-0.06	0.04
GBK 003705	0.29	0.00	-0.05	0.11	0.15	0.06	-0.02	-0.04	-0.04	-0.30	0.05	0.10	0.12	0.00	-0.02	0.07
GBK 003706	-0.17	-0.05	0.14	0.02	0.17	-0.24	-0.16	-0.22	-0.07	-0.03	-0.05	-0.02	0.10	0.14	-0.10	0.15
GBK 003707	0.21	-0.02	0.34	-0.22	-0.14	0.27	-0.21	-0.04	0.25	0.07	0.18	0.15	-0.04	0.09	0.03	0.11
GBK 003709	-0.34	0.02	-0.15	0.14	-0.23	0.33	0.12	0.01	-0.14	0.02	0.22	-0.01	0.03	0.07	-0.06	0.08
GBK 003711	-0.15	-0.02	-0.16	-0.39	0.05	-0.21	-0.20	0.03	-0.06	-0.10	-0.25	0.11	-0.13	0.08	0.00	-0.25
GBK 003711	0.10	0.31	0.05	0.08	-0.33	-0.33	0.28	0.10	0.14	0.16	-0.08	0.01	-0.07	-0.02	0.00	-0.01
GBK 003714	-0.04	-0.34	-0.12	0.11	0.13	0.00	0.01	0.07	-0.09	0.04	-0.43	0.16	-0.13	-0.06	-0.08	-0.17
GBK 003717	-0.08	-0.37	-0.14	0.20	-0.03	0.02	0.02	0.00	0.14	0.14	-0.23	-0.11	0.06	-0.14	0.17	-0.08
GBK 003718	0.17	-0.09	0.07	-0.25	0.24	-0.11	0.17	0.13	-0.03	0.14	0.04	-0.10	0.03	0.09	-0.09	-0.01
GBK 003720	0.25	-0.14	0.12	0.11	0.01	-0.03	-0.16	-0.10	-0.21	-0.06	0.09	-0.11	0.01	-0.18	0.07	-0.32
GBK 003723	0.00	0.03	0.21	0.18	-0.12	-0.04	0.28	0.04	0.09	-0.22	-0.03	0.15	0.31	0.21	-0.22	-0.18
GBK 003724	-0.47	0.17	0.04	0.10	0.09	0.00	0.09	0.03	-0.09	-0.09	0.13	0.31	0.00	-0.03	0.10	0.05
GBK 003726	-0.24	-0.40	0.13	0.09	0.16	0.03	-0.13	0.15	-0.07	0.00	-0.10	0.29	-0.13	0.14	0.05	0.01
GBK 003727	0.05	0.27	0.14	0.07	-0.32	-0.33	-0.11	-0.01	0.03	0.00	-0.21	-0.21	-0.06	-0.08	-0.04	-0.02
GBK 003780	-0.01	-0.02	-0.18	-0.27	0.14	0.00	-0.17	0.13	0.13	0.15	-0.01	-0.14	-0.16	0.14	-0.13	0.05
GBK 003796	-0.10	0.22	0.35	0.12	0.11	0.07	0.11	0.12	0.12	0.00	0.04	0.00	-0.03	0.21	0.35	-0.04
GBK 003804	-0.09	0.34	0.22	-0.12	0.19	-0.02	-0.14	-0.15	-0.18	-0.01	0.06	-0.02	0.18	0.05	-0.04	-0.01

Axis No.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
GBK 003814	-0.38	0.21	-0.38	0.04	-0.02	-0.20	-0.18	0.13	0.18	-0.01	0.07	-0.06	-0.04	-0.07	-0.02	-0.08
GBK 003816 A	0.05	0.43	-0.14	-0.18	0.08	0.01	0.29	0.02	-0.06	0.15	-0.01	0.05	0.06	-0.03	0.02	-0.02
GBK 003816 B	0.22	-0.28	0.10	-0.17	0.09	-0.14	0.09	-0.25	-0.05	0.05	0.17	-0.13	-0.21	0.07	-0.10	-0.09
GBK 003820	0.00	-0.33	0.21	-0.22	-0.18	-0.10	0.09	0.14	-0.07	-0.05	0.20	-0.13	-0.03	-0.14	0.02	0.12
GBK 003876	-0.19	-0.40	-0.20	0.11	0.04	-0.12	0.25	-0.09	-0.01	-0.03	0.23	0.02	0.01	-0.24	-0.14	0.11
GBK 003888	0.26	0.06	-0.09	-0.11	0.15	0.19	-0.17	0.03	-0.04	-0.06	-0.20	-0.09	0.13	-0.01	-0.03	0.06
GBK 003916	0.18	0.06	-0.06	0.37	0.18	-0.12	-0.04	0.05	0.20	0.08	0.16	-0.02	-0.08	0.00	-0.03	-0.13
GBK 003985	-0.23	-0.31	-0.43	-0.03	-0.17	0.02	-0.10	-0.11	0.00	-0.11	0.09	0.08	-0.24	0.04	-0.13	-0.05
GBK 005173	0.00	-0.12	0.07	-0.17	0.27	0.26	-0.28	0.10	0.09	-0.18	-0.05	0.09	-0.06	0.01	-0.15	-0.07
GBK 005173 A	-0.03	-0.19	-0.02	-0.23	-0.15	-0.12	0.16	-0.19	-0.22	0.03	-0.23	-0.08	0.02	0.04	0.07	-0.08
GBK 005173 B	0.00	0.18	-0.16	-0.40	-0.27	0.06	-0.11	-0.07	0.09	-0.11	0.09	0.07	0.14	-0.09	0.03	0.08
GBK 027036	-0.13	-0.31	0.18	-0.33	-0.05	0.06	-0.05	0.07	-0.17	0.09	0.14	0.06	0.11	0.22	-0.02	-0.14
GBK 027079	0.16	0.14	-0.10	-0.05	0.11	-0.19	-0.12	0.09	-0.21	-0.02	0.25	-0.01	0.13	-0.10	-0.19	-0.15
GBK 027089	-0.39	0.00	0.15	-0.29	0.29	0.08	0.07	-0.03	0.14	0.10	-0.05	0.30	-0.13	0.18	-0.01	0.00
KAT 1	0.13	0.09	-0.14	0.12	0.15	-0.25	0.08	-0.04	-0.10	0.03	0.24	0.09	-0.23	0.00	0.00	-0.10
KAT 3	0.01	0.33	0.09	0.03	-0.45	0.00	-0.03	-0.31	-0.10	0.02	0.05	0.14	0.08	-0.06	-0.04	0.09
KOL 1	-0.25	0.27	0.09	-0.21	0.22	0.06	-0.20	0.02	0.00	-0.13	0.08	-0.07	-0.03	-0.13	-0.05	-0.04
KOL 5	-0.43	0.24	-0.14	-0.04	-0.06	0.13	0.13	-0.03	0.26	0.30	0.14	0.15	0.06	0.03	0.20	-0.13
KOL 6	0.34	0.27	-0.17	0.18	0.07	0.14	0.06	-0.02	-0.06	0.00	0.03	0.03	-0.13	0.03	0.05	0.00
KOL 8	-0.39	-0.03	-0.01	0.24	-0.12	0.03	-0.02	0.25	-0.05	0.10	0.00	-0.26	-0.03	0.22	-0.06	0.02
KOL 9 B	-0.11	-0.09	0.13	-0.23	0.05	-0.23	0.08	0.13	-0.13	-0.21	-0.03	-0.07	0.01	0.07	0.14	0.07
MAC 1	-0.32	-0.13	-0.34	-0.28	-0.08	-0.08	0.02	0.03	0.07	0.10	0.00	0.16	0.10	-0.15	0.12	0.00

Axis No.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
MAC 2	-0.07	-0.14	0.11	-0.08	0.12	-0.30	0.24	-0.02	-0.14	-0.16	-0.01	-0.20	0.04	-0.05	-0.05	0.21
MAC 3	-0.30	-0.07	0.23	0.36	0.22	-0.25	0.00	0.03	0.04	0.16	-0.07	0.04	0.07	-0.15	0.18	0.02
MAC 3	-0.10	0.03	0.00	-0.11	-0.18	0.26	0.12	0.08	-0.24	-0.05	0.04	-0.20	-0.06	-0.05	0.15	-0.08
GBK 026941 A	0.25	0.22	-0.17	0.21	0.01	0.14	-0.05	0.01	-0.18	-0.13	-0.03	0.02	0.02	-0.06	0.02	0.00
GBK 026942 B	0.34	-0.15	-0.24	-0.14	-0.01	0.08	0.16	0.04	0.04	0.28	0.05	0.06	0.14	0.01	0.13	-0.02
GBK 026958 A	0.12	-0.12	-0.07	-0.14	0.14	0.37	0.11	-0.06	0.15	0.26	-0.13	-0.06	0.06	-0.10	0.02	0.03
GBK 026958 B	0.14	-0.14	-0.20	0.01	-0.08	-0.01	0.04	0.31	-0.11	-0.11	-0.06	0.09	0.05	0.09	0.14	0.09
GBK 046540	-0.29	0.14	0.23	0.17	0.02	0.03	-0.09	-0.35	0.06	0.00	0.09	-0.17	0.15	0.00	0.04	-0.11
K80	0.07	-0.06	0.28	-0.26	-0.06	0.01	0.37	-0.31	0.05	-0.11	-0.14	0.10	-0.12	0.04	-0.04	-0.24
KAR 1	0.37	-0.25	0.06	-0.02	0.11	-0.02	-0.03	-0.19	0.03	0.05	0.11	-0.11	-0.09	0.05	0.16	-0.02
KENKUNDE	0.31	0.19	0.03	0.06	-0.02	-0.06	-0.18	0.18	0.16	0.30	-0.07	-0.19	-0.07	-0.02	0.00	-0.09
KVU-27-1	0.09	0.21	-0.15	-0.12	0.03	-0.05	0.39	-0.08	0.00	-0.04	-0.11	0.06	0.03	0.11	0.05	0.13
M66	0.28	0.14	0.09	-0.10	0.01	0.04	0.03	-0.23	0.08	-0.10	-0.35	0.09	-0.24	0.12	0.02	0.04
KAB 1	-0.06	0.25	-0.09	-0.15	0.20	-0.01	0.00	-0.14	0.35	0.10	-0.20	-0.21	0.05	0.07	-0.09	0.00
KAB 3	0.00	0.33	0.13	-0.19	0.21	-0.04	-0.08	-0.10	-0.14	-0.11	0.02	-0.11	0.09	-0.12	-0.04	-0.07
KIP 1	0.21	0.32	-0.19	0.07	0.03	0.05	0.14	-0.07	-0.11	0.00	0.09	-0.05	-0.14	0.08	-0.08	-0.02
KIP2	0.28	-0.31	0.29	-0.02	-0.26	-0.04	0.02	0.03	-0.03	-0.02	-0.04	0.02	0.06	-0.23	0.01	0.05
LAM 4	-0.35	-0.03	-0.32	0.10	-0.16	0.26	0.17	0.04	-0.07	-0.07	0.16	0.01	-0.14	-0.17	0.02	-0.01
MAR.2	0.32	-0.02	0.37	0.11	-0.03	-0.14	0.16	0.19	-0.02	0.16	0.04	0.00	-0.24	-0.21	-0.04	0.12
MAR.3	0.40	-0.01	-0.25	0.08	0.06	-0.09	0.00	0.00	0.01	0.03	-0.03	0.04	-0.07	0.15	0.04	0.09
MAR.5	-0.14	-0.07	0.00	-0.18	0.11	-0.31	-0.14	-0.02	-0.06	-0.26	0.00	0.01	-0.14	0.03	0.18	0.04
MBL	-0.40	-0.15	0.19	0.05	-0.06	0.34	0.06	-0.06	-0.18	-0.04	0.20	-0.03	-0.13	0.10	-0.13	-0.08

Publications

1. Munyao R. K, Mamati E. G, Githiri S.M, Ateka E.M 2019. Genotypic Diversity among Cowpea Genotypes from the Lower Eastern Region of Kenya. International Journal of Agronomy and Agriculturaral Research14(5), 9-19.