UNIVERSITY FOR DEVELOPMENT STUDIES

EVALUATION OF NEW COWPEA (*Vigna unguiculata* L. Walp) LINES FOR STRIGA (*Striga gesnerioides* Willd) RESISTANCE AND YIELD PERFORMANCE

SHAIBU ALHASSAN

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SHAIBU ALHASSAN (BSc. BIOTECHNOLOGY AND MOLECULAR BIOLOGY)

(UDS/MBT/0003/19)

THESIS SUBMITTED TO THE DEPARTMENT OF BIOTECHNOLOGY AND MOLECULAR BIOLOGY, FACULTY OF BIOSCIENCES, UNIVERSITY FOR DEVELOPMENT STUDIES, IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE AWARD OF MASTER OF PHILOSOPHY DEGREE IN BIOTECHNOLOGY

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DECLARATION

Candidate's Declaration

I hereby declare that this thesis is the result of my own original work and that no part of it has been presented for another degree in the university or elsewhere. Works that were consulted have been duly acknowledged by way of references.

…… ……..……

Shaibu Alhassan **Date**

Supervisors' Declaration

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

…… ……

Dr. Damba Yahaya **Date**

(Principal Supervisor)

…… ……..……

Dr. Francis Kusi **Date**

(Co-Supervisor

…… ……..

Dr. Abraham Kusi Obeng **Date**

(Head of Department)

ABSTRACT

One of the most significant food mainstays in tropical Africa is the cowpea. However, parasitic weeds such as *Striga gesnerioides*, which has several distinct races, significantly reduces its productivity. The most dependable method for battling this parasite is the cultivation of resistant genotypes. Twenty new cowpea genotypes developed in the Coastal Savannah were evaluated under the Sudan Savannah condition for yield performance and resistance to *Striga gesnerioides.* The objectives were to: determine the agronomic and yield characteristics; Identify *Striga* resistant and susceptible lines among the genotypes as well as assess their morphological difference. The measured agronomic traits were days to flower initiation, days to 50% flowering, days to first maturity, maturity (90%), plant height, canopy size, leaf length, leaf width, number of pods per plant, number of pods per peduncle, pod length, seeds per pod, seed length, seed width, seed thickness, hundred seed weight (HSW), pod weight and grain yield per hectare. SSR-1 marker was used to screen these genotypes in the biotechnology laboratory at SARI. Most traits had significant coefficients of variation, and genotype variability was also substantial. Except for the number of pods per peduncle, all the features were likewise linked to high broad-sense heritability. The results of the study showed that 55% of the susceptible genotypes performed poorly in terms of hundred seed weight (HSW) yield, and this can be associated to *Striga* infestation. The results showed that only one genotype (UG-14) was resistant to the parasitic weed. This study also revealed high morphological variation among the tested genotypes. The non-susceptible line (UG-14) should be screened alongside other known *Striga* resistant genotypes to determine their genetic relatedness and with more *Striga* resistant markers.

Keywords: *Striga*, resistant, genotypes, susceptible and cowpea

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DEDICATION

This work is dedicated to my dear mother, Madam Rabiatu Baako, Sheikh Alhassan Kailan Baako and my sisters, Shaibu Khadijah and Shaibu Halimatu Sadia for their countless encouragement and support.

Table of Contents

LIST OF FIGURES

LIST OF TABLES

LIST OF ACRONYMS

%	Percentage
Cm	Centimetres
µL	Microlitre
mM	Millimolar
LSD	Least Significant Difference
RILs	Recombinant Inbred Line
IITA	International Institute of Tropical Agriculture
SARI	Savvana Agriculture Research Institute
PGRRI	Plant Genetic Resource Research Institute
CTAB	Cetyl Trimethylammonium Bromide
DNA	Deoxyribonucleic Acid
T.E	Tris EDTA
PCR	Polymerase Chain Reaction
TAE	Tris Acetate EDTA
SSR	Simple Sequence Repeat
Bp	Base Pairs
QTL	Quantitative Trait Loci
cM	Centimorgan
UG	University of Ghana
TA	Annealing Temperature
LG	Linkage Group
MGDw	Molecular Grade Distilled Water

PAGE	Polyacrylamide Gel Electrophoresis
TBE	Tris Borate EDTA
SMA	Single Marker Analysis
ANOVA	Analysis of variance
PIC	Polymorphism Information Content
MAS	Marker Assisted Selection
RAPD	Random Amplified Polymorphic DNAs

CHAPTER ONE
INTRODUCTION

1.1 Background of the study

Cowpea [*Vigna unguiculata* (L.) Walp] is an annual herbaceous legume that performs well in sandy soil. It can tolerate low rainfall, unlike most crops found in the tropical zones of the African continent (Obatolu, 2003). Also, cowpeas are well suited for poor-resource farmers and those who practice intercropping since it improves soil fertility via nitrogen fixation. Cowpea is one of the commonly grown legumes mostly in the savannah and transition zone of Ghana. According to Kebede and Bekeko (2020), over 14.5 million hectares of land are reported to be used for cowpea farming each year, which results in an annual yield of 6.2 million metric tonnes.

Africa is the leading global producer of cowpea with West Africa accounting for over 80% of the total production (Kebede and Bekeko, 2020). Cowpea seeds are high in calories, vitamins, and minerals, and they are a good source of plant protein (25%) (Goncalves *et al.,* 2016). It is extensively used in agriculture as a green manure crop that fixes nitrogen, as well as a cover crop to reduce erosion, and as livestock feed, according to Oelke *et al.* (1991). Oelke *et al.* (1991) revealed that the soft green leaves are also a common food source in Africa, where they are prepared similarly to pot herbs like spinach.

However, growth and yields of cowpea are severely lowered by a range of biotic and abiotic agents (Timko and Singh, 2008). It is reported that the 'witch-weed' (*Striga gesnerioides*) can cause yield losses of up to 100% in cowpea production (Asare *et al*., 210). As a result,

food insecurity and poverty levels rise in the areas impacted, which has a detrimental impact on cowpea output and revenue of rural farmers. Meanwhile, cowpea crop is one of our major cheap sources of protein which saves the poor from protein deficiency in their diets. While most cowpea varieties are susceptible to *Striga* parasitism, resistance has been shown in several local landraces and wild accessions, according to Lane et al. (1993); Lane et al. (1997), and Singh & Emechebe (1990). Development of various *Striga* resistant cowpeas was based on these lines (Omoigui *et al*., 2007; Omoigui *et al*., 2017; Singh & Emechebe, 1991).

However, most of the *Striga* resistant cultivars lack important seed qualities to satisfy the primary consumers. For instance, IT97K-499-35, a crossbreed of B301, is resistant to *S. gesnerioides* and *Alectra vogelii* but does not meet the consumer's preference as it produces small-sized seeds (Singh et al., 2002). Molecular genotyping and host-differential response investigations have previously identified at least seven different races of *S. gesnerioides* in West Africa (Botanga and Timko, 2006; Dubé and Belzile 2010). SSR-1, an SSR marker, has been found to be closely connected to *S. gesnerioides* resistance (Li and Timko, 2009).

1.2 Problem Statement of the study

Cowpea has the ability to increase revenue, food security, and soil quality; yet, a number of biotic and abiotic factors significantly hamper their production. The most catastrophic biotic factor among them is *Striga gesnerioides* (Asare *et al.,* 2013). Several attempts have been made to control *Striga* using cultural practices (hand-picking of emerged shoots before flowering), spraying with chemicals as well as conventional biological control methods. But seemingly, all these modalities are expensive, ineffective, and labor-intensive (Boukar

et al., 2004). As a result, developing cultivars that can withstand *Striga's* infection is the best approach.

1.3 Justification of the study

The multi-purpose use of cowpea has made it a cultural and a very significant crop within the African farming systems (Chweya and Eyzaguirre, 1999). This calls for the need to work relentlessly towards developing new varieties with good yield and agronomic performance. However, this cannot be successful if factors contributing to low yield in cowpea crops are not appropriately tackled. Therefore, the only effective method is to use host plant resistant genotypes which will be less costly compared to others. That seems to be a lasting solution to disturbances of the witch-weed, *Striga*.

1.4 Objectives of the study

The main objective of the study was to evaluate 20 inbred lines of cowpea for *Striga gesnerioides* resistance and yield performance in *Striga* endemic dry Sudan Savannah zone of Ghana.

The specific objectives of the study are:

i. To determine agronomic and yield characteristics of the cowpea lines
ii. Assess morphological differences of the cowpea lines
iii. Identify *Striga* resistant and susceptible lines among the cowpea lines

CHAPTER TWO
LITERATURE REVIEW

2.1 Origin and distribution of cowpea

Cowpea is one of the world's oldest crops, grown mostly for grain and fodder (Davis *et al*., 1991; Chivenge *et al.*, 2017). Contrary to other significant crops, not much is known about the development of cowpea farming (Xiong *et al*., 2016). However, the crop was given the name cowpea because it was primarily utilized as of feed for cows across the globe, including the south-eastern United States (Timko *et al*., 2007). Researchers in the scientific community have been unable to reach a consensus on where cowpea originated due to differing perspectives on its genesis. Although many people assume Africa is the birthplace and distribution hub for the cowpea crop, there is no compelling archaeological evidence to support this claim (Davis *et al*., 1991; Ogunkanmi et al., 2005 and 2006).

Around 1450-1000 BC, the remains of a rock shelter at Kintampo in Ghana were unearthed, which represents the oldest potential archaeological evidence of cowpea genesis and domestication in Africa (Flight, 1976). Based on the morphological characteristics of the plant, Africa and Asia are separate centers of cowpea origin (Timko and Singh, 2008). Faris (1963) proposed Nigeria as the origin of cowpeas in West Africa, based on cytological and morphological examination of the crop. Similar research on cowpea has led some researchers to assume that West Africa is where the crop originated and was domesticated, as wild cousins of the crop can be found on the outskirts of its forest (Pernes, 1984). Nonetheless, Coulibably *et al*. (2012) suggested that it was domesticated in north eastern Africa. On the contrary, it was hypothesized that, like millet and sorghum, the crop originated in Africa and spread over the Indian subcontinent over a period of nearly 2000

to 3500 years according to Alayande and others in 2012. Prior to 300 BC, cowpea was supposed to have been discovered in Asia and then introduced into North Africa and Europe, reported by Summerfield and others (1974), Tindall (1983) and Coetzee (1995). According to Perrino *et al*. (1994), the first written information regarding cowpea was stored in 300 BC and could have been transported to Central and North America during the slave trade period, which lasted from the 17th to the 19th centuries.

2.2. The cytology of cowpea

The cowpea plant has 2n=2x=22 chromosomes and is a diploid plant (Mukherjee, 1968; Sahay and Shukla, 2015). Mukherjee (1968) went on to say that one of these chromosomes has a small length (19 m), seven have a moderate length (26-36 m), and three have a somewhat long length (41-45 m). In the cowpea plant, the chloroplast is inherited maternally (Coniveau and Coleman, 1988). However, certain varieties of cowpea and their distant wild ancestors have 2n=22 chromosomes, according to a study (Rachie and Roberts, 1974). The black-eyed pea, southern pea, niebe and crowder pea are common names for cultivated cowpeas.

2.3 Cowpea taxonomy

Vigna unguiculata is a member of the *Vigna* (peas and beans) genus. The Latin word *unguiculata* means "little claw," referring to the flower petals' tiny stalks. Common names for cultivated cowpeas include: black-eyed pea, southern pea, niebe and crowder pea. However, the genus, *Vigna* is further broken down into sub-genera based on physical characteristics, the degree of hybridization, and the geographic distribution of the species.

Table 1 : Classification of cowpea (Vigna unguiculata (L.) Walp)

TAXONOMIC PLACEMENT	SCIENTIFIC NAME
Kingdom	*Plantae*
Division	*Magnoliophyta*
Class	*Magnoliopsida*
Order	*Fabales*
Family	*Fabaceae*
Sub-Family	*Faboideae*
Tribe	*Phaseoleae*
Sub-Tribe	*Phaseolinae*
Genus	*Vigna*
Section	*Catiang*
Species	*Unguiculata*
Botanical Varieties	*1.Vigna unguiculata var. unguiculata* *2.Vigna unguiculata unguiculata var. spontana*

Source : Verdcourt 1970

2.4 Morphology

Cowpea, a perennial herb that grows in a variety of shapes can be erect, trailing, climbing, or bushy, and it is mostly indeterminate especially when conditions are favorable. Depending on the cultivar, the canopy height might range from 30 to 60 cm.

2.4.1 Leaves

According to Valenzuela (2012), cowpea leaves start off simple and opposite, but as they progress, they become trifoliate and petiolate and are arranged in an alternate pattern. The oval leaflets on the trifoliate leaves range between 6 cm and 15 cm in length and 4 to 11 cm wide. The leaves of cowpea are typically dark green in hue, according to Feedipedia in 2015. The oval leaflets on the trifoliate leaves are 4 to 11 cm wide and 6 to 15 cm long.

2.4.2 Inflorescence

Cowpea has very attractive, self-pollinating blooms with corollas that range in color from white to pink to pastel blue to purple and are borne on short pedicels. Fery (1985) also reported that cowpea plant's blossom ranges between ten and thirty-centimeters in length. There is a rachis, which extends from the end of the peduncle and has each node carrying two flowers as well as an additional cushion of floral nectaries that attract insects. The blossoms bloom late at night and close late in the morning in cultivated varieties, with the anthers dehiscence occurring many hours before the flower opens. Despite the fact that it is considered autogamous, out-crossing which rates as high as 5% have been reported, necessitating certain measures in the preparation of breeder and foundation seeds to avoid out-crossing (Timko and Singh, 2008).

2.4.3 Stems

Cowpea is a fast-growing plant that can reach up to 20 cm more above in ideal conditions. The stem is hollow and hairless, and it stands straight. It measures approximately 0.4 or 2/5

inch (1 cm) in width. Aveling (1999) stated that the stems have a purple tint and are frequently crinkled or silky.

2.4.4 Fruit and Seeds

Cowpea pods come in a variety of sizes, colors, shapes, and textures. When fully ripe, they are often yellow but can also be different hues. They can be upright, crescent-shaped, or coiled. Cowpeas can have about four or more pods per peduncle.

2.4.5 Roots

Cowpea has a strong primary root with multiple lateral roots on the surface of the soil that can grow as deep as 244 cm into the earth to find moisture during droughts (Sustainable Agriculture Green Manure Crops August 2002). Cowpea roots have smooth, spherical globular nodules with a diameter of about 5 mm. The principal (tap) root has a large number of nodules, while the lesser roots have a smaller number (Chaturvedi *et al*., 2011).

2.5.0 Environmental requirements

2.5.1 Temperature

The cowpea is a warm-season annual plant that requires temperatures of at least 18°C during its entire life cycle, with a growing temperature of approximately 28°C (Craufurd *et al*., 1997). The cowpea plant tolerates a wide range of temperatures (warm-season plant). Cowpea grows well at a variety of temperatures (warm-season plant). The response of different cowpea types to day length varies, with some being insensitive to day length and

flower in 30 days after planting at around 30°C. Extremely warm or moist conditions usually prolong or extend flowering (even in early maturing cultivars), resulting in non-uniform growth. In addition, adverse blooming and flower defoliation brought on by hotter altitudes can have a negative impact on pod development. Never, flower abscission may occur in some cultivars due to high night temperatures. In conditions above 19 degrees Celsius, germination can occur quickly, although at lower temperatures it takes longer (Hall *et al*., 2002).

2.5.2 Rainfall

Cowpea is more drought resistant when compared to its companion crops (such as Bambara beans, chickpea, soya beans, etc.). It thrives in a range of 400 mm to 700 mm of annual rainfall. They may also flourish in areas with maximum rainfalls (of up to 2,000 mm per year), although as soil moisture increases, so does the rate of infection by fungi, according Cook *et al*. (2005). The cowpea's elongated taproot system has several strategies that increase its water retention, including rotating the leaves upward to reduce heating and sealing the stomata (Van Rij, 1999). Cowpea crops are highly important in the Sahelian and arid zones because of these characteristics.

2.5.3 Soil types needed

There are many different soil types and conditions where cowpea can thrive, although it likes sandy loams and soils better with adequate drainage. In contrast to other soil types, sandy soils, according to Hall (2002), support appropriate root growth and are less restrictive. It thrives on soils that are slightly acidic to a little bit salty. It is also less resistant

to salt, nevertheless it grows well in aluminum-rich soils. Cowpea exhibit vigorous growth on high fertile soils, although this does not guarantee substantial production of grains. Cowpeas have been shown to perform badly in cold soils when compared to regular beans (Cook *et al*., 2005). Despite the fact that the grain yield is not noticeably higher than it would be with a nitrogen application rate of 30 kg/ha, cowpeas frequently respond favorably to additional phosphorus (Agbenin *et al*., 1990).

2.5.4 The use of fertilizers in cowpea cultivation

The amount of fertilizer needed on cowpea-growing soils is mostly determined by the soil's fertility and the predicted yield during production (Davis *et al*., 1991). Because of the high weathered soils and limited nutrient reserves in tropical agriculture, fertilizer application is very important as it improves production levels (Stewart *et al*., 2005). However, current methods advocate for increase in fertilizer application over the world (Bumb, 1989). Due to the high cost of available fertilizers, there was a decline in fertilizer application in Sub-Saharan Africa some years back (Bumb and Baanante, 1996). While applying fertilizer in Ghana, cereals are given a lot of consideration (Camara and Heinemann, 2006), whereas cowpea receives less. The majority of farmers in Ghana mostly fertilize cereal crops and infrequently focus on leguminous plants (Zingore *et al*., 2008). Such cowpea growers mistakenly believe that inorganic fertilizers are not necessary for the healthy growth and development of leguminous crops (Kanankuka, 1999). Cowpea's nitrogen requirement can be improved through fertilization of the soil (Chiezey and others (1990); Kan‟‟ankuk‟‟a, (1999) and FAO, (2005). Cowpeas, meanwhile, typically thrive in low-nitrogen environments. For soils with low N content, a beginning N rate of 27 kg per hectare is frequently necessary (Rupela and Saxena, 1987; Bluementhal *et al*., 1992). In an article

from SARI (2013), it is recommended to apply 20 kg of N and 40 kg of P_2O_5 of fertilizer per hectare on ancient land (land that has been continuously farmed), where the proportion of organic component may be as little as 1%.

2.6 Weeds

Weeds are among the many components that hinder good yield in our cultivated crops as they compete with them for light, nutrients and water in order to survive. They raise the cost of crop production by requiring the use of numerous inputs, including weedicides. Furthermore, weeds reduce growth pace, grain quality, and quantity, all of which reduce production costs (Akobundu, 1980; Ghanizadeh *et al*., 2011). In Ghana, witch-weed can result in output declines, ranging from 30 percent to nearly 100 percent (Asare *et al*., 2010). Apart from the decline in crop yield, weeds host insects, diseases and nematodes. It was demonstrated that without weeding the cowpea field, the damage caused by insects alone rose up to 15.8% (Moody, 1973).

To combat weed disturbances, a weed management system was developed, but it requires certain basic knowledge about the weed (Tollenaar *et al*., 1994). It is also underlined that using crops that can tolerate competition from other plants is an important component of an integrated weed management scheme (Lemerle *et al*., 1996). The suppressive mechanisms used by planted crops to prevent the growth of weeds is highly preferable in as much as we try to minimize the use of herbicides which often increases cost of production (Bilalis *et al*., 2009). Factors to consider about weed-crop interactions include; rates of growth, leaf area, crop height, tillering capability, long stems, high biomass, allelopathy, and shading ability (Lemerle *et al*., 2001)

2.7.0 Importance and Uses of Cowpea

Cowpea offers numerous advantages, including improving the lifestyles of relatively impoverished people in the tropical areas of developing countries, particularly where animal protein is scarce. Commonly consumed in many nations, with great nutritional and nutraceutical qualities, as well as a number of agronomic, environmental, and economic benefits that support food security and environmental preservation. Carneiro da Silva and others (2018) reported that, cowpea is an essential crop for improving both health and availability of food on all continents.

2.7.1 Provision of nutritious food and high-quality feed

According to Langyintuo *et al*., (2003) and Asare *et al*. (2013), cowpea is one of Africa's most economically significant native crops, owing to its high protein content when used as food or feed for humans and animals. Cowpea grains contain about 25% protein, as well as a variety of vitamins and minerals (IITA, 2017). Fresh, immature pods, on the other hand, can be boiled and consumed like a vegetable. Consumers can also preserve dried leaves and eat them as a meat replacement. In Ghana, cassava, plantain, oatmeal, and yoghurt's nutritional content are all enhanced by the addition of cowpea. It is also used to make Apapransa, cowpea pie, Yikponos (cowpea biscuits), cowpea stew, and other dishes.
Cowpea is high in a variety of nutrients, including a substantial amount of protein.

Cowpea seeds are a low-cost source of protein in the diet when used as a seed vegetable. Apart from cowpea being a relatively cheap source of protein to solve malnutrition problems, it is also rich in nutraceutical compounds such as dietary fiber, antioxidants,

polyunsaturated fatty acids, and polyphenols that confer good health to the body. Omoigui *et al*. (2007) and Asare *et al*. (2013) reported that cowpea's high protein level makes it a useful supplement in the food for many Africans who are not able to purchase the high cost animal protein. The proteins from cowpea have effective emulsifying, foaming, and solubilizing characteristics, and can thus be used as a substitute for soy protein isolates for those who are allergic to it (such as infants).

2.7.2 Importance of cowpea in soil fertility management and cropping systems

Cowpea cultivation is very beneficial to smallholder farming systems due to the ability of the crop to nourish the soil with nutrients through nitrogen fixation (Kyei-Boahen *et al*., 2017). Thus, it cuts down on the cost of input materials. According to Crops Research Institute (CRI, 2006), cowpea can fix about 240 kg/ha of atmospheric nitrogen while supplying 60-70 kg/ha of nitrogen to subsequent crops grown in rotation with it.

2.7.3 Economic importance of cowpea

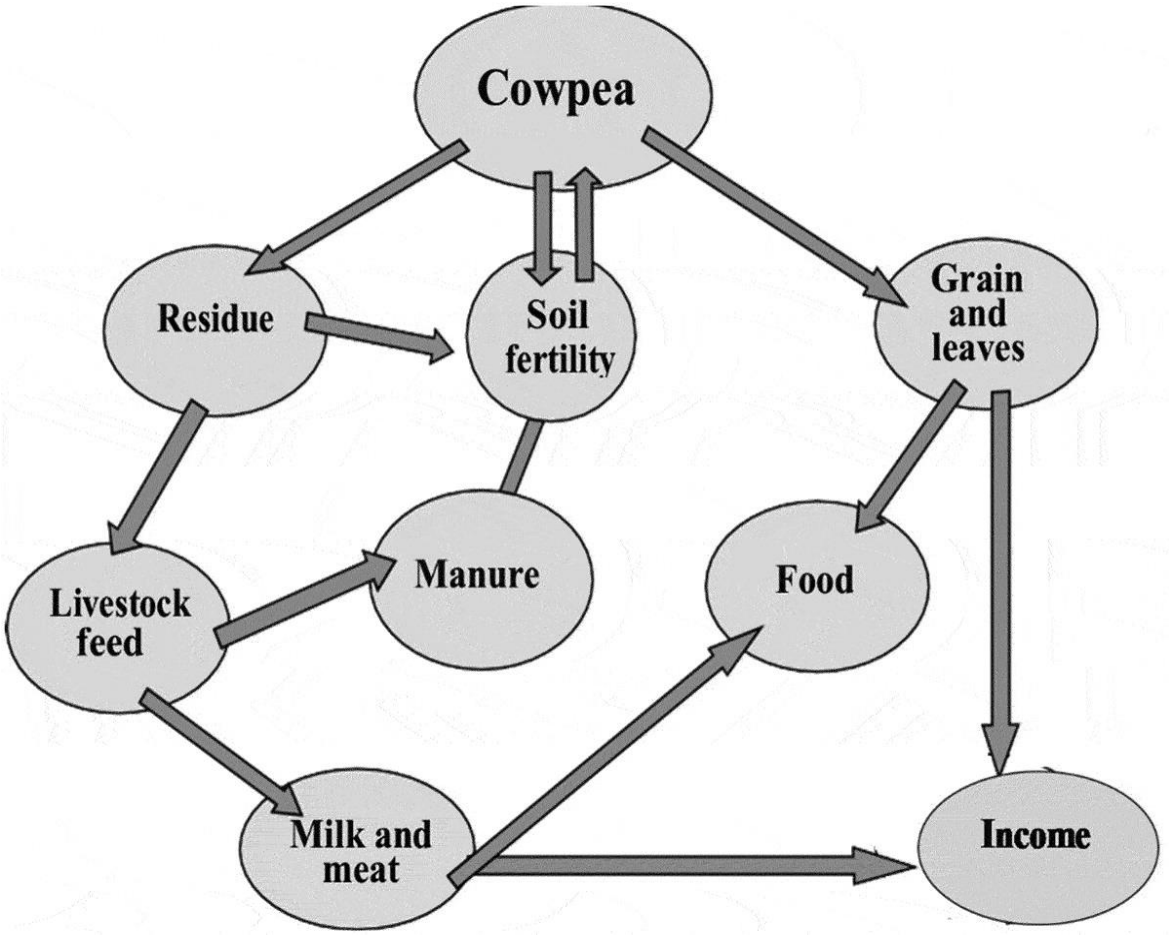
Cowpea has economic value as a source of income due to the sale of the grain and leaves, provision of food, improvement of soil fertility, and provision of forage (Alemu *et al*., 2016). Cowpeas are utilized as a vegetable as well as a grain. The semi-spreading varieties are often used as vegetables. Cowpea haulms can be traded for food by both large and small ruminants, which can be profitable. Cowpea is a valuable grain legume that is marketed in practically all local marketplaces, particularly in Africa. Farmers, small and medium-sized businesses, and entrepreneurs can make money from trading in cowpea products (Timko & Singh, 2008). It was observed that both rural and urban populations, particularly women,

can make some money by dealing in fresh cowpea leaves, fresh produce and processed items, by Ngalamu and others (2015).

Table 2 : Some new formations for utilization of cowpea flour in Ghana

Product	Description	Product	Description
Adunlei	Cowpea straw	Agonam	Cowpea pie
Akla	Fried cowpea paste	Apranpransa	Thick cowpea porridge
Atwomo	Cowpea twisted cake	Atwomo	Cowpea twisted cake
Ayikaklo	Fried plantain mixture	Ayitale	Fried cowpea/plantain
Ayiwonu	Cowpea vegetable soup	Cowpea-pap	Mix
Cowpea-pap	Mix	Frido	Cowpea cutlet
Cowpea cake	Cake	Gbalegbale	Cowpea pancake
Cowpea stew	Stew	Kitikiti	Cowpea chips
Cowpea fritter	Fritter	Kpeblo	Cowpea rock buns
Danwake	Cowpea dumpling	Mapele	Cowpea pudding
Tseke	Steamed flour cowpea	Majula	Cowpea doughnuts

Source: Randolph *et al.*, 1981



Source: Fatakun *et al.* (2002); Kebede and Bekeko, (2020)

Figure 2.1 : Uses of cowpea

Table 3 : Nutritional composition of cowpea (%)

Nutritional components	Seeds	Hay	Leaves
Carbohydrate	56-66	-	8
Protein	22-24	-	4.7
Water	11	18	85
Crude fibre	5.9-7.3	9.6	2
Ash	3.4-3.9	23.3	-
Fat	1.3-1.5	11.3	0.3
Phosphorus	0.146	2.6	0.063
Calcium	0.104-0.076	-	0.256
Iron	0.005	-	0.005

Source: (Kay, 1979; Tindall, 1983; Quass, 1995)

2.8.0 Cowpea Production

The cowpea is a well-known legume crop that thrives predominantly in tropical and subtropical regions of the world. It is grown using a range of cropping techniques, including solitary cropping, intercropping, and mixed cropping. Cowpea is primarily farmed for its edible seeds, pods, and leaves, which are fed to people and animals and serve as a source of income for households. While a growing percentage of farm households produce cowpea on marginally fertile and infertile soils, the output of the crop has persistently lagged behind global averages and has generally remained below the crop's capability.

2.8.1 Production of cowpea in Ghana

Apart from peanuts, cowpea is the second most farmed leguminous crop in Ghana in terms of land area utilized and annual yield (Egbadzor *et al*., 2013). Ghana is the fifth-largest producer of cowpea in Africa, producing an average of 143,000 million tons of the crop year on about 156,000 hectares of land (ICRISAT, 2012). The major production zone in Ghana is the Guinea savannah, Northern and Upper West Regions (Al-Hassan and Diao, 2007). Other potential production locations include the Sudan savanna zone (Upper East Region) and some districts in the Brong Ahafo and Ashanti Regions' transitional zones.

2.8.2 Production in Africa

Considering some places of West Africa, crop production are mostly focused on small-scale subsistence farming practices. Ajeibe and Singh (2006) reported that cowpea is typically intercropped with cereals in Africa. Surely, cowpea is a versatile crop that provides various benefits to producers (farmers), particularly in Africa: it feeds its companion crops with nutrients (during intercropping), as well as people and cattle. Farmers can choose to use more inputs to increase grain yields and produce more income, or they can use fewer inputs and gather more foliage but fewer grains. In this situation, the decreased grain yield would be offset by greater animal feed production, which might result in more meat and milk being produced by the fed cattle. According to Imrie B. (2000), the United States seems to be the most active producer and exporter of cowpea among developed nations.

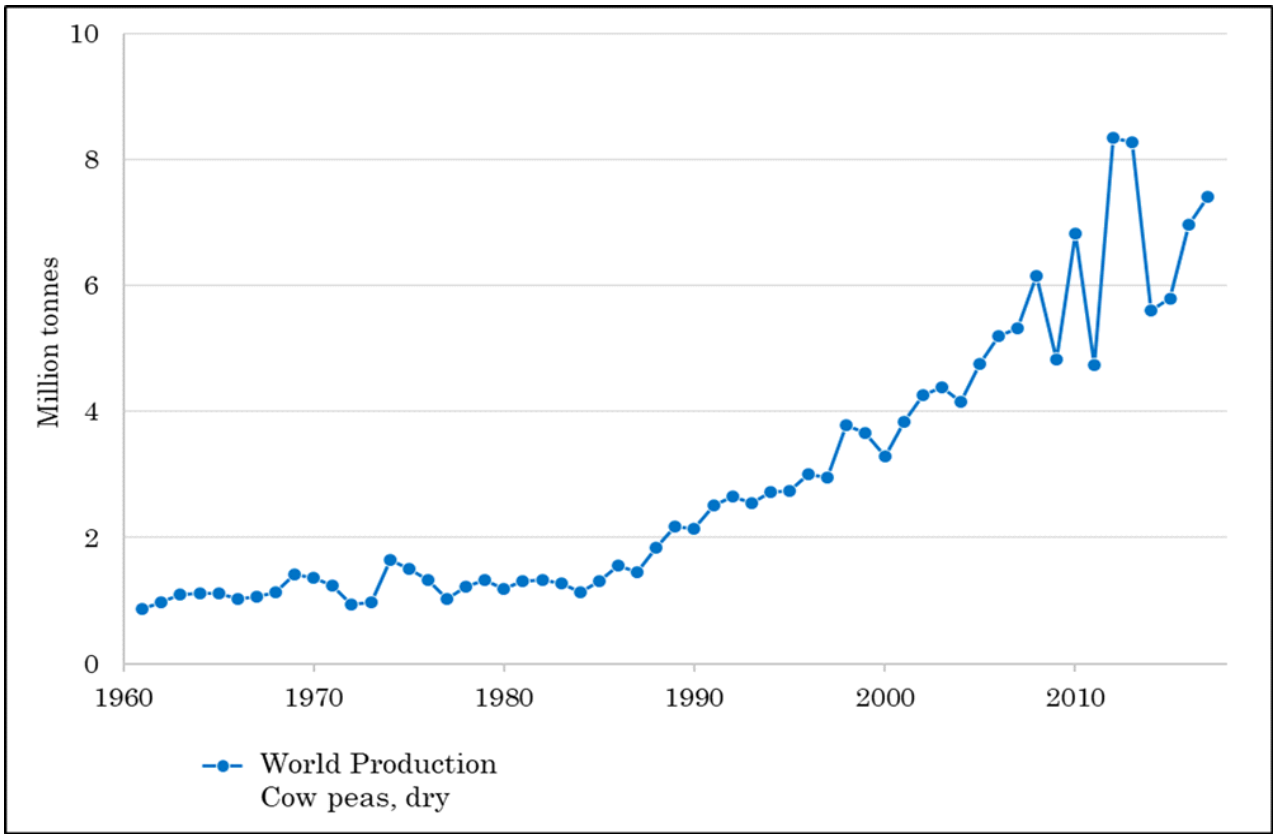
2.8.3 World Cowpea Production

According to Raina and Khan cowpea (2023) revealed that, approximately 14.4 million hectares of land are used for cultivating cowpea each year, yielding a total grain of 8.9 million tons, but only a small percentage of this reaches the international market (FAO, 2004). Africa accounts for 98 percent of total production area (12.25 million hectares) and 64 percent of the expected 3 million tons of dry grains (Fery, 2002; Timko & Singh, 2008; IITA, 2017). Cowpea grains are produced at over 7.4 million tons per year worldwide, with almost 7.1 million tons produced in Africa (IITA, 2017). West and Central Africa is Africa's and the world's top producer of cowpea. The biggest cowpea grower in the world is Nigeria, with Brazil coming in second. Nigeria accounts for 48% of African output and 46% of the global market, making it both the world's greatest producer and consumer (IITA, 2017). A total of 6.2 million metric tons of cowpea are produced annually on an estimated 14.5 million ha of planted land worldwide. According to Boukar and others (2016). Cowpea production has increased globally over the past three decades at an average rate of 5%, with yearly area growth of 3.5% and yield growth of 1.5% (Boukar *et al*., 2016). About 84% of the world's production area and 83.4% of the world's overall production of cowpea is from Africa, with over 80% of African production in West Africa.

Table 4 : Top cowpea producing countries in the world (2014)

Rank	Country	Production (tons)	Area (ha)	Yield (Kg/ha)
1	Nigeria	2,137,900	3,701,500	578
2	Niger	1,593,166	5,325,168	299
3	Burkina Faso	573,048	1,205,162	475
4	United Republic of Tanzania	190,500	197,323	965
5	Cameroon	174,251	209,019	834
6	Mali	149,248	353,382	422
7	Kenya	138,673	281,877	492
8	Myanmar	115,200	132,000	873
9	Mozambique	103,837	377,900	275
10	Sudan	80,000	260,000	308
11	D R C	70,042	159,945	438
12	Senegal	64,088	153,142	418
13	Malawi	35,903	81,753	439
14	Haiti	29,895	41,525	720
15	United States of America	21,591	12,060	1,790
16	Peru	17,588	12,779	1,376
17	Serbia	16,189	4,777	3,389
18	Sri Lanka	15,281	11,519	1,327
19	China, mainland	13,500	13,000	1,038
20	Uganda	10,100	25,000	404

Source: Boukar *et al*. (2018)



Source: (FAO, 2019)

Figure 2.2 : Increasing worldwide production of the cowpea, 1961-2017.

2.9 Cowpea Production Constraints

The low productivity of cowpea can be due to a wide array of abiotic and biotic stresses including socio-economic constraints.

2.10 Abiotic factors

Low soil quality, dryness, heat, acidification, and damage from inter-cropping with cereal crops are the most significant biotic variables that seriously jeopardize cowpea output according to Singh & Tarawali (1997) and Singh & Ajeigbe (2002).

2.10.1 Drought and heat stresses

One of the main factors causing food insecurity around the world is a lack of rainfall (Barters and Nelson, 1994). Drought has a significant impact on morphological and physiological aspects of plant development and growth, reported by Dulai *et al*. (2006). Cowpea yields may be severely reduced as a result of drought. This was supported by a study of monoculture legume yield responses to drought in field circumstances between 1980 and 2014, which indicated that the amount of water lost in the soil was linked to cowpea yield reduction (Agbicodo *et al*., 2009). Depending on the cultivar, heat stress beyond a threshold temperature of 16 degrees Celsius can reduce pod set and grain yield by 4 to 14 percent (Hall, 2004). The mechanisms used by plants to withstand drought stress can be categorized into three, namely: *drought escape* (the ability of plant complete its life cycle before soil and plant deficit occur), *drought avoidance* (the ability of plant to relatively high tissue water potential during shortage of soil moisture) and *drought tolerance* (the ability of plants to withstand water-deficit with low tissue water potential) (Mitra, 2001). Crops may sometimes require more than one of these mechanisms to survive under drought stress.

All the aforementioned mechanisms have been observed in cowpea. Compared to other leguminous plants, cowpeas are better at utilizing the moisture in the soil and can withstand droughts (Ehlers and Hall 1997; Singh and others, 1997; Kuykendall and others, 2000; Martins and others, 2003). Cowpeas react to serious moisture stress by limiting growth (especially leaf growth) and reducing leaf area by changing leaf orientation and closing the stomata. Flower and pod abscission during severe moisture stress also serves as a growth-

restraining mechanism. Despite the inherent tolerance to drought stress, cowpeas still suffer significant damage from persistent rainlessness in the Savannah regions because of low-volume, altered precipitation events, according to Singh and others (1997). Only early-maturing types have reportedly been known to frequently avoid the terminal drought (Singh, 1997). But they struggle under intermittent moisture stress during the early phases of vegetative growth, according to Mai-Kodomi and others in 1999a. Hence, a lot of work has been done to develop cultivars that are tolerant to low rainfall conditions. Moreover, according to Thiaw and others (1993), cultivars that mature quickly are able to avoid the early stages of the reproductive phase's drought stress (Thiaw *et al*., 1993). Unfortunately, studies on drought resistance using modern technology are more advanced in other crops such as common beans and soybeans. Nonetheless, scientists from all over the world are working together to develop more unsusceptible crops (Hall and others, 1997a; Turk & Hall, 1980).

2.10.2 Low soil fertility

One of the major causes of food shortages is loss of fertility on farmlands (Bationo *et al*. 2003a). Despite the fact that a large portion of West Africa is semi-arid (Voortman and Brouwer, 2003). Soil infertility is also one of the limitations to high yields in cowpea production. It is a more important yield-limiting factor than even rainfall. Due to the high cost and/or scarcity of chemical fertilizers, they are unavailable for purchase or access by peasant producers (Trolove *et al*., 2003). That appears to have remained unchanged over the years (Payne, 2006). When there is adequate soil P availability, Cowpea is a plant that does well in the arid Sahelian climate, which includes low soil quality, extreme heat, and

dryness, according to Hiler and others (1972), and Turk *et al*. (1980). Despite the fact that several studies have shown that cowpea crop respond positively to P fertilizer, the inorganic forms of it are not considered economically viable in rural communities (Trolove *et al*., 2003; Smalberger *et al*., 2004) due to their high cost and limited availability in such areas (Akhtar *et al*., 2006; Akhtar *et al*., 2007).

2.11 Biotic factors

Cowpea plants at the seedling are frequently attacked by a variety of insect such as aphids, Leafhoppe and foliage beetles (Tazerouni, *et al.*, 2019). These insect peat spread disease of the cowpea including the cowpea mosaic virus which aphids act as vector**.** The plant is infected with bacteria, viruses, and fungi, which cause a variety of diseases. The parasitic types of weeds, *Alectra* and *Striga*, also prevent the growth of cowpea plants. The complex of this crop's illnesses is undeniably a major stumbling block to more intensive and higher production. Although chemical control approaches exist for several diseases, they are unlikely to be technically or economically practical at the peasant farmer level, with the exception of seed dressing treatments.

2.11.1 Cowpea *Colletotrichum* Disease

Colletotrichum sp. causes serious illnesses to cowpea when grown under humid conditions, namely, anthracnose and brown blotch. These diseases are induced by two different species of the genus *Colletotrichum*. Emechebe and Florini (1997) suggested that the cowpea anthracnose pathogen is a different species from *Colletotrichum lindemuthianum* (the Phaseolus bean anthracnose pathogen). Latunde-Dada *et al*. (1999) proved that the

anthracnose pathogen of cowpea forms part of *Colletotrichum destructivum* O "Gara instead, and this has been accepted and adopted by Allen and Lenne (1998). In the savannah agro-ecologies, cowpea blotch disease is caused by *Colletotrichum capsci* (Allen and Lenne, 1998; Emechebe and Shoyinka, 1985). Nonetheless, *Colletotrichum truncaum* (Schew) induces brown blotches of cowpea under humid conditions (Adebitan, 1984). The signs of this disease on the cowpea plant include purplish dark discoloration on pods that spreads to the peduncles, petioles, and leaf veins. Pod infection frequently causes poor pod growth and deformation. (Allen *et al*., 1998). Emechebe and McDonald (1979) discovered that these diseases are seed-borne. The infection is estimated to cause yield losses in cowpea crops ranging from 46% to 74%, based on the degree to which the genotype of cowpea employed for the evaluation is susceptible (Alabi, 1994). Many cowpea genotypes still have a high level of susceptibility to the *Colletotrichum* diseases, hence the infection as one of the most devastating barriers to cowpea growth in humid climates. It is observed that brown blotch infection is high in intercropped cowpeas compared to monocrops, according to Adebitan *et al*. (1996). Furthermore, broad separation between cowpeas decreases the frequency and severity of brown blotch in comparison to plants planted with little spacing, either as monocrops or intercrops in humid zones. However, Adebitan and Ikotun (1996) revealed that the severity and incidence of anthracnose disease is lower in intercropped cowpeas as against mono-cropped ones, whereas reducing the spacing of crops increases the infection rate. Meanwhile, only a few cowpea plants are recommended for each acre of land when applying the spacing method as a control measure for the brown blotch disease.

2.11.2 Smut disease of cowpea leaves

In Nigeria, *protomycopsis phaseoli* is what causes cowpea smut leaf disease (Adejumo and others, 2000) Williams and Allen (1976) later made the discovery after IITA (1975) made the initial discovery in Nigeria. Lesions caused by the infection have a diameter of 3 to 10 mm, are dark ash to sooty gray, and have yellow haloes around newly formed lesions. Fake smut frequently results in the chalkiness of grains, which reduces grain weight. Moreover, it hinders seed germination. According to reports by Allen (1979); Singh and Allen (1979) and Adejumo & Ikotun (2003), fake smut primarily occurs in humid conditions and highly fertile soil, leading to output declines. According to Ajibade and Amusa (2001), about 65% of the 71 cowpea genotypes evaluated during the 1999 cropping season had leaf smut infection. It is suggested to remove leaf debris before crop emergence, rotate crops for a long time, and plant without tillage in an effort to ward off the infection.

2.11.3 Web blight and related diseases

Web blight usually affects leaves and pods. The symptoms of the disease in infected leaves are water-soaking, followed by browning or necrotic circular lesions, resulting in the dying and falling of the infected leaf. While infected, pods show irregular lesions that are brown in color. Nonetheless, numerous other immature stem tissues are infected by the web blight pathogens. *Rhizoctonia solani* causes damping-off, root rot, crown and stem rot, and web blight on a wide range of ornamental hosts. Web blight is induced by aerial types, usually belonging to AG-1, while the strains that induce root rots or seedling diseases are strongly soil-borne, in contrast to the aerial strain, which has only a transient association with the soil.

The two forms of the disease complex have been found to be seed-transmitted (Emechebe & McDonald, 1979). These diseases are often severe under localized, waterlogged conditions in the humid forest of south-western Nigeria. In humid environments, lesions grow quickly and clump together, resulting in significant burning and loss of leaves as suggested by Allen & Lenne in 1998. In the forest area of West Africa, the two illnesses are recognized as being serious and economically significant diseases (Emechebe & McDonald, 1979). Similar to web blight, which affects cowpeas in hot, humid regions of India and Latin America, web blight is described as a disease that causes the plant to die, according to Lin & Rios (1985) and Verma & Mishra (1989).

2.11.4 White mold

This is usually white but gradually gets darken. Usually, infected plants wilt and die, which causes the grown cowpea harvests to lose nearly all of their grain (Adejumo and Ikotun, 2003). *Sclerotium* rot is more concentrated in endemic regions of infected crops. However, it does not pose a significant production barrier for cowpea.

2.11.5 Charcoal rot (damping off)

The soil-borne fungus Macrophomina phaseolina (Tassi) Goid, which causes the root and stem disease known as "charcoal rot disease," is a significant biotic stressor that globally restricts cowpea output. Along with causing damping-off, the infections can also cause wilt, according to Abdon *et al*. (1980) and Singh *et al*. (1990). Reuveni *et al*. (1983) and Short *et al*. (1980) reported that sources of pathogen's main inoculum include seeds, soil, and

plant debris. The occurrence of charcoal rot has caused significant yield losses of cowpea in Nigeria (Singh *et al*., 1990).

2.11.6 Parasitic nematodes of cowpea

About 51 species of parasitic nematodes from 23 genera have been connected to cowpea plants. (1985; Caveness & Ogunfowora). Nevertheless, Florini (1997) revealed that cowpea hosts roughly nine different types of parasitic nematodes. Meloidogyne incognita, a species of Meloidogyne harmful to cowpea, is the most worrying, according to Sarmah & Sinha (1995); Khan *et al*. (1996) and Adegbite *et al*. (2005). Anonymous (1961) revealed that the root knot nematodes such as *M. incognita*, *Meloidogyne javanica*, and *Meloidogyne areneria* were first reported in Nigeria on cowpea in 1958 and documented in 1960. Meanwhile, *M. incognita* and *M. javanica* have been reported to be predominant in the southern forest zone of Nigeria (Olowe, 1976). It was observed that those root knot nematodes are responsible for the yield reduction in cowpea. Caveness (1979) and Ogunfowora (1976) reported yield losses of 20 and 59%, respectively, due to infestation by *M. incognita*. Another evaluation demonstrated that root knot nematodes caused about 69.6% yield losses of cowpea grains (Babatola & Omotade, 1991). When root knot nematode infestation is severe in cowpea plants, it might result in crop damage (Olowe, 1981; Adegbite *et al*., 2005).

2.12.0 Phytophthora Stem Rot (*Phytophthora vignae*)

In Queensland, Australia, cowpeas with root and stem rot were the first plants from which *Phytophthora vignae* was identified and characterized by Purss in 1957. When the weather

is damp, stem rot develops, and affected plants become yellow. The root of the sunken brown lesions extends upward from the ground level. Infected plants wilt and die in dry conditions.

2.12.1 Wilt (*Fusarium oxysporum*)

Fusarium oxysporum is a soil-borne fungal pathogen that infects cowpeas with vascular wilt disease (Armstrong and Armstrong, 1981). Fusarium wilt can be a challenge wherever cowpea crops are cultivated. The side effects of fusarium wilt differ from those of *phytophthora* stem rot with the absence of sores outside the stem (Quinn, 2014).

2.12.2 Powdery Mildew

It is an infection that occurs under dry conditions or in late-planted crops. The infection starts with a fluffy substance on the leaf. As it matures it creates some colored patches on the leaves. The leaf at this stage can easily fall prematurely when stressed, according Schwartz *et al*. (2005).

2.12.3 Parasitic Weeds

A key challenge in many tropical agricultural systems is parasitic weeds. The plant *striga*, commonly called "witchweed," is part of the *orobachaceae*, which was originally called *scrophulariaceae*. *Striga* species number in the hundreds, but only around five are economically significant in Africa today. Due to taxonomic confusion and multiple sub-species, the precise number of species is unknown (Table 1). They parasitize African cereal

crops, including maize, rice, millet, and sorghum, with the exception of *Striga gesnerioides.* Berner *et al*. (1997) stated *Striga gesnerioides*, a parasitic weed, affects cowpea and other legumes. *Striga gesnerioides* has a higher influence on people's livelihoods than any other parasite angiosperm since the suitable-hosts tend to be major food crops in some areas, according to Singh (2000).

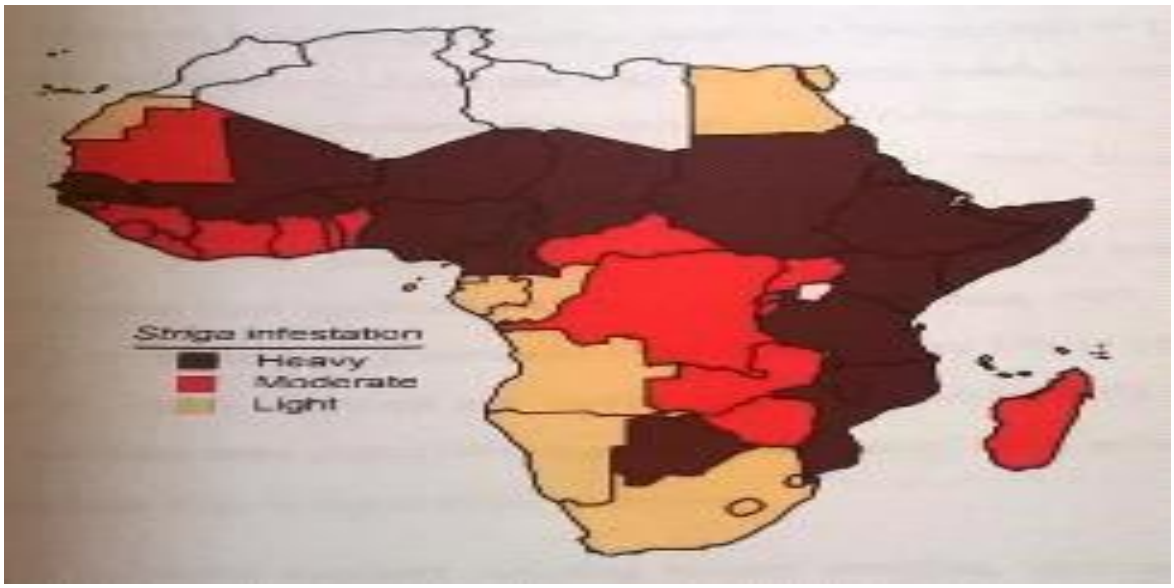
Striga's seed germination can be aided by root exudas from crop plant. As they continue to expand, the seeds that have already started to germinate cling to the host plant's roots and take up nutrients. Farmers are able to discern between striga damage on two different levels (aboveground and underground). But the underground level causes more harm.

Striga is completely reliant on its host as a parasite. According to Singh (2000), *Striga* parasitic weeds may pose a greater biological constraint to food production in Sub-Saharan Africa than any other biotic factor. Additionally, throughout some areas of the Sahel and Sudan, *Striga gesneriodes* preys on cowpea, according to Ramaiah *et al*., (1983), and Musselman & Parker (1982). On the Guinea Savannah of Benin, Ghana, Togo, and Sierra Leone, as well as in the coastal savannas near the Atlantic Ocean (RENACO, 1990). *Striga* has been linked to cowpea production losses ranging from a few kilograms per hectare to complete crop failure in northern Nigeria (Obilana, 1987). In Ghana, witch-weed might lead to yield losses ranging from 30% to 100% (Asare *et al*., 2010). *Striga* can withstand a broad variety of soil and climatic conditions. It flourishes in regions with yearly rainfall of 25 to 150 cm, with lesser rainfall, deficient nutrient, and repeated cultivation of suitable-host's crop (Musselman & Ayensu, 1984).

2.12.4 Geographical Distribution and Races of *Striga gesnerioides*

When it comes to *striga* species and their preferred hosts, there are two broad groupings (Pieterse, 1985; Mohamed *et al*., 2001). *Striga hermonthica*, *Striga aspera*, and *Striga asiatica* belong to the first group. The *Poaceae* family, which includes essential food and forage grains, is largely parasitized by this group (corn, sorghum, rice, and millet). *S. gesnerioides*, the most widely spread of the witch-weeds, belongs to the second group. *S. gesnerioides* isolates from various locations can be distinguished by their various hues and dimensions size, as reported by Musselman (1980), Musselman & Parker (1981), Mohamed (1984), and Mohamed and colleagues (2001). At present, there are not enough morphological distinctions between isolates to justify classifying them as separate species or subspecies (Mohamed *et al*., 2001). The variability of host specificity is substantial. According to Lane and others in 1996, races of *S. gesnerioides* exhibit genetic variation, which affects how susceptible various host species are to various samples of species.

According to research, the Ghanaian strain of *S. gesnerioides* displays virulence qualities similar to other known ones, as reported by Asare *et al*. (2010). However, one or more parasite species can be found in practically all African countries south of the Sahara, in croplands and/or grasslands (Gressel *et al*., 2004). One race of *S. gesnerioides*, according to Cardwell and Lane (1995), can be found in every nation of West Africa. Its evolutionary location and potential effects are unknown because the parasite from Ghana has not been studied previously.



Source: Essem *et al*., 2019.

Figure 2.3 : Striga infestation distribution in Africa

2.12.5 *Striga* species' taxonomy

There are 17 groups among the approximately 3,000 parasitic weed plant species (Kuiper et al., 1998). Both cereals and legumes could have these parasites (Botanga & Timko, 2005). According to Mohamed *et al*. (2001), *Striga* is mostly an African genus, with around 30 native species inhabiting the continent. The family *Scrophulariaceae*, which has roughly 50 species, includes the genus, according to Botanga and Timko (2005).

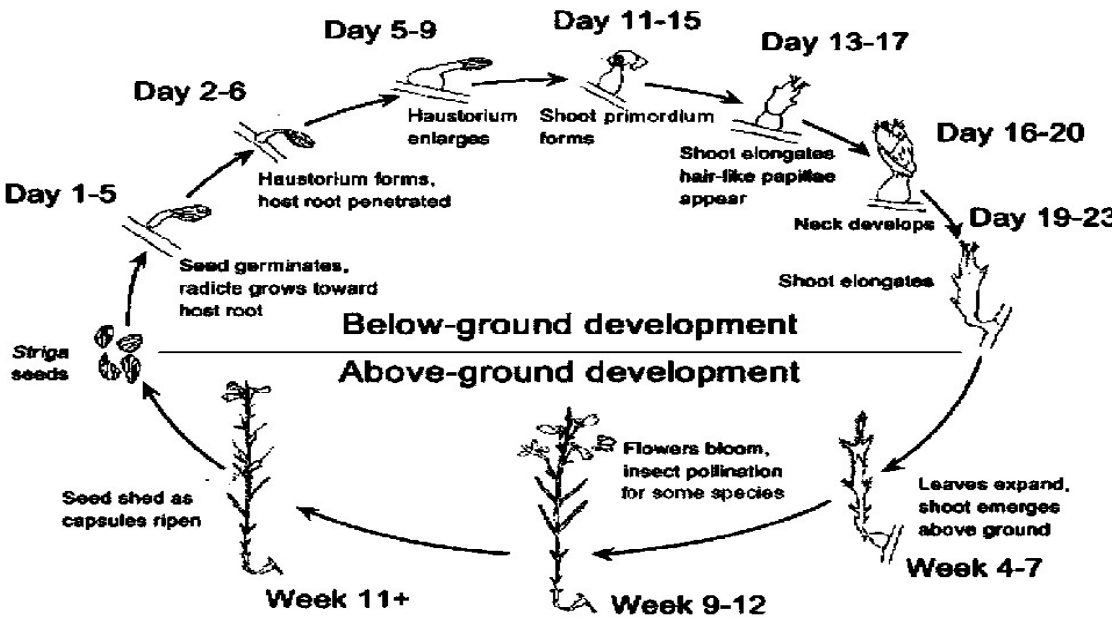
Although some are hemiparasitic (with chlorophyll and the ability to synthesize food through photosynthesis), the majority of *Scrophulariaceae* members are holoparasitic (obtain nutrients from their host) (Matusova *et al.,* 2005). Chlorophyll is present, but it is obscured by other colors. The plants resemble *Orobanche* species in color, being white or reddish. According to Matusova *et al.* (2005), due to aerial photosynthetic activity that occurs after *Striga* emerges from the soil, Hemiparasites include the 13 *Orobanchaceae*

species of *Striga*. By the time these parasitic weeds emerge to be noticed, the crop has already been ruined by their underfoot attacks on their hosts. Their destructive nature may have given them the Latin moniker "*Striga*," which means "hag" or "witch." Hosts are "bewitched" in this way because the farmer is ignorant of the parasites until they appear. Meanwhile, only *S. gesnerioides* infects broadleaf hosts, posing a threat to dicotyledonous species, especially cowpea (Berner & Williams, 1998).

2.13.0 The life cycle and biology of *Striga gesnerioides*

Striga gesnerioides has a life cycle that includes a sequence of growth phases that correspond to the host plant's developmental stages (Lane & Bailey, 1992). There are molecular cues that establish a tight link between *Striga's* life cycle and that of its hosts (Matusova *et al*., 2005). *Striga* seeds require 6 to 7 months of post-harvest before they can finish their physiological phase (Thalouran & Fer, 1993). When it is either below or above 25 or 35 degrees Celsius, the seeds remain dormant (Kuiper *et al*., 1996). *Striga* seed germination is best at temperatures between 30 and 35 degrees Celsius in a wet environment. Before the seeds can germinate, they must be imbibed for 10 to 21 days (Okonkwo, 1991; Lane & Bailey, 1992). *Striga* seed germination is aided by *strigolactones*, which are signaling molecules found in the exudates of the host root. The roots of the host encourage the seeds to grow, according to Lane & Bailey, (1992) and Matusova *et al*., 2005). The *haustorium* is formed during germination by separating the reticular apex. The parasitic weed successfully develops a vascular link, allowing it to access water and nutrients necessary so that it can develop (Dubé & Olivier, 2001). *Striga* radical, nevertheless, cannot endure for longer than seven days, if it does not establish a bond with

the host because seeds' tiny size limits the amount of nutrients they can contain, according to Berner & Williams (1998). *Striga* seeds weigh between 4 and 7 g and have smaller sizes (between 0.20 mm and 0.35 mm), making them incredibly tiny (nano sized). (Dubé & Olivier, 2001). The seeds' nature, on the other hand, makes them easy to spread by animal vectors via water, wind, and soil. Human interaction, as well as technology, tools, and clothes, are the principal sources of seed dissemination (Mohamed *et al*., 2001). *Striga* lowers crop plant growth and significantly affects crop plant architecture as a result of its connection with the crop plant.



Source: Aggarwal *et al*., 1988

Figure 4.4 *:* A diagrammatic representation of *Striga gesnerioides'* life cycle

2.13.1 Measures to control *Striga gesnerioides*

Striga management is time-consuming because a large portion of its life cycle occurs underground. Before seedlings break through the soil, the germination and development of *striga* seeds cannot be seen. It occurs prior to the point at which crop infestation begins to show off (www.wyoug.nsw.gov.au/environment/weeks). Managing pest with chemical methods is expensive for peasant farms, whereas cultural measures provide fundamentally long-term benefits. In accordance with Berner & Williams (1998) and Berner *et al.* (1997), causing suicidal germination with the use of germination stimulants for *Striga* seeds can be an efficient technique of managing the parasitic plant. Meanwhile, the cost of these techniques is exorbitant for Sub-Saharan African smallholder farmers. *Striga* seed stock in the soil can also be reduced by trapping it. It has been observed that a sorghum bicolor variation known as *Bagauda Farafara* is one of the most effective germination stimulants for *S. gesnerioides* (Berner & Williams, 1998). According to several studies, delaying black-eyed pea planting helps lessen the severity of the *Striga* infection as reported by Lagoke and others (1991), and Toure and others (1997). However, Parker (1990) suggested that the most successful strategy for small-scale farmers to control *Striga gesnerioides* is to use resistant genotypes. Infestation with *S. gesnerioides* was also found to reduce the rate of nitrogen fixation (Alonge *et al*., 2004).

2.14 Socio-economic constraints

Non-availability of market preferred varieties, low yield potential, high cost of farmland preparation, lack of improved production and harvesting tools, high cost and absence of labor, high cost and adulteration of pesticides, poor harvest prices, and underdeveloped

marketing channels are some of the socio-economic constraints affecting cowpea production in Sub-Saharan Africa listed by Horn *et al*. (2015) and *Ibro et al*. (2014).

2.15. Plant resistance mechanisms

2.15.1 Antibiosis

A biological process known as an antibiosis explains how the nature of an organism that has inhabited a resistant crop is altered. Antibiosis effects can be induced by chemical and morphological plant defenses. Antibiosis resistance has a range of consequences, from minor impacts that affect fertility, development time, and body size to severe direct effects that result in the organism's mortality (Kogan & Omar, 1978). Antibiosis can be brought on by the presence of dangerous substances, a deficiency in essential nutrients, or an imbalance in an organism’s diet.

2.15.2 Antixenosis

A defense mechanism used (often by a plant) to stop or discourage pest infestation is known as antixenosis. The resistance mechanism can be morphological (e.g., leaf hairs, surface wax, tissue thickness), chemical (e.g., repellants), or antifeedant in nature. The insects' non-preference for refuge, oviposition, and eating is caused by host plant resistance. It refers to the presence of morphological or chemical factors that change the behavior of insects or pests, resulting in poor insect or parasite establishment. According to Kogan and Omar (1978), plants with such resistance mechanisms are less likely to be infested by insects than vulnerable ones.

2.15.3 Tolerance

Tolerance involves a plant's ability to withstand stress (disease, infection, or physiological challenge) while sustaining a degree of loss that is below the economically feasible level (a degree of loss that doesn't limit the product's potential). Plant vitality, regrowth of injured tissue, and the production of extra branches to compensate for the loss are all thought to be factors.

2.16 Genetics of *Striga gesnerioides* Resistance in Cowpea

Striga gesnerioides has been classified into seven distinct races (Lane *et al*., 1996; Botanga & Timko, 2006). Except for some regional races, which appear to have a unique gene that makes them hostile to some particular *Striga* races (Timko *et al*., 2007), many cowpea species are susceptible to *Striga* infestation (Aggarwal *et al*., 1984; Toure *et al*., 1997). The symbols such as Rsg1, Rsg2, Rsg3, and Rsg4 are often used to represent *Striga generioides* resistance genes. Some cowpea resistance to *S. gesnerioides* race-SG1, race-SG2, race-SG3, and race-SG4 is monogenic, according to early investigations (Touré *et al*., 1997, Atokple *et al*., 1993; Moore *et al*., 1995). A recessive gene controls the growth of *S. hermonthica* and *S. asiatica* (Touré *et al*., 1997). Singh & Emechebe (1990b) and Singh *et al*. (1997) assert that a single dominant gene, Rsg, and two duplicate dominant genes, Rav1 and Rav2, control the cowpea genotype B301's resistance to *Striga and Alectra*.

2.17 Cowpea seed sizes

The features of cowpea seeds are extremely crucial to African farmers and consumers as well as to the global community. Farmers search for a variety of features in cowpeas, including overall form, seed coat color, and seed size, in order to achieve effective commercial production. The cowpea seed size is arguably the most crucial of these three factors for both consumers and farmers (both commercial and subsistence). Seed size which ranges from medium to large, is critical for commercial production of the crop in Ghana. Seed size has a number of agronomic implications. When large cowpea seed is planted deeply, there is improved emergence (up to 5 cm) causing the seed to germinate more quickly and during the early stages of development, bigger plants are produced (Lush & Wien, 1980).

Seed size is a characteristic of several crops, such as wheat (Giura & Saulescu, 1996), soybean (Cober *et al*., 1997), cowpea (Drabo *et al*., 1984), and mung bean (Drabo *et al*., 1984), and is largely stable and heritable (Fery, 1980). In cowpea, several genes are known to regulate seed quality including size inheritance. Two significant, unconnected genomic areas were found by Fatokun *et al.* (1992), among which has an orthologous QTL for the size of a mung bean seed. The quantitative inheritance of seed size may be influenced by at least eight loci (Drabo *et al*.1984). Furthermore, according to Fatokun *et al*. (1984), at least eight loci may have an impact on the quantitative transmission of grain size. Seed size is frequently compromised when novel features from several collections are introduced into progeny. Because grain size has such a high market value, regaining proper grain size after elite exotic crosses is a critical goal.

2.18 Heritability of seed size in Cowpeas

Heritability of seed traits, especially size in cowpea plants is controlled by some number of genes, or quantitative trait loci, and has a substantial impact on grain yield (Xian-Jun *et al*., 2007). Floral induction is the first step in seed development, and it is influenced by a variety of elements such as the plant's age, environmental circumstances, and dry matter accumulation, among others. According to *Li et al*. (2008), genes may also influence the final seed size. These genes limit the length of time that cells can proliferate, determining the seed's maximum size. Different authors and for different crops have reported a number of genes that influence seed size. Some authors, however, use the terms "seed weight" and "seed size" interchangeably. For different crops, there may be differences in seed size inheritance. Cowpea has eight genes that affect seed size, according to Drabo *et al.* (1984), and five, according to Lopez *et al*. (2003). Nonetheless, several authors have reported controlling the trait using six, ten, and other numbers of genes as reported by Aryeetey and Laing in 1973, and Lopes and others in 2003).

2.19 Molecular markers and cowpea breeding

Traditional selection makes extensive use of phenotypic variation. Yet, environmental factors swiftly affect morphological markers, which can possibly lead to epistasis, according to Meglic and Staub (1996). DNA molecular markers are made from individual nucleotide sequence changes, which provide a precise depiction of genetic variations at the DNA level. This technique makes use of technologies like single nucleotide polymorphisms (SNP), restriction fragment length polymorphisms (RFLP), amplified fragment length

polymorphisms (AFLP), single sequence repeats (SSR), random amplified polymorphic DNA (RAPD), and others. The simple sequence repeat (SSR) and single nucleotide polymorphism (SNP) markers are now the two most reliable marker systems commonly used in cowpea breeding.

2.20 Genetic Markers

Molecular markers have made it possible to identify variance (due to a change in the DNA site). According to Xu (2010), molecular markers employed in plant breeding fall into two categories, DNA markers and Mendelian markers. Morphological, cytological, and biochemical components are all included in Mendelian (classical) markers. As a result, various DNA markers, such as RFLP, AFLP, RAPD, SSR, and SNP, have evolved into a variety of techniques, according to Collard *et al*., (2005). These morphological markers indicate genetic diversity that is easily detected and controlled. They are frequently used in this way to create phylogenetic trees of organisms. DNA sequences can be utilized as alternative selection criteria to enhance breeding because they are connected to other agronomic traits (Xu, 2010). Karyotype and bands are cell-based markers that can be used to see chromosomal architecture (Xu, 2010). These chromosomal features are used not only to distinguish between normal and mutation analysis, but also for linkage group detection and physical mapping. Protein markers and biochemical markers are two categories of molecular markers. The latter, on the other hand, are frequently mistaken for DNA markers. Isozymes are auxiliary or optional forms of a molecule that follows the same metabolic pathway while having varied molecular weights and electrophoretic mobilities.

2.21 Simple Sequence Repeat (SSR) markers

SSRs are PCR-based markers that are also known as short tandem repeats (STRs) or microsatellites. They're random tandem repeats (2–6 bp/nucleotide length) with short nucleotide patterns. Plant and animal genomes include large amounts of di-, tri-, and tetra-nucleotide repeats such as (GT), (AAT), and (GATA). Different species have different numbers of duplicates in these repeats, which can cause diversity in plants. PCR primers created particularly for these loci are employed because the DNA sequences surrounding microsatellite sites are typically conserved (Song *et al*., 2010). Microsatellite loci, which are utilized as molecular markers, are special in that they have a great deal of allelic variability. In order to enhance the number of SSR alleles by PCR, special primers can be created using the unique sequences surrounding SSR motifs as a guide.

2.22 Heritability

Heritability, which ranges from 0% to 100%, measures the degree to which progeny share a particular trait with their parents. Heritability is a measurement of how strongly an individual's phenotypic traits (performance) and genotypic traits (breeding value) are linked. Breeding value is determined by the combination of the cumulative effects of alleles at the loci. When choosing parents for the future generation, heritability informs how much reliance to put on the performance of the phenotype (Provine, 2001). Heritability is a key factor in predicting genetic advancement as a result of genetic enhancement through selection. As a result, the percentage of observed variation that may be attributable to genetics is known as heritability. There are two kinds of heritability: broad and limited sense heritability. In its broadest meaning, the total genetic influences are what is referred

to as heritability, according to Wray and Visscher, (2008). The entire genetic variance is expressed as a percentage and is not broken down into its constituent parts. Heritability is a poor indicator of potential genetic advancement or breeding success in the broadest sense. The population under consideration will determine its usefulness.

On the other hand, narrow sense heritability relates to the proportion of genetic variance caused by additive gene action. Narrow sense heritability is always less than or equal to broad sense heritability because broad sense heritability includes all genetic influences whereas narrow sense heritability only contains additive effects. The utility of broad versus narrow sense heritability is determined by the population's generation and reproductive system. Because only additive gene action can generally be transferred to children, broad-sense heredity is less advantageous than narrow-sense heredity (Wray and Visscher, 2008). But as the early generations combine features from both parental plants, both desirable and unattractive qualities may be inherited. In order to minimize the selection of undesired features, a breeder must evaluate all the progeny and choose lines with the desired characteristics. Next, in an effort to transfer more of its desirable traits into the subsequent generations, he crosses the chosen offspring back to one of the initial parent plants. Back-crossing is the word for this process, which typically takes several years until the offspring have all the desired characteristics and none of the undesirable ones of the parental ones.

2.23 Restrictions on Traditional Breeding

In conventional breeding methods, 1,000 genes are passed on in every crossover, some of which might be advantageous in addition to the target species' desired genes. Barriers to gene transfer caused by incompatibility are another fundamental constraint of traditional breeding. However, perfect alleles with a minor impact, especially for highly complex attributes, have often remained hidden, making it impossible to use them for genetic improvement. This is despite the fact that trait selection has often been effective in finding genes that have a substantial effect on the phenotype, according to Morgante and Salamini (2003). As a result, the masking effect of the environment may reduce selection efficiency, resulting in the loss of important alleles during the selection process. For several important crops, the rate of genetic yield gain that was tested during the twentieth century may be hard to sustain if just current conventional breeding techniques are applied (Araus *et al*., 2008).

CHAPTER THREE

MATERIALS AND METHODOLOGY

3.1 Experimental Materials and the Study Location

The CSIR-SARI Manga Station's fields, which are located between Latitude 11° -01° N and Longitude 00° -16° W, were the site of the experiment. It is elevated at 249 m above sea level with an average rainfall of 800 mm-1000 mm (Sarpong, 2001). Mainly, the soil type is sandy and sandy-loamy with low organic matter content, low pH and low fertility. Hence the place often experiences erosion when there is a heavy down pour.

3.2 Parental sources of the 20 genotypes

The twenty (20) genotypes were developed from the following two separate bi-parental crosses:

Cross I: Solid Black X Black Eye

Cross II: Solid Red X Dark Mottled.

As a result of the above crosses, the twenty (20) genotypes were selected based on their seed characteristics (especially seed color and seed size). An aspect of the description of these parental seeds is shown in Table

Table 5 : Description of planting materials

Description	Parents			
	Solid Black	Black Eye	Solid Red	Dark Mottled
Seed coat pattern	Solid	Eyed	Solid	Mottled
Seed coat color	Black	White	Red	Dark with grey background
Seed size	Relatively large	Relatively small	Relatively large	Relatively small

3.2 Experimental design and cultural practices

The material was evaluated using augmented design (Federrer, 1956). The design consisted of 4 blocks containing 8 genotypes in each with 5 entries and 3 check entries. The total field area was 114.24 meters square. Each genotype was represented by a plot size of 2.26 x 1.58-meter dimensions with three lines. The plants were spaced planted by using a planting distance of 20 x 60 centimeters dimensions for optimal expression of traits. Data was collected from five (5) randomly selected plants within the inner rows of each plot on various morphological, maturity, yield and yield contributing traits. In each block, the checks were allotted randomly. Off-type plants were detected and uprooted through critical assessment of the seedlings. Since the study was conducted under irrigation between October and December 2020, every morning and evening, or as needed, the soil was regularly watered to keep it moist.

3.3 Field evaluation

Based on the detailed "descriptors of Cowpea" provided by Biodiversity International, data was gathered on the plants in the inner rows of each plot.

3.3.1 Parameters measured

Eighteen (18) parameters were determined. These are:

Days to first flower initiation: Number of days between sowing and the first flower development for each genotype.

Days to 50% flowering: This was recorded as the number of days between sowing to when half of genotypes had flowered.

Days to first maturity: This was recorded as number of days between sowing and the first pod development.

Days to 90% maturity: This was calculated as the number of days between sowing and the maturity of 90% of the genotypes.

Canopy size (cm): This was measured with a ruler, as the proportion of fixed area of ground covered by the upper part of plant.

Plant height (cm): Plant height was taken as the perpendicular height of the plant from the top soil level to the end of the top most leaf of the plant using a tape measure.

Leaf width (cm): A ruler was used to measure the broad part of the leaf blade, starting from one point to the other.

Leaf length (cm): A ruler was used to determine the length of each leaf from its pointed tip at one end to its junction with the stalk at the other.

Number of pods per plant: The total harvestable pod per individual plant were counted after harvest.

Number of pods per peduncle: The number of pods developed by the individual tagged or selected plant from each genotype was counted and then averaged.

Mean number of seeds per pod: Five (5) pods were randomly selected and the number of seeds each pod contained was counted. The mean number was then estimated by dividing sum of their seed numbers by 5.

Seed length (cm): This was determined by using a caliper.

Seed width (cm): This was determined by using a caliper.

Seed thickness (cm): This was determined by using a caliper.

Hundred seed weight (g): From each genotype's individual plant, 100 seeds were chosen at random and its weight was measured.

Total seed weight (g): The total grains obtained from individual plants of each genotype were weighed.

Grain yield (kg/ha): The total seed weight was used to estimate tones of the grain per hectare

3.4 Molecular Analysis

Young leaf of a plant from each genotype was harvested and placed in a silica gel for genomic DNA extraction using the CTAB protocol in the biotechnology laboratory of SARI, Nyankpala station.

3.4.1 DNA Extraction

The young leaf-samples were preserved in an incubator after mixing with silica gel for about three days. Then about 20 mg of each sample was ground in 2.0 ml micro tubes into fine powder using metal beads. This was followed by the addition of 800 µl of 2% CTAB with 0.1% of mercaptoethanol and the mixture was incubated in a sand bath at 65ºC for 30 minutes with intermittent vortexing. The sample was cooled and equal volume (800 µl) of chloroform isoamyl alcohol (24:1) was then added. The tubes were inverted to ensure appropriate mixing before subjecting them to centrifugation at 14000 rpm for 15 minutes. Afterwards, aqueous phase of the resulting components was transferred into clean 1.5 ml tubes. Nucleic acid was precipitated by adding 400 µl of ice-cold isopropyl alcohol and shaken gently. The mixture was stored at -20ºC for overnight and centrifuged at 14000 rpm for 5 minutes to pellet nucleic acids. After decanting the isopropyl alcohol, the particle was washed with 400 liters of 80% ethanol and then centrifuged at 6000 rpm for 4 minutes. The ethanol was decanted, and the pellets of nucleic acid were left to dry. RNase was now added to digest and remove any RNA components. The resulting DNA components were transferred into new 1.5 ml tubes and mixed with a loading dye. This mixture was subjected to a PCR machine for amplification. The quality of the DNA isolated from the samples was then evaluated using 0.8% (w/v) agarose gel electrophoresis.

3.4.2 Polymerase Chain Reaction

Materials used for the polymerase chain reaction include; a master mix = 5 µl, Nuclease free H_2O =3 µl, DNA = 1 µl and primer = 1 µl. The Thermocycler used had the following conditions: denaturation at 94 degrees Celsius for 30 seconds, followed by 35 cycles of

denaturation, annealing, and extension at 59 degrees Celsius for 30 seconds each. Using a horizontal gel electrophoresis device and polyacrylamide gel in 1 x TAE buffer, the PCR products were resolved at 120 V for three hours. Ethidium bromide staining was used to color the gels, viewed on a CHROMATO-VUE using a Trans-illuminator and photo-documented. The DNA molecular weight size marker employed contained 50-bp.

3.4.3 Markers for Simple Sequence Repeats (SSRs)

A microsatellite marker (SSR), which has been linked to cowpea resistance to *S. gesnerioides*, was employed. These markers are highly polymorphic and widely distributed throughout the genome. They only need a minimal amount of genomic DNA and have easy interpretation when used in genotyping. Precisely, the SSR marker used for this experiment was SSR-1.

Table 6 : Description of SSR marker for Striga resistance

Marker	**Primer sequences**			
	Forward sequence (5'–3')	**Reverse sequence (5–3')**	**Anealing temperature**	***Striga* race specificty**
SSR-1	CCTAAGCTTTTCTCCAACTCCA	CAAGAAGGAGGCGAAGACTG	57.7°C	Linked-SG3

Source: Li and Timko, 2009

3.4.4 Agarose Gel Electrophoresis Band Scoring

The EOS REBEL T2i Utility was used to score the bands on the agarose gel. The Deoxy ribonucleic Acids' materials obtained from the test genotypes and checks were added to each gel along with a 50-bp DNA ladder as a molecular weight size marker. Those that

matched the marker's product size were rated as present (+), whereas those that fell below or over the marker's molecular weight or had no discernible DNA band were marked as absent (-).

3.5 Pot experiment for confirmation of resistance to *Striga gesnerioides*

A pot experiment was conducted to confirm whether there was no *Striga* attachment to roots of genotypes found without *Striga* emergence during the field experiment. Eight (8) pots were artificially infested with about five grams (5 g) of *Striga* seeds. Three holes were made in each pot and two seeds sown in each hole making six seeds per pot. Two weeks later, the plants were thinned to three plants per pot.

3.6 Data analysis

Data was taken based on nine quantitative traits related to seed yield namely, days to flowering, days to maturity, plant height canopy size, number of pods per plant, pod length, seed per pod, hundred seed weight and seed yield per plant. Using R studio (version 4.03; 2020-10-10), these data were put through an analysis of variance (ANOVA). The Least Significant Difference (LSD) test was used to compare the variance means at a 5% level of confidence. The adjusted treatment means of the various parameters from the statistics were used to construct tables.

CHAPTER FOUR

RESULTS

4.1 Response of cowpea genotypes to *Striga gesnerioides* in the field

The results of the experiment on the Recombinant Inbred Lines (RILs) of advanced cowpea genotypes are presented in Table 10. Only one (1) out of the 20 Recombinant Inbred Lines was resistant to the parasitic weed, *S. gesnerioides.* All susceptible genotypes had emergence (or attachment) of *Striga* plantlets from the soil. The symptoms expressed by these susceptible genotypes are; stunted growth, leaf necrosis, defoliation and reduced size of young leaves and senescence.

Figure 4.5 : *Striga* attachment to roots of a susceptible host cowpea genotype

Table 7 : Reaction of cowpea RILs based on molecular screening and field trials

Genotypes(checks/RILs)	Genotypic Reaction (molecular screening)	Phenotypic Reaction (field screening)
Apagbala	+	S
KT benga	-	R
UG-01	+	S
UG-02	+	S
UG-03	+	S
UG-04	+	S
UG-05	+	S
UG-06	+	S
UG-07	+	S
UG-08	+	S
UG-09	+	S
UG-10	+	S
UG-11	+	S
UG-12	+	S
UG-13	+	S
UG-14	-	R
UG-15	+	S
UG-16	+	S
UG-17	+	S
UG-18	+	S
UG-19	+	S
UG-20	+	S
Wang Kae	-	R

R: Resistant, **S**: Susceptible, **+**: Present, **-**: Absent

4.2 Response of *Striga* Promising Lines to Artificial *Striga gesnerioides* in a Pot Experiment

A pot experiment was conducted in order to ascertain whether the cowpea RIL (UG-14) which emerged to be *Striga* resistant during the field trial truly carry this feature **(Figure 4.6).** However, the result of this pot experiment confirmed that the genotype was resistant (no *Striga* emergence or *Striga* attachment) to *Striga.*

Figure 4.6 : No *Striga* emergence upon artificial inoculation

4.3 Grain quality attributes

Aside yield, grain quality is one of the most preferred traits by farmers, processors and even consumers. In this study, three (3) main grain qualities were considered which are; seed color, seed texture and seed size. Seed texture and seed size were sharply categorized into two (rough/smooth and large/small) whiles seed color was grouped into five (5) categories (white/cream, red, mottled, mixture and holstein).

The white/cream seed-coat was the dominant color which represented 55% of the total seeds obtained. The red color represented 25% of the total seeds while 10% were multi-colored (mixture of seeds with different colors) **(Figure 4.7).** However, a few of the grains were mottled (5%) and holstein (5%). Also, 75% of the grains had smooth texture while 25% of them had rough texture **(Figure 4.8).** Again, higher percentage (80%) of the grains exhibited small seed size whiles few percentage (20) had small seed sizes **(Figure 4.9).**

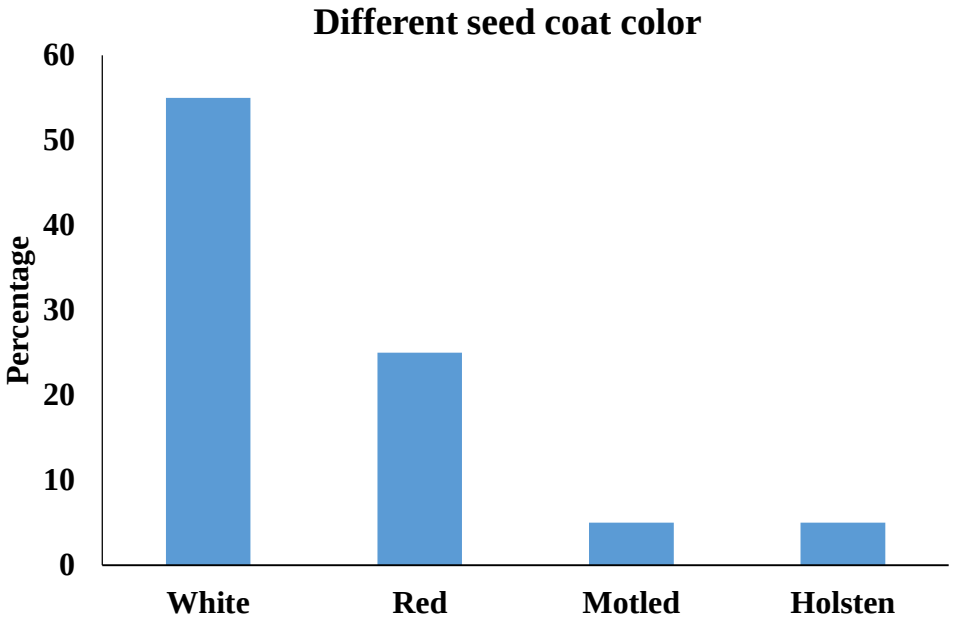


Figure 4.7 : Seed coat colors recorded for the progeny genotypes

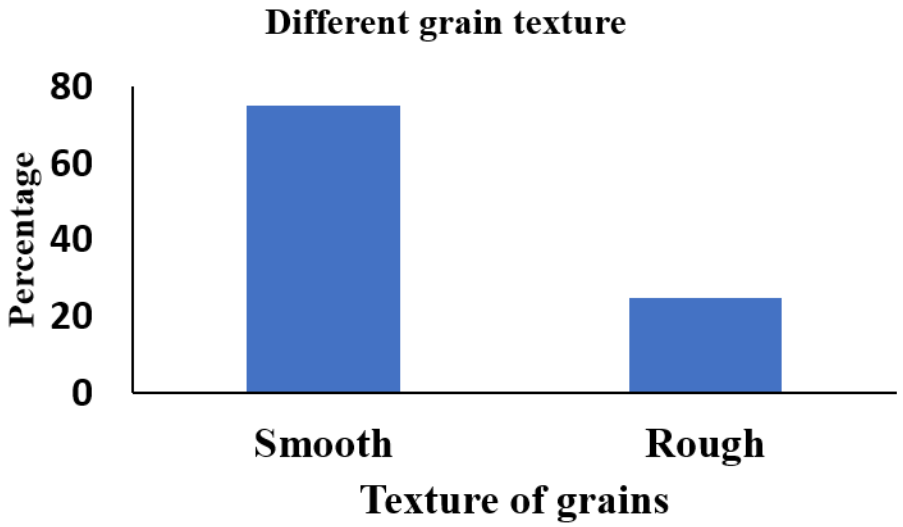


Figure 4.8 *:* Seed textures recorded for the progeny genotypes

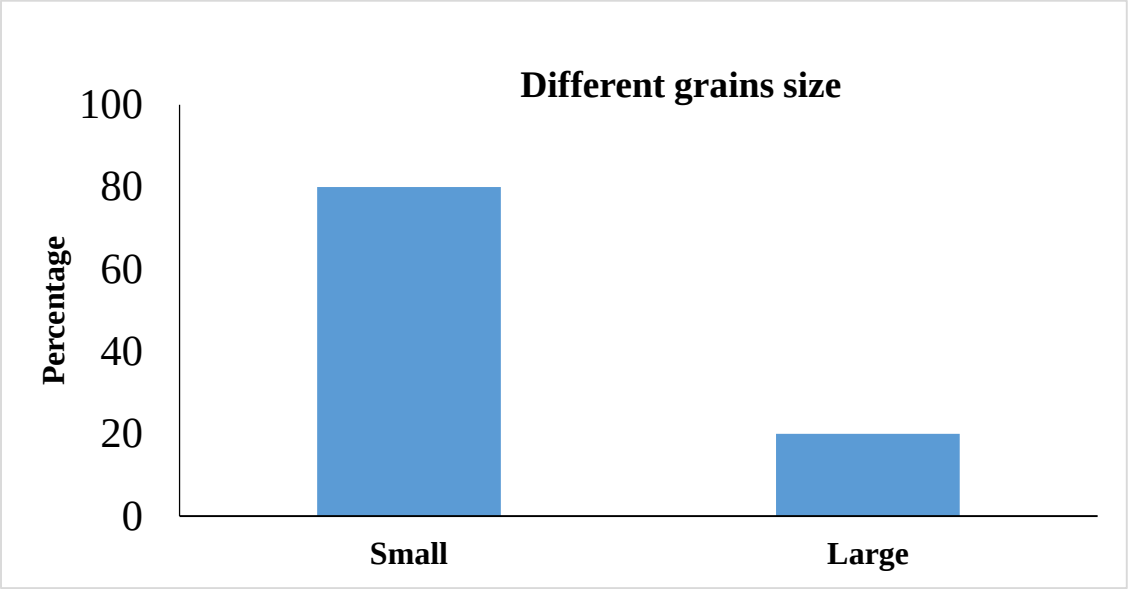


Figure 4.9 : Sizes of grain recorded for the progeny genotypes

4.4 Physiological and Agronomic Traits

4.4.1 Days to flowering and maturity

The analysis of variance revealed a significant mean sum of squares for flowering and maturity with respect to different sources of variation. The Block (unadjusted) effect and Treatment effects (adjusted and unadjusted) were significant for days to flowering and maturity. Similarly, the effects due to checks and check v/s varieties were significant.

The mean number of days to flower initiation varied between 32 and 40 days whiles average number of days to 50% flowering ranged from 35 to 47 days (**Table 8**). The days to maturity ranged between 51 and 66 days. The genotypes UG-12, UG-08 and UG-20 took the lowest mean period to initiate flowering and also attain 50% flowering. Whereas UG-14 and UG-19 recorded the highest mean number of days for first flowering and to gain 50% flowering. Similarly, the genotypes UG-20 and UG-08 attained 90% maturity earliest than all the test treatments with an average of 64 days. While, the genotype UG-14 recorded the maximum

number of days for 90% maturity with an average of 66 days. Most of the test treatments respectively performed far better than all the checks used with regards to days to flowering and days to maturity. The checks (Apagbala and KT benga) for these traits flowered and matured within the ranges of 40.5-67 days and 40.5-71 days.

Table 8 : Mean number of days to flowering and days to maturity

Genotypes (checks/RIs)	Days to 1st flowering	Days to 50% flowering	Days to 1st maturity	Days to 90% Maturity
Apagbala	36	41	58	67
KT benga	36	41	59	71
UG01	36	42	58	68
UG02	37	41	54	68
UG03	34	39	54	67
UG04	39	42	59	69
UG05	34	38	58	71
UG06	36	40	58	71
UG07	36	42	53	71
UG08	33	38	58	64
UG09	35	39	58	65
UG10	35	41	57	71
UG11	37	42	58	67
UG12	33	35	55	67
UG13	34	40	58	67
UG14	40	44	66	76
UG15	36	41	58	70
UG16	35	40	57	67
UG17	39	39	56	72
UG18	37	42	59	71
UG19	43	46	59	69
UG20	32	35	51	64
Wang Kae	40	43	67	74

4.4.2 Plant height and pods per peduncle

The statistical results showed that adjusted treatment effects as well as test entries and checks were significant for plant height (Table 15). Only checks versus varieties as well as checks differed significantly for plant height, whiles all sources of variation had significant effects for canopy size except adjusted block. Similarly, apart from the checks, none of the sources of variation showed significant difference for pods per peduncle.

Plant height ranged from 10.65 cm to 26.2 cm, canopy size varied from 28.20 cm to 97 cm whiles number of pods per peduncle ranged from 3.4 to 14.6 (Table 9). The genotype UG-09 recorded the highest plant height with 26.2 cm whiles Apagbala showed the lowest plant height with 10.65 cm. Also, the genotype UG-08 record the highest value (97 cm) for canopy size and the lowest value (28.20 cm) was found in UG-05. Similarly, UG-20 recorded the maximum pod number on each peduncle with 14.6 whereas the lowest number 3.4 was observed in UG-19.

Table 9 : Mean of plant height and pods per peduncle

Genotypes (checks/RIs)	Plant height (cm)	Canopy size (cm)	Number of peduncle per plant
Apagbala	10.65	34.10	11.25
KT benga	17.75	44.65	8.65
UG01	20.8	57	8.2
UG02	19.8	38.60	6
UG03	18.8	41.60	4.6
UG04	12.4	45.80	7.4
UG05	13.2	28.20	7.8
UG06	18.4	35.80	4
UG07	22.8	38.40	10.8
UG08	21	97	11.4
UG09	26.2	75	7.8
UG10	14.2	35.20	5.6
UG11	18.4	47.40	9.8
UG12	12.6	29.20	7.6
UG13	14.8	37.40	10.2
UG14	17.4	33.80	6.8
UG15	21.6	42.40	4.4
UG16	25.6	40.20	7.4
UG17	22	37	5.2
UG18	23.8	40.80	4.6
UG19	21.4	41.60	3.4
UG20	15	62.20	14.6
Wang Kae	16.35	42.05	6.8

4.4.3 Leaf width and length

There were significant variations for leaf length and leaf width. Adjusted block effects were not significant for leaf length, whiles both (adjusted as well as unadjusted block) effects were not significant for leaf width.

The means of leaf length and leaf width ranged from 6.5 cm to 11.64 cm and 3.82 cm to 6.52 cm, respectively. The maximum values for leaf length and leaf width were recorded for UG-19 and UG-04, respectively, whereas the genotype UG-20 exhibited the lowest values for these traits (Table 10).

Table 10 : Means of Leaf length and leaf width

Genotypes (checks/RILs)	Leaf length (cm)	Leaf width (cm)
Apagbala	7.69	3.57
KT benga	10.57	4.98
UG01	11.34	5.34
UG02	9.16	5.36
UG03	9.52	5.9
UG04	11.2	6.52
UG05	8.48	3.82
UG06	9.82	5.64
UG07	10.37	6.16
UG08	10.98	6.08
UG09	9.7	5.86
UG10	10.68	6
UG11	10.76	5.42
UG12	8.62	5.36
UG13	9.66	5.34
UG14	9.98	5.36
UG15	11.02	6.12
UG16	9.8	5.54
UG17	9.52	5
UG18	10.98	6.24
UG19	11.64	6.28
UG20	6.5	3.82
WangKae	10.59	4.79

4.4.4 Pod per plant, pod length and Seed per pod

The results of analysis of variance revealed that all the sources of variation had significant impacts on the number of pods plant^{-1} (Table 15), except checks v/s varieties. Similarly, all the sources of variation showed significant effects for number of seeds in each pod, except blocks (adjusted as well as unadjusted) and checks. However, only checks differed significantly for pod length.

The number of pods per plant ranged from 4 to 28.8 whiles number of seeds per pod ranged from 7.2 to 14.2 (Table 11). The greatest pods plant $^{-1}$ was found for UG-20 which is 28.8 but the lowest number, 4 was recorded for UG-19. Also, the highest number of seeds per pod, 14.2 was observed in UG-19 whiles the lowest value, 7.2 for this trait was found in UG-10. The average pod length varied from 17 cm to 37.9 cm. The longest pod length was identified in UG-01, and the shortest pod length was discovered in UG-12.

Table 11 : Mean number of pods per plant, length of each pod and number of seed per Pod

Genotypes (checks/RIs)	Pod per plant	Pod length (cm)	Seed per pod
Apagbala	15.5	20.45	9.25
KT benga	12.45	30.48	14
UG01	13.8	37.90	10.8
UG02	9.4	23.10	12.2
UG03	5.8	22.80	9.2
UG04	10	32.80	13.6
UG05	11.2	20.60	9.8
UG06	5.6	25.50	10.4
UG07	15.2	29.60	10
UG08	17.8	25.10	13.6
UG09	11.2	29	13.8
UG10	7	17.10	7.2
UG11	13	31	11.8
UG12	11.2	17	11.8
UG13	13.4	23.80	12
UG14	10.8	35.40	10.8
UG15	5.6	23.60	13.2
UG16	10.6	31.0	13.8
UG17	8.4	28.20	10.2
UG18	5.8	23.60	13.6
UG19	4	24.90	14.2
UG20	28.8	25.60	10.2
WangKae	9.5	27.53	13

4.4.5 Mean of seed length, seed width and seed thickness

The statistical analysis of variance showed variations from different sources for seed thickness, seed length and seed width. For seed thickness all the sources varied significantly except adjusted blocks. Meanwhile, block effects were not significantly different for seed length and seed width.

The means of seed thickness varied from 4.14 cm to 5.7 cm, seed length ranged from 6.46 cm to 9.27 cm whereas seed width differed from 4.77 cm to 6.67 cm as shown in Table 12. The genotype UG-17 which came next to the best check KT benga (5.76 cm) recorded the maximum seed thickness among the test treatments with 5.62 cm, whiles the minimum seed thickness value, 4.14cm was found in UG-19. Similarly, the maximum seed length value (9.27 cm) among the tested genotypes was observed in UG-18 which surpassed only one of the checks, Apagbala (9.8 cm) whereas the minimum seed length value (6.46 cm) was recorded for UG-20. Also, the topmost seed width value (6.67 cm) was found in UG-15 which surpassed the best check, KT benga (6.63 cm).

Table 12 : Mean seed thickness, seed length and seed width

Genotype (checks/RILs)	Seed thickness (cm)	Seed length (cm)	Seed width (cm)
Apa	4.56	9.31	5.84
KT benga	5.76	9.8	6.63
UG-01	5.16	9.8	6.03
UG-02	5.14	7.5	5.91
UG-03	4.46	8.6	6.21
UG-04	4.86	8.38	5.63
UG-05	5.38	9.1	6.51
UG-06	5.24	8.48	6.03
UG-07	5.12	7.14	5.75
UG-08	4.78	8.92	6.47
UG-09	4.54	7.88	6.01
UG-10	5.06	8	5.55
UG-11	4.82	7.76	5.63
UG-12	5.16	8.6	6.01
UG-13	5.58	8	5.97
UG-14	5.34	9.16	6.39
UG-15	5.02	7.86	6.67
UG-16	4.64	7.4	5.85
UG-17	5.62	9.19	6.61
UG-18	4.88	9.27	6.07
UG-19	4.14	7.48	5.65
UG-20	3.6	6.46	4.77
Wangkae	5.49	9.97	6.59

4.4.6 Total pod weight and total seed weight

The analysis of variance revealed that all causes of variation for total pod weight and total seed weight were significantly different, except adjusted blocks and checks versus varieties. Total pod weight ranged from 178 g to 870 g whiles total seed weight varied from 98.2 g to 479.98 g. The highest mean values for total pod weight and total seed weight were recorded for UG-08 followed by UG-20, while UG-06 had the minimum values for the two characters (Table 13).

Table 13 : Means of Total pod weight and total seed weight

Genotypes (checks/RILs)	Pod weight (g)	Total seed weight (g)
Apagbala	375	206.89
KT benga	575.75	317.64
UG01	696	383.98
UG02	431	237.78
UG03	389	214.61
UG04	566	312.26
UG05	651	359.16
UG06	178	98.2
UG07	353	194.75
UG08	870	479.98
UG09	700	386.19
UG10	402	221.78
UG11	661	364.67
UG12	658	363.02
UG13	651	359.16
UG14	533	294.06
UG15	235	129.65
UG16	581	320.54
UG17	479	264.26
UG18	392	216.27
UG19	542	299.02
UG20	861	475.01
WangKae	498.75	275.16

4.4.7 Hundred-seed weight and Grain yield (per hectare)

The ANOVA outputs revealed that every source of variance was substantially different for grain yield and seed weight at 100 seeds (Table 18), except adjusted block which was not significant for 100-seed weight.

The average 100-seed weight differed from 7.8 g to 20.9 g whiles the mean grain yield ranged from 425.64 kg/ha to 1995.68 kg/ha (Table 14). The highest average 100-seed weight among all the treatments was recorded for UG-01 with 20.9 g followed by the two resistant checks, KT benga (20.8 g) and Wang kae (19.5 g). The resistant test genotype, UG-14 (18.6 g) then came next in the rank. However, UG-20 scored the lowest value for 100-seed weight with 7.8 g followed by UG-11 (12 g). In this case only UG-01 performed better than all the checks, although few of the test treatments recorded better 100-seed weight values as compared to the susceptible check, Apagbala (14.4 g). Also, the genotype UG-20 had the maximum grain yield with 1995.68 kg/ha, followed by UG-08 (1828.65 kg/ha) and UG-05 (1758.94 kg/ha). Nonetheless, the minimum grain output was observed in UG-06 which had 425.64 kg/ha.

Table 14 : Mean values of Hundred-seed weight and Grain_yieldha^{-1}

Genotypes (checks/RILs)	Hundred-seed weight (g)	Grain yield (kg/ha)
Apagbala	14.4	862.03
KT benga	19.5	1323.51
UG01	20.9	1492.26
UG02	13.3	883.1
UG03	12.8	722.94
UG04	14.3	1563.53
UG05	17.5	1758.94
UG06	15.5	425.64
UG07	12.1	827.93
UG08	14.1	1828.65
UG09	13.3	1437.86
UG10	13.2	816.43
UG11	12	1411.81
UG12	17.5	1341.32
UG13	13.7	1512.97
UG14	18.6	1241.72
UG15	12.4	802.65
UG16	13	1164.31
UG17	16.8	1363.53
UG18	14.6	793.47
UG19	16.4	1508.36
UG20	7.8	1995.68
Wang Kae	20.8	1146.5

Table 15 : Means of sum of squares for quantitative traits in the 20-cowpea genotype

Source of variation	df	DTFFI	DTFF	DTFM	DTNM	CD	PH	LL	LW	PD/Ped	PD/P	PDL	PDWT	TSWT	S/PD	SL	SW	ST	100SWT	G_YLD/Ha
Blocks (ignoring treatments)	3	25.78*	10.781*	1.2	19.46*	183.37*	10.27	1.31*	0.4	18.077	64.03*	11.9	446852**	221559*	2.875	0.73	0.3	0.11*	2.94	190760
Treatment (eliminating blocks)	22	6.67	6.354*	24.02*	11.85	230.98**	25.18	2.18**	1.056**	8.511	25.42	34.93	392157**	161095*	4.889*	1.34*	0.27	0.38***	15.8***	172355
Checks	2	17.58*	5.333	105.58***	53.58**	120.84*	56.57*	11.16***	2.33**	19.99	36	106.17**	359930*	86547	1.103	0.46	0.80*	1.58***	46.16***	216812
Blocks (eliminating	3	1.64	3.222	0.53	3.64	13.71	1.82	0.21	0.031	9.178	25	4.85	125451	80707	0.91	0.074	0.04	0.052	0.67	110069
Entries (ignoring blocks)	22	9.96	7.385*	24.11*	14.01*	254.11**	26.33	2.33**	1.11**	9.725	30.74*	35.89	435985**	180302**	5.16*	1.43*	0.30*	0.39***	16.11***	183358
Varieties	19	9.31	7.839*	9.22	8.72	271.79**	17.92	1.47*	0.59*	8.244	30.86*	30.36	465596**	197687**	3.57	0.78*	0.21	0.24**	8.29**	182402
Checks v/s varieties	1	7.25	2.852	144.1	35.21*	184.76*	125.67**	1.042	8.48***	17.328	18.1	27.81	25472	37483	43.44**	15.66***	0.99*	0.87***	104.63**	167909
Residual	6	3.14	1.556	3.69	3.14	19.38	8.45	0.21	0.092	5.714	7.01	9.67	40467	23971	1.24	0.194	0.078	0.015	0.78	68761

4.5 Genetic variability

The coefficient of variation (CV) ranged from 2.42 to 30.7%. The maximum CV was recorded for Pod per peduncle and the lowest CV was recorded for Seed thickness. In every characteristic examined, phenotypic variance (PV) exceeded genotypic variation (GV). In line with this, for every characteristic examined, the phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV). The PCV percentages were between 4.28% and 53.08% while values for GCV ranged from 3.42% to 50.72%. The highest PCV and GCV values were recorded for seed weight whereas their lowest value was found in days to 90% maturity. Furthermore, the maximum coefficient of variation due to the environment, ECV (31.54) was estimated for Pod on each peduncle whiles the lowest ECV (2.57) was recorded for Days to 90% maturity. The biggest genetic advance, or GA (1285.33), was found in seed weight, while the lowest GA (0.61) was found in seed width. The highest genetic advance as percentage of mean i.e. GAM (99.98) was recorded for Seed weight whiles the lowest GAM (5.65) was recorded for Days to 90% Maturity.

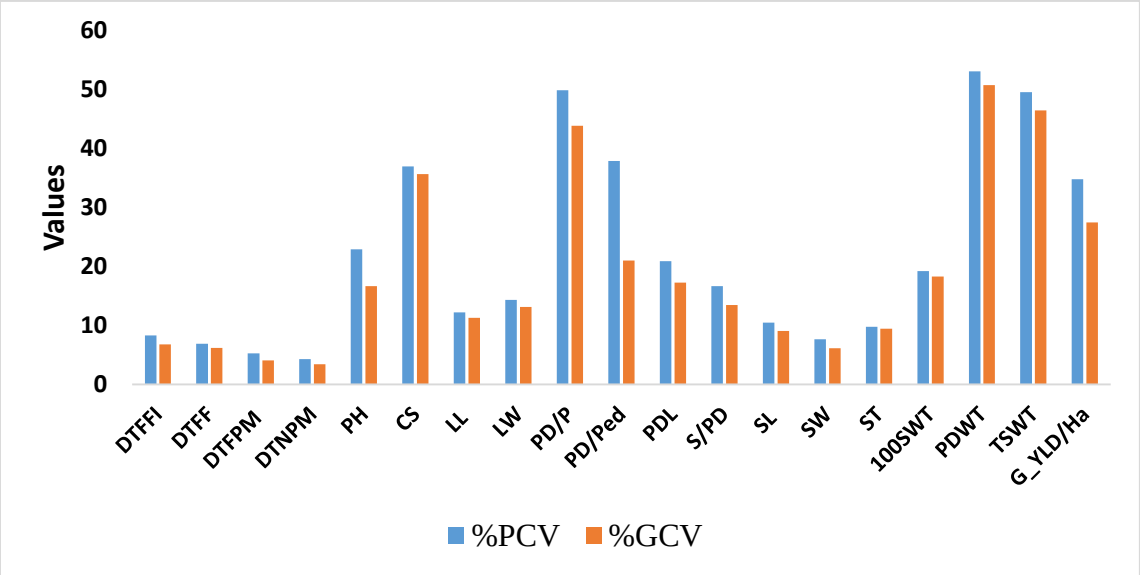


Figure 4.10 : Genotypic coefficient of variation and phenotypic coefficient of variation

4.6 Broad sense heritability (H ^{2}bs) of the cowpea traits

The broad sense heritability estimates of attributes for the genotypes is shown in Fig. 11 below. For the eighteen (18) attributes, the broad sense heritability calculated as percentages was between 30.68 and 93.62%. (Fig. 4.7). According to Singh (2001), there are four levels of heritability: low (40%), medium (40-59%), high (60-79%) and extremely high (80%). Among the traits studied, seed thickness exhibited the highest broad sense heritability (93.62%) whiles Pod per peduncle recorded the least broad sense heritability (30.68 %).

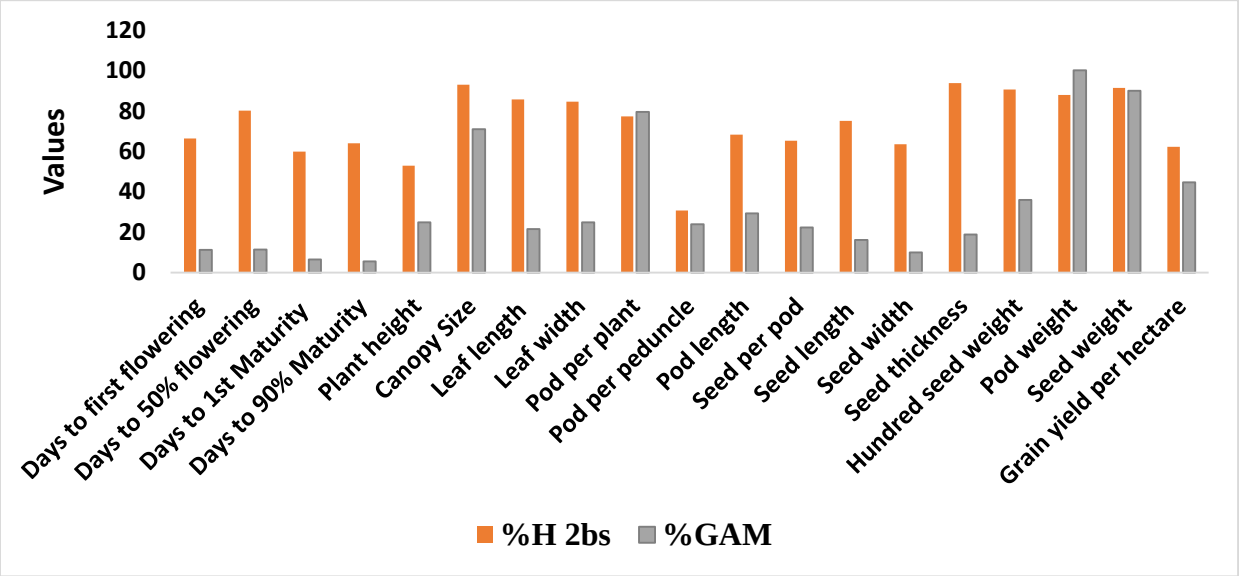


Figure 4.11 : Heritability (Broad sense) and Genetic advance as percent of the mean for traits

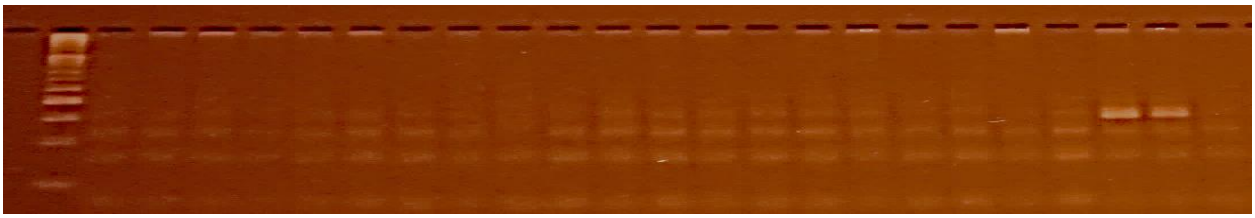
Table 16 : Mean, variability and genetic parameters for the quantitative characters

Parameter	Mean	%CV	PV	%PCV	GV	%GCV	EV	%ECV	GA	%GAM	%H 2bs
DTFFI	36.73	4.79	9.31	8.31	6.17	6.76	3.14	4.82	4.17	11.35	66.26
DTFF	40.63	3.06	7.84	6.89	6.28	6.17	1.56	3.07	4.63	11.4	80.16
DTFPM	57.77	3.27	9.22	5.26	5.53	4.07	3.69	3.33	3.75	6.5	59.93
DTNPM	69.03	2.55	8.72	4.28	5.58	3.42	3.14	2.57	3.9	5.65	64.02
PH	18.48	16.64	17.92	22.91	9.46	16.65	8.45	15.74	4.61	24.97	52.82
CS	44.58	10.15	271.79	36.98	252.41	35.64	19.38	9.87	31.59	70.85	92.87
LL	9.94	4.66	1.47	12.21	1.26	11.3	0.21	4.62	2.14	21.58	85.69
LW	5.37	5.92	0.59	14.3	0.5	13.14	0.09	5.64	1.34	24.92	84.46
PD/P	11.13	23	30.86	49.9	23.84	43.86	7.01	23.79	8.86	79.54	77.27
PD/Ped	7.59	30.07	8.24	37.89	2.53	20.99	5.71	31.54	1.82	23.98	30.68
PDL	5.37	11.82	30.36	20.91	0.5	17.27	0.09	11.8	7.75	29.41	68.16
S/PD	11.33	10.38	3.57	16.68	2.33	13.47	1.24	9.84	2.54	22.44	65.22
SL	8.43	5.02	0.78	10.47	0.59	9.07	0.19	5.23	1.37	16.21	75.07
SW	6.03	4.57	0.21	7.67	0.14	6.12	0.08	4.64	0.61	10.06	63.51
ST	4.97	2.42	0.24	9.75	0.22	9.44	0.02	2.46	0.94	18.84	93.62
100SWT	14.98	5.56	8.29	19.23	7.51	18.3	0.78	5.9	5.38	35.92	90.57
PDWT	1285.54	15.82	465597	53.08	425129	50.72	40467.1	15.65	1285.33	99.98	87.87
TSWT	897.24	17.6	197687	49.55	173716	46.45	23971.4	17.26	806.03	89.83	91.31
G_YLD/Ha	1227.18	21.95	182402	34.8	113641	27.47	68760.7	21.37	548.93	44.7	62.3

4.7 *Striga gesnerioides*-related SSR Markers in cowpea genotypes

SSR-1 markers successfully separated the various genotypes of cowpeas into Striga-resistant and susceptible cowpeas by segregating with the *Striga*-resistant allele(s). However, one resistant genotype (UG-14) could not be recognized by the SSR-1 markers. Any one of the markers indicated the presence of the *Striga* resistance allele in a cowpea (s). A marker's presence (+) indicates resistance, whereas its absence (-) indicates vulnerability. The marker's resolution on polyacrylamide gel across the cowpea genome is illustrated in Figure 4.12.

L 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 WK KT AP



L: 50 bp ladder, 1-20: UG-1 to UG-20.

Figure 4.12 : Results from molecular analysis. All samples of UG-1 to UG-20 do not have the striga resistant band. The checks WK and KT benga have the band.

CHAPTER FIVE

5.0 DISCUSSION

5.1 Differences in field screening and laboratory screening results for *Striga* resistance

In this study, the field screening projected results which contradicted the genotyping outcome in terms of *Striga* resistance in the tested genotypes. Some of the tested genotypes (UG-14) showed resistance with no *Striga* emergence or attachment to its root at all, whiles the marker (SSR-1) for PCR amplification during genotyping, recognized it as susceptible (due to absence of SSR marker band for UG-14). The SSR marker is a known functional marker which is highly polymorphic and very robust. Previous studies discovered that the disadvantage of examining genotypes under natural conditions is the unequal distribution of *Striga* seeds in the field which often enable some cultivars to escape infestation (Kim *et al*., 2002). In addition, pot screening was chosen over field evaluation by Baptiste *et al*. (2013), showing its reliability. In order to get rid of false conclusion, the resistance potential of UG-14 was confirmed through pot screening with eight replications. Hence, the lack of band can be associated with a possible recombination which might have occurred between the markers and the targeted *Striga* resistant genes. As reported by Zhang *et al*., (2012), if a marker lost its contact with a gene of interest, recombination can occur resulting in Type 1 error. Also, it could be that, the *Striga* resistance genes contained by the genotype (UG-14) is not associated with SSR markers hence causing its failure to bind to it. Among the seven reported *S. gesnerioides* race variants, SSR marker SSR-1 has been demonstrated to be closely associated with SG3 resistance, as revealed by Li & Timko (2009).

5.2 Variation in agronomic traits among genotypes

In the analysis of variance, the mean sum of squares for the majority of the features for the various sources of variation were found to be highly significant, demonstrating the sufficient genetic diversity of these experimental materials. The success of a crop's genetic improvement depends on the diversity of its quantitative features. For current and upcoming breeding efforts, crop germplasm, particularly that of the cowpea, represents a priceless source of genetic variation. For all examined qualities, the evaluated genotypes varied significantly, and the majority of traits showed strong broad sense heritability. Morphological traits have become the target of many breeders who want to capture the phenotypic differences among genotypes in several crops worldwide including cowpea (Artea *et al*., 2019; Lee and Park, 2017; Menssen *et al*., 2017 and Ouaja *et al*., 2021). These traits are used to estimate variations and select parental lines for crossing (Lee and Park, 2017).

5.2.1 Crop phenology (flowering and maturity)

Early flowering is advantageous for crops with an indeterminate growth habit, such as cowpeas, because it allows for simultaneous vegetative growth, flowering, pod development, and pod filling. The genotypes can take advantage of the soil moisture and nutrients that are available and avoid biotic and abiotic challenges that develop late in the growth season by flowering and maturing early. The present study revealed that the genotypes exhibited significant variability.

Many of the test genotypes performed better than the checks in terms of first flower initiation, although the latest flowering genotype emerged from the test treatments. It's possible that differences in their genetic make-up, environmental conditions, and genotype by environment

interactions are responsible for the observed broad range among genotypes for days to 50% flowering. This crucial stage is extremely vulnerable to temperature changes since they have a negative impact on pollen viability and pollination, which could lead to poor fertilization and a low seed set. According to Devasirvatham *et al*. (2012), flowering time is one of the significant factors which affects pod set, seed set and yield. Early maturity is highly preferred in places where farmers intercrop cowpea with maize, cassava, yam, millet, and sorghum (Singh *et al*., 1997). Early maturity is highly preferred in places where farmers intercrop cowpea with maize, cassava, yam, millet, and sorghum (Singh *et al.,* 1997). It was also revealed that early flowering and early maturing contributed to higher grain yield under drought area (Rehman *et al.* 2011) because such crops are able to escape dehydration during the sensitive and grain filling periods. Moreover, the length of the pod filling process and pod size may be the cause of the observed significant variance for days to 90% maturity.

Thus, early genotypes along with those medium reproductive duration and reasonable yield traits can be candidates for potential breeding material in future improvement of cowpea in various regions.

5.2.2 Leaf length and width

There were differences across the various genotypes especially between the check varieties for both of these characters. The outstanding long leaves were discovered among the genotypes. Large leaves have greater surface area which would allow them to absorb more sunlight for photosynthesis when coupled with a ready supply of water. At the same time, a large area would allow for a large amount of water loss. This means that early flowering and maturity should have been experienced in genotypes with larger leaves, but it did not reflect that way in this study.

Because UG-20 had the shortest and the narrowest leaves but formed part of the genotypes that attained 90% maturity of pods using shorter periods.

5.2.3 Plant height

The findings revealed significant genetic variation among the genotypes examined for plant height. The large range of variation in plant height may be caused by interactions between genotype and environment, as well as genetic factors. One of the desirable traits of cowpeas is plant height, which lowers the lodging impact and increases the final seed output. Crop height has a significant impact on lodging resistance and directly impacts crop output (Liu *et al.*, 2018). Extreme plant dwarfism produces little grains, semi-sterile panicles, and deformed panicles, all of which reduce yield and biomass production (Asano and others, 2009; Liu and others, 2018; Sazuka and others, 2009). Their findings coincide with those from this work where greater plant height translated into high yield and yield components.

5.2.4 Canopy sizes

There was a significant variation in the genotypes with regards to their canopies' sizes. It's possible that genetic, environmental, and genotype by environment interactions are responsible for the trait's high degree of variability. The enhancement of photosynthesis has frequently been suggested as a major objective for raising crop productivity (Simkin *et al*., 2019; Weber & Bar-Even, 2019; Wu *et al*., 2019). Experiments with enhanced CO_2 for a variety of crops provide evidence for the benefit of increased photosynthetic activity for seed yield (Ainsworth & Long, 2005)

Optimizing cowpea crops to increase carbon dioxide (CO_2) assimilation and light absorption across the canopy may increase yield (Digrado *et al*., 2020). Improved light penetration within the canopy may also prolong the senescence of leaves in the lowest layer of the canopy (Liebsch and Keech, 2016), maintaining leaf area later in the season and ultimately resulting in a better yield (Koester, Skoneczka, Cary, Diers, & Ainsworth, 2014; Liu *et al*., 2015). This implies that the high yield can be associated with canopy sizes as suggested by Digrado *et al*., (2020). However, to ascertain the efficacy of breeding for high canopy and how it translates to high yield, more research is required. Therefore, genotypes with large canopy sizes is very useful in improving cowpea's yield.

5.2.5 Number of pods per plant and Number of pods per peduncle

The quantity of pods per plant could affect the cowpea plant's growth behavior and yield output. The number of pods per plant and per peduncle differed between genotypes which showed existence of genetic variation. Similar results have been reported by some other researchers such as Hegde and Mishra (2009) in cowpea. The variations in the number of pods produced by each plant may result from genotypes, environments, or interactions between genotype and environment. The number of pods is one of the most substantial yield component and it is affected by environmental stress factors such as heat or drought that causes the death of pollen grains and destruction of tissues (Al-Assafi and Abed, 2014; Abed, 2017). Morakinyo (2000) and N'gbesso and others in 2013 reported that number of pods per plant significantly and positively correlated with seed yield. However, Alidu *et al.*, (2013) discovered that the two traits were not significantly correlated. Consequently, genotypes like UG-20 and UG-08 that have an exceptionally high

number of pods per plant or per peduncle can be used to hybridize cowpea with early blooming and maturing features to increase output.

5.1.6 Pod length and Seed pod^{-1}

The current research discovered significant variations across all the treatment genotypes with regards to pod length and the number of seeds per pod, except for the checks which showed no substantial differences in the number of seeds contained in each of their pods. Most of the test treatments surpassed the control treatments with regards to the average number of seeds recorded in their pods. All the genotypes which exhibited greater pod lengths also recorded high number of seeds per pod showing the relationship between these traits. Similar results were reported by Venkatesen *et al*. (2003), Patil *et al*. (2004), Kumawat and Raje (2005), and Manggoel *et al*. (2012). This implies that improving pod length could result in high seed yield with other important agro-morphological traits. Hence, in cowpea breeding programs, selection should give top attention to pod length and seed pod^{-1}.

5.1.7 Total pod weight and Seed weight

One of the most crucial characteristics of seed-consuming pulse crops, such as cowpea, is seed weight. Results in this study showed significant variation among genotypes with regards to pod weight as well as seed weight. Clearly, genotypes which recorded the highest pod weights had the greatest seed weights and the vice versa. The poor values recorded in UG-10 for these traits could be due to disease infection along with drought and *Striga* weed infestation. Seven UG-10 plant stands were completely loss to an infection. The results in this study are similar to that of Imamura (2019), Ajibade and Morakinyo (2000).

5.1.8 Hundred Seed weight

The results showed substantial variations for 100_seed weight amongst varieties examined (Table 16). The usage of different genotypes with varying pod sizes and pod filling times, which alter seed size (weight) due to late-occurring biotic (*Striga gesnerioides*, insects) and abiotic stressors (drought), could be the cause of the very large variations. The quantity of pods per plant might potentially be a factor because of competition for the scarce soil nutrients and moisture. This might lead to smaller seeds. This research made it clear that genotype UG-20 which had the highest number of pods per plant (29 pods per plant) recorded the lowest 100 seed weight. Therefore, the lower value observed in UG-20 for 100-seed weight is clearly due to smaller seed size in terms of seed thickness, seed length and seed width. Generally, seed set, pod filling, and consequently seed weight may be influenced by genetics, the environment, or a combination of genetics and the environment. The findings showed that the analyzed cowpea varieties had the ability to produce genotypes with high 100_ seedweight, significant yield, and associated attributes. Thus, genotypes with high 100_seed weight from this study could be applied in the region's upcoming cowpea breeding programs.

5.2 Susceptibility of the Cowpea Genotypes to *Striga gesnerioides* and Yield Performances

Analysis of variance projected non-significant means sum of squares for grain yield, indicating the insufficient genetic variability of the genotypes in terms of yield performance. Apart from UG-14, all the tested genotypes in addition to the susceptible check, Apagbaala exhibited different levels of susceptibility to the *Striga* parasite. However, resistance to *Striga* did not translate to higher yield in UG-14. This is because most of the susceptible genotypes performed better than the resistant genotypes (UG-14, KT Benga and Wangkae) in terms of grain outputs including other

related traits. The response to *Striga* varied among genotypes suggesting that differences exist in the ability of these plants to recognize the pest and to activate defense response mechanisms (Godwa *et al*., 1999). Therefore, the high yield performance exhibited by some of these susceptible genotypes (UG-20 and UG-08) could be linked to their extra early maturity potential through which they were able to escape the severe attacks of the parasitic weed. The poor yield performances by the resistance genotypes can be due to low fertility and drought stress only. The overall poor yield performances of the susceptible genotypes can be associated with the effects of *Striga* infestation. Botanga and Timko (2005) reported that incompatibility occurs when the parasite is unable to initiate a strong connection with the host plant. The resistant genotypes in this instance were unsuitable hosts.

5.3 Seed quality

In cowpea, seed quality traits include seed size, seed coat color, seed coat texture, and cooking time. According to a survey conducted across the markets in Ghana, most of the imported cowpea varieties are large size grain with white or cream seed coat color (Quaye *et al*., 2011). Interactions with the farmers revealed that imported cowpea varieties do not perform better than the indigenous ones in terms of yield, yet they are highly demanded by consumers (Egbadzor *et al*., 2014). The seed sizes ranged from small to large. The results in this research showed that majority of the genotypes (80%) exhibited large size seeds. The trait is polygenic and additive gene effects are predominant in its control (Drabo *et al*., 1984). Cowpea seed coat color varies with variety. The current study categorized seed coat color into cream, red, ash speckle, Holstein and mixture (multi-colored). The dominated seed coat color was cream (55%) followed by red (25%). The topmost yielding genotypes (UG-12 and UG-08) in the present study segregated to produce seeds with non-

uniform coat colors. According to Drabo *et al*. (1988) seed coat color is controlled by five genes whiles Egbadzor *et al*. (2014) suggested several genes may control the trait.

The findings discovered two seed coat textures in the cowpea genotypes namely; smooth and rough. Most of the genotypes showed smooth seed coat texture whiles few of them exhibited a rough texture. Seed yield in cowpea is the product of components including the number of pods per plant, the number of seeds per pod, and the mean seed weight.

5.4 Genetic variability of traits

Genetic variability in breeding materials is essential for a successful plant breeding program. For yield improvement projects to be chosen and managed successfully, genetic diversity in a given crop population is essential as reported by Idahosa & others (2010) and Ndukauba & others (2015). The notable variations found in all of the genotypes suggest the existence of inherent genetic variability among them. This present study suggests that the phenotypic coefficient of variation (PCV) was relatively higher than the corresponding genotypic coefficient of variation (GCV). However, the differences between PCV and GCV were narrow indicating little influence of environment on the expression of these traits and considerable amount of variation was observed for the traits studied. This outcome was consistent with the research by Reshma and others (2019). A considerable relative degree of variability between crop plant attributes is compared using the coefficient of variation (%CV) according to Sharma (1988). In this experiment, the Pod per peduncle, Pod per plant, and Pod weight, in that order, had the largest coefficient of variation. This result suggests that, compared to the other investigated qualities, these traits exhibited higher levels of genetic variability that may be exploited. Also, choosing certain qualities above others has a

higher chance of leading to favorable advancement (Eid, 2009; Ndukauba.& others, 2015). Contrarily, the character with lower %CV were found to be Seed thickness and Days to 90% Maturity. These traits had low levels of exploitable genetic variability and, as a result, had a lower chance of favorably advancing under selection than other traits.

For every trait, the size of the genotypic variants was greater than the matching environmental variances. This suggests that the predominant source of overall variation in the variables under study was the genotypic component of variance. The Seed_weight, Pod plant^{-1} and Pod_weight recorded maximum phenotypic coefficient of variation (PCV) while the least was recorded for Days to 90% Maturity. Depending on the level of variability present, high PCV suggests that there is a wider range of selection for the trait under consideration, according to Khan and others (2009). So, it is anticipated that selecting for these traits among the genotypes of cowpeas under study will have a larger chance to express in progenies. For Days to 90% maturity, however, there is a limited range of selection because of the lesser diversity. The characters such as pod weight, seed weight, pod per plant and grain yield recorded high values for GCV and PCV **(Figure 4.1),** indicating the availability of great genetic variability for these traits in the tested genotypes.

The genotypic coefficient of variation (GCV) provides a measure of genetic variability that exists in different quantitative traits. The highest GCV was obtained for the Seed weight followed by Pod weight, and Pod per plant; the lowest GCV was recorded for Days to 90% Maturity. High GCV indicates the presence of exploitable genetic variability for the traits, which can facilitate selection (Yadav *et al*., 2009). Although estimates for PCV were higher than those for GCV, they were close, implying that genotype contributed more than environment in the expression of these

characters and selection based on phenotypic values is therefore feasible. The results of the study were in conformity with the findings of Reshma *et al*. (2019) who reported high value of PCV and GCV for seed yield per plant and Pod per plant. In addition, Manggoel, *et al*. (2012) and Mofokeng, *et al*. (2020) also reported high PCV and GCV for days to flowering, pod per plant, pod weight per plant, seed per pod, hundred seed weight and seed yield in cowpea.

Polygenic variation can be phenotypic, genotypic, or environmental and the relative values of these three coefficients for a trait will provide information about the magnitude of variability (Nausherwan *et al*., 2008; Ndukauba *et al*., 2015).

5.4 Heritability Estimates for the traits

Heritability estimates provide an insight into the extent of genetic control to express a particular trait and phenotypic reliability in predicting its breeding value (Ndukauba *et al*., 2015). High heritability indicates less environmental influence in the observed variation (Eid, 2009). Broad-sense heritability (h^2bs) only indicates whether or not there is sufficient genetic variation in a population, which implies whether or not a population will respond to selection pressure (Gatti *et al*., 2005; Milatovic *et al*., 2010; Ullah *et al*., 2012). However, broad sense heritability is not enough to guarantee a successful selection of character under a particular selection pressure since it comprises of both fixable (additive genes) and non-fixable genes. According to Johnson and others (1995), a heritability which is strong coupled with high genetic advance clearly is a sign that a character is mainly controlled by additive genes. On that basis, the high heritability values combined with high genetic advance recorded for these traits is an indication of their usefulness in selection for better cowpea cultivars. These traits can therefore be given special attention for selections aimed at cowpea improvement. To access a more effective trait selection, heritability

accompanied by genetic advance is more useful than heritability alone (Ullah *et al*., 2012). Similarly, Manggoel *et al*. (2012); Thorat and Gadewar, (2013); Khan *et al*. (2015); Khanpara *et al*. (2016); Reshma *et al*. (2019) and Mofokeng *et al*. (2020) reported high heritability values in cowpea.

CHAPTER SIX

6.0 CONCLUSION AND RECOMMENDATION

6.1 Conclusion

All the newly tested genotypes with the exclusion of UG-14 recorded *Striga* emergence indicating their susceptibility to the parasitic weed. However, the study showed that resistance did not correlate with yield performance since UG-14 and the resistant checks did not perform better than all the susceptible genotypes in terms of yield and yield traits. The findings from the study indicated that most of the tested genotypes performed better than the best checks in terms of days to flowering, days to maturity, plant height, canopy diameter, number of seeds per pod, number of pods per plant, 100-seed weight and grain yield per hectare. Besides, there were strong inheritance values observed for these characters coupled with high genetic advance which indicates that there is high possibility of the genes being transfered to the next filial generation for crop improvement. This study also projected an enormous morphological variability between the cowpea genotypes grown. This diversity is important since it could help to lay the foundation for successful cowpea breeding programs that are needed to design elite varieties that could survive the most common biotic and abiotic stress in local farming environments. Moreover, heritability estimates reported are low, high or very high depending on the trait. Breeding for the traits considered can be successful if adequate methods are used.

Generally, the study identified the following genotypes for further genetic studies:UG-14 based on *Striga* resistance; UG-9, UG-12 and UG-20 based on early flowering and maturity; UG-09, UG-16, UG-18, UG-15, UG-07 and UG-17 based on plant height; UG-20, UG-08, UG-09, UG-07, UG-13 and UG-12 based on number of pods per plant; UG-08, UG-09, UG-18, UG-15, UG-

16, UG-18 and UG-19 based on number of seeds per pod and UG-08, UG-20, UG-09, UG-11, UG-12, UG-13, UG-14, UG-16 and UG-19 considering the maximum weight of seed obtained, grain output on each hectare, hundred-seed weight of each plant, and quantity of seeds per plant.

6.2 Recommendations

Based on this study, the following recommendations have been outlined:

1. Promising early flowering and maturing genotypes among the test treatments which have appreciable yield performance should be utilized to improve the genetics of cowpea in various regions.
2. Genotype UG-14 should be evaluated on other *Striga* infested fields.
3. All the new genotypes should be assessed with multiple markers to ascertain or confirm their reaction with other *Striga* resistance molecular markers.
4. *Striga* infested and non-infested data should be compared to ascertain the effects of *Striga* on yield and yield components.

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APPENDIX

List of Striga species

***Striga* species**	**Authority**	**Distribution**
S. aequinoctialis	Chev. Ex Hutch. & Dalz.	W. Africa
S. angolensis	K. I. Mohamed & L. J. Musselman	Angola
S. angustifolia	(Don) Saldanha	E. Africa, Asia, Indonesia
S. asiatica syn. *S. lutea* (Asiatic witchweed, red witchweed)	(L.) Kuntz Loureiro	Africa, Arabian Peninsula, India, Burma, China, Indonesia, Philippines, Malaysia, New Guinea, USA (introduced)
S. aspera	(Willd.) Benth.	Africa
S. bilabiate ssp. *barteri*	(Thunb.) O. Ktze. (Engl.) Heper	Africa
ssp. *bilabiata*	Kuntze	

ssp. *Ledermannii*	(Pilger) Hepper	
ssp. *linearifolia*	(Schum. & Thonn.) Mohamed	
ssp. *rowlandii*	(Engl.) Hepper	
S. brachycalyx	Sckan	Africa
S. chrysantha	A. Raynal	Central Africa
S. dalzielii	Hutch.	W. Africa
S. elegans (elegant witchweed)	Benth.	Angola, Malawi, S. Africa, Zimbabwe
S. forbesii (giant mealie witchweed)	Benth.	Africa, Madagascar
S. gastonii	A. Raynal	Chad and Central African Republic

S. gesnerioides syn. *S. orobanchoides* (cowpea witchweed, tobacco witchweed)	(Willd.) Vatke Benth.	Africa, Arabian Peninsula, India, USA (introduced)
S. gracillima	Melch.	Tanzania
S. hermonthica syn. *S. senegalensis* (purple witchweed)	(Del.) Benth. Benth.	Senegal to Ethiopia, Democratic Republic of Congo and Tanzania, Angola, Namibia
S. hallaei	A. Raynal	Gabon, Democratic Republic of Congo
S. hirsuta	Benth.	Madagascar
S. junodii	Schinz	S. Africa, Mozambique
S. klingii	(Engl.) Skan	W. Africa, Nigeria, Ghana, Cameroon, Togo
S. latericea	Vatke	E. Africa, Ethiopia, Somalia
S. lepidagathidis	A. Raynal	Senegal, Guinea, Guinea Bissau.

S. lutea	Lour.	Sudan, Ethiopia
S. macrantha	(Benth.) Benth.	W. Africa, Nigeria, Ivory Coast, Togo
S. passargei	Engl.	W. & C. Africa, Arabian Peninsula (?)
S. pinnatifida	Getachew	Ethiopia
S. primuloides	A. Chev.	Ivory Coast, Nigeria
S. pubiflora	Klotzsch	Somalia
S. yemenica	Musselman and Hepper	Ethiopia

Source: (Mohamed *et al*., 2001) Note: list is not complete