GENETIC STUDIES OF GRAIN YIELD AND OTHER AGRONOMIC TRAITS OF COWPEA (*VIGNA UNGUICULATA)* (L.) Walp) IN WATER STRESS AND NON-STRESS CONDITIONS

BY

ABUBAKAR, HASHIM
(P16AGPS8077)

DEPARTMENT OF PLANT SCIENCE
FACULTY OF AGRICULTURE
AHMADU BELLO UNIVERSITY,
ZARIA, NIGERIA

NOVEMBER, 2019

GENETIC STUDIES OF GRAIN YIELD AND OTHER AGRONOMIC TRAITS OF COWPEA (*VIGNA UNGUICULATA)* (L.) Walp) IN WATER STRESS AND NON-STRESS CONDITIONS

BY

ABUBAKAR, HASHIM
B.Sc. BIOLOGY (A.B.U) 2008
(P16AGPS8077)

A DISSERTATION SUBMITTED TO THE SCHOOL OF POSTGRADUATE STUDIES AHMADU BELLO UNIVERSITY IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE AWARD OF A MASTER DEGREE IN PLANT BREEDING

DEPARTMENT OF PLANT SCIENCE,
FACULTY OF AGRICULTURE,
AHMADU BELLO UNIVERSITY,
ZARIA, NIGERIA

NOVEMBER, 2019

DECLARATION

I declare that the work in this thesis entitled "GENETIC STUDIES OF GRAIN YIELD AND OTHER AGRONOMIC TRAITS OF COWPEA (*VIGNA UNGUICULATA)* (L.) Walp) IN WATER STRESS AND NON-STRESS CONDITIONS" has been carried out by me in the Department of Plant Science. The information derived from literature has been duly acknowledged in the text and a list of references provided. No part of this thesis was previously presented for another degree or diploma at this or any other Institution.

Hashim Abubakar   ….……………   ………………………
Student   Signature   Date

CERTIFICATION

The dissertation entitled "GENETIC STUDIES OF GRAIN YIELD AND OTHER AGRONOMIC TRAITS OF COWPEA (*VIGNA UNGUICULATA)* (L.) Walp) IN WATER STRESS AND NON-STRESS CONDITIONS" by ABUBAKAR HASHIM meets the regulations governing the award of the degree of Master of Science in Plant Breeding of Ahmadu Bello University, and is approved for its contribution to scientific knowledge and literary presentation.

Prof. M. Yeye   …………………..   ……………………
Chairman, Supervisory Committee   Signature   Date

Prof. C.A Echekwu.   ……………………   ………..………….
Member, Supervisory Committee   Signature   Date

Prof. M.D. Katung.   ……………………   …………………….
Member, Supervisory Committee   Signature   Date

Dr. Alhassan Usman   …………………..   …………………….
Head, Department of Plant Science   Signature   Date

Prof. Sani Abdullahi   ……………………   ……….………….
Dean, School of Postgraduate Studies   Signature   Date

DEDICATION

To Allah (S.W.T) for wisdom, sound health, favor, guidance and protection during the course of my study and throughout my life and His noble Prophet Muhammad (Peace Be upon Him). This work is dedicated to my parents. I pray may Almighty Allah give them long life and prosperity, Ameen.

ACKNOWLEDGEMENTS

ABSTRACT

The study on the genetic studies for grain yield and other agronomic traits under water non-stressed and water stressed conditions in cowpea was carried out using five parental lines comprising three drought resistant (IT98K-628, IT99K-7-21-2-2, SAMPEA-10) and two drought susceptible genotypes (SAMPEA-8, BIU LOCAL) which were crossed to develop F_1s. The F_1s were advanced to F_2s and backcrosses made to the two (2) parents. The eighteen generations obtained were evaluated along with a commercial check Dan'ila in Randomized Complete Block Design (RCBD) with replications at the Institute for Agricultural Research (IAR), Samaru, Zaria. Significant differences in mean performance among the parents and the F_1s suggests sufficient variability across the generations for the characters studied. The three parameter model was adequate to explain variations observed in the inheritance of days to fifty percent flowering, plant height, number of seeds per plant and root length. It was however inadequate to explain the variations observed in the inheritance of days to pod maturity, pod yield per plant and hundred seed weight. For these the six parameter model of Jinks and Jones was fitted. Non-allelic gene interactions were significant for number of matured pod per plant and pod yield per plant under the two different conditions. High broad sense heritability was obtained (95%). These showed the importance of the above traits in selection. Correlation had been found to be high and significant (positive and negative). The genotypic correlation coefficients exceeded those of the corresponding phenotypic correlation coefficient for most of the character pairs indicating that the correlation were more

genetic than environmental in the three sets of cowpea crosses studied, indicating; positive response, repeatable and transmit ability of these traits in selection.

TABLE OF CONTENT

CHAPTER ONE

CHAPTER TWO

LIST OF TABLES

LIST OF ABBREVIATIONS

D50%F- Days to fifty percent flowering

PH- Plant height

DPM- Days to pod maturity

NMPP- Number of matured pod per plant

NSPD- Number of seeds per pod

PYYP- Pod yield per plant

HSW- Hundred seed weight

RL- Root length

FAOSTAT - Food and Agricultural Organization Statistics

ICRISAT - International Crops Research Institute for the Semi-Arid Tropics

IITA - International Institute of Tropical Agriculture

DF- Degree of Freedom

CV- Coefficient of Variation

BCP- Backcross to Parent

F_1- First Filial Generation

F_2 - Second Filial Generation

CHAPTER ONE

1.0 INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp] is the most economically important indigenous African grain legume producing a source of economic livelihood and nutritional well-being for rural poor and urban consumers (Agbicodo *et al.,* 2009; Langyintuo *et al.,* 2003; Timko, 2006).

Cowpea plays a critical role in the lives of millions of people in Africa and other parts of the developing world, where it is a major source of dietary protein that nutritionally complements staple low-protein cereal and tuber crops, and is a valuable and dependable commodity that produces income for farmers and traders (Singh, 2002; Langyintuo, *et al.*, 2003). Cowpea is a valuable component of farming systems in many areas because of its ability to restore soil fertility through nitrogen fixation, for succeeding cereal crops grown in rotation with it (Carsky *et al.,* 2002; Tarawali *et al.,* 2002; Sanginga *et al.,* 2003). The N contribution to a cropping system by a cowpea cover crop was reported to be about 145.7 kg N/ha per season if the crop is turned under (Valenzuela and Smith, 2002). Early maturing cowpea varieties can provide food earlier than any other crop (in as few as 55 d after planting), thereby shortening the "hunger period" that often occurs prior to harvest of other crops in farming communities in the developing world. Cowpea haulms and chaff are used as livestock feeds and are also beneficial in maintaining soil fertility thus making it an important component of any cropping system (Sanginga *et al.,* 2000, Muchero *et al.,* 2003). Cowpea is a valuable component of farming systems in many areas because of its

ability to restore soil fertility through nitrogen fixation, for succeeding cereal crops grown in rotation with it (Carsky *et al.,* 2002; Tarawali *et al.,* 2002; Sanginga *et al.,* 2003). The N contribution to a cropping system by a cowpea cover crop was reported to be about 145.7 kg N/ha per season if the crop is turned under (Valenzuela and Smith, 2002). Early maturing cowpea varieties can provide food earlier than any other crop (in as few as 55 d after planting), thereby shortening the "hunger period" that often occurs prior to harvest of other crops in farming communities in the developing world. Cowpea haulms and chaff are used as livestock feeds and are also beneficial in maintaining soil fertility thus making it an important component of any cropping system (Sanginga *et al.,* 2000, Muchero *et al.,* 2008). Dry grain for human consumption is the most important product of the cowpea plant; these grains can either be boiled or converted into other food products such as moin-moin, akara, bean soup etc. in Nigeria. The green leaves/twigs are also used in preparing nutritious vegetable soup; the fresh pods and peas are used for salad in vegetarian diets (Timko *et al.,* 2007).

The estimated world cowpea production area is over 14.5 million ha, with an annual production estimated at about 7.64 million tonnes. Out of this estimate, West and Central Africa (WECA) account for over 9 million ha and 3 million tonnes. West Africa is the key cowpea production zone, mainly from the dry savanna and semi-arid agro-ecological zones. In West Africa, Nigeria and Niger Republics are the major cowpea producers with Nigeria contributing over 60% of the total production (FAOSTAT, 2015). Compared with many other crops, cowpea is reported to thrive in places considered too dry for the production of

other grain legumes but because it is mostly grown under rain-fed conditions on sandy soils having low water-holding capacity in the drier regions that receive between 300 - 600 mm annual rainfall, its productivity is adversely affected by erratic rainfall patterns which occur frequently in these areas (Belko *et al.,* 2013).

Droughtcan cause direct reduction of about 50 - 67% in cowpea grain yield (Fatokun *et al.,* 2012; Sanda and Maina, 2013). In addition to the direct effect on yield, many aspects of plant growth are affected by drought stress (Hsaio, 1973), including leaf expansion, which is reduced due to the sensitivity of cell growth to water stress. Water stress also reduces leaf production by promoting senescence and abscission (Karamanos, 1980), resulting in decreased total leaf area per plant. Reduction in leaf area reduces crop growth and thus biomass production. Seed production, which is positively correlated with leaf area (Rawson and Turner, 1982), may also be reduced by reduction in leaf area caused by drought stress.

There are various ways of reducing the effect of drought or addressing the problem of drought stress including irrigation and breeding. However, irrigation requires large capital outlay and availability of water throughout the growing season, especially at flowering and pod filling stages. This makes it less feasible especially for small scale farmers in Africa. Developing drought tolerant varieties is a more sustainable option of managing drought since there would be no additional cost to the farmer once drought tolerant seeds are available. Breeding for drought tolerance and grain yield however is complex because they are governed by minor genes whose effects are often confounded by interaction of morphological, physiological and biochemical characters of the crop with the

environment thus making genetic improvement of these traits in crops a slow and difficult process (Fatokun *et al.,* 2012; Mir *et al.,* 2012).

In cowpea research, drought tolerant factors have been separated into shoot and root tolerance using simple, rapid and cheap screening methods (Singh and Matsui, 2002; Hall *et al.,* 2003). For selection, two classical approaches are followed when breeding for drought tolerance: (i) utilization of grain yield as selection criteria, and (ii) identification of physiological traits that might contribute to yield production under drought (Singh et al., 2003; Hamidou *et al.,* 2007; Badu-Apraku *et al.,* 2011).

In cowpea research, drought tolerant factors have been separated into shoot and root tolerance using simple, rapid and cheap screening methods (Singh and Matsui, 2002; Hall *et al.,* 2003). For selection, two classical approaches are followed when breeding for drought tolerance: (i) utilization of grain yield as selection criteria, and (ii) identification of physiological traits that might contribute to yield production under drought (Singh *et al.,* 2003; Hamidou *et al.,* 2007; Badu-Apraku *et al.,* 2011).

Although grain yield between 2500 kg/ha to 4000 kg/ha is achievable for cowpea, several constraints have kept farmers' yields constantly low at levels between 350 and 700 kg/ha(Ajeigbe *et al.,* 2010a). If the yield barrier is to be overcome, strategies to improve the genetic potential of cowpea plants by introducing novel genes is required. For this to be achieved, genotypes with potential for higher yield and other desirable traits are needed as parent lines to develop improved varieties (Aremu, 2005).

4

The identification of suitable parental genotypes, potentially generating superior lines with traits contributing to the overall yield of a crop, is an important step in the development of improved varieties because if parents are precisely selected, the desired recombinants will be found in the segregating generations (Moalafi *et al.,* 2010; Ayo-Vaughan *et al.,* 2013). Knowledge of the genetic control of complex quantitative traits and the magnitude of genetic variability that exists among available germplasm are therefore important for selection and genetic improvement of crop plants. Selection of parents based on combining ability has been used as an important breeding approach in crop improvement. The combining ability and gene effects of yield and its components have been studied by many researchers.

This research work is therefore focused on the studies of the inheritance of drought tolerance information necessary to assist in developing promising cowpea genotypes with tolerance to drought. This can be achieved through the following specific objectives:

1. Assess the genetic variability for resistance to drought and other agronomic traits of cowpea in water stress and non-stress condition
2. Determine the gene effects involved in the inheritance of drought resistance of cowpea in water stress and non-stress condition
3. Assess the relationship between seed yield and other quantitative traits of cowpea in water stress and non-stress conditions.

CHAPTER TWO

2.0   LITRATURE REVIEW

2.1   Cowpea taxonomy, origin, domestication and economic importance

Cowpea, [*Vigna unguiculata*(L.) Walp] is a *Dicotyledoneae* belonging to the order Fabales, family Fabaceae, subfamily Faboideae, tribe Phaseolaeae, sub tribe Phaseolinae, genus *Vigna* and section Catiang (Verdcourt, 1970; Marechal *et al.,* 1978). The genus *Vigna* has many species varying according to authors but all cultivated cowpeas are under *Vigna unguiculata*. The species *unguiculata* is subdivided into four culti-groups viz: (1) *unguiculata* which is the common form, (2) *biflora* or *catjang* with small erect pods; (3) *sesquipedalis*or yard-long beans characterized with very long pods and consumed as green snap bean; (4) *textilis* characterized with its long peduncles which is used for fibers (Padulosi and Ng, 1997).

Information based on range of variation and number of varieties found in wild cowpea as well as their primitive characteristics suggested that cowpea originated from the southern Africa regions encompassing Namibia, Zambia, and Zimbabwe but further distributed through the Western Africa regions (Ng, 1995). Cowpea is considered to have been domesticated in Africa from its wild ancestral form, *V. unguiculata* subsp. *Dekindtiana* (Harms) Verdc. (Ng and Marechal, 1985). The center of maximum genetic diversity of cultivated cowpea is considered to encompass region of Nigeria, southern Niger, and part of Burkina Faso, northern Benin, Togo and northwestern part of Cameroon (Ng, 1995).

Cowpea is a vegetable legume which provides an inexpensive source of protein complementing staple cereal and starchy tuber crops and minerals for the urban

and rural populations of SSA where it is predominantly cultivated and consumed. According to Ehlers and Hall (1997), dry grain for human consumption is the principal product of the cowpea plant, but leaves (many parts of eastern Africa), fresh peas (the southern USA and Senegal) and fresh green pods (humid regions of Asia and Caribbean) are consumed. The crop is also used for green manure (southern USA and Australia) and fodder (parts of the Sahel). Cowpea cultivars differ in nutritional composition and cooking characteristics. For example, seed protein ranged from 23 to 33% on dry weight basis (Nielsen et al., 1993); fat content ranged from 1.4 to 2.7% and cooking time ranged from 21 to 62 minutes (Ehlers and Hall, 1997).

Cowpea is favoured by farmers for its diverse uses which include: rich protein source feed for livestock feed, its ability to improve soil fertility through its nitrogen fixing ability and its ability to control erosion and as an intercrop with cereals like millet and sorghum thus making it an important integral part of crop farming system in West Africa (WA). It also provides household benefits in the form of cash and income diversity for farmers (Eaglesham *et al.,* 1992; Fabunmi *et al.,* 2012). Demand for cowpea and low-cost nutritive food is increasing because of population increase and more knowledge on healthy nutrition (Singh *et al.,* 2003; Yewande and Thomas, 2015).

2.2 Cowpea production, productivity and production constraints
At present, cowpea is grown throughout the tropic and subtropic areas around the whole world where rainfall resources are characteristically low (300-600 mm) (Fatokun *et al.,* 2012) and variable (Fussell *et al.,* 1991). Information available on the Food and Agriculture Organization (FAO) database estimated that cowpea

is now cultivated on at least 11.3 million hectares worldwide with an annual production of 5.7 million tonnes with 95%being produced in Africa. Although cowpea is widely cultivated throughout the tropics, West and Central Africa (WCA) account for over 64% of the area (9.2 million hectares) followed by about 2.4 million hectares in Central and South America, 1.3 million hectares in Asia and about 0.8 million hectares in Eastern and South Africa. A substantial part of cowpea production from WCA comes from the drier parts of northern Nigeria (about 3.2 million ha from 2.5 million tonnes), and southern Niger Republic FAOSTAT (2015).

Cowpea in WCA is traditionally often intercropped with cereals like sorghum, maize or millet by small-holder farmers. Fertilizers and pesticides are generally not used and when used, farmers do not apply the adequate dosage needed for optimum yield potential of the crop because these inputs are expensive and/or not readily available for the small-holder farmers (Ajeigbe *et al.,* 2010b).

The large differences between on-farm yield of cowpea in WCA (0.025 to 0.3 tonnes/ha) and the potential yield reported from experimental stations (1.5 to 3 tonnes/ha) (Ajeigbe *et al.,* 2010a) showed that the high production estimate arising from these regions mainly comes from increase in land area rather than the genetic potential of the crop (Singh *et al.,* 1997; van Ek *et al.,* 1997). For instance, average cowpea yield in the United States of America is 1.9 tonnes/ha while it is 0.97 tonnes/ha for WCA (FAOSTAT, 2015). Several biotic and abiotic factors such as insect pests, diseases (fungal, viral, bacterial and parasitic weeds), poor soil fertility, metal toxicity and drought contribute to the reduction of cowpea yield potential in SSA (Singh and Tarawali, 1997; Wang *et al.,* 2001;

Emechebe and Lagoke, 2002; Singh and Ajeigbe, 2002). Other factors contributing to low yield in SSA include lack of improved varieties that can withstand these stresses and lack of adequate production practices and inputs needed for higher productivity and profitability. This yield gap therefore can be bridged if improved varieties and production practices are available to farmers through participatory on-farm training and evaluation with farmers (Ajeigbe *et al.,* 2010a, b).

Drought is one of the most important abiotic constraints threatening food security in the world. This is so because the economies of African nations depend largely on rain-fed agricultural systems which are seriously affected during periods of severe drought thus making drought a serious natural disaster in Africa (Oladipo, 2008). Drought conditions can either be intermittent when they occur at one or more intervals due to limited periods University of Ghana http://ugspace.ug.edu.gh of inadequate rain or irrigation during the crops' growing period or terminal when there is progressive decrease in available soil water resulting in severe drought stress at the later period of crop growth at grain-filling stage.

Crop response to water stress at various stages of growth is related to crop species, stage of growth, economic portion of the crop, the duration and intensity of the stress (Shouse, 1979, 1981). Cowpea is reported to be more tolerant to drought (Whitbread and Lawrence, 2006) however; it still suffers considerable damage due to frequent drought in the Savanna and Sahel sub-region. Studies have indicated that cowpea could maintain good seed yield when subjected to drought at vegetative stage provided subsequent conditions were conducive for

flowering and pod set (Ziska and Hall, 1983a, b; Singh *et al.,* 1997; Akyeampong, 2012). However, Akyeampong (1986) showed that the crop is highly sensitive to water deficits during flowering and pod filling stages. To this end, early maturing varieties have been developed to escape terminal drought (Singh, 1987) but they have been reported to perform poorly if exposed to intermittent moisture stress occurring at the vegetative growth stage (Mai-Kodomi *et al.,* 1999; Fatokun *et al.,* 2012).

Moreover, these early varieties tend to be sensitive to drought that occurs during the early stages of the reproductive phase (Thiaw *et al.,* 1993). Cowpea is a dual-purpose crop; it is grown for the purpose of green manure as much as for its grains. Early moisture stress that can reduce the quantity of green manure is sometimes unavoidable because cowpea solely grown under this system is terminated at the vegetative (Fabunmi *et al.,* 2012). Therefore, genetic enhancement of cowpea for tolerance to both vegetative and terminal drought will be a most effective method for ensuring sustainable and improved yield under variable and changing climate.

2.3. Impact of drought on agriculture and food security

Agricultural production remains the main source of livelihood for rural communities in Sub- Saharan Africa, providing employment to more than 60% of the population and contributing about 30% of gross domestic product. Agriculture production and productivity are highly sensitive to changes in climate and weather conditions. Therefore, the climatic variability has been implicated in affecting local as well as global food, fiber and forest production (Easterling *et al.,* 2007). Food security in its most basic form is the access of all

people to the food needed for a healthy life at all times. It refers to the availability of food and one's access to it. A household is considered food secure when its occupants do not live in hunger or fear of starvation while a country is considered as food-secure when food is not only available in the quantity needed by the population consistent with decent living, but also when the consumption of the food does not pose any health hazard to the citizen. (Baro and Deubel, 2006; Pinstrup-Andersen, 2009).

Drought is a naturally occurring phenomenon that exists when precipitation is significantly below normal recorded levels, causing serious hydrological imbalances that adversely affect land resource production systems (UNCCD, 2011). It can be attributed to inadequate seasonal precipitation, a prolonged dry season or a series of sub-average rainy seasons (Sheikh and Soomro, 2006). In agricultural terms, drought is said to occur when there is not enough moisture available at the right time for the growth and development of crops. It often results from insufficient and/or poor distribution of rainfall when crops are still growing in the field (Nhlane, 2001; Ganapathy and Ganesh, 2008). As a result, yields and/or absolute production decline (Sharfiq-ur-Rehman *et al.,* 2005). Drought is especially problematic in developing countries where agriculture is predominantly rain-fed. It is considered the most serious threat to world agriculture and food security because it is the main cause of desertification, major cause of severe food shortages resulting in malnutrition and famine (Mir *et al.,* 2012). It therefore affects the four pillars of food security: availability, stability, access and utilization (FAO, 2009).

In the agricultural sector, its effects include: crop losses, lower yields in both crop and livestock production, increased livestock deaths, increases in insect infestation and plant and animal diseases, damage to fish habitat, forest and range fires, desertification and soil erosion. Its impacts on human health include increased risk of food and water shortages, increased risk of malnutrition and higher risk of water and food borne diseases. Economic impacts include: income losses, high prices of food products as supplies are reduced, with severe effects on the poorest and most vulnerable. Shortfalls in food production leads to substantial increases in imports to meet local needs, which can result in increased fiscal pressure on national budgets (Oladipo, 2008). Twelve million hectares are lost globally annually (23 hectares/minute), where 20 million tonnes of grain could have been grown as a result of drought and desertification (http://www.un.org/en/events/desertificationday/ background.shtml accessed 28/10/2014 at 1.15pm). For instance, during the drought of 1972–73 in the northeastern Nigeria about300,000 animals representing 13% of the livestock population of the region were reported dead, while agricultural yield dropped to between 12% and 40% of the annual averages (Fagbemi, 2002). The effects of drought in terms of reduced food production have been even more severe during 1982 - 84 than 1972 - 74. In some parts of Borno State (then, comprising Borno & Yobe States) nearly 100% crop losses were recorded (Enabor, 1987). Agriculture consumes the largest available water through irrigation and in 2004 it was reported that 80% of world available water was consumed alone by irrigated agriculture (Condon *et al.,* 2004). With expected increase in world population by 2025 to 9.6 billion, agricultural water consumption will have to decrease which in turn will affect agricultural production and productivity (Ribaut *et al.,* 2009).

2.4 Adaptive traits for drought tolerance in cowpea

Breeding improved genotypes for the arid and semiarid tropics by selection solely for seed yield is difficult, because of the variability in amount and temporal distribution of available moisture from year to year. The relatively low heritability for grain yield under drought conditions has resulted in the use of other efficient traits that are indirectly related to grain yield (Omae *et al.,* 2007; Singh *et al.,* 2004, 2007; Sharma *et al.,* 2007). These traits are referred to as secondary traits and are highly heritable, cheap and easy to measure thus making selection for drought tolerance easier and faster.

In cowpea, traits such as stem greenness at vegetative stage (Muchero *et al.,* 2008) or DLSC (during pod-filling) stage (Fatokun *et al.,* 2012); number of pods and seeds per plant (Ajibade and Morakinyo, 2000) are frequently used as secondary traits to identify tolerant genotypes under water limited conditions. Recently, precision phenotyping for drought tolerance using more sophisticated instruments (Mir *et al.,* 2012) that can give accurate measurement of the health of green tissues of plants are now being employed to complement visual scoring for the stay green trait which though convenient is subjective (Joshi *et al.,* 2007). The instruments provide measurements of the normalized difference vegetation index (NDVI) of the crop growing under stress. NDVI is a mathematical formula derived to form a single spectral-based number, which is more sensitive than justa single wavelength and it is a measure of greenness (Sembiring *et al.* 2000; Hazratkulova *et al.,* 2012).

2.4.1 Stem greenness or Delayed leaf Senescence

Maintenance of green stem was shown to be an important criterion for seedling stage drought tolerance in cowpea (Muchero *et al.,* 2008) while maintenance of DLSC trait has been shown to be important for mid-season and terminal drought tolerance in cowpea (Fatokun *et al.,* 2012). Studies have demonstrated a link between late-season DLSC, a trait similar to 'stay-green' in cereals and grain yield in cowpea (Gwathmey, 1992a, b). Recent studies have also described field and greenhouse protocols to screen for DLSC at seedling stage in cowpea (Mai-Kodomi, 1999; Muchero *et al.,* 2008; Muchero *et al.,* 2009). Plants exhibiting this phenotype are characterized by maintenance of green leaf area under drought stress. It is believed that the maintenance of green leaf area contributes to continued carbohydrate formation during drought and faster recovery following a rainfall event (Borrell *et al.,* 2000). Therefore, selection for DLSC in cowpea genotypes allows more photosynthates to be synthesized and distributed leading to production of higher yields.

2.4.2 Number of pods per plant and number of seeds per pod

In cowpea, variations in yield due to environmental stresses were mainly due to variations in number of pods per unit area but drought occurring at pod-filling stage reduced the number of pods per plant and poor pod-filling (Turk *et al.,* 1980; Bala Subramanian and Maheswari 1992). Decrease in number of pods per plant is mainly due to the abscission of flowers and pods of cowpea under drought stress. This detrimental effect at flowering and pod-filling stage is rather not reversible by re-watering (Ziska *et al.,* 1985). Higher number of pods per

plant and seeds per pod and good pod-filling (big seed size) is therefore a reflection of tolerance to drought (Gwathmey *et al.,* 1992a).

2.4.3 Root systems

Root systems cannot be overlooked because it is through them that the plant obtains its water and mineral requirements for growth and unavailability of these resources often impose limit on productivity. Screening for root characteristics confirming drought tolerance have been studied in cowpea using the 'pin-board root-box' (Matsui and Singh 2003), herbicidal band screening (Robertson *et al.,* 1985; Khalfaoui and Havard, 1993) and polyethylene glycol (PEG) (Badiane *et al.*, 2004) methods. However, 'pin-board root-box' is not as widely accepted as the wooden box technique for vegetative screening probably because it is not practical for screening large numbers of plants (Matsui and Singh, 2003). Limited progress has been made on root system and drought tolerance in cowpea perhaps because some studies have reported that deeper and larger root systems may not be of additional advantage for the areas of cowpea production that are characterized by sandy soils with only about 8% of soil water and secondly, possession of larger roots require additional carbohydrates and energy for their construction and maintenance (Hall *et al.,* 2012). Studies have, however, been more directed towards the water saving traits in cowpea (Belko *et al.,* 2013).

2.5 Genetics of drought tolerance in cowpea

Understanding the nature of genes controlling a specific trait of interest is the baseline of any breeding programme. Genetic information regarding the gene effects and magnitude of gene action controlling such traits must be determined and well understood (Hinkossa *et al.,* 2013). Traits like drought and yield are

polygenically controlled and affected by environmental factors which are not transmissible from parents to offspring. It is therefore important to determine the genetic factors affecting these traits for an efficient breeding programme.

There are three types of gene effects i.e. additive, dominance and epistatic (Gamble, 1961). The dominance and epistatic constitute the non-additive part. The dominance can either be ambidirectional, a situation of positive and negative dominance at different gene loci or unidirectional, dominance in one direction (Kearsey and Pooni, 1998). Epistasis refers to interaction of alleles at different loci. Epistatic gene action occurs when the additive dominance model cannot explain variation alone (Derera, 2005). The additive gene effects reflect the degree to which progenies are likely to resemble their parents, as reflected in narrow-sense heritability (Derera, 2005).

Estimation of the relative proportion of additive genetic effects (or general combining ability of a line, GCA) and non-additive genetic effects (or specific combining ability of a cross, SCA) controlling the drought-adaptive traits and their interactions with the environment is useful for designing breeding programmes and assembling germplasm for population advancement (Shahi and Singh, 1985).

2.6 Heritability and genetic advance

Heritability is an index of the transmission of characters from parents to their offspring. It is generally expressed in percentage. The estimation of heritability helps the plant breeder in selection of elite genotypes. It also measures the degree of resemblance between relative and correspondence between phenotypic and

breeding value. The genetic advance is the deviation in the characters of selected population over the base population. Gain under selection or genetic advance is a measure to predict the expected progress under selection. The genetic advance helps to evaluate the selection procedures. If the value of genetic advance is more than in the succeeding generation, there will be good progress over population mean. The estimation of heritability along with genetic advance is more applicable than the heritability value alone.

Johnson *et al.* (1955) reported that in study of estimated heritability in conjunction with genetic advance would provide more reliable information than the study of heritability alone. Rangaiah and Mahadevu (2000), Two F_2 populations of 2 crosses of cowpea cultivars (v16 x c152 (C1) and v16 xs-488 (C2)) were grown during the kharif seasons maintaining a 45 x 20 cm row spacing. Plant height (PH), number of branches per plant (NB), number of clusters per plant (NC), number of pods per plant (NP), pod length (PL), number of seeds per plant (NS), pod weight (PW), total seed weight (TSW) and 100-seed weight (SW) were determined. The heritability and genetic advance (GA) were calculated. The difference between PCV and GCV was narrow with respect to NS in both crosses resulting in high heritability coupled with high GA. C2 had high GA (36.052%) and heritability of 76.418 for SW.

Borah *et al.,* (2000) reported that highly heritable characters i.e., number of branches and leaves, stem and leaf dry weight, and plant height, also exhibited high genetic advance as a percentage of mean, indicating additive gene action. The crude protein content, days to 50 percent flowering, stem thickness and leaf length and width exhibited low genetic advance with high heritability estimates.

Oluwatosin (2000) inheritance of black, brown and red seed coat colours was studied in crosses between 8 selected cowpea lines and Ibadan BPC, a branched peduncle cowpea mutant, carrying homozygous recessive alleles at the seed coat colour and eye pattern loci. Black and brown coat colours were digenically dominant to cream coat colour, while red coat colour was monogenically dominant to cream coat colour. The results suggest that cowpea genotypes with the same cream coat colour could behave differently in crosses with other coat colours.

Shinde (2000) reported that the characters crude protein percentage, weight of pod, yield per ha and yield per plant had high heritability values coupled with high percentage of genetic advance indicating additive gene effects and greater scope for selection.

 Nehru *et al.* (2001) studied fourteen cowpea genotypes grown to determine genetic variability for yield and yield components. High PCV coupled with high heritability resulted in high genetic advance expressed as per cent of mean for pods per plant and moderate for plant height, 100-seeds weight and yield per plant.

Kehind (2001) studied the segregation pattern of genes governing the expression of pigmentation on vegetative parts; flower, fresh pod and dry pod. Different gene actions were observed to be in operation. For flower colour, dry pod colour and pigmentation on vegetative parts, monogenic gene action was involved, while for fresh pod colour, complementary gene action was observed. Various symbols are proposed for these genes. Those characters under single gene action could be used as markers in genetic and breeding experiments.

Ramesh *et al.,* (2002) revealed moderate to high heritability for plant height, pod length, 100 seed weight, number of branches and number of pods per plant indicating the role of additive gene effect in controlling these traits in cowpea. Pathak and Jamwal (2002) reported that the high heritability, coupled with high genetic advance (GA) was recorded for pod yield per plant. Moderate GA was recorded for number of days to 50% flowering and plant height, indicating the role of additive gene action for the inheritance of these characters. High heritability with low GA was observed for number of days to first picking, pod length and average pod weight.

Santosh *et al.,* (2002) conducted an experiment using 5 cowpea cultivars and exhibited high genetic advance for green pod yield, plant height and days to 50 percent flowering. Venkatesan *et al.,* (2003) revealed that twenty genotypes of cowpea grown and evaluated for variability, heritability and genetic advance for 12 traits viz. (number of days to first flower, plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod yield per plant, pod length, number of seeds per pod, 100-seed weight, seed yield per plant, and dry matter production). Plant height, number of pods per plant, pod length, 100-seed weight, seed yield, and dry matter production were characterized by very high heritability. High heritability coupled with high genetic advance was recorded for plant height, dry matter production, and seed yield, indicating the importance of additive gene effects in these characters.

Pal *et al.,* (2003) an experiment reported that high heritability with moderate to high genotypic coefficient of variation and genetic advance were observed for

plant height, peduncle length, number of primary branches per plant, number of peduncles per plant and green pod per plant, which could be improved by simple selection in the early generation. Days to 50 percent flowering, days to first green pod picking, pod diameter, number of seeds per plant and 100-seed weight manifested high heritability with low genotypic coefficient of variation and genetic advance.

Vinieta *et al.,* (2003) studied in cowpea and reported that heritability and genetic gain were high for seed yield per plant, and number of pods and clusters per plant. Nigude *et al.,* (2004) reported that heritability in broad sense was higher for all the characters. Genetic advance was highest for all characters except number of seeds per pod.

Anbumalarmathi *et al.,* (2005), High heritability and high genetic advance for days to 50% flowering, plant height, branches per plant, clusters per plant, pods per plant, pod length, seeds per pod, 100-seed weight and single plant yield.

Malarvizhi *et al.,* (2005) an experiment studies on variability, heritability and genetic advance were carried out with 60 genotypes of cowpea [*Vigna unguiculata (L.)* walp]. Heritability and genetic advance was high for the character number of branches per plant, number of leaves per plant, dry weight of leaves, dry weight of stem. Hence the selection was more effective.

Kumawat *et al.,* (2005) observations were recorded for days to 50 percent flowering, reproductive period (days), days to maturity, plant height, branches per plant, clusters per plant, pods per plant, pods per cluster, pod length, seeds per pod, 100-seed weight, seed yield per plant, biological yield per plant and

harvest index. High estimates of heritability along with high genetic advance as percentage of mean were recorded for harvest index and seed yield per plant. Girish *et al.,* (2006) reported that the magnitude of phenotypic and genotypic coefficient of variation, heritability and genetic advance was high for seed yield per plant, number of pods per plant and plant height in cowpea.

Days to first flower opening, days to 50% flowering and days to maturity had a low genetic advance. Seema *et al.,* (2006) revealed that most of the yield components showed high heritability values. Seed yield expressed high genetic advance, moderate heritability indicating the preponderance of additive gene effects for this trait. The 100-seed weight also showed high heritability coupled with high genetic advance, suggesting the suitability of direct selection for this trait.

Sheela *et al.,* (2006) observed high heritability coupled with high genetic advance for characters plant height, number of branches, number of leaves, leaf length, stem thickness, leaf weight, stem weight, leaf stem ratio, green fodder yield, dry matter yield and crude protein content in cowpea.

Lal *et al.,* (2007) showed that higher estimates of heritability coupled with the higher genetic advance for number of peduncles per plant, number of days to flower, number of pods per plant and pod yield per plant indicated that heritability is mainly due to additive genetic effects. Eswaran *et al.,* (2007) studied that high estimates of genetic variability coupled with high heritability and genetic advance were observed for plant height at the time of first flowering, plant height at the time of 50 percent flowering and plant height at the time of 50 percent maturity, indicating their dependability for effecting selection.

Sharma *et al.,* (2007) revealed that the heritability and genetic advance were high for plant height and moderate for pods per plant and pod yield per plant indicating the additive and non-additive gene action for their expression, respectively. Bhandari and Verma (2008) revealed that heritability were high and coupled with high to moderate genetic advance for plant height, days to 50%flowering, number of leaves per plant, crude protein content and green forage yield in cowpea.

Suganthi *et al.,* (2008) was recorded high heritability for seed yield per plant, followed by number of seeds per pod, pod length and 100-seed weight. Genetic advance as percent of mean was highest for seed yield per plant, followed by number of pods per plant and number of clusters per plant. Bertini *et al.,* (2009) were recorded high heritability (90%) in cowpea for pod length, number of pods per plant, number of seeds per pods, weight of 100seeds, total yield per plant. It indicates the possibility of genetic improvement through selection.

Choudhary *et al.,* (2010) revealed that the high estimates of heritability, genotypic coefficient of variation and genetic advance were observed for plant height, number of pods per plant and green pod yield per plant. These characters can be effectively improved through selection. Singh *et al.,* (2012) reported that the high heritability (in narrow sense) estimates were recorded for pods per plant, seed yield per plant and biological yield per plant. High genetic advance was recorded for plant height, pods per plant, productive branches per plant, and seeds per pod, biological yield per plant and seed yield per plant.

2.7 Correlation

Correlation Coefficient is a statistical measure which is used to find out degree and direction of relationship between two or more variables. A positive value of correlation shows that changes of two variables are in the same direction whereas in the negative correlation movements of two variables are in the opposite direction Kalaiyarasi and Palanismy (2001) studied correlation for among 9 traits. The result indicated that seed yield per plant showed strong positive correlation with 100 seed weight, number of seed per pod, plant height, crude protein content, number of pods per plant and number of branches per plant and crude fiber content showed strong negative correlation with seed yield.

Pathak and Jamwal (2002) reported that the genotypic correlation coefficients were generally higher than the corresponding phenotypic correlation coefficients. At the phenotypic level, pod yield per plant was positively correlated with number of pods per plant, plant height and average pod weight. Positive associations were also observed between number of days to 50% flowering and number of days to first picking, number of pods per plant and plant height, pod length and number of seeds per pod and average pod weight. Thus, high-yielding cultivars may be developed via selection for greater number of pods per plant, plant height, average pod weight, pod length and number of seeds per pod.

Venkatesan *et al.,* (2003) reported that, the number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, and pod yield were positively correlated with seed yield at the genetic and phenotypic levels. The magnitude of genetic correlation was higher than that of phenotypic correlation.

Kutty *et al.,* (2003) an experiment showed the number of pods per plant, number of pickings, average weight of pods and pod length were positively and significantly correlated with yield per plant both at phenotypic and genotypic levels. Number of days to first picking showed significant negative correlation with number of pickings.

Vinieta *et al.,* (2003) studied in cowpea and reported that seed yield per plant was positively correlated with number of clusters and pods per plant, and 100-seed weight, but it was negatively correlated with days to maturity. Nigude *et al.,* (2004) reported that grain yield per plant was significantly and positively associated with all the characters except pod length and test weight at both levels. Xiao-Jie (2004) revealed that negative correlation was observed among the number of branches. Highly significant negative correlation was observed between the number of peduncles per plant and node length. A positive correlation was observed between the number of peduncles per plant and number of branches per plant, and between pod length and pod width. The correlation between the length of fruit and pod length was highly positive.

Singh *et al.,* (2004) found that green pod yield per plant was positively and significantly associated with number of primary branches per plant, pod length, pod diameter, number of pods per plant, number of seeds per pod and 100-seed weight. Days to 50 percent flowering and days to first green pod picking showed significant negative correlation with green pod yield per plant, indicating that selection should be based on these traits.

Anbumalarmathi *et al.,* (2005) revealed that single plant yield had positive and significant association with clusters per plant, pods per plant, pod length, seeds per pod and 100-seed weight as indices for improving yield in cowpea.

Chakraborty *et al.,* (2005) studied correlation coefficient between nine symbiotic traits in treatment combinations of nine genotypes of *Vigna* species and five Rhizobium strains of cowpea group with an uninoculated control. They reported that grain yield was positively correlated with total N content, Legheamoglobin content, nodule fresh weight, 100 seed weight, number of pods per plant, number of nodules per plant and chlorophyll content.

Patil *et al.,* (2005) revealed that seed yield per plant had positive and highly significant correlation with plant height at genotypic levels and number of pods per plant at both phenotypic and genotypic levels. Alege (2007) reported that positive correlations were obtained between leaf number and stem diameter, leaf number and number of seeds per pod, number of branches and plant height. Negative correlation existed between number of pods per plant and number of seeds per pod.

Dahiya *et al.,* (2007) study revealed that the seed yield per plant showed significant and positive association with No. of clusters per plant, No. of pods per plant, pod length, No. of seeds per pod, 100-seed weight and harvest index while it was negatively correlated with plant height.

Eswaran *et al.,* (2007) reported that Seed yield per plant had high significant positive correlation with total dry matter production and harvest index both at phenotypic and genotypic levels. Lal *et al.,* (2007) Correlation analysis pointed out the importance of number of peduncles per plant, number of pods per plant,

average pod weight and pod length towards pod yield. Sharma *et al.,* (2007) revealed that the positive association of pod yield per plant with pods per plant, pod length, seeds per pod and total soluble solids.

Suganthi *et al.,* (2008) reported that the seed yield had a positive and significant association with pod length in cowpea. Nehru *et al.,* (2009) the experiment was showed significant differences among the genotypes evaluated for all the characters. Correlation studies revealed that seed yield was correlated positively with all the characters during early kharif, but during late kharif, it was correlated only with the plant height.

Correa *et al.,* (2010) studied in cowpea and observed that positive and significant genetic correlations between all the traits and dry bean yield and the highest for days to flowering, mass of pods and number of seeds per pod. Singh *et al.,* (2011) reported that the numbers of pods per plant, plant height, number of primary branches per plant, 100 seed weight and number of clusters per plant were the major characters contributing to grain yield as these traits were significantly and positively associated with grain yield per plant.

 Cholin *et al.,* (2012) found that number of clusters per plant, pods per plant had positive correlation with seed yield whereas, clusters per plant, pod lengthand test weight had a positive direct effect on seed yield and days to maturity has negative direct effect on seed yield in cowpea. Manggoel *et al.,* (2012) reported in cowpea that Positive correlation between grain yield and number of peduncles per plant, flowers per plant, pods per plant and 100-seed weight.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Description of Experimental Site

The research was conducted at the Institute For Agricultural Research (IAR) Farm, Samaru, Ahmadu Bello University (ABU) Zaria (11^0 11' N: 7^0 38' E, 686m) in Northern Guinea Savanna of Nigeria in 2011/2012.

3.2 Description of the Plant Materials

The plant materials of this research consisted of five (5) genotypes, presented in Table 3.1. Four genotypes were obtained from the cowpea unit of IAR/ABU Zaria. The other two were obtained from the International Institute for Tropical Agriculture (IITA) Ibadan. The genotypes comprised three drought tolerant (IT98K-628, IT99K-7-21-2-2 and SAMPEA-10), two drought susceptible (SAMPEA-8(IT452-1) and BIU-LOCAL) and one check (Dan'ila).

3.3 Development of genetic populations and crosses

The genetic populations were developed in the screen house and evaluated in the field. The F_1s and the backcross populations were generated by emasculation and the parental materials were denoted as P_1, P_2, P_3 for female parent and P_4, P_5 for male parent. The male parent were crossed to the female parent to generate the F_1 populations. The F_1s were selfed to generate the F_2 populations and the F_1s were backcrossed to both the male and female parent to generate the backcross populations denoted as BC_1P_1 and BC_1P_2 for all the population studied.

Table 3.1 The source and description of the parental materials used in the experiment

Genotypes	Parents	Origin	Description
IT98K-628	P1	IITA	Drought tolerant, white large rough seed, high yielding with medium maturity (80-95 days).
IT99K-7-21-2-2	P2	IITA	Drought tolerant, high yield, white large rough seed grain medium maturity (85-90 days).
SAMPEA-10	P3	IAR	Drought tolerant and white large rough seed medium maturity (85-95 days).
SAMPEA-8(IT452-1)	P4	IAR	Drought susceptible, high yielding, white large black eye seed, famers preference, and medium maturity (85-95) days
BIU LOCAL	P5	IAR	Drought susceptible, white large black eye seed, farmers' preference and medium maturity (80-92 days).
DAN'ILA	CHECK	IAR	Drought tolerant and white medium smooth seed size medium maturity (85-95 days).

Source: IITA = International Institute of Tropical Agriculture; and IAR= Institute for Agricultural Research.

Paired crosses were made using five parents through hand emasculation by biparental mating design at the screen house of Plant Science Department, Ahmadu Bello University Zaria as follows; IT98K-628 x SAMPEA-8(IT452-1) (P_1 x P_4), IT99K-7-21-2-2 x SAMPEA-8(IT452-1) (P_2 x P_4), SAMPEA-10 x BIU LOCAL (P_3 x P_5), to obtain three F_1s. (Table 3.2)

The F_1s hybrids were advanced to obtain three F_2 generations through selfing. Six backcrosses were also obtained by reciprocal crosses to their respective parents at institute for Agricultural Research screen house Samaru. The Table 3.2 represents the crosses generated.

Table 3.2 Crosses, F_1, F_2 and Backcrosses developed.

Female parent	Male parent	F_1	F_2	Backcrosses	
P_1	P_4	$P_1 \times P_{4\ (cross\text{-}1)}$	$(P_1 \times P_4) \times (P_1 \times P_4)$	$BC_1 P_1$	$BC_1 P_4$
P_2	P_4	$P_2 \times P_{4\ (cross\text{-}2)}$	$(P_2 \times P_4) \times (P_2 \times P_4)$	$BC_1 P_2$	$BC_1 P_4$
P_3	P_5	$P_3 \times P_{5\ (cross\text{-}3)}$	$(P_3 \times P_5) \times (P_3 \times P_5)$	$BC_1 P_3$	$BC_1 P_5$

3.4 Experimental Design and Procedure

The three F_1 hybrids, three F_2, six backcrosses, five parental lines along with a commercial check (Dan'ila) making a total of eighteen entries were laid out in a Randomized Complete Block Design (RCBD) with three replications of one row/plot each of 5m in length with an inter and intra row spacing of 0.75cm and 0.25cm, respectively. Evaluation was conducted under the following conditions at the Institute for Agricultural Research Farm Samaru Zaria:

1. Water non-stress: continued to receive irrigation water once every week until physiological maturity.

2. Water Stress: water stress was imposed by withdrawing irrigation water as from 5 weeks after planting to ensure drought stress at flowering stage. Banziger *et al.,* (2000).

The two conditions were separated from each other by 2.5m alley to prevent spill-over at the water stress plots during the period of imposed water stress at the beginning and end of each replication; non experimental lines were raised to minimize the edge border effects. Irrigation water was applied to field capacity once every week to all the conditions during the first 5 weeks (35 days) after sowing. Apart from the targeted stress, the management of the trials was the same in all the two conditions. Two seeds were planted per/hill and later thinned to one plant after emergence. Weed control was done manually three times at two, five and seven weeks respectively after sowing.

3.5 Data collection.

Data were collected on the following characters base on five randomly selected plants per plot.

- **Days to 50% flowering:** the days after planting when 50% of the plants have bloomed.

- **Plant height (centimeter):** the length from ground level to the tip of the main axis was measured using meter rule shortly before harvest.

- **Days to pod maturity:** From planting to when 50% of the plants reach physiological maturity.

- **Number of mature pods per plant**: Total number of mature pod was counted at harvest from a random sample of five plants to calculate the mean number of pods per plant.

- **Number of seeds per pod:** The average number of seeds obtained from a random sample of five mature pods per plant was counted.

- **Pod yield per plant (PYPP) (g)**: matured pod on a plant were dried, cleaned and then weighed using a weighing balance.

- **Hundred seed weight (HSW) (g):** A random sample of hundred seeds was taken from the harvested bulk seed of each genotype and weighed using Mottler PM16 -N weighing balance of model ISCO7501.

- **Root length (cm).** At harvest, roots were separated from the shoots and were gently removed from the soil mass and measured using a meter rule from the base to the tip end of the tap root.

3.6 Statistical Analysis

The data collected from the different genetic populations were subjected to Analysis of Variance (ANOVA) and appropriate statistical tools. Mean separation was undertaken using Duncan's Multiple Range Test at 5% level of probability.

Analysis of variance (ANOVA) model for RCBD is;

$$y_{ik} = \mu + \alpha_i + \ + \ell_{ik}$$

Where; y_{ij} = an observation in treatment i

μ = The overall mean

α = The effect of treatment i

e_{ijk} = Random error

Table.3.3 Form of Analysis of Variance for Randomized Complete Block Design for one location

Sources	Df	MS	EMS
Replication	(r-1)		
Genotype	(g-1)	MS_1	$\sigma^2_e + r\,\sigma^2_g$
Error	(r-1)(g-1)	MS_2	σ^2_e
Totals	(rg-1)		

Where; r = number of replications, g = number of genotype

$$\sigma^2_g = \frac{MS_2 - MS_1}{r},$$

MS_g = mean squares due to genotypes

σ^2_g = genotypic variance

MS_e = error mean square

σ^2_e = error variance

r = number of replications.

3.6.1 Coefficient of variation

The coefficient of variation was calculated to measure the relative variability. The coefficient of variation (CV) was calculated thus:

$$CV = \left(S \middle/ \bar{X} \right) \times 100$$

Where

S = Standard deviation, and

$\bar{X}$ = mean

3.6.2 Joint scaling test

The model described by Cavalli (1952) was used to estimate the parameters of the model viz., m (mean), a (additive) and d (dominance), and to test the goodness of fit of the model.

$$\overline{p_1} = m - a$$

$$\overline{p_2} = m + a$$

$$\overline{F_1} = m + d$$

$$\overline{F_2} = m + \frac{1}{2}(d)$$

$$\overline{BCP_1} = m - \frac{1}{2}(a) + \frac{1}{2}(d)$$

$$\overline{BCP_2} = m + \frac{1}{2}(a) + \frac{1}{2}(d)$$

Where; m = mean

a = value of additive gene effects

d = value of dominance gene effects

3.6.3 Generation Mean Analysis (GMA)

Generation mean analysis was performed separately for each cross following the procedure described by Kang (1994). The calculation was done for the six generations of each cross. To determine the mode of inheritance of grain yields, the notation of Gamble's (1962) notations were used as:

$Y = m + \alpha a + \beta d + \alpha 2aa + 2\alpha\beta ad + \beta 2dd.$

Where

Y is the observed generation mean;

m is F_2 mean;

a is additive gene effects;

d is dominance gene effects;

aa is additive x additive epistatic gene effects;

ad is additive x dominance epistatic gene effects; and

dd is dominance x dominance epistatic gene effects.

α and β represent the coefficients for the genetic effects for the particular generation being estimated (Hayman, 1958; Mather and Jinks, 1982).

Means of six generations *viz.,* P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2 were used to estimate the six parameters model by following the equation given by Hayman (1958).

$m = F_2$

$d = BC_1P_1 - BC_1P_2$

$h = 2BC_1P_1 + 2BC_1P_2 + F_1 - 4F_2 - \frac{1}{2} P_1 - \frac{1}{2} P_2$

$i = 2BC_1P_1 + 2BC_1P_2 - (1/2 P_1) + \frac{1}{2} P_2$

$j = BC_1P_1 - BC_1P_2 - (1/2 P_1) + \frac{1}{2} P_2$

$l = P_1 - P_2 + \frac{1}{2} F_1 + 4F_2 - 4BC_1P_1 - 4BC_1P_2$

The variances of the estimates of gene effects were obtained as follows.

$Vm = VF_2$

$$V(d) = VBC_1P_1 + BC_1P_2$$

$$V(h) = 4(BC_1P_1 + BC_1P_2) + VF_1 + 16VF_2 + \tfrac{1}{2}(VP_1 + VP_2)$$

$$V(i) = 4(BC_1P_1 + BC_1P_2) + 16V\,F_2$$

$$V(j) = VBC_1P_1 + VBC_1P_2 + \tfrac{1}{4}(VBC_1P_1 + VP_2)$$

$$V(l) = VP_1 + VP_2 + 4VF_1 + 16(VF_2 + VBC_1P_1 + VBC_1P_2)$$

Where, Vm, V(d), V(h), V(i), V(j) and V(l) were variances of m, d, h, i, j and l, respectively. VP_1, VP_2, VF_1, VF_2, VBC_1P_1 and VBC_1P_2 were variances of the mean of these estimates that provided standard errors for testing the significance of corresponding estimates.

The significance of the above parameters is tested with the help of 't'. To test the significance of the estimates, the 't' values were calculated for each component by dividing the gene effect of respective components by their standard error (SE) as given below.

$$t(m) = \frac{m}{SE(m)} \qquad t(d) = \frac{d}{SE(d)} \qquad t(h) = \frac{h}{SE(h)}$$

$$t(i) = \frac{i}{SE(i)} \qquad t(j) = \frac{j}{SE(j)} \qquad t(i) = \frac{i}{SE(1)}$$

The calculated' values were compared with table 't' value at 5 and 1 percent level of significance, respectively at pooled degrees of freedom.

3.6.4 Heritability

Heritability is a measure of the efficiency of a selection system in separating genotypes. The quantitative traits are largely influenced by environments; therefore, those are not highly heritable. High, moderate and low heritability are not rigidly defined as it varies with character to character, but the following values are widely accepted (Robinson *et., al.* 1949). 1. Low heritability: 0 – 30 % 2. Moderate heritability: 30 - 60 % 3. High heritability: > 60 %. Both broad and narrow sense heritability estimates were calculated and presented in tabular data but heritability in narrow sense may be more helpful in the selection of segregating populations and that is why the genetic advance was calculated on the basis of narrow sense heritability to ascertain more reliable results.

In its broad sense, heritability was calculated in accordance with the procedures outlined by Allard (1960). Heritability in the narrow sense was calculated in accordance with the procedures outlined by Warner (1952).

Narrow sense heritability was estimated as follows:

$$H_{ns} = \frac{2\sigma^2 F_2 - \left(\sigma^2 BCP_1 + \sigma^2 BCP_2\right)}{\sigma^2 F_2} \times 100 \quad \text{(Warner, 1952)}$$

Where:

H_{ns} = Narrow sense Heritability

$\sigma^2 F_2$ = Variance of F_2 population

$\sigma^2 BC_1 P_1$ = Variance of the backcross to parent1

$\sigma^2 BC_2 P_2$ = Variance of the backcross to parent2

$\sigma^2 F_2$ = Variance of F_2 population

$\sigma^2 F_2 = {}^1\!/_2 A + {}^1\!/_4 D + E$

$\sigma^2B_1 + \sigma^2B_2 = {}^1\!/_2A + {}^1\!/_2D + E$

$2\,\sigma^2F_2 - \sigma^2B_1 - \sigma^2B_2 = A + {}^1\!/_2D + 2E - ({}^1\!/_2A + {}^1\!/_2D + 2E) = {}^1\!/_2A$

A = Additive genetic variance

D = Dominance variance

E = Environmental variance

B_1 = Backcross to parent P_1

B_2 = backcross to parent P_2

Assumptions are:

i.   Independence of genotypic and environmental variances

ii.   Additivity of genetic effects over the various loci.

iii. The F_2 and the two backcross variances are of comparable magnitude.

Broad sense heritability was estimated as follows:

$$H_{BS} = \frac{\sigma^2F_2 - \left(\sigma^2P_1 + \sigma^2P_2 + \sigma^2F_1\right)/3}{\sigma^2F_2} \times 100 \quad \text{(Allard, 1960)}$$

$\sigma^2F_2 = \sigma^2G + \sigma^2E \;\; \sigma^2F_1 = \sigma^2E_3 \;\; \sigma^2P_1 = \sigma^2E_1$

$\sigma^2F_2 = \sigma^2E_2$ In these relationships:

H_{BS} = Broad sense heritability

σ^2F_2 = Variance of F_2 population

σ^2P_1 = Variance of parent1

σ^2P_2 = Variance of parent2

σ^2F_1 = Variance of Fist filial generation

σ^2E = Environmental variance

Dabholkar (1992) classified heritability estimate as low (5% to 10%), medium (11% to 30%) and high (> 30%).

3.6.5 Genetic Advance (GA)

Genetic Advance (GA) was calculated in accordance with the method illustrated by

Allard (1960) as:

$$\text{GA or } G_s = K \times \sigma_e^2\, F \times h^2_{(n)}$$

Where:

G_s = Expectation of genetic advance under selection

K is the standardized selection differential, at 10 % selection intensity, K = 1.755

$\sigma^2 F$ = variance of F_2 population of a cross

$h^2_{(n)}$ = narrow sense heritability estimate.

The value of expected genetic advance for various characters is demarcated into three categories viz., low, moderate and high, as follows (Johnson *et al.,* 1955)

1. Low genetic advance: 0 - 10%

2. Moderate genetic advance: 10 - 20 %

3. High genetic advance : > 20 %

3.7 Correlations

Phenotypic and genotypic correlations were used to investigate the association among characters studied. correlation coefficients were calculated from component of variance and covariance according to the Shivaji and Gritton (1975) the genotypic components were computed by equating the genotypic variances and covariance to the expected mean square and set products, and hence genotypic correlations were computed by this formula:

$$r_g = \frac{COV_{g12}}{\sqrt{(\sigma^2_{g1})}\sqrt{\sigma^2_{g2}}}$$

r_g = Genotypic correlation coefficients (COV)

COV_{g12} = Estimate of genotypic variance of character 1 and 2.

σ^2_{ph1} = Estimate of phenotypic variance of character 1

σ^2_{g2} = Estimate of genotypic variance of character 1

Phenotypic correlations were computed by this formula:

$$r_p = \frac{COV_{ph12}}{\sqrt{(\sigma^2_{ph1})}\sqrt{\sigma^2_{ph2}}}$$

r_p = phenotypic correlation coefficients (COV)

COV_{ph12} = Estimate of phenotypic variance of character 1 and 2.

σ^2_{ph1} = Estimate of phenotypic variance of character 1

σ^2_{ph2} = Estimate of phenotypic variance of character 2

Decision of significance was made using error degree of freedom at 5% and 1%

4.0 RESULTS

4.1 Mean Squares.

The mean squares for water non-stress conditions from the analysis of variance are presented in Tables 4.1. The results from this study indicated highly significant differences among the genotypes (P < 0.01) for all the traits measured for cross-1, except for days to fifty percent flowering and root length. Cross-2, was found to be highly significant (P < 0.01) except for number of matured pods per plant and root length, also highly significant (P < 0.01) except for hundred seed weight and root length in cross-3. Table 4.2, under water stressed condition, showed high significant (P < 0.01) among the three sets of crosses except for days to 50% flowering, hundred seed weight in cross-1, number of matured pod per plant, hundred seed weight in cross-2 and hundred seed weight, root length in cross-3 that were not significant.

4.2 Mean Performance.

The mean, range and coefficient of variation for the traits studied in the three crosses are presented in the Tables 4.3 and 4.4. As presented in Table 4.3. In cross IT98K-628 X SAMPEA-8, the parent SAMPEA-8 flowered earlier (38.70 days) than the parent IT98K-628 (45.20days) with coefficient of variation of 10.01% and 9.89% respectively. The resistant parent was significantly different having the longest days to 50% flowering than the susceptible parent. However, the F_1 flowered earlier (36.47days) than both parents with coefficient of variation 7.82%. Among the generations backcross to both parents. F_2, BC_1P_1, and BC_1P_4 showed to be significantly different.

In cross-2 IT99K-7-21-2-2 flowered earlier (41.20days) than SAMPEA-8 (42.00 days) with coefficient of variation 8.26% and 8.80% respectively but both parents were statistically similar despite the susceptible parent having the highest mean value among parents. However, the F_1 flowered earlier (39.17days) than both parents with coefficient of variation 9.60% showed to be statistically similar to the resistant parent and backcross to parent one.

In the cross SAMPEA-10 x BIU LOCAL (cross-3) showed that BIU LOCAL flowered earlier (36.33days), than the resistant parent SAMPEA-10 (44.20days) it showed to be statistically different from the susceptible parent despite having the longer days to 50% flowering across the six generations with coefficient of variation 6.62% and 8.89% respectively. Among crosses F_2 and BC_1P_5 were statistically similar and F_1 and the susceptible parent were statistically the similar. However, F_1 flowered almost the same time with SAMPEA-10 (37.00days) with the susceptible parent BIULOCAL coefficient of variation 4.20%.

For plant height, days to pod maturity, number of seeds per pod, pod yield per plant and hundred seed weight as shown in Table 4.3. In the cross IT98K-628 x SAMPEA-8, the resistant parent, IT98K-628   had a mean height of 46.96cm and a range between 19cm and 49cm been the tallest among the six generations and statistically different from the susceptible parent and the crosses .

Table 4.1 Mean squares observed from three crosses for eight agronomic traits of cowpea under water non-stress condition grown in IAR farm, Samaru in 2013.

Cross	Source of variation	df	D50%F	PH	DPM	NMPP	PYPP	NSPP	HSW	RL
1	Rep	2	15.33	0.84	0.56	0.43	1.49	0.58	0.92	0.11
	Genotype	16	64.73	319.63**	284.10**	12.48**	6.62**	183.02**	2.26	3.69**
	Error	32	52.21	55.32	52.78	5.56	2.92	20.63	1.41	4.85
2	Rep	2	17.45	0.97	0.43	0.67	1.58	0.72	0.39	0.20
	Genotype	16	70.10**	299.60**	254.19**	12.50	5.72**	172.11**	2.96	3.19**
	Error	32	52.21	55.32	52.78	5.56	2.92	20.63	1.41	4.85
3	Rep	2	12.20	1.11	0.33	1.10	2.42	0.60	1.09	0.15
	Genotype	16	87.23**	301.57**	244.18**	18.27**	7.29**	190.82**	2.77	2.89
	Error	32	47.29	50.35	71.20	4.99	2.97	21.23	1.49	4.89

**Highly significant at 1% level of probability, Cross 1= IT98K-628 X SAMPEA-8, Cross 2=IT99K-7-21-2-2 X SAMPEA-8, Cross 3= SAMPEA-10 X BIU LOCAL, D50%F: Days to fifty percent flowering, PH (cm): Plant height, DPM: Days to pod maturity, NMPP: Number of mature pod per plant, NSPD: Number of seeds per pod, PYPP: Pod yield per plant, HSW: Hundred seed weight, RL: Root length.

Table 4.2 Mean squares observed from three crosses for eight agronomic traits of cowpea under water stress condition grown in IAR farm, Samaru in 2013.

Cross	Source of variation	df	D50%F	PH	DPM	NMPP	PYPP	NSPP	HSW	RL
1	Rep	2	11.19	0.87	0.66	0.53	2.01	0.38	0.97	0.10
	Genotype	16	62.13	299.63**	270.10**	10.49**	6.69**	183.92**	2.36	3.87**
	Error	32	50.11	59.37	48.70	1.56	2.90	20.44	1.47	4.22
2	Rep	2	14.00	0.82	0.16	0.47	1.69	0.88	0.71	0.42
	Genotype	16	74.88**	290.60**	244.13**	12.40	5.39**	170.17**	2.90	3.12**
	Error	32	46.00	55.15	52.70	5.59	2.90	20.22	1.31	4.60
3	Rep	2	12.10	1.55	0.39	1.30	2.57	0.63	1.19	0.55
	Genotype	16	77.50**	278.57**	260.22**	18.97**	5.21**	189.82**	3.07	2.99
	Error	32	67.85	58.40	62.90	7.21	1.99	20.40	1.58	4.80

**Highly significant at 1% level of probability, Cross 1= IT98K-628 X SAMPEA-8, Cross 2=IT99K-7-21-2-2 X SAMPEA-8, Cross 3= SAMPEA-10 X BIU LOCAL, D50%F: Days to fifty percent flowering, PH (cm): Plant height, DPM: Days to pod maturity, NMPP: Number of mature pod per plant, NSPD: Number of seeds per pod, PYPP: Pod yield per plant, HSW: Hundred seed weight, RL: Root length.

Table 4.3. Range, mean and CV of eight agronomic traits, for parents, F_1, F_2 and   backcross populations of three cowpea crosses evaluated under water non-stress condition at IAR farm, Samaru 2013.

Generation/Cross	Days to 50% Flowering			Plant Height (cm)			Days to Pod Maturity		
	Range	Mean	CV(%)	Range	Mean	CV(%)	Range	Mean	CV(%)
IT98K-628 X SAMPEA-8									
IT98K-628 (R)	35-46	45.20a	9.89	19-49	46.96a	8.69	70-108	84.43a	8.25
SAMPEA-8 (S)	27-39	38.70c	10.01	25-46	44.30b	9.22	72-110	73.03d	7.96
F_1	22-37	36.47d	7.82	28-44	38.21c	11.48	78-101	80.52b	1.44
F_2	39-44	43.11b	8.36	24-40	37.76cd	6.01	68-99	81.19bc	9.74
BC_1P_1	30-42	38.94cd	8.32	20-38	34.98d	10.3	74-100	75.40c	9.87
BC_1P_4	35-39	37.29de	6.47	25-37	33.04de	7.63	71-101	72.64de	8.52
IT99K-7-21-2-2 X SAMPEA-8									
IT99K-7-21-2-2 (R)	38-49	41.20ab	8.80	19-47	40.96a	8.69	70-108	89.43a	8.01
SAMPEA-8 (S)	36-44	42.00a	8.26	22-40	39.07ab	8.04	75-109	78.09c	7.91
F_1	35-46	39.17bc	9.60	25-39	37.02b	6.21	71-100	80.75b	9.28
F_2	33-39	34.88c	7.95	19-39	34.15c	8.84	72-98	75.21d	6.48
BC_1P_2	30-42	40.50b	9.89	18-37	33.09cd	9.99	74-108	79.56bc	9.66
BC_1P_4	30-41	34.59cd	8.73	21-38	31.32d	5.97	73-115	74.45de	23.72
SAMPEA-10 X BIU LOCAL									
SAMPEA-10 (R)	34-48	44.20a	8.89	19-47	40.96b	8.69	70-108	78.39de	8.25
BIU LOCAL (S)	35-47	36.33cd	6.62	24-39	37.77cd	7.01	77-111	92.62a	7.26
F_1	34-40	37.00c	4.20	21-40	35.59de	8.12	69-117	80.07d	5.51
F_2	30-41	40.67b	7.93	19-48	46.12a	9.28	76-103	89.95bc	7.89
BC_1P_3	33-40	35.50d	9.11	19-39	36.69d	9.82	35-100	91.32ab	6.33
BC_1P_5	37-43	39.50bc	9.63	21-42	37.98c	7.10	43-102	91.19b	8.92

R = resistant, S = susceptible, CV = coefficient of variation, F_1 = first filial generation, F_2 = second filial generation

Table 4.3 Continued under water non-stress condition

Generation/Cross	Number of seeds per plant			Pod yield per plant			Hundred seed weight (g)		
	Range	Mean	CV(%)	Range	Mean	CV(%)	Range	Mean	CV(%)
IT98K-628 X SAMPEA-8									
IT98K-628 (R)	4.51-19.20	17.20c	6.89	19-27	20.96c	4.69	30-58	56.43a	2.25
SAMPEA-8 (S)	5.37-24.10	20.70ab	7.98	15-26	19.35cd	9.22	20-44	43.03de	4.96
F_1	8.20-20.13	18.47d	1.29	13-23	14.25e	2.48	38-52	50.52b	2.44
F_2	8.29-22.04	21.11a	8.36	14-26	23.76b	3.01	26-46	43.19d	3.74
BC_1P_1	7.20-17.20	14.94d	8.32	10-27	25.98a	5.30	25-51	47.40bc	4.87
BC_1P_4	4.83-19.82	17.29bc	6.47	15-29	19.04d	1.63	38-49	48.64bc	8.52
IT99K-7-21-2-2 X SAMPEA-8									
IT99K-7-21-2-2 (R)	4.05-18.20	17.20b	2.89	19-21	20.01a	1.60	29-49	48.10b	1.25
SAMPEA-8 (S)	6.10-19.90	18.00ab	5.26	12-26	19.07ab	2.04	19-51	48.09bc	2.91
F_1	5.20-16.66	14.87c	4.60	15-21	17.02bc	6.21	21-45	40.75d	5.28
F_2	3.66-19.31	18.81a	5.95	13-29	14.15d	5.84	20-57	55.21a	3.48
BC_1P_2	2.90-15.21	14.50cd	3.89	15-21	18.09b	1.99	24-41	39.56e	2.61
BC_1P_4	5.30-18.01	16.56bc	3.73	10-23	11.32e	2.97	23-46	40.45de	2.11
SAMPEA-10 X BIU LOCAL									
SAMPEA-10 (R)	5.5-17.8	15.20cd	1.89	9-20	10.96f	1.14	30-49	46.43c	3.20
BIU LOCAL (S)	6.3-20.7	15.33c	6.62	14-26	17.77d	7.11	37-56	52.62b	2.01
F_1	5.9-19.3	18.00a	4.10	11-27	25.59a	3.82	21-43	40.77e	5.52
F_2	4.3-17.9	15.67bc	1.08	19-21	20.12c	1.47	36-52	43.35d	3.89
BC_1P_3	5.7-18.4	16.50b	4.22	13-29	22.69b	4.01	35-71	69.31a	3.99
BC_1P_5	9.1-19.1	16.86ab	2.67	11-23	15.98de	5.10	33-47	40.19ef	3.33

R = resistant, S = susceptible, CV = coefficient of variation, F_1 = first filial generation, F_2 = second filial generation

The susceptible parent SAMPEA-8 had a mean of 44.30cm with a range between 25cm and 46cm. The F_1 hybrid had a mean of 38.21cm with a range between 28cm and 44cm is statistically similar to F_2. There were segregation among the F_2 population with the range of the F_2 being 24cm and 40cm coupled with the CV of 6.01% and mean height of 37.76cm. Mean Plant height for the backcrosses, BC_1P_1 and BC_1P_4 were 34.98cm and 33.04cm, respectively were statistically similar. In the second cross: IT99K-7-21-2-2 x SAMPEA-8, the parent IT99K-7-21-2-2 had a mean plant height of 40.96cm statistically similar from the second parent and range between 19cm and 47cm. The F_1 generation from this cross had a mean plant height of 37.02cm. The F_2 population for the cross had a range from 19cm to 39cm with mean of 34.15cm and CV of 8.84%, F_1 and F_2 were statistically different. The BC_1P_2 and BC_1P_4 had mean values of 33.09cm and 31.32cm, respectively showed to similar statistically. In the (cross-3) SAMPEA-10 x BIU LOCAL, SAMPEA-10 had a mean plant height of 40.96cm, with the range of 19cm to 47cm, showed to be statistically different from BIU LOCAL with a mean plant height of 37.77cm and range of 24cm - 39cm. The F_1 mean was 35.59cm with a range of 21cm – 40cm, the F_2 ranges from 19cm - 48cm with mean plant height of 46.12cm and CV of 9.28%. The BC_1P_3 and BC_1P_5 had mean values of 36.69cm and 37.98cm, respectively. Across the generations BIU LOCAL, F_1 and BC_1P_3 were statistically similar despite the susceptible parent being the tallest. While SAMPEA-10, and F_2 were statistically different across the generations, also BIU LOCAL and BC_1P_5 were statistically similar.

Pod yield per plant F_1 had a mean value of 14.25g, with range of 13g – 23g and CV of 2.48% showed to be statistically different across the generations. The F_2 recorded mean of 23.76g, range of 14g – 26g and CV of 3.01%. BC_1P_1 mean was 25.98g with CV of 5.30% and range of 10g- 27g, while BC_1P_4 of the same cross had mean of 19.04g, CV of 1.63% and range of 15g – 29g. Significantly, both the two parents were statistically similar, the F_1 and BC_1P_1 were statistically similar. In (cross-2) IT99K-7-21-2-2 x SAMPEA-8, the F_1 mean was 17.02g, with range of 15g – 21g and CV of 6.21%. F_2 has mean of 14.15g, range of 13g – 29g and CV of 5.84%. BC_1P_2 mean was 18.09g with CV of 1.99% and range of 15g- 21g, while BC_1P_4 of the same cross had mean of 11.32g, CV of 2.97% and range of 10g – 23g. For the cross; SAMPEA-10 x BIU LOCAL, the F_1 had the mean pod yield per plant of 25.59g, with range of 11g – 27g and CV of 3.82%. The F_2 recorded mean of 20.12g, range of 19g – 21g and CV of 1.47%. BC_1P_3 mean was 22.69g with CV of 4.01% and range of 13g- 29g, while BC_1P_5 of the same cross had mean of 15.98g, CV of 5.10% and range of 11g – 23g.

100 seed weight recorded 50.52g mean for F_1, with range of 38g – 52g and CV of 2.44%. The F_2 mean of 43.19g, range of 26g – 46g and CV of 3.74%. BC_1P_1 mean was 47.40g with CV of 4.87% and range of 25g- 51g, while BC_1P_4 of the same cross had mean of 48.64g, CV of 8.52% and range of 38g – 49g. For the cross; IT99K-7-21-2-2 x SAMPEA-8, F_1 had the mean weight of 40.75g, with range of 21g – 45g and CV of 5.28%. The F_2 recorded mean of 55.21g, range of 20g – 57g and CV of 3.89%. BC_1P_2 mean was 39.56g with CV of 2.61% and range of 24g- 41g, while BC_1P_4 of

the same cross had mean of 40.45g, CV of 2.11% and range of 23g – 46g. Cross

between SAMPEA-10 x BIU LOCAL, the F_1 weight 40.77g, with range of 21g – 43g

and CV of 5.52%. The F_2 recorded mean 100 grain weight of 43.35g, range of 36g –

52g and CV of 3.89%. BC_1P_3 mean was 69.31g with CV of 3.99% and wide range of

33g-71g, while BC_1P_5 of the same cross had mean of 40.19g, CV of 3.33% and range

of 33g – 47g.

(Table 4.4). The cross IT98K-628 X SAMPEA-8 showed that SAMPEA-8 flowered

earlier (37 days) than IT98K-628 (38 days) with the mean and coefficient of variation

of 44.70d and 5.90% and 40.90d and 6.19% respectively. However, the F_1 flowered

almost the same time with BC_1P_4 (36 days) with the mean and coefficient of 38.47d

and 8.29%. IT99K-7-21-2-2 x SAMPEA-8 showed that IT99K-7-21-2-2 flowered

earlier (35days) than susceptible SAMPEA-8 (37days) parent with the mean and

coefficient of 38.20d and 7.89% and 40.00d and 8.26% respectively. For cross-3,

SAMPEA-10 flowered earlier (35 days) than BIU LOCAL (37 days) with the mean

and coefficient of variation of 40.20d and 7.89% and (44.33 and 6.62) respectively.

However, in these cross F_1 flowered almost the same time with SAMPEA-10 (35

days) with the mean and coefficient of variation 42.00d and 4.20%.

Plant height for the cross IT98K-628 x SAMPEA-8, the resistant parent, IT98K-628

had a mean height of 32.35cm and a range between 20cm and 36cm. SAMPEA-8 had

a mean of 33.35cm with a range between 22cm and 35cm. The F_1 hybrid had a mean

height of 34.25cm taller than both the two parent with a range between 26cm and

40cm.

Table 4.4 Range, mean and CV of Range, mean and CV of eight agronomic traits, for parents, F_1, F_2 and backcross populations of three cowpea crosses evaluated, under water stress condition at IAR farm, Samaru 2013.

Generation/Cross	Days to fifty percent flowering			Plant height (cm)			Days to pod maturity		
	Range	Mean	CV(%)	Range	Mean	CV(%)	Range	Mean	CV(%)
IT98K-628 X SAMPEA-8									
IT98K-628 (R)	38-43	40.90cd	6.19	20-36	32.35e	8.69	80-108	96.43a	7.25
SAMPEA-8 (S)	37-48	44.70a	5.90	22-35	33.35cd	9.22	79-120	83.03c	6.96
F_1	36-46	38.47e	8.29	26-40	34.25bc	9.48	80-112	82.52cd	6.44
F_2	39-44	40.11de	7.36	26-38	33.76c	9.01	78-126	79.19e	8.74
BC_1P_1	34-44	43.94ab	8.32	20-39	35.90b	7.33	75-111	77.40ef	7.87
BC_1P_4	36-44	41.29c	6.47	25-40	39.04a	8.63	84-124	88.64b	8.52
IT99K-7-21-2-2 X SAMPEA-8									
IT99K-7-21-2-2									
(R)	35-40	38.20bc	7.89	31-43	41.96d	8.09	80-108	98.43a	6.25
SAMPEA-8 (S)	37-42	40.00ab	8.26	22-51	49.07a	7.04	79-100	88.09b	6.91
F_1	35-46	39.87b	6.60	25-49	47.00b	6.21	71-105	80.75d	5.28
F_2	33-37	34.81d	5.95	28-45	44.11c	5.33	82-101	85.21c	5.99
BC_1P_2	39-42	40.50a	7.89	34-45	43.00cd	6.99	64-108	79.56e	8.66
BC_1P_4	32-41	34.56de	6.73	21-42	41.01de	7.97	63-102	80.45de	6.72
SAMPEA-10 X BIU LOCAL									
SAMPEA-10 (R)	35-43	40.20d	7.89	20-44	40.12d	8.69	70-108	76.43d	7.25
BIU LOCAL (S)	37-47	44.33a	6.62	26-48	47.70ab	7.14	77-111	82.62ab	6.26
F_1	35-41	42.00b	4.20	21-39	38.59e	8.82	71-117	80.77b	5.51
F_2	33-43	40.67c	5.93	21-47	46.00b	7.98	69-123	83.35a	9.89
BC_1P_3	38-42	40.50cd	4.11	19-43	42.69c	9.82	75-117	79.91c	5.33
BC_1P_5	37-45	41.56bc	6.63	21-49	47.98a	6.11	73-102	80.19bc	6.92

R = resistant, S = susceptible, CV = coefficient of variation, F_1 = first filial generation, F_2 = second filial generation

Table 4.4 Continued under water stress condition

Generation/Cross	Number of seeds per pod			Pod yield per plant			Hundred seed weight (g)		
	Range	Mean	CV(%)	Range	Mean	CV(%)	Range	Mean	CV(%)
IT98K-628 X SAMPEA-8									
IT98K-628 (R)	5.4-16.0	13.26cd	6.89	8.7-23	9.96de	5.69	30-58	46.47a	1.29
SAMPEA-8 (S)	6.3-18.2	16.72a	1.98	9.2-14	10.35d	2.01	21-40	33.03e	2.96
F_1	4.4-19.8	14.47b	1.29	12–16	14.25bc	1.88	28-41	40.52c	1.44
F_2	9.4-16.0	14.11bc	2.31	13-20	16.76a	3.87	31-46	43.19b	0.74
BC_1P_1	8.2-17.5	13.91c	2.37	13-19	15.98ab	1.93	25-39	37.40d	4.07
BC_1P_4	7.3-13.4	12.20d	1.40	12-19	14.84b	1.69	28-44	38.64cd	2.15
IT99K-7-21-2-2 X SAMPEA-8									
IT99K-7-21-2-2 (R)	5.8-12.0	10.20e	1.20	9.4-17	10.96cd	1.39	28-58	41.43b	1.35
SAMPEA-8 (S)	8.3-15.4	14.90cd	1.26	11-15	12.07bc	1.04	19-49	38.09de	1.91
F_1	6.6-17.8	15.07c	1.66	13-18	14.00ab	5.20	21-45	40.75bc	4.18
F_2	6.7-20.8	18.44a	0.95	12-17	14.15a	5.80	22-47	45.21a	2.41
BC_1P_2	7.7-18.4	17.51ab	3.89	12-20	13.79b	2.99	34-48	39.56c	2.60
BC_1P_4	5.5-16.3	14.76d	3.73	10-15	11.32c	1.90	23-42	39.45cd	2.10
SAMPEA-10 X BIU LOCAL									
SAMPEA-10 (R)	5.5-19.9	15.29c	1.79	14-18	16.96a	5.68	30-48	36.43d	1.87
BIU LOCAL (S)	5.1-17.0	15.33bc	2.62	14-19	15.77ab	3.14	37-51	42.62ab	2.21
F_1	6.5-18.6	17.00a	1.99	10-20	11.59d	5.82	31-57	40.77b	4.81
F_2	4.3-17.7	15.67b	2.93	12-26	14.12bc	2.98	36-44	43.35a	3.89
BC_1P_3	5.1-19.7	16.59ab	1.71	13-22	14.69b	2.09	35-47	39.31bc	2.11
BC_1P_5	6.9-16.9	14.56cd	2.03	11-20	12.98cd	3.16	33-49	36.19de	1.99

R = resistant, S = susceptible, CV = coefficient of variation, F_1 = first filial generation, F_2 = second filial generation

There were high level of segregation among the F_2 populations with the range of 26cm and 38cm couple with the CV of 9.01% and mean height of 33.76cm. For the backcrosses, BC_1P_1 and BC_1P2 were 35.90cm and 39.04cm, respectively. The cross: IT99K-7-21-2-2 x SAMPEA-8, IT99K-7-21-2-2 had a mean plant height of 41.96cm and range between 31cm and 43cm. The F_1 generation from this cross had a mean plant height of 47.00cm. F_2 population had a range from 28cm to 45cm with mean of 44.11cm and CV of 5.33%. The BC_1P_2 and BC_1P_4 had mean values of 43.00cm and 41.01cm, respectively. The cross between SAMPEA-10 x BIU LOCAL, SAMPEA-10 had a mean plant height of 40.12cm, with the range of 20cm - 44cm. BIU LOCAL had a mean plant height of 47.70cm, with the range of 26cm - 48cm. The F_1 mean was 38.59cm, and the F_2 ranges from 21cm - 47cm with mean plant height of 46.00cm and CV of 9.28%. The BC_1P_3 and BC_1P_5 had mean values of 42.69cm and 47.98cm, respectively.

The mean pod yield per plant in the cross IT98K-628 X SAMPEA-8 was recorded of 14.25g, with range of 12g – 16g and CV of 1.88% F_1. The F_2 recorded mean of 16.76g, range of 13g – 20g and CV of 3.87%. BC_1P_1 mean was 15.98g with CV of 1.93% and range of 13g- 19g, while BC_1P_4 of the same cross had mean of 14.84g, CV of 1.69% and range of 12g – 19g. For the cross; IT99K-7-21-2-2 x SAMPEA-8, the F_1 mean was 14.00g, with range of 13g – 18g and CV of 5.20%. The F_2 recorded mean of 14.15g, range of 12g – 17g and CV of 5.80%. BC_1P_2 mean was 13.79g with CV of 2.99% and range of 12g- 20g, while BC_1P_4 of the same cross had mean of 11.32g, CV of 2.90% and range of 10g – 15g. SAMPEA-10 x BIU LOCAL, the F_1 had mean of 11.59g, with range of 10g – 20g and CV of 5.82%.

The F_2 recorded mean of 14.12g, range of 10g – 20g and CV of 2.98%. BC_1P_3 mean was 14.69g with CV of 2.09% and range of 13g- 22g, while BC_1P_5 had mean of 12.98g, CV of 3.16% and range of 11g – 20g.

For 100 seed weight recorded 40.52g for F_1, with range of 28g – 41g and CV of 1.44%. The F_2 mean weight 43.19g, range of 31g – 46g and CV of 0.74%. BC_1P_1 had a mean 37.40g with CV of 4.07% and range of 25g- 39g, while BC_1P_2 of the same cross had mean of 38.64g, CV of 2.15% and range of 28g – 44g. For the cross; IT99K-7-21-2-2 x SAMPEA-8, the F_1 had the mean 100 seed weight of 40.75g, with range of 21g – 45g and CV of 4.18%. The F_2 recorded mean weight of 45.21g, range of 22g – 47g and CV of 2.41%. BC_1P_2 mean was 39.56g with CV of 2.60% and range of 34g- 48g, while BC_1P_4 of the same cross had mean of 39.45g, CV of 2.10% and range of 23g – 42g. For the third cross; SAMPEA-10 x BIU LOCAL, the F_1 had mean of 40.77g, with range of 31g – 57g and CV of 4.81%. The F_2 recorded mean of 43.35g, range of 36g – 44g and CV of 3.89%. BC_1P_3 mean was 39.31g with CV of 2.11% and range of 35g- 47g, while BC_1P_5 of the same cross had mean of 36.19g, CV of 1.99% and range of 33g – 49g.

SAMPEA-8 recorded the highest mean for days to 50% flowering (44.70) and hundred seed weight (46.47g) in the cross IT98K-628 x SAMPEA-8, BIU LOCAL recorded the highest mean for plant height (47.70cm) in the cross SAMPEA-10 x BIU LOCAL, IT99K-7-21-2-2 recorded the highest mean for days to pod maturity (98.43d) in the cross IT99K-7-21-2-2 x SAMPEA-8 , SAMPEA-8 recorded the highest mean for number of seeds per pod in the cross IT98K-628 x SAMPEA-8,

SAMPEA-10 recorded the highest mean for pod yield per plant (16.96) in cross SAMPEA-10 x BIU LOCAL. There was segregation among the F_2 and backcross populations. F_2, BC_1P_1, and BC_1P_4 showed significant differences for plant height, days to pod maturity, number of seeds per pod, pod yield per plant and hundred seed weight as shown in Table 4.4.

4.3 Estimates of Gene Effects

The estimates of the genetic effects and their magnitudes for each trait for Joint scaling tests under water non-stress condition are presented in Tables 4.5, 4.6 and 4.7. Data were subjected to three parameter model under joint scaling tests to test the adequacy of additive-dominance model, under non-stress condition. The calculated chi-square at 3 degree of freedom was not significant for cross-2 and cross-3. There was significance for number of matured pods per plant, pod yield per plant and hundred seed weight in cross-1. Haymen's (1958) six parameter model was followed to estimate gene interaction effects based on mean values of the six generations.

The six-parameter model for cross-1 (Table 4.5) showed that additive effects were highly significant ($p < 0.01$) and positive for number of matured pods per plant and pod yield per plant but negative and highly significant ($p < 0.01$) for hundred seed weight. Dominant effects and additive-by-additive epistasis were non-significant for all the traits. Additive-by-dominant effects were highly significant ($p < 0.01$) and negative for number of matured pod per plant, and pod yield per plant. Dominant-by-dominant effects were highly significant ($p < 0.01$) and positive only for pod yield per plant.

55

Gene effects for cross-2 (Table 4.6), showed that mean effects of the three parameter model were highly significant (p < 0.01) and positive for all the eight agronomic traits evaluated the additive effect were highly significant (p < 0.01) and positive only for number of matured per plant but non-significant for the traits while non-significant for dominant effects.

Table 4.5. The estimates of gene effects for eight quantitative characters for cross-1 evaluated in water-non stress at Samaru, 2013.

Parameters	D50%F	PH(cm)	DPM	NMPPP	PYPP	NSPP	100SW(g)	RL(cm)
Three parameters								
M	4.4 ± 2.9**	39.2 ± 3.4**	109.4 ± 5.1**	13.8 ± 5.6	7.2 ± 4.8	6.7 ± 4.5**	47.2 ± 4.5**	0.16±0.21 *
D	-3.2 ± 1.2	-0.8 ± 1.4	-4.2 ± 2.4	112.1 ± 2.2**	1.2 ± 2.2	11.0 ± 9.0	-14.2±3.1**	0.26±0.01**
H	-8.2 ± 3.1	-9.2 ± 4.4	-7.2 ± 3.3	7.8 ± 5.1	11.0 ± 9.0	-0.8 ± 0.9	4.2 ± 1.9	0.20±0.04**
X^2	1.6	3.0	4.0*	14.7**	14.0**	0.4	17.9**	0.1
Six parameters								
m			109.2 ± 10.4	43.8 ± 15.0	31.0 ± 14.0		78.5±24.2**	
d			-9.2 ± 1.5	12.8 ± 1.8**	11.0 ± 1.7**		-14.5±1.8**	
h			-25.0 ± 11.5	-23.8 ± 35.0	-32.0 ± 29.1		-117.2±54.1	
i			0.8 ± 12.11	-73.8 ± 5.9	-21.0 ± 9.0		32 ± 22.4	
j			6.2 ± 10.1	-23.8±12.6**	-41.0±14.0**		3.3 ± 19.5	
l			19.2 ± 10.6	-3.8 ± 12.6	2.0 ±2 9.0**		97.3 ± 44.8	

cross 1= IT98K-628 x SAMPEA-8. Estimates of gene effect were significantly different from zero at 0.05 (*) and 0.01 (**) probability level. m=mean effect, d=additive gene effect, h=dominance gene effect, i=additive x additive gene effect, j=additive x dominance gene effect, l=dominance x dominance gene effect, X^2=chi-square.

100 seed weight was also highly significant ($p < 0.01$) but negative. (Table 4.6) Dominant effects and dominant-by-dominant effects were non-significant for all the traits in the cross. Additive-by-additive epistasis was highly significant ($p < 0.01$) and positive for number of matured pods per plant. Additive-by-dominant effects were highly significant ($p < 0.01$) and positive for hundred seed weight.

Additive effects were highly significant ($p < 0.01$) but negative for number of matured pods per plant and hundred seed weight (Table 4.7). Dominant effects were highly significant and positive ($p < 0.01$) for number of matured pods per plant and pod yield per plant. Additive-by-additive epistases were highly significant ($p < 0.01$) and positive for number of matured pods per plant and pod yield per plant. Additive-by-dominant effects were non-significant for all the traits. Dominant-by-dominant effects were significant ($p < 0.05$) and negative for number of matured pods per plant, and pod yield per plant.

The result from the analysis of six parameter model in the cross-3 SAMPEA-10 x BIU LOCAL showed that mean effect for 100 seed weight were highly significant and positive ($p < 0.01$). The dominant effect were highly significant and positive ($p < 0.01$) for number of matured pods per plants and pod yield per plant, Additive-by-additive was highly significant and positive ($p < 0.01$) for number of matured pods per plants and 100 seed weigh.

Table 4.6. The estimates of gene effects for eight quantitative characters for cross-2 evaluated in water-non stress at Samaru, 2013.

Parameters	D50%F	PH(cm)	DPM	NMPPP	PYPP	NSPP	100SW(g)	RL(cm)
Three parameters								
M	36.2 ±1.4**	38.1 ± 3.1**	110.2 ± 3.4**	121.1 ± 4.3**	14.2 ± 3.2**	13.7 ± 3.2**	54.2 ± 6.3**	0.62±0.2 *
D	-1.2 ± 0.4	2.2 ± 1.4	-2.6 ± 2.0	6.8 ± 2.3**	4.7 ± 3.9	7.2 ± 6.0	-8.2 ± 2.6	0.10±0.2
H	-0.5 ± 1.8	-2.3 ± 3.1	-6.2 ± 4.4	-6.8 ± 8.6	10.2 ± 6.0	-0.7 ± 1.5	-1.8 ± 3.2	0.51±0.4 *
X^2	0.7	3.1	4.2*	6.2*	5.3*	0.3	23.8**	0.1
Six parameters								
m			89.6 ± 14.3	11.8 ± 15.2	17.2±15.0		56.4±23.2**	
d			-3.6 ± 1.8	6.8 ± 3.6**	7.0± 6.2**		-6.5 ± 3.0**	
h			39.2 ± 22.2	33.8 ± 45.6	30.2±4 6.4		-134.2±63.8	
I			29.2 ± 14.1	1.8 ± 15.6**	1.7 ±1 6.8		5.2 ± 32.2	
j			16.2 ± 9.4	-14.9 ± 14.8	-17.2±14.5		14.0 ± 3.2**	
l			-29.2 ± 12.4	-33.8 ± 35.9	-30.0±26.9		54.9 ± 43.2	

 Cross 2= IT99K-7-21-2 x SAMPEA-8. Estimates of gene effect were significantly different from zero at 0.05 (*) and 0.01 (**) probability level. m=mean effect, d=additive gene effect, h=dominance gene effect, i=additive x additive gene effect, j=additive x dominance gene effect, l=dominance x dominance gene effect, X^2=chi-square,

Table 4.7. The estimates of gene effects for eight quantitative characters for cross-3 evaluated in water-non stress at Samaru, 2013.

Parameters	D50%F	PH(cm)	DPM	NMPPP	PYPP	NSPP	100SW(g)	RL(cm)
Three parameters								
M	39.4 ± 1.6**	35.2 ± 3.0**	102.7 ± 4.1**	23.8 ± 5.0*	16.2 ± 4.0**	17.9 ± 4.1**	36.2 ± 4.8**	0.36±0.11
D	-0.7 ± 0.5	-1.8 ± 1.6	-3.2 ± 2.0	-4.8 ± 2.1	-6.2 ± 0.9	-1.8 ± 0.6**	-3.2 ± 1.0**	0.86±0.33*
H	1.9 ± 1.8	9.2 ± 3.4	-3.2 ± 5.0	-11.8 ± 4.6	-6.9 ± 3.8	-0.9 ± 1.8	-19.8±2.5**	0.86±0.17
X^2	1.8	0.4	6.6*	22.2**	18.7**	0.5	4.7*	0.2
Six parameters								
m			110.2 ± 15.2	-63.8 ± 23.6	-40.9 ± 32.2		9.2 ± 12.2	
d			4.2 ± 3.1	-5.2 ± 1.6*	-6.9 ± 2.8		-4.0 ± 0.9**	
h			-19.8 ± 22.0	213.8±55.6**	216.9±63.5**		50.2 ± 34.0	
i			-19.1 ± 12.8	70.1 ± 55.6**	96.9 ± 23.9**		26.5 ± 14.0	
j			-29.2 ± 12.1	13.1 ± 9.5	14.9 ± 19.8		-12.2 ± 11.0	
l			39.2 ± 10.9	- 139.8 ±45.6*	-126.1±48.7*		-36.2 ± 24.0	

Cross 3=SAMPEA-10 x BIU LOCAL. Estimates of gene effect were significantly different from zero at 0.05 (*) and 0.01 (**) probability level. m=mean effect, d=additive gene effect, h=dominance gene effect, i=additive x additive gene effect, j=additive x dominance gene effect, l=dominance x dominance gene effect, X^2=chi-square,

Under water stressed, the calculated chi-square at 3 degree of freedom was not significant for days to 50% flowering, plant height, number of seed per pod and root length.

In the cross IT98K-628 x SAMPEA-8 additive gene effects was highly significant and positive for pod yield per plant also highly significant ($p < 0.01$) and negative for hundred seed weight. Dominant and Dominant-by-dominant gene effects were non-significant for all the traits. Additive-by-additive epistatics were highly significant ($p < 0.01$) and positive for number of matured pods per plant. Additive-by-dominant effects were highly significant ($p < 0.01$) and positive for pod yield per plant. Additive effects were highly significant and positive ($p < 0.01$) for number of matured pods per plant and pod yield per plant also highly significant ($p < 0.01$) and negative for hundred seed weight. Dominant effects, additive-by-additive epistatics, dominant-by-dominant effects were non-significant for all the traits. Additive-by-dominant effects were highly significant ($p < 0.01$) and negative for number of matured pods per plant in the cross IT99K-7-21-2-2 x SAMPEA-8. In the cross-3. Additive gene effects were highly significant and negative ($p < 0.01$) number of matured pods per plant and highly significant ($p < 0.05$) and negative hundred seed weight. Dominant effects were highly significant and positive ($p < 0.01$) pod yield per plant. Additive-by-additive epistatics were highly significant and positive ($p < 0.01$) for number of matured pods per plant and pod yield per plant. Additive-by-dominant gene effects highly significant ($p < 0.01$) and negative number of matured pods per plant. Dominant-by-dominant effects were non-significant for all the traits.

Table 4.8. The estimates of gene effects for eight quantitative characters for cross-1 evaluated in water stress at Samaru, 2013.

Parameters	D50%F	PH(cm)	DPM	NMPPP	PYPP	NSPP	100SW(g)	RL(cm)
Three parameters								
M	4.2 ± 1.8**	30.2 ± 3.0**	109.4±5.1**	10.8 ± 5.3	7.1 ± 4.3	5.7 ± 4.9	37.8 ± 3.8**	0.19±0.25
D	-3.8 ± 1.2	-0.7 ± 1.3	-3.2 ± 2.4	110.1±2.0**	1.5 ± 2.5	14.0 ± 6.4	-16.8±3.3**	0.28±0.11**
H	-8.0 ± 3.9	-9.2 ± 4.4	-6.2 ± 3.3	6.8 ± 5.1	10.0 ± 9.0	-1.9 ± 0.5	3.2 ± 1.6	0.25±0.09
X^2	1.4	2.8	3.7*	12.7**	12.0**	0.7	18.9**	0.3
Six parameters								
m			100.2 ± 9.2	99.2 ± 15.2	40.0 ± 11.0		58.5±22.2**	
d			-8.2 ± 1.4	4.8 ± 3.1	10.0 ± 1.5**		-14.5±1.2**	
h			-28.0 ± 11.1	-29.8 ± 22.0	-42.0 ± 19.0		-108.2±44.0	
i			0.9 ± 12.10	20.1±11.8**	-28.0 ± 10.0		29 ± 20.4	
j			7.2 ± 12.1	-29.2 ± 12.1	-31.0±15**		3.9 ± 12.1	
l			18.2 ± 10.0	29.2 ± 10.0	5.0 ±239.0		90.3 ± 40.2	

Cross 1= IT98K-628 x SAMPEA-8. Estimates of gene effect were significantly different from zero at 0.05 (*) and 0.01 (**) probability level. m=mean effect, d=additive gene effect, h=dominance gene effect, i=additive x additive gene effect, j=additive x dominance gene effect, l=dominance x dominance gene effect, X^2=chi-square.

Table 4.9. The estimates of gene effects for eight quantitative characters for cross -2 evaluated in water stress at Samaru, 2013.

Parameters	D50%F	PH(cm)	DPM	NMPPP	PYPP	NSPP	100SW(g)	RL(cm)
Three parameters								
M	34.2 ± 1.1**	35.1 ± 2.1**	105.2±3.4**	111.0±4.3**	12.1 ± 3.0**	16.7 ± 3.8**	44.8 ± 8.3**	0.72±0.8*
D	-1.4 ± 0.4	2.2 ± 1.4	-2.2 ± 2.0	6.4 ± 2.9**	2.7 ± 3.9	7.7 ± 6.0	-9.2 ± 2.2	0.17±0.5
H	-0.7 ± 1.8	-2.3 ± 3.8	-6.9 ± 4.4	-6.8 ± 8.6	9.2 ± 6.9	-0.8 ± 4.1	-1.6 ± 3.8	0.81±0.8**
X^2	0.9	3.0	4.0*	5.8*	5.0*	0.4	20.8**	0.4
Six parameters								
m			79.6 ± 14.4	45.8 ± 15.9	15.2 ± 13.5		43.0±20.2**	
d			-3.5 ± 1.8	12.8 ± 1.8**	5.1 ± 6.5**		-6.8 ± 1.0**	
h			30.2 ± 22.0	-23.8 ± 35.0	25.2 ±3 6.1		-115.0±53.8	
i			24.2 ± 14.9	33.8 ± 5.1	1.5 ±1 6.0		5.8 ± 22.8	
j			16.2 ± 9.8	-23.8±12.6**	-12.4 ± 10.5		12.0 ± 2.2**	
l			-29.2 ± 12.4	-3.8 ± 13.8	-25.0 ± 26.0		40.9 ± 33.4	

Cross 2= IT99K-7-21-2 x SAMPEA-8. Estimates of gene effect were significantly different from zero at 0.05 (*) and 0.01 (**) probability level. m=mean effect, d=additive gene effect, h=dominance gene effect, i=additive x additive gene effect, j=additive x dominance gene effect, l=dominance x dominance gene effect, X^2=chi-square,

Table 4.10. The estimates of gene effects for eight quantitative characters for cross-3 evaluated in water stress at Samaru, 2013.

Parameters	D50%F	PH(cm)	DPM	NMPPP	PYPP	NSPP	100SW(g)	RL(cm)
Three parameters								
M	29.4 ± 1.6**	32.2 ± 3.0**	100.7±4.1**	20.8 ± 5.1*	14.2 ± 4.9**	14.2 ± 4.9**	31.2 ± 4.4**	31.2 ± 4.4**
D	-0.7 ± 0.8	-1.8 ± 1.5	-3.2 ± 2.6	-4.8 ± 2.1	-9.2 ± 0.2	-9.2 ± 0.2	-3.3 ± 1.5**	-3.3 ± 1.5**
H	1.9 ± 1.8	9.7 ± 3.4	-3.2 ± 5.8	-10.2± 4.6	-9.9 ± 3.3	-9.9 ± 3.3	-22.8±2.3**	-22.8±2.3**
X^2	1.6	0.8	5.4*	21.8**	16.0**	16.0	4.2*	4.2
Six parameters								
m			100.2 ± 15.1	11.8 ± 15.0	-38.9 ± 32.9		6.2 ± 10.8	
d			3.2 ± 3.9	6.8 ± 3.6**	-5.1 ± 1.5		-8.0 ± 0.4**	
h			-19.8 ± 25.9	30.8 ± 35.6	106.2±43.5**		45.2 ± 24.0	
i			-18.1 ± 12.7	1.9 ± 15.2**	84.9 ± 33.0**		22.5 ± 11.0	
j			-25.2 ± 12.2	-14.9±14.8**	24.9 ± 29.0		-14.2 ± 13.1	
l			32.2 ± 10.4	-33.8 ± 35.2	-141.1 ± 48.0		-32.0 ± 18.2	

Cross 3=SAMPEA-10 x BIU LOCAL. Estimate of gene effect were significantly different from zero at 0.05 (*) and 0.01 (**) probability level. m=mean effect, d=additive gene effect, h=dominance gene effect, i=additive x additive gene effect, j=additive x dominance gene effect, l=dominance x dominance gene effect, X^2=chi-square,

4.4 Heritability and genetic advance

Heritability estimates and genetic advance for the traits studied are shown in Table 4.11 and 4.12. Narrow sense heritability estimates and broad-sense heritability estimate for all the traits across the three sets of crosses were moderate to high under water stressed and water non-stressed conditions.

For cross-1, IT98K-628 X SAMPEA-8. Broad sense heritability estimates ranged from 0.0% for number of matured pods per plant to 80% for hundred seed weight. Narrow sense heritability ranged from 0.0% for number of matured pods per plant and 60% for hundred seed weight. Genetic advance ranged from 0.0% for number of matured pods per plant to 20.4% for days to 50% flowering. The character hundred seed weight has the highest value for narrow sense and broad sense heritabilites while the trait days to 50% flowering has the highest value for genetic advance.

Broad sense heritability estimates ranged from 40% for root length to 82% for 100 seed weight. Narrow sense heritability ranged from 30% number of mature pods per plant to 65% for 100 seed weight to in the cross IT99K-7-21-2-2 X SAMPEA-8 (cross-2). Genetic advance ranged from 7.5% root length to 24.2% for hundred seed weight. The character hundred seed weight has the highest value for narrow sense heritability, broad sense heritability and genetic advance. In the cross between SAMPEA-10 X BIU LOCAL (cross 3). Broad sense heritability estimates ranged from 45% for root length to 95% for hundred seed weight. Narrow sense heritability ranged from 28% for number of seeds per pod to 70% for hundred seed weight. Genetic advance ranged from 4.9% for root length to 23.5% for hundred seed weight

65

Table 4.11. Estimates of heritability and genetic advance of eight agronomic traits of three cowpea crosses evaluated at IAR farm Samaru under water non-stress condition in 2013

Crosses	D50%F	PH(cm)	DPM	NMPP	PYPP	NSPP	HSW(g)	RL(cm)
IT98K-628 X SAMPEA-8 (cross 1)								
H (B)(%)	65	54	54	0.0	60	54	80	40
h (N)(%)	52	52	28	0.0	40	44	60	32
G.A	20.4	18.3	9.8	0.0	15.2	15.8	19.5	5.2
IT99K-7-21-2-2 X SAMPEA-8 (cross 2)								
H(B) (%)	54	52	53	62	63	50	82	40
h(N)(%)	43	50	34	30	54	35	65	35
G.A	14.8	18.0	11.0	14.3	15.9	15.5	24.2	7.5
SAMPEA-10 X BIU LOCAL (cross 3)								
H(B) (%)	58	53	52	65	55	62	95	45
h(N)(%)	48	32	29	52	38	28	70	40
G.A	17.3	18.0	10.2	10.5	15.0	15.1	23.5	4.9

D50%F: Days to fifty percent flowering, **PH (cm)**: Plant height, **DPM**: Days to pod maturity, **NMPP:** Number of mature pod per plant, **NSPD**: Number of seeds per pod, **PYPP**: Pod yield per plant, **HSW**: Hundred seed weight, **RL**: Root, H(B): Broad sense heritability, h(N): narrow sense heritability. G. A: Genetic Advance.

The character hundred seed weight has the highest value for broad sense and narrow sense heritability and genetic advance. The heritability estimates and genetic advance under water stress condition represented in Table 4.12.

For cross-1, IT98K-628 X SAMPEA-8. Broad sense heritability estimates ranged from 50% for number of seeds per pods to 70% for hundred seed weight. Narrow sense heritability ranged from 25% for days to pod maturity and number of matured pod per plant for number of matured pods per plant to 60% for hundred seed weight. Genetic advance ranged from 5.5% for root length to 20.1% for days to 50% flowering. The character hundred seed weight has the highest value for narrow sense and broad sense heritability while the trait days to 50% flowering has the highest value for genetic advance. Broad sense heritability estimates ranged from 0.0% for number of matured pods per plant to 68% for 100 seed weight. Narrow sense heritability ranged from 0.0% number of mature pods per plant to 55% for 100 seed weight to in the cross IT99K-7-21-2-2 X SAMPEA-8 (cross-2).

Genetic advance ranged from 0.0% root length to 21.0% for hundred seed weight. The character hundred seed weight has the highest value for narrow sense heritability, broad sense heritability and genetic advance. In the cross-3 between. Broad sense heritability estimates ranged from 50% for pod yield per plant to 82% for hundred seed weight. Narrow sense heritability ranged from 28% for number of seeds per pod to 63% for hundred seed weight. Genetic advance ranged from 5.2% for root length to 17.2% hundred seed weight.

Estimates of heritability and genetic advance of eight agronomic traits of three cowpea crosses evaluated at IAR farm Samaru under water stress condition in 2013.

Crosses	D50%F	PH(cm)	DPM	NMPP	PYPP	NSPP	HSW(g)	RL(cm)
IT98K-628 X SAMPEA-8 (cross 1)								
H(B) (%)	63	55	55	53	65	50	70	52
h(N) (%)	50	51	25	25	43	32	60	48
G.A	20.1	17.5	9.2	11.9	14.9	11.6	14.2	5.5
IT99K-7-21-2-2 X SAMPEA-8 (cross 2)								
H(B) (%)	50	54	52	0.0	60	52	68	45
h(N) (%)	41	40	30	0.0	48	45	55	30
G.A	13.2	17.2	10.7	0.0	13.5	13.5	21.0	4.0
SAMPEA-10 X BIU LOCAL (cross 3)								
H(B) (%)	55	52	54	65	50	62	82	52
h(N)	47	50	28	32	40	44	63	45
G.A	14.3	14.0	9.1	12.0	12.7	12.9	17.2	5.2

D50%F: Days to fifty percent flowering, **PH (cm)**: Plant height, **DPM**: Days to pod maturity, **NMPP:** Number of mature pod per plant, **NSPD**: Number of seeds per pod, **PYPP**: Pod yield per plant, **HSW**: Hundred seed weight, **RL**: Root, H(B): Broad sense heritability, h(N): narrow sense heritability, G. A: Genetic Advance.

4.5 Genotypic and phenotypic correlations

Estimates of phenotypic and genotypic coefficient of correlations for the traits studied under non-water stress and water stress conditions are presented in table 4.13. The genotypic coefficient of correlations for the cross IT98K-628 X SAMPEA-8, negative and highly significant correlations were obtained between days to 50% flowering and number of matured pods per plant, pod yield per plant and number of seeds per plant. Plant height showed negative and highly significant correlation with number of seeds per pod but correlated positively and highly significantly with days to pod maturity. There was negative and highly significant correlation between number of matured pod per plant, pod yield per plant, number of seeds per pod and correlate positive and highly significant correlation with hundred seed weight. Positive and highly significant correlations were indicated between number of matured pods per plant and pod yield per plant also number of seeds per plant, hundred seed weight and pod yield per plant correlate positive and highly significant with number of seeds per plant and hundred seed weight. Number of matured pod per plant, pod yield per plant and days to 50% flowering were positively correlated with number of seeds per plant while days to pod maturity was negative and highly significant to days to pod maturity. There were negative and highly significant associations between number of matured pods per plant and hundred seed weight. Significant and positive associations between number of matured pod per plant and days to pod maturity. Negative and highly significant associations were obtained between number of seeds per plant and days to pod maturity. Positive and significant associations were obtained between number of

matured pods per plant and number of seeds per plant. Hundred seed weight and days to pod maturity were positively and significantly correlated.

Phenotypic coefficient of correlation under non stress condition for cross-1 showed that Number of matured pods per plant, pod yield per plant was highly significant and positively correlated with days to 50% flowering and highly significant and negatively correlated with number of seeds per plant. Under stress condition hundred seed weight was significant and positively correlated with days to 50% flowering. Root length was significant and negatively correlated with plant high under water stress condition. Number of seeds per plant and hundred seed weight were highly significant and positively correlated with days to pod maturity, significant and positive with number of matured pods per plant. Non-stress condition was highly significant and negatively correlated with number of matured pods per plant.

Correlations among traits in cross-2 IT99K-7-21-2-2 X SAMPEA-8. Under non-stress condition are presented in Table 4.14. The results indicated significant and negative correlations between number of matured pods per plant, pod yield per plant, number of seeds per plant and hundred seed weight. Days to 50% flowering are significant and positively correlated with days to pod maturity. Plant height showed high significant and negative correlation with number of matured pods per plant. Number of seeds per plant showed significance and negative correlation with pod yield per plant but correlated positively with days to pod maturity and hundred seed weight.

Table 4.13: Genotypic (above diagonal) and phenotypic (below diagonal) correlations for yield and other quantitative characters in cowpea Cross 1 = (IT98K-628 x SAMPEA-8) evaluated under non-water stress (values above each box) and water stress (values below each box) condition at IAR farm Samaru.

	Days to fifty percent flowering	Plant height (cm)	Days to pod maturity	Number of matured pods per plant	Pod yield per plant (g)	Number of seeds per plant	Hundred seed weight(g)	Root length (cm)
Days to fifty percent flowering		0.36	0.81**	-0.85**	-1.00**	-1.00**	-0.60**	0.04
		0.26	0.50*	-0.35	0.36	-0.60**	0.15	0.01
Plant height (cm)	0.47		0.90**	-0.16	-0.40	-1.00**	0.19	-0.33
	0.11		0.63**	-0.23	0.11	-0.56*	0.15	-0.11
Days to pod maturity	-0.15	0.23		-0.69**	-0.46*	-0.94**	0.82**	0.17
	0.13	-0.14		0.12	-0.82**	-0.42	0.63**	0.14
Number of matured pods per plant	0.63**	-0.01	0.02		0.73**	0.62**	0.93**	-0.15
	0.18	0.14	0.48*		0.10	0.33	0.61**	0.11
Pod yield per plant (g)	0.78**	-0.01	-0.21	0.06		0.92**	0.65**	-0.27
	0.44	0.11	-0.28	0.12		0.44	0.20	-0.01
Number of seeds per plant	-0.84**	0.41	-0.77**	0.11	-0.01		0.14	-0.11
	-0.10	-0.28	0.68**	0.54*	0.25		0.10	-0.01
Hundred seed weight(g)	-0.12	0.27	-0.16	-0.81**	0.04	-0.17		-0.06
	0.50*	0.22	0.77**	0.33	0.01	-0.29		-0.02
Root length (cm)	0.34	0.22	-0.02	-0.12	0.07	-0.16	0.39	
	0.28	-0.49*	0.14	-0.33	-0.00	-0.11	0.17	

At $p \leq$ or $= 0.05(*)$, r=0.468 and at $p \leq$ or $= 0.01(**)$, r=0.590.

Highly significant and negative correlation was observed between number of matured pod per plant and number of seed per plant. However days to pod maturity recorded positive and significant correlation with hundred seed weight. There was high significant and positive correlation between pod yield per plant, number of seed per plant, hundred seed weight and number of matured pods per plant. Pod yield also correlate positively significant with hundred seed weight and number of seed per plant.

Genotypic correlations showed that days to 50% flowering were negative and highly significant with pod yield per plant and number of seeds per plant. Days to pod maturity and hundred seed weight are positively correlated. Plant height showed significant and negative correlations with number of seeds per plant and number of matured pods per plant respectively. Days to pod maturity showed high significant and negative correlations with number of matured pods per plant and number of seeds per plant respectively. The numbers of matured pods per plant were positive and significantly correlated with pod yield per plant. It was negatively correlated with days to pod maturity. Positive correlations were obtained between pod yield and hundred seed weight. IT99K-7-21-2-2 X SAMPEA-8 under non-stress condition indicates positive and highly significant associations between number of matured pod per plant, pod yield per plant and days to 50% flowering. Significant and negative associations were obtained between number of matured pods per plant and hundred seed weight.

Table 4.14: Genotypic (above diagonal) and phenotypic (below diagonal) correlations for yield and other quantitative characters in   cowpea Cross 2= (IT99K-7-21-2 x SAMPEA-8) evaluated under non-water stress (values above each box) and water stress (values below each box) condition at Samaru.

Each cell contains two values: non-water stress (upper) / water stress (lower).

	Days to fifty percent flowering	Plant height (cm)	Days to pod maturity	Number of matured pods per pod	Pod yield per plant (g)	Number of seeds per plant	Hundred seed weight(g)	Root length (cm)
Days to fifty percent flowering		0.36 / 0.24	0.92** / 0.58**	-0.80** / -0.50**	-0.75** / -0.55**	-0.95** / -0.83**	-0.88** / 0.70**	-0.09 / -0.01
Plant height (cm)	0.40 / 0.08		0.69** / 0.44	-0.88** / -0.62**	-0.59** / -0.42	-1.00** / -0.53**	0.65** / 0.11	-0.07 / -0.12
Days to pod maturity	-0.28 / -0.11	-0.08 / -0.25		-0.70** / -0.55**	-0.41 / 0.23	-1.00** / -0.83**	0.52** / 0.42	0.04 / -0.22
Number of matured pods per plant	0.13 / 0.11	-0.27 / -0.10	-0.13 / -0.52**		0.82** / 0.50**	0.62** / 0.15	0.63** / 0.12	-0.03 / -0.00
Pod yield per plant (g)	0.10 / 0.00	-0.08 / -0.09	-0.17 / -0.04	-0.19 / 0.22		0.58** / 0.40	0.75** / 0.52**	-0.22 / -0.19
Number of seeds per plant	-0.13 / -0.09	-0.11 / -0.10	-0.16 / -0.48**	-0.07 / -0.27	-0.01 / -0.28		0.24 / 0.11	-0.15 / -0.25
Hundred seed weight(g)	-0.05 / -0.02	-0.28 / -0.09	-0.05 / -0.21	-0.45** / -0.59**	0.04 / 0.12	-0.17 / -0.22		-0.09 / -0.25
Root length (cm)	-0.08 / -0.09	0.02 / 0.40	-0.15 / -0.19	-0.08 / -0.01	0.07 / 0.11	-0.40 / -0.33	-0.28 / 0.19	

At $p \leq$ or $= 0.05(*)$, r = 0.468 and at $p \leq$ or $= 0.01(**)$, r = 0.590.

For phenotypic coefficient of correlations under water stressed condition presented in Table 4.14 indicates negative and significant associations were obtained between days to pod maturity, number of seeds per plant and days to 50% flowering. Negative and significant associations were obtained between number of seeds per plant, number of matured pods per plant and days to pod maturity. Significant and negative associations were obtained between hundred seed weight and number of mature pods per plant.

Genotypic coefficients of correlations under water stress condition are presented in (Table 4.15) for SAMPEA-10 x BIU LOCAL. The results showed significance and negative correlation between number of matured pods per plant, pod yield per plant, number of seeds per plant and days to 50% flowering. Plant height showed negative and highly significant correlation with number of matured pods per plant. Number of seeds per plant showed positive and highly significant correlation with pod yield per plant. Highly significant and negative correlations were observed between numbers of matured pods per plant, pod yield per plant. Days to pod maturity indicate positive and highly significant correlation with hundred seed weight. There were positive and highly significant correlation between pod yield per plant, number of seed per plant, hundred seed weight and number of matured pods per plant. Pod yield also correlated positively with hundred seed weight.

In SAMPEA-10 x BIU LOCAL, days to 50% flowering was negative and highly significant correlation with number of matured pods per plant and pod yield per plant. Plant height showed negative significant correlations with number of seeds per plant.

Table 4.15: Genotypic (above diagonal) and phenotypic (below diagonal) correlations for yield and seven other quantitative characters in cowpea Cross 3= (SAMPEA-10 x BIU LOCAL.) evaluated under non-water stress (values above each box) and water stress (values below each box) condition at Samaru.

	Days to fifty percent flowering	Plant height (cm)	Days to pod maturity	Number of matured pods per pod	Pod yield per plant (g)	Number of seeds per plant	Hundred seed weight(g)	Root length (cm)
Days to fifty percent flowering		0.29	0.44	-0.95**	-0.72**	-0.83**	-0.04	-0.14
		0.40	0.17	-0.81**	-0.61**	-0.45	-0.13	-0.11
Plant height (cm)	0.47		0.63**	-0.76**	1.00**	-1.00**	0.15	-0.33
	0.57*		0.41	-0.28	0.43	-0.55*	0.40	0.07
Days to pod maturity	-0.53*	-0.69**		-0.54*	-0.62**	-0.25	0.84**	0.08
	0.18	-0.01		-0.30	-0.47*	-0.22	0.51*	0.10
Number of matured pods per plant	-0.09	-0.26	0.02		0.73**	0.62**	0.93**	-0.09
	-0.18	-0.41	0.22		0.49*	0.40	0.27	-0.38
Pod yield per plant (g)	-0.07	-0.11	0.13	0.41		-0.41	0.90**	-0.31
	-0.12	-0.27	0.29	0.33		-0.25	0.50*	-0.12
Number of seeds per plant	-0.04	0.02	0.18	-0.24	-0.53*		0.24	-0.20
	-0.19	0.21	0.14	-0.55*	-0.62**		0.11	-0.13
Hundred seed weight(g)	-0.11	-0.04	-0.12	-0.51*	0.04	-0.27		-0.15
	-0.09	-0.02	-0.07	-0.29	0.02	-0.14		-0.19
Root length (cm)	-0.15	0.11	0.13	-0.15	0.07	-0.16	0.40	
	0.24	0.10	0.21	-0.19	0.03	-0.22	0.11	

At $p \leq$ or $= 0.05$(*), r= 0.468 and at $p \leq$ or $= 0.01$(**), r= 0.590.

Days to pod maturity showed negative and significantly correlated with pod yield per plant and also positive with hundred seed weight. Number of matured pods per plant showed positive and significant correlation with pod yield per plant. Positive and significant correlations were also obtained between pod yield per plant and hundred seed weight.

Phenotypic coefficient of correlations (Table 4.15) for the cross SAMPEA-10 x BIU LOCAL was highly significance and negative between number of matured pods per plant and pod yield per plant. Days to 50% flowering indicated negative correlation with days to pod maturity. Negative and significant associations were also obtained between number of matured pods per plant and hundred seed weight. Under water stress condition, positive and significant associations between, plant height and days to 50% flowering was indicated. Similarly, negative and significant associations were obtained between number of seeds per plant, number of matured pods per plant and days to pod maturity. Negative and highly significant associations were obtained between number of seeds per pod and number of mature pods per plant.

CHAPTER FIVE

5.0 DISCUSSION

Differential performance of genotypes in segregating populations has often been used by geneticists to indicate the presence of heritable variation. The degree of variation among the different populations for days to 50 % flowering, plant height, days to pod maturity, 100 seed weight, pod yield per plant strongly suggest the existence of genetic differences for these traits. Similar results have been reported for yield and related characters by Jatasara *et al.,* (1982) , Wein and Summerfield (1980), Tyagi *et al.,* (1978), Sharma and Singhania (1992), and Nehru and Manjunath, (2000), in fodder cowpea and by Rekha (1995) and Sharma (1999) in grain cowpea. The thee sets of crosses considered in this study, the means of the parents was extreme and contrasting than the means of the F_1 and F_2 for the measured traits. The heritable differences that abound among the parents, offered an opportunity to elucidate the genetic nature of the inheritance for these traits, the segregation pattern of the F_2 population gives the possibility of selection for advancement of days to 50 % flowering, plant height, days to pod maturity, 100 seed weight, pod yield per plant and hundred seed weight.

The presence of heritable variation within different genotypes in an evaluation has always been used by geneticists and plant breeders. In this study, the degree of variation among the different populations such as parents and their generations, strongly suggests genetic differences among them. These were in agreement with Wein and Summerfield (1980), Tyagi *et al*., (1978),

Highest mean days to 50% flowering imply that selection for this character can be made. The means of days to 50% flowering, of the F_1 progeny were lower than their mid-parent mean values and close to the susceptible parent (SAMPEA-8). In a self-pollinated crop such as cowpea a departure of F_1 mean value from its mid-parent value for days to 50% flowering indicates the effect of dominance or partial dominance. This agrees to the findings of Brittingham (1950) who stated that early maturity is dominant or partially dominant over late maturity. According to Mather and Jinks (1982), the phenotypic difference between the parental lines is of the utmost importance for inheritance studies, aiming at obtaining the most precise estimates of genetic parameters. The mean plant heights for the F_1 hybrid in the entire cross were similar to the mid parental value. This indicated the preponderance of additive gene action for plant height. The height of F_2 plants were distributed over the range of both parents with continuous distribution, suggesting the involvement of more than one gene controlling the inheritance of the trait and it also suggests that gene controlling the trait, are dispersed among the parents. Also from the result, the mean plant heights for the backcrosses (BC_1P_1 and BC_1P_2) skewed towards their respective recurrent parents.

The mean plant heights for the F_1 hybrid in the entire cross were similar to the mid parental value. The height of F_2 plants were distributed over the range of both parents with continuous distribution, suggesting polygenic inheritance of the trait. Mean values of the F_1 hybrids in the three crosses, for root lengths were similar to their respective susceptible parents as in the case of non stress. The distributions of

the segregating F_2 populations in the crosses. The resistant parent IT99K-7-21-2-2 and SAMPEA-10 had the highest days to pod maturity and pod yield per plant with mean value 98.43days and 16.96g respectively. Some of the F_2 populations segregated outside their parental range in the three sets of crosses for number of matured pods per plant, pod yield per plant and root length under the two conditions. This was in conformity with the works of Oseni *et al.,* (1992) who reported that the role of pods per plant was apparent in the determination of seed yield, similarly Sawant (1994), observed that pods per plant had highest positive direct effect on seed yield.

In general, the narrow sense heritability estimates were less in magnitude than the broad-sense heritability estimates in the three crosses for few traits studied. Following the classification above, the broad and narrow sense estimates for days to fifty percent flowering under stress and non-stress condition were high in the three crosses. High values of heritability estimate is an indication the phenotype of that trait strongly reflects its genotype (Sivakumar *et al*., 2013).Days to 50% flowering, Pod yield per plant and number of matured pods per plants studied are highly heritable and selection for improvement in the early generation will be effective in improving early maturity in cowpea. High heritability estimates have been reported for days to flowering and days to pod maturity in cowpea by Sharma and Singhania (1992); Adeyanju and Ishiyaku (2007); Suganthi and Murugan, (2008) and Sivakumar *et al*. (2013). However, heritability in the broad sense in self-pollinating crops is less informative than heritability in the narrow sense which is a direct measure of additive variance (Caviness, 1969; Strickberger, 1976; Tsuchiya, 1986).

The high narrow sense heritability observed in the crosses under the two conditions for hundred seed weight confirms the presence of additive genetic variability for the trait as observed in the generation means analysis. Similar result was obtained by Showemimo (2005), Obilana, (1984). The high broad sense heritability observed in all the crosses for the trait used in the study, indicates that the trait has sufficient genetic variability and that there would be high probability of success in selecting for drought resistance in the early generation using this trait. Generally, the high heritability values estimated in this study indicated that the traits are highly heritable and selection can be done to improve the characters. This finding agreed with the findings of (Upadhyaya et al., 1997). According to Johnson and Frey (19 67), phenotype is a good index of genotypic merits for characters with high heritability, so that genetic gain can be made easily through selection.

The gene effect showed that additive (a) gene effect was larger in magnitude in the three crosses than other epistatic gene effects. This was in agreement with the findings of Pathmanathan et al., (1997) who reported that both additive (a) and dominance (d) effects were larger and of more importance in the inheritance of seed yield and pods weight. Root length was predominantly under duplicate gene effect for the three crosses. The epistatic effects, additive × additive (aa), dominance × dominance (dd) magnitude were large enough in the three crosses; this suggests that the contribution of the epistatic effects to the inheritance of seed yield is greater than that of additive but less than that of dominance effect. On individual basis, epistatic effect, the dominance × dominance (dd) estimate were the largest for other

traits. The additive × dominance (ad), and dominance × dominance (dd) epistatic effects for the first cross (IT98K x SAMPEA-8) and additive × additive (aa) and dominance × dominance (dd) epistatic effects were of large magnitude and importance. The implication was that the contribution of epistatic effects to the inheritance of yield, were greater than additive (a) and dominance (d) gene effects. Jatasara, (1980) in his work with cowpea reported that most of gene governing yield (either seeds, fodder etc.) act additively. Mitra *et al.,* (2001), using generation mean analysis reported that fodder, seeds, pods per plant appeared to be influenced by both additive and non additive gene action. They also reported that complementary gene action was predominantly involved in inheritance of most characters (days to 50 % flowering, plant height, days to pod maturity, 100 seed weight, pod yield per plant).

Dominance gene action being negative suggests it was toward the susceptible parent (SAMPEA-8). Additive × additive (*aa*), additive × dominance (*ad*) gene action being significant in both cases suggest additive × additive and additive × dominance epistasis also played an important role in the inheritance of the trait. According to Khattack *et al.* (2002), traits with additive × additive (*aa*) type of epistasis can be exploited by standard hybridization and selection procedures for days to pod maturity, 100 seed weight, pod yield per plant.

There was no dominance × dominance (*dd*) epistastic effect on the inheritance of the traits studied. In addition, the negative signs of (*a*) and (*d*) for all the parameters used in these study suggest that duplicate type of epistasis played a role in days to

50% flowering, days to first pod maturity and number of matured pods per plant. This finding was in perfect agreement with that of Akhshi *et al.,* (2014), who studied generation mean analysis to estimate genetic parameters for morphological traits in common bean (*Phaseolus vulgaris* L.). This is in agreement with reports by Ojomo, (1971) and Adeyanju and Ishiyaku (2007) who indicated that duplicate epistasis between two major genes in the presence of some minor modifying genes are responsible for medium to early maturity in cowpea. Inheritance of medium maturity in cowpea is quantitatively inherited and hence under polygenic control. Brittingham, (1950) and Ishiyaku *et al.,* (2005) had already pointed out that maturity in cowpea is quantitatively inherited and therefore conditioned by at least seven major genes with other modifyer genes.

In genetic studies, two types of correlation between characters are recognized, genotypic and environmental. Correlation analysis gives a picture of association pattern of different yield related characters among themselves. Yield is a complex quantitative character governed by a large number of genes. For a rational approach towards improvement of the yields, selection has to be made for the component of the yield. Genetic correlation between different characters of plant often arises because of either linkage or pleiotropy. If a negative association between characters is due to pleiotropic effects it would be very difficult to obtain the desired combinations, while if linkage is involved special breeding programmes are needed to break the linkage (Al-jibouri *et al.,* 1958; Pandey and Gritton, 1975) The correlation pattern is expected to differ with material that is studied since it is a reflection of the genetic makeup of the population. Indirect selection of one trait to

improve another is for the phenotypic correlations between characters of interest. But phenotypic and genotypic correlation may differ in magnitude and sign. One may be negative and the other positive or on the other hand one low and the other high. Selection for one of the character here would result in greater changes in the other character than would be expected if the genotypic correlation were assumed equal to the phenotypic correlation. This is for the assumption that differences indicated between genotypic and phenotypic correlations are true differences and not due to sampling variation alone (Johnson *et al.,* 1955). In general, the results in this study indicate that the two of water stress and non-stress, genotypic correlations were higher than phenotypic correlations with few exceptions. This is in agreement with the findings of Johnson *et al.,* (1955); Doku (1970); Aryeetey and Laing (1973); Waldia *et al.,* (1980); Yunus and Paroda (1980) and Sharma (1984) who reported strong inherent associations between characters. The negative highly significant association of days to 50% flowering with other characters in all the crosses implies that indirect selection will dry reduced the yield, the same trend was noticeable in the cross two: days to 50% flowering with hundred seed weight. These correlations agreed with those reported by Trehan *et al.,* (1970), Virupakshappa *et al.,* (1980) and Sigh *et al.,* (1982), meaning that direct selection for these characters to improve yield would be effective. Many researchers reported positive, highly significant or not correlations partaining to yields and its components in cowpeas. Patil *et al.,* (1989) reported that grain yield near highly correlated with pods per plant, seed weight, and days to flowering. Saddique and Gupta (1991) observed highly significant correlation of seed weight per plant and

days to flowering. Oseni *et al.,* (1992) revealed that there is a positive correlation with seed yield and days to flowering, and also positive correlation between days to flowering and other yield components such as dry and green fodder yield. Sawant (1994) found that seed yield was significantly and positively correlated with inflorescence per plant, and pods per plant. Tamiselvan and Das (1994) reported that pod weight, and seed weight, should be used as criterions in the development of high yielding genotypes in cowpeas. Singh and Singh (1957) reported that parameters such as seed weight and total biomass made greater directional contribution to seed yield in 45 cowpea genotypes. Rangaiah *et al.,* (1999) reported that total biomass was positively and significantly correlated with all traits except plant height.

CHAPTER SIX

6.0 SUMMARY, CONCLUSIONS AND RECOMMENDATIONS

6.1 SUMMARY

The study was carried out using six cowpea genotypes, three tolerant varieties: IT98K-628, IT99K-7-21-2-2 and SAMPEA-10 and two susceptible varieties: SAMPEA-8 and BIU LOCAL with a commercial check (Dan'ila) which is also drought tolerant at Institute for Agricultural Research (IAR), farm Samaru, in 2012/2013. Population development was carried out in the screen house at IAR Samaru using biparental mating design in 2012. The F_1 hybrids in each cross were advanced to F_2, and were backcrossed to their respective parent to generate BC_1P_1 and BC_1P_2. Evaluation of the genetic populations (P_1, P_2, F_1, F_2, BCP_1, and BCP_2) was done at the irrigation plot in IAR farm Samaru research field in 2013.The research work is therefore focused on the studies on the inheritance of drought tolerance information through the specific objectives, to assess the genetic variability for resistance to drought and other agronomic traits in cowpea, to determine the gene action involved in the inheritance of drought resistance in cowpea and to assess the relationship between seed yield and other quantitative traits under water non-stress and water stress conditions. Days to 50% flowering, plant height, days to pod maturity, number of matured pods per plant, number of seeds per pod, pod yield per plant, and hundred seed weight and root length were the parameters measured in the study. Analysis of variance revealed highly significant differences among the genotypes for all the traits measured under non stress and stress conditions. The mean squares from the indicated ample

variations among the genotypes for all the characters. The range of variability suggests the possibility for improving the characters for drought tolerance.

The three male parents (IT98K-628, IT99K-7-21-2-2 and SAMPEA-10) were tolerant, though their mean values for the traits studied were lower in magnitude due to their poor agronomic qualities compared to the female parents (SAMPEA-8 and BIU LOCAL), but the performance of IT98K-628 proved to be better under non stress among male parents and SAMPEA-8 performed better among female parent under the two conditions. From the research, SAMPEA-8 showed some level of tolerance because it recorded good performance under non-stress and stress conditions. Estimates of the six parameters for the various gene effects showed that additive, dominance and epistatic gene effects contributed significantly to the inheritance of the traits studied, with more preponderance of additive gene effects. Additive gene action and epistasis appeared to control the inheritance of drought tolerance in the cowpea genotypes used.

The high broad sense heritability estimates and genetic advance obtained in some of the traits (days to 50 % flowering, plant height, days to pod maturity, 100 seed weight, pod yield per plant) studied, signified positive responses, repeatability and transmit ability of these traits in selection, thus, the traits can easily be selected for further improved. The genotypic correlation coefficients exceeded those of the corresponding phenotypic correlation coefficients for most of the character combinations in the three sets of crosses studied.

6.2 CONCLUSIONS

Based on the observations in the study conducted, the following conclusions were made;

- For the two conditions (water stress and water non-stress), results showed partial dominance and over dominance were jointly and severally recorded in the traits studied. The genetic variability was also found in the material used. Both additive and non additive gene effects were significant in the expression of drought tolerance traits in the crosses. Additive x Additive (*aa*) and additive x dominance (*ad*) and epistasis were of great importance in the expression of the trait, indicating that breeding procedures that make good use of these gene interactions can be employed to improve drought tolerance in cowpea. Finally moderate to high heritabity (broad and narrow), and how the traits studied correlated showed that selection can be done on such trait in order to increase yields in cowpeas.

6.3 RECOMMENDATIONS

Resistant varieties are used as a component in integrated programme for drought improvement, it is therefore recommended that:

- The resistance indicated by the three parents especially IT98K-628 and the cross IT98K X SAMPEA-8 used in this study and the F_2 sergregants could be used as resistance sources to increase and diversify resistance in commercial cowpea varieties.

87

- Presence of non-additive gene action for most of the yield related characters implies that conventional selection procedure may not be effective enough for improvement of yield for drought resistance. Therefore, postponement of selection in later generations or inter mating among the selected segregants followed by one or two generations of selfing is suggested to break the undesirable linkage and allow the accumulation of favorable alleles for the improvement of desirable traits.

- Pedigree, single seed decent and backcross breeding should be complemented with marker assisted selection to reduce long periods of time associated with these conventional methods and also improve on the accuracy of results.

REFERENCES

Abdou-Razakou, I. B., Mensah, B., Addam Kiari, S., & Akromah, R. (2013). Using morpho-physiological parameters to evaluate cowpea varieties for drought tolerance. *International Journal of Agricultural Science Research,* 2(5): 153-162.

Acquaah, G. (2012). Breeding hybrid cultivars. In: *Principles of Plant Genetics and Breeding, Second Edition*. Pp. 355-373.

Agbicodo, E.M., Fatokun, C.A., Muranaka, S., Visser, R.G.F. & van der Linden, C.G. (2009). Breeding drought tolerant cowpea: Constraints, accomplishments, and future prospects. *Euphytica*, *167*: 353–370.

Ajeigbe, H.A., Oseni, T.O. & Singh. B.B. (2006). Effect of planting pattern, crop variety, and insecticide on the productivity of cowpea–cereal systems in Northern Guinea Savanna of Nigeria. *Journal of Food, Agriculture and Environment,* 4(1):145–150.

Ajeigbe, H.A., Singh, B.B., Adeosun, J.O. & Ezeaku, I.E. (2010b). Participatory on-farm evaluation of improved legume cereals cropping systems for crop-livestock farmers: Maize-double cowpea in Northern Guinea Savanna Zone of Nigeria. *African Journal of Agricultural Research,* 5(16): 2080-2088.

Ajeigbe, H.A., Singh, B.B., Musa, A. Adeosun, J.O., Adamu, R.S. & Chikoye, D. (2010a). Improved cowpea–cereal cropping systems: cereal–double cowpea system for the northern Guinea savanna zone. International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria, pp 17. University of Ghana http://ugspace.ug.edu.gh

Akyeampong, E (2012). Some responses of cowpea to drought stress. www.fao.org/wairdocs/ilri/x5488e/x5488e0d.htm. Assessed 1/12/2015 at 12.22pm.

Akyeampong, E. (1986). Some responses of cowpea to drought stress. In *Potentials of Forage Legumes in Farming Systems of Sub-Saharan Africa: Proceedings of a Workshop Held at ILCA, Addis Ababa, Ethiopia, 16-19 September 1985* (p. 141). ILRI (aka ILCA and ILRAD).

Aryeetey, A. N., and Laing, E. (1973). Inheritance of Yield Components and their Correlation Studies in Cowpeas *(Vigna unguiculata* (L.) Walp.). *Euphytica,* 22: 386-392.

Badu-Apraku, B., Oyekunle, M., Akinwale, R. O., Lum, A. F. (2011). Combining ability of early-maturing white maize inbreds under stress and nonstress environments. *Agronomy Journal,* 103: 544-557.

Bala Subramanian, V., & Maheswari. M. (1992). Compensatory growth responses during reproductive phase of cowpea after relief of water stress. *Journal of Agronomy Crop Science,* 168: 85-90.

Baro, M., & Deubel, T. F. (2006). Persistent hunger: Perspectives on vulnerability, famine, and food security in sub-Saharan Africa. *Annu.al Review of Anthropology*, 35: 521-538.

Baro, M., & Deubel, T. F. (2006). Persistent hunger: Perspectives on vulnerability, famine, and food security in sub-Saharan Africa. *Annu.al Review of Anthropology*, 35: 521-538.

Belko, N., Zaman-Allah, M., Cisse, N., Diop,N.N., Zombre, G., Ehlers, J.D. & Vadez, V. (2012) Lower soil moisture threshold for transpiration decline under water deficit correlates with lower canopy conductance and higher transpiration efficiency in drought-tolerant cowpea. *Functional Plant Biology,* 39(4):306-322.

Belko, N., Zaman-Allah, M., Diop, N.N., Cisse, N., Zombre, G., Ehlers, J.D. & Vadez, V. (2013). Restriction of transpiration rate under high vapour pressure deficit and non-limiting water conditions is important for terminal drought tolerance in cowpea. *Plant Biology,* 15: 304–316.

Bhatnagar-Mathur, P., Rao, S., Vadez, V. & Sharma, K. K. (2010). Transgenic strategies for improved drought tolerance in legumes of semi-arid tropics. *Journal of Crop Improvement,* 24**:** 92-111.

Blokhina, O., Virolainen, E., Fagerstedt, K.V. (2003). Antioxidants, oxidative damage and oxygen deprivation stress. *Annals of Botany:* 91:179-194.

Blum, A. (2005). Drought resistance, water-use efficiency, and yield potential—are they compatible, dissonant, or mutually exclusive? *Australian Journal of Agricultural Research,* 56**:** 1159-1168.

Borrell, A. K., Hammer, G. L., & Douglas, A. C. (2000). Does maintaining green leaf area in sorghum improve yield under drought? I. Leaf growth and senescence. *Crop Science*, *40*(4): 1026-1037.

Boyer, J.S. (1996). Advances in drought tolerance in plants. *Advances in Agronomy:* 56: 189–218.

Brosché, M., Overmyer, K., Wrzaczek M, Kangasjarvi (2010). Stress signaling III: Reactive oxigen species (ROS). In: Pareek, A., Sopory, S.K., Bohnert, J.H. & Govindjee (Eds.), (pp. 91-102). *Abiotic stress adaptation in plant.* Springer, Dordrecht.

Caliskan, S., Caliskan, M. E., Arslan, M. & Arioglu, H. (2008). Effects of sowing date and growth duration on growth and yield of groundnut in a mediterranean-type environment *Field Crops Research,* 105: 131-140.

Carsky, R.J., Vanlauwe, B., & Lyasse, O. (2002) Cowpea rotation as a resource management technology for cereal-based systems in the savannas of West Africa. In: Fatokun, C.A., Tarawali, S.A., Singh, B.B., Kormawa, P.M., Tamo, M. (Eds.), (pp. 252-266). *Challenges and Opportunities for Enhancing Sustainable Cowpea Production.* International Institute of Tropical Agriculture, Ibadan, Nigeria.

Chaves, M.M., Maroco, J.P. & Pereira, J.S. (2003). Understanding plant responses to drought from genes to the whole plant. *Functional Plant Biology,* 30(3):239-264.

Cissé, N., Ndiaye, M., Thiaw, S., & Hall, A.E. (1997). Registration of 'Melakh' cowpea. *Crop Science:* 37: 6

Condon, A.G & Hall, A.E. (1997). Adaptation to diverse environments: variation in water-use efficiency within crop species. In: Jackson, L.E. (Ed.), (pp. 79-116). *Ecology in Agriculture*. Singh BB (1994) Breeding suitable cowpea varieties for West and Central African savanna. In: Menyonga, J.M., Bezuneh, J.B., Yayock, J.Y. & Soumana, I. (Eds.), (pp. 77-85). *Progress in food grains research and production in semiarid Africa.* OAU/STRCSAFGRAD, Ouagadougou.

Derera, J. (2005). Genetic effects and association between grain yield potential, stress tolerance and yield stability in Southern African maize (*Zea mays* L.) base germplasm. PhD Thesis, University of KwaZulu-Natal, 175pp.

Eaglesham, A.R.J., Ayanaba, A., Rama, V.R. & Eskew, D.L. (1992). Mineral N effects on cowpea and soybean crops in a Nigeria soil: Amounts of nitrogen fixed and accrual to the soil. *Plant and Soil,* 68: 183-186.

Easterling, W., Aggarwal, P., Batima, P., Brander, K., Bruinsma, J., Erda, L., Howden, M., Kirilenko, A., Morton, J., Pingali, P., Soussana, J.F., Tubiello, F., Antle, J., Baethgen, W., Barlow, Chhetri, C., N., des Clers, S., Killman, W., Mader, T., O'Brien, K., Schmidhuber, J. & Sedjo, R. (2007). In: Sweeney, J., Singh, T.P. & Kajfež-Bogataj, L. (Eds.), *Food, Fibre, and Forest Products 3*. (pp 1-59).

Ehlers, J.D. & Hall, A.E. (1997). Cowpea (*Vigna unguiculata* L. Walp.). *Field Crops Research,* 53: 187-204.

Ekanayake, I., Garrity, J, & Masajo, D. (1985). Inheritance of root characters and their relations to drought resistance in rice. *Crop Science:* 25:927-933.

Emechebe, A.M. & Lagoke, S.T.O. (2002). Recent advances in research on cowpea diseases. In: Fatokun, C.A., Tarawali, S.A., Singh, B.B., Kormawa, P.M. & Tamo, M. (Eds.), (pp 94- 123). *Challenges and opportunities for enhancing sustainable cowpea production.* Proceedings of the World Cowpea Conference III held at the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria, 4-8 September 2002. IITA, Ibadan Nigeria.

Enabor, E.E. (1987). "*Socio-economic Aspect of the Effect of Drought on Natural Resources and the Environment*". In: Ecological Disasters in Nigeria: Drought and Desertification. Published by the Federal Ministry of Science and Technology, Lagos, Nigeria. Pp 210–212.

Fabunmi, T.O., Gbadamosi, B. K. & Adigbo, S.O. (2012). Seed Hydro-Priming and Early Moisture Stress Impact on Biomass Production and Grain Yield of Cowpea. *International Journal of Applied Science and Technology, 2*(10): 112-122

Fagbemi, K. (2002). "Disaster Management and Data Needs in Nigeria". National Emergency Management Agency (NEMA), Lagos, Nigeria.

FAO (2009). "World summit on food security", Food and Agriculture Organization of the United Nations, Rome. www.fao.org/wsfs/world-summit/en/ Accessed 3/12/2015 at 13.26.

FAOSTAT, (2015). Food and Agricultural Organization Databases. Available production data for year 2013. http://faostat3.fao.org/download/Q/QC/E Accessed 18th October 2015 at 21.13.

Fatokun, C. A., Boukar, O., & Muranaka, S. (2012). Evaluation of cowpea (*Vigna unguiculata* (L.) Walp.) germplasm lines for tolerance to drought. *Plant Genetic Resources,* 10(3): 171 – 176.

Fukai, S. & Cooper, M. (1995). Development of drought-resistant cultivars using physio-morphological traits in rice. *Field Crops Research,* 40: 67–87.

Fussell, L.K., Bidinger, F.R. & Bieler, P. (1991). Crop physiology and breeding for drought tolerance: Research and development. *Field Crops Research,* 27: 183-199.

Gamble, E. E. (1961). Gene effects in corn (*Zea mays L.*) separation and relative importance of gene effects for yield. *Canadian Journal of Plant Sciences,* 42**:** 339-348.

Ganapathy, S., & Ganesh. S.K. (2008). Heterosis for physio-morphological traits in relation to drought tolerance in rice (*Oryza sativa* L.). *World Journal of Agricultural Sciences,* 4(5): 623-629.

Gaur, P. M., Krishnamurthy, L. & Kashiwagi, J. (2008). Improving drought-avoidance root traits in chickpea (*Cicer arietinum* L.) - current status of research at ICRISAT. *Plant Production Science,* 11**:** 3-11.

Gwathmey, C.O. & Hall, A.E. (1992c). Adaptation to midseason drought of cowpea genotypes with contrasting senescence traits. *Crop Science,* 32: 773–778.

Gwathmey, C.O., Hall, A.E. & Madore, M.A. (1992a). Adaptive attributes of cowpea genotypes with delayed monocarpic leaf senescence. *Crop Science,* 32: 765–772.

Gwathmey, C.O., Hall, A.E., & Madore, M.A. (1992b). Pod removal effects on cowpea genotypes contrasting in monocarpic senescence traits. *Crop Science,* 32: 1003–1009.

Hall, A. E., Cisse, N., Thiaw, S., Elawad, H. O., Ehlers, J. D., Ismail, A. M., Fery, R.L., Roberts, P.A., Kitch, L.W., Murdock, L.L., Boukar, O., Phillips, R.D. & McWatters, K.H. (2003). Development of cowpea cultivars and germplasm by the Bean/Cowpea CRSP. *Field Crops Research*, *82*(2): 103-134.

Hamidou, F., Zombre, G. & Braconnier, S. (2007). Physiological and biochemical response of cowpea genotypes to water stress under glasshouse and field condition, *Journal of Agronomic Crop Science,* 193: 229-239.

Hazratkulova, S., Ram, C.S., Alikulov, S., Islomov, S., Yuldashev, T., Ziyaev,Z., Khalikulov, Z., Ziyadullaev, Z. & Turok, J. (2012). "Analysis of genotypic variation for normalized difference vegetation index and its relationship with grain yield in winter wheat under terminal heat stress." *Plant Breeding,* 131(6): 716-721.

Herbinger, K., Tausz, M., Wonisch, A., Soja, G., Sorger, A, & Grill, D. (2002). Complex interactive effects of drought and ozone stress on the antioxidant defence systems of two wheat cultivars. Plant Physiol. *Biochemistry,* 40(6):691-696.

Hinkossa, A., Gebeyehu, S. & Zeleke, H. (2013). Generation mean analysis and heritability of drought resistance in common bean (Phaseolus vulgaris L.). *African Journal of Agricultural Research,* 8**:** 1319-1329.

Hsaio, T. C. (1973). Plant responses to water stress. *Annual Review of Plant Physiololology,* 24: 519-570.

Jackson, R.B., Sperry, J.S. & Dawson, T.E. (2000). Root water uptake and transport; using physiological processes in global predictions. *Trends in Plant Science,* 5: 482-488.

Jatasara, D. S., Gupta, P.C., and Singh, K. (1982). Studies on Forage Production Potential and Quality of Different Varieties of Cowpea. *Forage Research,* 8. 141.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. 1955. Gnotypic and phenotypic correlations in soybean and their implications in selection. *Agron. J.,* 47: 477-483

Joshi, A. K., Kumari, M., Singh, V. P., Reddy, C. M., Kumar, S., Rane, J. & Chand, R. (2007). Stay green trait: variation, inheritance and its association with spot blotch resistance in spring wheat (*Triticum aestivum* L.). *Euphytica,* 153: 59–71.

Kararnanos, A, S. (1980). Water stress and leaf growth of field beans (Vicia faba) in the field: leaf number and total area. *Annals of Botany,* 32: 1393 – 1402.

Kearsey, M. & Pooni, H., S. (2005). *The genetical analysis of quantitative traits.* Chapman and Hall, U.K.

Kheradnam, M., Bassiri, A., and Nikrejad, M. (1975). Heterosis, Inbreeding Depression, and Reciprocal Effects for Yield and Yield Components in Cowpea (*Vigna unguiculata* (L.) Walp.). *Crop Science*,15: 689-690.

Kramer, P. J. (1981). Carbon dioxide concentration, photosynthesis, and dry matter production. *BioScience*, *31*(1): 29-33.

Langyintuo, A.S., Lowenberg-DeBoer, J., Faye, M., Lambert, D., Ibro, G., Moussa, B., Kergna, A., Kushwaha, S., Musa, S., & Ntoukam, G. (2003.) Cowpea supply and demand in West Africa. *Field Crops Research,* 82:215–231.

Lauer, J. G., Bijl, C. G., Grusak, M. A., Baenziger, P. S., Boote, K., Lingle, S., Carter, T., Kaeppler, S., Boerma, R., Eizenga, G., Carter, P., Goodman, M., Nafziger, E., Kidwell, K., Mitchell, R., Edgerton, M.D., Quesenberry, K. & Willcox, M.A. (2012). The scientific grand challenges of the 21st century for the Crop Science Society of America. *Crop Science,* 52:1003–1010.

Lawan, R.J. (1983). Responses of four grain legumes to water stress in higher plants. *Annual Review of Plant Physiology,* 35: 299– 319.

Lawlor, D.W. & Tezara, W (2009). Causes of decreased photosynthetic rate and metabolic capacity in water deficient leaf cells: A critical evaluation of mechanisms and integration of processes. *Annals of Botany,* 103(4): 561– 579.

Lin, K.H., Tsou, C.C., Hwang, S.Y., Chen, L.F.O. & Lo, H.F. (2006). Paclobutrazol pre-treatment enhanced flooding tolerance of sweet potato. *Journal of Plant Physiology,* 163(7): 750-760.

Lu, Z., Percy, R.G., Qualset, C.O. & Zeiger, E. (1998). Stomatal conductance predicts yields in irrigated pima cotton and bread wheats grown at high temperatures. Journal of Experimental Botany, 49: 453-460.

Ludlow, M.M. (1989). Strategies of response to water stress. In: Kreeb, K.H., Richter, H. & Hinckley, T.M. (Eds.), (pp 269-281). *Structural and functional responses to environmental stresses.* SPB Academic, The Hague.

Mai-Kodomi, Y., Singh, B.B., Myers, O., Yopp, J.H., Gibson, P.J. & Terao, T. (1999). Two mechanisms of drought tolerance in cowpea. *Indian Journal of Genetics,* 59(3): 309-316.

Mak, C., and Yap, T.C. (1977). Heterosis and Combining Ability of Seed Protein, Yield and Yield Components in Long Bean. *Crop Science*, 17: 339-341.

Marechal, R., Mascherpa, J.M. & Stainer. F. (1978). Etude taxonomique d'un groupe complexe d'speces des genres *Phaseolus* et *Vigna* (Papilionaceae) sur la base de donnees morphologiques et polliniques, traitees par l'analyse informatique. *Boissiera,* 28: 191-193.

Mathur, R. (1995). Genetic Variability Studies in Cowpea .*Legume Research*, 22:65-66.

McCue, K.F, & Hanson, A.D. (1990). Drought and salt tolerance: Towards understanding and application.*Trends Biotechnology,* 8:358-362.

Mir, R.R., Zaman-Allah, M., Sreenivasulvu,N., Trethowan, R. & Varshney, R.K. (2012). Integrated genomics, physiology, and breeding approaches for improving drought tolerance in crops. *Theoretical and Applied Genetics,* 125:625-645.

Mitra, J. (2001). Genetics and genetic improvement of drought resistance of crop plants. *Current Science*, 80:758–763.

Mitra, J., Natarajan, S., and Jain, R. K. (2001). Gene Action for Fodder Yield and its Components in Cluster Bean (*Cyamopsiste tragonobola* (L.) Taub.). *Indian Journal of Genetics and Plant Breeding, 61(3): 253-255.*

Muchero W., Ehlers J.D., & Roberts P.A. (2008). Seedling stage drought-induced phenotypes and drought-responsive genes in diverse cowpea genotypes. *Crop Science, 48,* 541–552.

Muchero, W., Ehlers, J. D., & Roberts, P.A. (2010). Restriction site polymorphism-based candidate gene mapping for seedling drought tolerance in cowpea [Vigna unguiculata (L.) Walp.]. *Theoretical and Applied Genetics,* 120(3): 509 – 518.

Nehru, S. D., and Manjunath, A. (2001). Genetic Variability for Yield and Accessory Character in Cowpea (*Vigna unguiculata* (L.) Walp). *Indian Journal of Agriculture*, 45:99-101.

Ng, N.Q. 1995. Cowpea Vigna unguiculata (Leguminosae-Papilionoideae). In: Smartt, J. & Simmonds, N.W. (Eds.), (pp 326-332). *Evolution of crop plants.* 2nd editions. Longman, Harlow, UK.

Ng,N.Q. & Marechal, R. (1985). Cowpea taxonomy, origin and germ plasm. In: Singh, S.R. & Rachie, K.O. (Eds.), (pp. 11-21). *Cowpea Research, Production and Utilization*. John Wiley & Sons Ltd.

Nhlane, G. (2001). Selecting and breeding maize cultivars for drought tolerance in Malawi. Seventh Eastern and Southern Africa Regional Maize Conference 11 – 15 February, 2001. pp 305-307.

Nielsen, S. S., Brandt, W. E., & Singh, B. B. (1993). Genetic variability for nutritional composition and cooking time of improved cowpea lines. *Crop Science*, *33*(3): 469-472.

Oladipo, E. (2008). Climate Change and Sustainable Livelihoods – The Greening Options. Paper presented at the First National Summit on the Environment, Abuja Nigeria, 20 October 2008.

Omae, H., Kumar, A., Kashiwaba, K. & Shono, M. (2007). Assessing drought tolerance of snap bean (*Phaseolus vulgaris*) from genotypic differences in leaf water relations, shoot growth and photosynthetic parameters. *Plant Production Science*; 10:28–35.

Oseni, T., Lenge, D. D., and Pal, U. R. (1992). Correlation and Path Analysis of Yield Attributes in Diverse Lines cowpea, *Indian Journal of Agricultural Science,* 62: 365-368.

Padulosi, S. & Ng, N.Q. (1997). Origin, taxonomy, and morphology of *Vigna unguiculata* (L.) Walp. In: Singh, B.B., Mohan Raj, D.R., Dashiell, K.E. & Jackai, L.E.N. (Eds.), (pp 1-12). *Advances in Cowpea Research.* Copublication of International Institute of Tropical Agriculture (IITA) and Japan International Research Center for Agricultural Sciences (JIRCAS). Sayce, Devon, UK.

Parameshwarappa, S. G., & Salimath, P. M. (2007). Studies on genetic variability, character association and path coefficient analysis in greengram. *Crop Research-HISAR-*, *34*(1/3): 195.

Piepho, H.P.(2000). A mixture-model approach to mapping quantitative trait loci in barley on the basis of multiple environment data. *Genetics,* 156: 2043–2050.

Pinstrup-Andersen, P. (2009). Food security: definition and measurement. *Food security*, 1(1): 5-7.

Rawson, H. M. & Turner, N. C. (1982). Recovery from water stress in five sunflower *(Helianthus annus L.)* cultivars. I. Effect of timing of water application on leaf area and seed production. *Australia Journal of Plant Physiology,* 9: 437-448.

Reitz, L.P. (1974). Breeding for more efficient water use – is it real or a mirage? *Agricultural Water Management,* 14: 3-28.

Ribaut, J.M., Betran, J., Monneveux, P. & Setter, T. (2009). Drought tolerance in maize. In: Bennetzen, J.L., & Hake, S.C. (Eds.), (pp 311-344). *Handbook of Maize: Its Biology.* Springer Science Business Media, LLC.

Robinson, H. F., Comstock, R. E. and Harvey, V. H. 1949. Estimation of heritability and degree of dominance in corn. *Agronomy J.,* 41:353-359.

Sanda, A. R., & Maina, I. M. (2013). Effect of drought on the yields of different cowpea cultivars and their response to time of planting in Kano State, Nigeria. *International Journal of Environment and Bioenergy,* 6(3): 171-176

Sanginga N, Dashiell, K.E., Diels, J., Vanlauwe, B., Lyasse, O., Carsky, R.J., Tarawali, S., Asafo-Adjei, B., Menkir, A., Schulz, S., Singh, B.B., Chikoye, D., Keatinge, D.,& Ortiz, R (2003). Sustainable resource management coupled to resilient germplasm to provide new intensive cereal–grain–legume–livestock systems in the dry savanna. *Agriculture Ecosystem Environment*, 100: 305–314.

Sawant, D. S. (1994). Association and Path Analysis in Cowpea (*Vigna unguiculata* (L.) Walp.*).) Annals of Agriculture Research*, 15:134-139.

Scott, P (2000). Resurrection plants and the secrets of eternal leaf. *Annals of Botany,* 85(2):159-166.

Sembiring, H., H. L. Lees, W. R. Raun, G. V. Johnson, J. B. Solie, M. L. Stone, M. J. DeLeon, E. V. Lukina, D. A. Cossey, J. M. LaRuffa, C. M. Woolfolk, S. B. Phillips, & W. E. Thomason, (2000). Effect of growth stage and variety on spectral radiance in winter wheat. *Journal of Plant Nutrition,* 23: 141–149.

Shafiq-ur-Rehman, S., Harris, P.J.C. & Ashraf, M. (2005). Stress environments and their impact on crop protection. In: Ashraf, M & Harris, P.J.C. (Eds.), (pp. 3-18). *Abiotic stresses: plant resistance through breeding and molecular approaches*, The Haworth Press, NY, USA.

Sharma, C. D., and Singhania, D. L. (1992). Performance of cowpea genotypes for fodder traits. *Annals of Arid Zones,* 31: 65-66.

Sharma, K. D., Kumar, A., Singh, D., Salisbury, P. & Kumar, A. (2007). Assessing drought tolerance in *Brassica* species by root characteristics and plant water relations. In: *Proceedings: The 12*th *International Rapeseed Congress"Sustainable Development in Cruciferous Oilseed Crops Production": Wuhan, China, March 26- 30.* Tingdong, F. & Chunyun, G. (Eds.), (pp. 448-451). Science Press USA Inc.

Sharma, T. R. (1999). Genetic Variability Studies in cowpea. *Legumes Resources*, 22: 65-66.

Sharma, T. R. (1999). Genetic Variability Studies in cowpea. *Legumes Resources*, 22: 65-66.

Sheikh, B.A and Soomro, G.H (2006). Desertification: Causes, Consequences and Remedies. *Pakistan Journal of Agriculture, Agriculture Engineering and Veterinary Science,* 22(1): 44-51

Shouse, P.J. (1979). Effect of water deficit on the growth, yield and water use of field grown cowpea. *Agronomy Journal,* 72: 434-439.

Shouse, P.J., S. Dasberg, W.A. Jury and L.H. Stolzy. (1981). Effect of water deficits on water potential, yield and water use of cowpea. *Agronomy Journal,* 73: 333-339.

Singh, B.B. & Ajeigbe, H.A. (2002). Breeding improved cowpea varieties for different cropping systems and Agro-ecologies in West Africa. *Africa Crop Science Conference Proceeding,* 5: 35-41.

Singh, B.B. & Matsui, T. (2002). "Cowpea varieties for drought tolerance". In: Fatokun, C.A., Tarawali, S. A., Singh, B.B., Kormawa, P.M. & Tamò, M. (Eds.), (pp. 287-300). *Challenges and Opportunities for Enhancing Sustainable Cowpea Production.* IITA, Ibadan.

Singh, B.B. & Tarawali, S.A. (1997). Cowpea and its improvement: Key to sustainable mixed crop/livestock farming systems in West Africa. In: Renard C (Ed.), (79-100). *Crop Residues in Sustainable Mixed Crop/Livestock Systems.* CAB International in association with ICRISAT and ILRI, Wallingford, UK. pp.

Singh, B.B. & Tarawali, S.A. (1997). Cowpea and its improvement: Key to sustainable mixed crop/livestock farming systems in West Africa. In:

Renard C (Ed.), (79-100). *Crop Residues in Sustainable Mixed Crop/Livestock Systems.* CAB International in association with ICRISAT and ILRI, Wallingford, UK. pp.

Singh, B.B. (1987). Breeding cowpea varieties for drought escape: In: Menyonga, J.M., Bezuneh, T. & Youdeowei, A. (Eds.), *Food seed production in semi-arid Africa.* OAU/STRC-SAFGRAD. Ouagadougou, pp 299-306.

Singh, B.B. (1994). Breeding suitable cowpea varieties for West and Central African savanna. In: Menyonga, J.M., Bezuneh, J.B, Yayock, J.Y. & Soumana, I. (Eds.), *Progress in food grains research and production in semi-arid Africa.* OAU/STRC-SAFGRAD. Ouagadougou, pp 77-85.

Singh, B.B., Ajeigbe, H.A., Tarawali, S.A., Fernandez-Rivera, S., & Abubakar, M. (2003). Improving the production and utilization of cowpea as food and fodder. *Field Crops Research,* 84:169- 177.

Singh, D. P., Chaudhary, B. D., Kumar, A., Sharma, K. D. & Tyagi, P. K. (2004). Agro-physiological basis of resource management and crop improvement in drought prone environment. In: *Dryland Agriculture Research and Technologies in India: Issues and Strategies.* Shanwal, A. V., Panwar, K. S. & Raj, M. *(Eds.),* (pp. 99–119). CCS Haryana Agricultural University, Hisar, India.

Singh, D. P., Kumar, A. & Upadhyaya, S. D. (2007). Inter-linkages and association among stress tolerance traits and their utilization in crop improvement in stress environments. In: *Proceedings International Conference on Sustainable Crop Production in Stress Environments: Management and Genetic Options.* Singh, D. P., Tomar, V. S., Behl, R. K., Upadhyaya, S. D., Bhale, M. S. & Khare, D *(Eds.). (pp. 11-22). February 9-12,* Agrobios International, India.

Taiz, L. & Zeiger, E. (2006). Stress physiology. In: Taiz, L. & Zeiger, E. (Eds.), (671-681). *Plant physiology.* Sinauer Associates, Inc., Sunderland, MA.

Tarawali, S.A., Singh, B.B., Gupta, S.C., Tabo, R., Harris, F., Nokoe, S., Fernández-Rivera, S., Bationo, A., Manyong, V.M., Makinde, K., & Odion, E.C. (2002). Cowpea as a key factor for a new approach to integrated crop–livestock systems research in the dry savannas of West Africa. In: Fatokun, C.A., Tarawali, S.A., Singh, B.B., Kormawa, P.M., & Tamo, M. (Eds.), (pp. 233–251) *Challenges and Opportunities for Enhancing Sustainable Cowpea Production.* International Institute of Tropical Agriculture, Ibadan, Nigeria.

Thiaw, S., Hall, A.E. & Parker, D. R. (1993).Varietal intercropping and the yields and stability of cowpea production in semi-arid Senegal. *Field Crops Research,* 33, 217–233.

Timko M.P. (2006). *The cowpea genomics initiative*, 2nd Edition. Department of Biology, University of Virginia, United States of America.

Timko, M. P., Ehlers, J. D. & Roberts, P. A. (2007). Cowpea. In *Pulses, sugar and tuber crops* (pp. 49-67). Springer Berlin Heidelberg.

Tuberosa, R. & Salvi, S. (2006). Genomics-based approaches to improve drought tolerance of crops. *Trends in Plant Science,* 11: 405–412.

Turk, K.J. & Hall, A.E. (1980a). Drought adaptation of cowpea III. Influence of drought on plant growth and relation with seed yield. *Agronomy Journal,* 72: 428-433.

Turk, K.J., Hall, A.E. & Asbell C.W. (1980b). Drought adaptation of cowpea. I. Influence of drought on yield. *Agronomy Journal*, 72: 413–420.

Turner, N.C., Wright, G.C. & Siddique, K.H.M. (2000). Adaptation of grain legumes (pulses) to water-limited environments. *Advances in Agronomy,* 71:193–231.

Tyagi, I. D., Parihar, B. P. S., Dixit, R. K., and Singh, H.G. (1978). Component Analysis of Green Fodder Yield in Cowpea. *Indian Journal of Agricultural Science,48: 646-649.*

UNCCD, (2011). Desertification: A visual Synthesis. GRAPHI 4 Press, Bresson France. Pp: 1-52.

Valenzuela, H., & Smith, J. (2002). Cowpea. Sustainable Agriculture Green Manure Crops.SA-GM-6. http://www.ctahr.hawaii.edu/of/freepubs/pdf/GreenManureCrops/cowpea.pdf

Van Ek, G.A., Henriet, J., Blade, S.F. & Singh, B.B. (1997). Quantitative assessment of traditional cropping systems in the Sudan savanna of northern Nigeria II. Management of productivity of major cropping system. *Samaru Journal of Agricultural Research,* 14: 47-60.

Van Oosterom, E.J., Jayachandran, R.& Bidinger, F.R. (1996). Diallel analysis of the stay-green trait and its components in sorghum. *Crop Science*, 36: 549–555.

Verdcourt, B. (1970). Studies in the Leguminosae - Papilionoideae for the "Flora of Tropical East Africa IV". *Kew Bulletin,* 24:542-544.

Wang, W.X., Vinocur, B., Shoseyov, O. & Altman, A. (2001). Biotechnology of plant osmotic stress tolerance: physiological and molecular considerations. *Acta Horticulturae,* 560:285-292.

Watanabe, L., Terao, T. & Singh, B.B. (1995) Screening cowpea lines for drought tolerance. *Agronomy Abstracts* 1995. American Society of Agronomy, Madison, Wisconsin, USA, p. 101. American Society of Agronomy, Madison, Wisconsin, USA, p. 101.

Wein, H.C., and Summerfield, R.J. (1980). Adoptation of Cowpea: Effects of Photoperiod and Temperature Response in Cultivars of Diverse Origin. *In*: R.J. Summerfield, and A. H. Bunting (Eds), *Advances in Legumes Sciences*, pp. 405-417 HMSO London.

Yewande, B. A., & Thomas, A. O. (2015). Effects of processing methods on nutritive values of Ekuru from two cultivars of beans (Vigna unguiculata and Vigna angustifoliata). *African Journal of Biotechnology*, *14*(21): 1790-1795.

Yue, B., Xue, W., Xiong, L., Yu, X., Luo, L., Cui, K., Jin, D., Xing, Y. & Zhang, Q. (2006). Genetic basis of drought resistance at reproductive stage in rice: Separation of drought tolerance from drought avoidance. *Genetics*, 172(2):1213-1228.

Zaman-Allah, M., Jenkinson, D. & Vadez, V. (2011). A conservative pattern of water use, rather than deep or profuse rooting, is critical for the terminal drought tolerance of chickpea. *Journal of Experimental Botany,* 62**:** 4239-4252. University of Ghana http://ugspace.ug.edu.gh

Ziska, L. H., & Hall, A. E. (1983a). Seed yields and water use of cowpeas (*Vigna unguiculata* [L.] Walp.) subjected to planned-water-deficit irrigation. *Irrigation Science*, *3*(4): 237-245.

Ziska, L. H., & Hall, A. E. (1983b). Soil and plant measurements for determining when to irrigate cowpeas (*Vigna unguiculata* [L.] Walp.) grown under planned-water-deficits. *Irrigation Science*, *3*(4): 247-257.

Ziska, L.H., Hall, A.E & Hoove, R.M. (1985). Irrigation management methods for reducing water use of cowpea (*Vigna unguiculata* (L.) Walp.) and lima beans (*Phaseolus lunatus* L.) while maintaining seed yield at maximum levels. *Irrigation Science,* 6: 223–239.