



UNIVERSITY OF GHANA

COLLEGE OF BASIC AND APPLIED SCIENCES

SCHOOL OF BIOLOGICAL SCIENCES

DEPARTMENT OF PLANT AND ENVIRONMENTAL BIOLOGY

**LINKAGE DISEQUILIBRIUM AND ASSOCIATION MAPPING OF COWPEA (*VIGNA*
UNGUICULATA (L.) WALP) QUANTITATIVE TRAITS**

BY

AJARA SEIDU

10701967

**THIS THESIS IS SUBMITTED TO THE UNIVERSITY OF GHANA, LEGON IN
PARTIAL FULFILMENT OF THE REQUIREMENT FOR THE AWARD OF MPhil IN
BOTANY DEGREE**

OCTOBER, 2020

DECLARATION

I certify that this work was carried out under strict supervision of Professor I. K. Asante and Professor (Mrs.) Essie T. Blay and that this thesis does not contain any material previously presented or published either in whole or part for an award of a degree in any university except for references to works by other researchers which I have duly acknowledged to the best of my knowledge.



Ajara Seidu

(Student)

...2nd July, 2021...

Date



Professor Isaac K. Asante

(Supervisor)

...2nd July, 2021...

Date.



Professor (Mrs.) Essie T. Blay

(Supervisor)

...6th July, 2021...

Date

DEDICATION

This thesis is dedicated to the memory of my late parents (Mr. and Mrs. Seidu). As well as my husband (Mr. Zaidu Jabiru) and my entire family.

ACKNOWLEDGEMENTS

I express my sincere gratitude to Allah for His immense grace and protection throughout the program.

I am most grateful to my supervisors, Professor Isaac K. Asante and Professor (Mrs.) Essie T. Blay for their strict supervision, constructive criticisms, constant encouragement, guidance and support.

My sincere appreciation to the Head of Department and all the lecturers of the Department of Plant and Environmental Biology who contributed in one way or the other to the success of this work.

My heartfelt gratitude to Professor Alfred Oteng-Yeboah for his kind advice and constant encouragement.

I am most grateful to Mrs. Felicia Oppong and all the technicians of the department for their technical assistance. Not forgetting my colleagues, Ralieu Awura-Korkor Nortey, George A. Akwetey, Roy K. Gyamfi and Edem K. Adalet, who made this journey lively and competitive.

I am grateful to the Genetics group; Pearl Zoryeku, Kingsley Smith, Henry Mensah, Frank Yeboah, Adomako F. Twum-Barima and Benjamin D. Williams, for their support and encouragement.

I am thankful to the staff of Pesticide Residue Laboratory, Ghana Standard Authority (GSA) and the Laboratory of the Government Chemist (LGC) Limited, UK for their support in the laboratory analysis.

I am most grateful to my entire family and staff of Ofori Panin Senior High School (OPASS), for their understanding and support throughout the program.

My final appreciation goes to my children (Mahraj, Sufyan, Hamdiyyat and Abdul Hafidz of the Zaidu's family) for their patience, understanding and encouragement throughout the program.

ABSTRACT

A genome-wide association study (GWAS) was conducted using 187 cowpea germplasm to study linkage disequilibrium and association mapping of some cowpea quantitative traits. All the accessions with the exception of two which were obtained from the Department of Plant and Environmental Biology, were assembled from International Institute of Tropical Agriculture Germplasm Resources Information Centre. These accessions comprised 94 cultivated types and 93 wild relatives. Data on morpho-agronomic traits were collected using the Cowpea Descriptor by the International Board for Plant Genetic Resources. A total of 32 morpho-agronomic traits and 46 SNPs markers were assessed. Ethanol extracts of pulverized dried cowpea seeds were used to determine the amino acid concentrations. Data analysis involved descriptive statistics, Pearson's correlation, principal component analysis (PCA), cluster analysis, Nei's genetic diversity of subpopulations, likelihood ratio test for Hardy Weinberg equilibrium, F statistics and gene flow, population structure and genetic distance analysis. High variation was observed in the morpho-agronomic traits. A total of one hundred and thirty-six (136) significant pairwise correlations were observed in the quantitative traits. Out of the forty-six (46) SNPs markers, forty-three (43) were polymorphic. Means for the quantitative traits studied were as follows: days to 50% germination was 3.93 ± 0.26 days. Mean days to first leaf stage was 12.40 ± 0.24 days. Mean chlorophyll content was 1.44 ± 0.02 mg/liter. Mean days to 50% flowering was 65.97 ± 1.97 days. Mean number of flowers per plant was 8.95 ± 0.55 flowers. Mean peduncle length per plant was 13.39 ± 0.45 cm. Mean number of pods per peduncle was 1.97 ± 0.01 pods. Mean days to 50% pod maturation was 81.86 ± 1.97 days. Mean number of pod per plant was 7.09 ± 0.54 pods. Mean pod length per plant was 11.53 ± 0.28 cm. Mean average seed per pod was 9.86 ± 0.24 seeds. Mean 20 seed weight was 1.5580 ± 0.07 grams. Mean seed yield per plant was 70.31 ± 5.65 seeds. Mean seed abortion rate per

plant was 2.14 ± 0.08 percent. All the 19 amino acids analyzed for the seed quality traits were present in the accessions, except L-Cysteine which was beyond detection. However, some accessions recorded 0.00 for Iso-Leucine and Trans-4-Hydroxyl-Proline. Mean concentrations for the amino acids was generally low in the wild relatives. It ranged between $21623.03 \pm 5299.45 \times 10^{-5}$ ppm (L-Tryptophan) to $17.52 \pm 5.36 \times 10^{-5}$ ppm (L-Methionine) while that for the cultivars varied from $3953909.00 \pm 7143.39 \times 10^{-5}$ ppm (L-Tryptophan) to $18266.33 \pm 2524.18 \times 10^{-5}$ ppm (L-Methionine). Mean Nei's genetic diversity for the overall population was 0.3001, mean Wright's Fixation coefficient for inbreeding (F_{IS}) was 0.8935, mean degree of differentiation within population (inbreeding at different level) (F_{IT}) was 0.9143, mean degree of genetic differentiation (F_{ST}) was 0.1952, mean gene flow (N_m) was 1.0309, mean observed heterozygosity was 0.0242 and mean frequency of cross pollination (C) was 0.0805. Analysis of population structure grouped the cowpea accessions into two clusters. Proportion of membership for cluster 1 was 0.551 and that for cluster 2 was 0.449. The mean F_{ST} value for cluster 1 was 0.064 and that for cluster 2 was 0.048. Intra chromosomal linkage disequilibrium estimate for SNPs loci revealed 12.64% and 15.38% at the threshold level of $r^2 \geq 0.1$ and $r^2 \geq 0.05$ respectively. The largest LD block observed was 25.0 bp between SNPs markers 6904_1061 and 9815_2051 at correlation co-efficient measure of variability between two loci (r^2) of 0.10 and the difference between the gamete frequencies at two different loci (D') of 0.89. Partial linkage disequilibrium decay was observed from a graph of r^2 values of LD (between 0.0 and 0.75) against map distance ranging from 0.0 to 38.75 cM. Significant marker-trait associations were identified with very high potential for exploitation in marker-assisted breeding for the important traits in cowpea. Number of flowers per plant, mean peduncle length, number of pods per peduncle, number of pods per plant, seed yield per plant and DL-Beta phenyl-Alanine were associated with different SNPs markers at 5 cM map distance while

20 seed weight, D-Proline, Iso-Luecine, L-Histidine and L-Serine were associated with different SNP markers at 0.0 cM map distance.

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LIST OF ABBREVIATIONS

AFLP	Amplified Fragment Length Polymorphism
ARC	Agricultural Research Council
C	Frequency of cross pollination
CRI	Crops Research Institute
CTC	Complex Trait Consortium
DPEB	Department of Plant and Environmental Biology
D'	Homogenized difference between the coupling and repulsion gamete
EST	Expressed Sequenced Tags
FAO	Food and Agriculture Organization
F _{IS}	Wright's Fixation coefficient for inbreeding
F _{IT}	Degree of differentiation within population (inbreeding at different level)
	frequencies at two different loci
F _{ST}	Degree of genetic differentiation
GBS	Genotyping by sequencing
GGT	Graphical genotype
GLM	General linear model
MLM	Mixed linear model
GSA	Ghana Standards Authority

GWAS	Genome-wide association studies
IBPGR	International Board for Plant Genetic Resources
IITA	International Institute of Tropical Agriculture
LD	Linkage disequilibrium
LGC	Laboratory of the Government Chemist
MOFA	Ministry of food and agriculture
MTA	Marker-trait association
N_m	Gene flow
NRA	Non-random association
Obs Het	Observed heterozygosity
PCA	Principal Component analysis
PCR	Polymerase chain reaction
PGC	Production Guidelines for Cowpea
PIC	Polymorphism information content
QTL	Quantitative trait loci
r^2	Correlation co-efficient of allele frequencies at significant threshold
RAPD	Random amplified polymorphic DNA
RFLP	Restriction fragment length polymorphisms.
SNPs	Single nucleotide polymorphisms
SSRs	Simple Sequence Repeats

STS	Sequence Tagged sites
UNU	United Nations University
UPGMA	Unweighted pair group method with arithmetic mean
USDA	The United States Department of Agriculture
WHO	World Health Organization

CHAPTER ONE

1.0 INTRODUCTION

Cowpea is an essential legume with several divergent species, both wild and cultivated relatives with remarkable associated groups. According to Onwueme and Sinha (1991), cited in Asante (1996), cowpea is regarded as the second most essential food grain fabaceous crop that can be consumed directly by humans (Kelly, 2010; Haruna *et al.*, 2018). It is believed to have originated from Sub-Saharan Africa, with Nigeria as the most leading producer (Asante, 1996). It is basically a self-fertilised crop with narrow genetic lines (Asare *et al.* 2010). Cowpea is a tap-rooted, dicotyledonous annual herbaceous leguminous plant with alternating trifoliate, ovate leaflets. It is a nutrient rich indigenous leafy vegetable grown by farmers. Cowpea exhibits several growth habits including erect, semi-erect, spreading and indeterminate. Dry cowpea beans are highly nutritious and important to the livelihoods of comparatively poor people in underdeveloped and developing countries of the tropics like Ghana and others particularly where animal protein is difficult to come by, thereby contributing immensely to the National Food Security Programs (Lupton *et al.*, 2002). Cowpea is a multifunctional grain crop that provides food for both man and livestock (Nweke, 1988), and also serves as a dependable and valuable commodity that can generate revenue in most parts of the world (MOFA, 2000). Cowpea is cheap and contains high levels of seed proteins, mainly arginine, tryptophan and lysine which ranges from 18% to 29% (Togola *et al.*, 2020), although research has proved that some varieties contain 23% to 32% and 18% to 35% protein in whole cowpea flour and dehulled defaltered cowpea flour respectively (Khalid *et al.*, 2012). Cowpea is rich in roughage (dietary fiber), phytochemicals and several micronutrients with reduced fat content (Siddhuraju and Becker, 2007). It has appreciable amount of vitamins (vitamin B and folic acid) and some minerals needed during pregnancy to prevent fetal

defects (Tan *et al.*, 2012) with high number of essential amino acids (Igbal *et al.*, 2006). Previous research revealed that frequent consumption of dry cowpea beans reduces blood cholesterol and helps to prevent chronic diseases such as cancer (Frota *et al.*, 2008), as well as improve metabolic processes and diabetic therapy that help to control weight (Winham *et al.*, 2007). Cowpea is widely used as an important food crop since the past decades in the Southern Africa of Sahara and sub-Saharan regions especially in West Africa. It contains high levels of proteins and minerals with less/ or no metabolites and other poisonous compounds (Nkewe, 1988). Cowpea is cultivated basically for its edible leaves, pods and dry seeds. Besides, it provides high quality feed for livestock with proteins in the form of forage, silage and hay. It also serves as cover crop and provides green manure which maintains soil fertility (Kabede and Bekeko, 2020). Root nodules of leguminous plants harbour nitrogen fixing bacteria called *Rhizobium* which help to fix atmospheric nitrogen into the soil to reimburse for the nitrogen loss removed by intercropped plants (Onwueme and Sinha, 1991; Haruna *et al.*, 2018). Spreading indeterminate and semi-determinate bushy growth of cowpea provides ground cover, reduces soil erosion, soil temperature and suppresses the growth of weeds. Plant residue left after harvesting decays, providing organic matter and nutrients to the soil (Haruna *et al.*, 2018).

Ghana is one of the developing countries with high increasing population growth rate. This has led to an increased demand for food to regulate and satisfy the growing population. Foliage leaves of cowpea as well as the dry beans are largely used by consumers. Several households in Ghana feed on cowpea which serves as a good source of protein that is cheap and readily available to the poor. It also has a very short life cycle. Despite the enormous benefits obtained from cowpea, its breeding creates a lot of challenges. This makes production of the crop inadequate to satisfy the increasing demand for the commodity domestically (MOFA, 2000). The main plant gene bank in Ghana with

the aim to collect, conserve and protect Ghana's genetic resources and those from abroad to prevent extinction is the Plant Genetic Resources Research Institute (PGRRI), located at Bunso. Domestication and diversification through evolutionary processes has led to significant deviations in allele and genotypic frequencies of individuals in a population. Evolution result in changes in genetic constitution of a population (Acquaah, 2012).

In order to enable the breeder locate the genes and identify an efficient method to trace the origin of these genes and to include them in breeding, there is the need to research into linkage disequilibrium and association mapping of cowpea quantitative traits. This will help to detect genes and quantitative trait loci (QTLs) and to diagnose molecular markers associated with complex agronomic traits in a mating population. As stated, cowpea is a major grain leguminous crop that contribute immensely to the development of healthy life, thereby satisfying and promoting the World's Food Security Programs. According to WHO & UNU (2007) on World Food Summit, Food Security is attained when "every individual, at all times can get economic and physical access to adequate, nutritious and safe food that is balanced and preferred for a healthy life". Evolution and domestication has resulted in genetic, physiological and morphological variations in plants. These domesticated species may be linked to tamed wild plants /or animals that has become pet (Acquaah, 2012). The use of association mapping based on linkage disequilibrium (LD) has been recommended to have high resolution for mapping quantitative trait loci (QTLs) to help dissect these complex genetic variations. It can also be used to identify genes associated with quantitative variation of agronomic traits (Acquaah, 2012).

The basic aim of studying genetics is to link heritable characters (genotypes) to the physical features (phenotypes). Association mapping based on linkage disequilibrium studies identifies specific variations in genes or chromosomal regions linked to differences in phenotypic traits to

encourage recognition of traits caused by polymorphisms in DNA sequence (Oraguzie and Wilcox, 2007). Association mapping based on linkage disequilibrium or genome-wide association studies (GWAS), is a technique used to identify markers associated with phenotypic traits. It makes use of familial recombination present in the gene pool of a species to identify marker-trait associations. Genome-wide association mapping is a valuable tool for the dissection of novel genes or quantitative trait loci (QTLs) of important agronomic characteristics. Gene-based markers are more accurate than linked markers for the prediction of phenotype, since the marker-trait association do not lost during segregation in the course of recurrent breeding selection cycles (Acquaah, 2012). This approach has the potential to identify a single polymorphism within a gene that is responsible for the difference in phenotype. Association mapping therefore helps in the following ways:

- Results from the analysis can be used to predict the best haplotype across one or multiple genes for optimum expression of the target trait.
- Association studies based on correlations between alleles at different sites or linkage disequilibrium can provide high resolution for the identification of genes that contribute to phenotypic variation in natural populations.
- Also, many plant species have high levels of diversity for which association mapping approaches are well suited to evaluate the numerous alleles available.

1.1 Main Objective of the study

The main objective of this research was to study linkage disequilibrium and association mapping of cowpea quantitative traits using 187 cowpea accessions.

1.2 Specific Objectives

The specific objectives of the research were to:

1. Assess 187 cowpea accessions for morpho-agronomic traits.
2. Carry out amino acids (seed quality traits) analysis of cowpea seeds.
3. Study genetic diversity and population structure of 187 cowpea accessions using SNPs markers.
4. Estimate linkage disequilibrium and linkage disequilibrium decay in the cowpea accessions
5. Conduct association mapping for morpho-agronomic and amino acids (seed quality traits)
6. Identify and select SNPs markers associated with cowpea morpho-agronomic traits and amino acids (QTLs).

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Botany and origin

Cowpea (*Vigna unguiculata*) is a dicotyledonous plant belonging to family Fabaceae. It is mainly cultivated in Africa, Asia, Brazil, Latin America and India (Ehlers *et al.*, 2002) with several growth habits including erect, semi-erect, prostrate, semi prostrate, climbing. Pods may be straight, round, coiled, linear or crescent. Pod length varies between 20 and 30 centimeters. There have been uncertainties about the exact origin and place of domestication. However, several evidences have proved that cowpea, originated from Africa, especially West Africa by some workers, because both wild and cultivated species thrive in the region. Others also believed that it originated from Southern Africa (Oruko *et al.*, 2011).

2.2 Production

Worldwide cowpea production was estimated at 2.7 million metric tons from 7.7 million hectares (Simon, 2018). It is cultivated in the semi-arid regions of Africa, Europe, Asia, and United states due to its adaptability to dry areas (Khalid *et al.*, 2012). Cowpea is one of the accredited crops strongly addressed by the International Institute of Tropical Agriculture (IITA). The most leading cowpea producing region worldwide is known to be the Western and Central Africa. This area produces about 64% of the rated 3 million metric tons of cowpea seeds cultivated annually (Zuma, 2016; Simon, 2018). Nigeria is known to be the world's foremost cowpea producing nation, where annual production is about 2 million metric tons followed by Niger (650,000 metric tons) and then, Brazil (490,000 metric tons) (Singh *et al.*, 2002; Beintema *et al.*, 2019; Chaminuka *et al.*, 2019).

Other major cowpea producing countries include Burkina Faso, Malawi, Kenya, Ghana, Uganda, Tanzania, Mali, Cameroon and Senegal (all in Africa) and India, Burma, Sri Lanka, Philippines, Bangladesh, Thailand, Indonesia. (Ng and Marechal, 1985)

2.3 Cowpea production in Ghana

According to Haruna *et al.* (2018), Ghana is known to be the fifth highest cowpea producing country in Africa with Guinea Savanna zone (Northern and Upper West Regions) of Ghana as the major producing areas. Annually, about 156,000 ha yielding an average of 143,000 MT cowpea is produced in Ghana. Other cowpea producing zones include Sudan Savanna (Upper East Region) and some localities in the Brong, Ahafo and Ashanti Regions. There are six agro-ecological zones present in Ghana for cowpea cultivation, (Asante, 1996). The crop is mainly cultivated in the savanna but also in all agro-ecological regions of Ghana (Bawa *et al.*, 2017). Cowpea is widely cultivated by small scale peasant farmers under dryland farming conditions (Oruko *et al.*, 2011), usually as an intercrop with cassava, millet, sorghum and yams. Cowpea production in Ghana is affected by parasitic weeds (Haruna *et al.*, 2018), pest or nematode infection, changes in agronomic practices and climatic conditions as well as consumer preference and industrial demands.

2.4 Principles of genetic mapping

According to Meksem and Kahl (2006) cited in Gómez *et al.* (2011); Salvi and Tuberosa (2007), there are two main aims for genetic mapping. These are:

- Detection and identification of genetic factors that control phenotypic traits and;
- Detection of recombination distance between the markers or loci.

One of the conditions for mapping is that, the trait to be investigated must be polymorphic. A way of detecting such polymorphisms is by the use of genetic markers (Gómez *et al.*, 2011).

2.5 Association mapping

Association mapping, also variously known as association genetics, genome-wide association studies (GWAS) and linkage disequilibrium is a way of analyzing and mapping quantitative trait loci (QTL) (Chakaborty and Weiss, 1988; Kruglyak, 1999). It is an approved strategy to identify and dissect important variants such as molecular markers involved in the transmission of complex traits (Oraguzie *et al.*, 2007; Agarwal, 2014). Association mapping aims at identifying specific significant markers associated with phenotypic differences in a character to help detect and identify the trait. Association mapping identifies specific variations in genes or chromosomal regions linked to phenotypic traits (Oraguzie and Wilcox, 2007). This is done by scanning the entire genome for strong linkages between a group of genetic markers such as SNPs and a significant phenotype. These associations are conducted to verify if they are closely or directly associated with the trait of interest (Gibson and Muse, 2009).

Association mapping requires a large number of genetic markers to generate genetic maps as well as locate the regions of interest related to the expression of the desired trait (Gómez *et al.*, 2011). Association mapping seeks to overcome majority of significant limitations of linkage mapping and does not involve building segregating or mapping population. It identifies statistical associations that exist between markers and a trait. (Gómez *et al.*, 2011). It is powerful and can map traits with very high resolutions (Yu *et al.*, 2008).

Differences between linkage mapping and association mapping

Association mapping involves the gathering of natural population that involves the use of loosely structured or unstructured population, mainly intraspecific. The fundamental condition for association like this is the identification of statistical non-random association of heritable trait variation and observed genetic polymorphisms (Acquaah, 2012) while linkage mapping involves segregating population.

2.6 Quantitative Trait Loci (QTL) Analysis

Quantitative trait loci (QTL) is a specific sequence of DNA which correlates with a particular phenotypic trait. Several QTLs may be linked to a single trait (Daware *et al.*, 2020). QTLs may be mapped by detecting or identifying, through appropriate statistical analysis or by sequencing to locate and determine molecular markers (e.g. SNPs) that are linked with the trait of interest (Gómez *et al.*, 2011). In identification of QTL in cowpea on chromosomes, gene models underlying QTL region can be used to determine the physical region of the QTL by positioning flanking SNPs in genome sequence (Lo *et al.*, 2020). Quantitative trait loci (QTL) analysis is a genomic tool in cowpea breeding programs and facilitates the improvement of cowpea breeding. It accounts for phenotypic variation which may differ from one trait to the other (Sobda *et al.*, 2017).

2.7 Morphological and phenotypic Variability in cowpea germplasm

The variability in cowpea germplasm can be influenced by the accession type. Variability is observed in accessions collected from Deciduous Forest regions and those from Sudan Savanna and Guinea Savanna with reference to germination, flowering and pod maturity periods (Asante *et*

al., 2006). High significant morphological variations with reference to growth habit, pod colour, seed coat colour / pattern, leaf colour and V-marking as well as phytochemical traits are also observed (Zoryeku, 2019). Significant low levels of phenotypic variability within population diversity are observed due to the fact that cowpea is a self-fertilized specie (Zoryeku, 2019). However, some quantitative traits may also have no morphological or phenotypical variation (Ghalmi *et al.*, 2010).

2.8 Amino acid variation in cowpea

Amino acid is an organic compound containing the elements: carbon, hydrogen, oxygen and nitrogen with few containing sulphur. It is the smallest unit of proteins containing both amine or amino (-NH₂) group and carboxyl (-COOH) group. According to Reeds (2000), there are about twenty-two known amino acids occurring naturally with pyrrolysine as the 22nd amino acid. Out of these, ten of them are considered to be essential while the remaining are non-essential. Essential amino acids are indispensable units of proteins that cannot be produced by organisms. They are required in large quantities and need to be supplemented in the diet. Amino acids that are not necessarily needed but can be synthesized by organisms are called non-essential amino acids (Kenji and Akira Okada, 1998; WHO & UNU, 2007). Current research has proved that cowpea (*Vigna unguiculata* L. Walp) contains nine out of the ten essential amino acids and eight non-essential amino acids (Ukpene and Imade, 2015). The essential amino acids include B-Threonine, DL-Beta_phenyl Alanine, Iso-Leucine, L-Histidine, L-Lysine, L-Methionine, L-Threonine, L-Tryptophan and L-Valine while the non-essential ones include DL-Alpha Alanine, D-Proline, Glutamine, Glycine, L-Asparagine, L-Aspartic Acid, L-Cysteine, L-Serine, L-Tyrosine and L-Trans-4-Hydroxyl-Proline. Cowpea is one of the important major source of plant proteins (Ukpene

and Imade, 2015). The main function of proteins is to provide our bodies with these dispensable (non-essential) and indispensable (essential) amino acids.

2.9 Population structure

Populations in their natural settings are classified into sub-groups which prevent complete random mating and this increases heterozygosity due to diverse genetic disparities among each other (Xiong et al., 2016). Sewall Green Wright, an American geneticist and a founder of population genetics developed F-statistics as a measure for deflections from Hardy-Weinberg equilibrium in sub-grouped populations. Measurement of linkage disequilibrium (LD) and possible association mapping (AM) can be carried out by the use of structured population generated from the studied sample. The effect of population structure depends on relationship between sampled individuals. The F-statistic comprises the following:

- Wright's fixation index (F), as a measure of heterozygote deficiency or excess
- Coefficient of inbreeding (F_{IS}). This refers to the measure of mating individuals within the local sub-population.
- Coefficient of inbreeding at different levels within populations (F_{IT}). It is a correlation between alleles among individuals with respect to the overall population.
- Degree of genetic differentiation (F_{ST}). This is a measure used for analyzing the total genetic divergence within the sub population. It refers to correlation between randomly selected alleles from the sub-population in relation to the overall population. .

Population structure assessment makes use of the following elements: genetic distances, clustering and differentiation between clusters or groups (Panda *et al.*, 2015). According to Panda *et al.* (2015), cited in Zoryeku (2019) Principal component analysis provides a reliable and important information for inferring population structure. It is used for the study of genetic distances between

individuals. It is also used to assess genetic differentiation among clusters or groups classified by dendrogram.

2.10 Molecular markers

The rapid advancement in the molecular genetics has led to the emergence of diverse techniques to analyze genetic variation (Karp *et al.*, 1996; Parker *et al.*, 1998). Different methodologies have been used for studying plant genetic resources. These include the use of morphological, biochemical and molecular markers to assess the level of genetic diversity (Zoryeku, 2019) as well as map the association between the phenotypes and genotypes. Even though genetic assessment has for decades relied on morphological markers, molecular markers however, have played a more reliable role in the genetic analysis in most plant species. Several different methods may be employed in molecular analysis. Genetic markers differ with respect to specific important features such as locus specificity, genome abundance, reproducibility, technical requirement and the level of polymorphism detected (Spooner *et al.*, 2005). The DNA based markers are classified into two groups namely hybridization and polymerase chain reaction (PCR) based markers. An example of hybridization based DNA markers is Restriction Fragment Length Polymorphisms (RFLP). PCR based markers include Random Amplified polymorphic DNA (RAPD), Amplified Fragment Length Polymorphism (AFLP), Simple Sequence Repeats (SSRs), Expressed Sequenced Tags (EST), Sequence Tagged sites (STS) and Single Nucleotide polymorphisms (SNPs). Molecular markers like all other genetic markers are based on differences in DNA sequence and are not influenced by the environment. They generally detect polymorphism by analyzing the total amount of DNA sequence variability in a genome (Barcaccia, 2010). Molecular markers are highly recognized tool for studying genetic biodiversity. DNA based markers are used to measure genetic

variation within populations to assess the genetic relatedness among sub-populations. This promotes the formation, implementation and use of germplasm programs (Barcaccia, 2010).

Single Nucleotide polymorphisms (SNPs) markers

Single Nucleotide polymorphisms (SNPs) is a molecular marker that detect variations in single nucleotide position (Spooner *et al.*, 2005). Several research work on cowpea have been done by using DNA based markers. Results from several researchers have proved that single nucleotide polymorphisms (SNPs) markers are highly efficient in differentiating between cowpea accessions than morphological techniques (Egbadzor *et al.*, 2014; Qin *et al.*, 2016). SNP markers are very informative in relation to polymorphisms, and present reliable, comprehensive and comparable data. It accounts for phenotypic variations when distributed along different chromosomal regions (Sobda *et al.*, 2017). They help to reconstruct genotypes and explain haplotypes by multiple analysis using preliminary sequence information (Barcaccia, 2010).

2.11 Genetic Diversity

Diversity refers to the wide range of differences that can be seen when considering large number of individuals in a population. Genetically, the two main forms of diversity widely known are genetic and phenotypic diversities. Genetic diversity involves the use of genetic markers while phenotypic diversity deals with the application of morphological markers. According to Mafakheri *et al.* (2017) genetic diversity plays an important role in the continual existence of species. Its assessment is very crucial to lessen the dangers of environmental variation. Knowledge on genetic diversity is utmost in breeding programs for the maximum utilization of genetic resources. The existence of genetic diversity within different plant species helps in the selection of those with desirable traits for crop improvement (Zoryeku, 2019). Several statistics are employed in estimating genetic diversity. The parameters estimated during genetic diversity assessment

include; Nei's genetic diversity and differentiation, likelihood ratio test for Hardy Weinberg, gene flow, percentage polymorphic loci, frequency of cross pollination and observed heterozygosity. The frequency of cross pollination determines the level of heterozygosity. Even though, cowpea is a self-fertilized crop, it exhibits some level of heterozygosity.

2.12 Linkage and Linkage disequilibrium

When two genes occur on the same homologous chromosomes, they are said to be linked. During meiosis, different chromosomes are assumed to segregate independently. As a result, two genes located on different chromosomes also segregate independently. Genes on the same chromosome that are transmitted and inherited together are said to be genetically linked (Acquaah, 2009). The probability of whether or not genetically linked genes found on the same chromosome will not separate during meiosis depends on how tightly or closely linked they are. However the likelihood that an allele (of one ancestor) at the same locus co-inherits with another at different locus is 0.5 and such genes are considered to be unlinked. The position of genetic markers or genes relative to one another can be detected through linkage mapping techniques. This can be estimated by calculating the value of recombination frequency among marker genes. The larger the value of the recombination frequency, the more separated the genes appear on the chromosome (Acquaah, 2009). Steps involved in the construction of this genetic linkage maps include; organizing mapping population data, polymorphism identification, and pair-wise recombination frequency calculated from mapping populations, linkage group establishment and map distance estimation (Acquaah, 2012). Different statistical models have been proposed for the evaluation of linkage disequilibrium (Hedrick, 1987). However, r^2 and D' are the most frequently used measures in association mapping analysis at two different loci (Stich and Melchinger, 2010). The r^2 represents the correlation coefficient of allele frequencies at significant threshold, while the D' represents the homogenized

difference between the coupling and repulsion gamete frequencies at two different loci (Stich and Melchinger, 2010).

Linkage Disequilibrium Decay

Linkage disequilibrium (LD) generally decreases rapidly in cross pollinated species than self-pollinated species. This is because, less effective recombination occur in self-pollinated species, where individual exhibit high levels of homozygosity than heterozygosity (Gupta *et al.*, 2005). According to Flint-Garcia *et al.* (2005), cited in Gómez *et al.* (2011), low levels of linkage disequilibrium (LD) are normally expected within large populations; and when the common ascendant among individuals in a population is far apart. Likewise, low linkage disequilibrium level is not uniformly distributed along the entire genome but is rather located within short distances around particular loci or markers which produce just critical co-occurrences within physically close loci. This increases the mapping resolution of the sampled population.

2. 13 Marker Trait Association

Some morphological markers facilitate the detection, identification and understanding of a specific trait. General linear model (GLM) and mixed linear model (MLM) are the two main statistical models which holds that any observed response is a linear sum of multiple individual underlying responses (Pouratian *et al.*, 2002; Al-Herz *et al.*, 2014). General linear model is a simple statistical model that is used to predict outcomes both for experimental and responding variables with distinct distributions and those that are not linearly associated to the predictors. It helps to understand, predict and analyze experimental data by comparing how different variables affect continuous variables (Stroup, 2016). General linear model also helps to identify relationship between response and covariate variables. Statistical model having both random and non-random effects useful in biological and physical sciences are employed in linear model analysis. Mixed linear model

(MLM) are add-on of general linear model (GLM) to enable both random and non-random (fixed) effects to be analyzed. These two models are valuable in various disciplines such as biological, physical as well as social sciences (Stroup, 2016). Mixed linear model (MLM) is more refined and has advantage of dealing with missing data values and are therefore usually preferred over other methods.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Experimental materials

The experimental materials used for the study were a total of 187 cowpea accessions, 93 from wild relatives and 94 from cultivated types collected from 32 countries were used in this study. The passport data and list of the accessions used for the study are presented in Table 3.1.

3.2 Sources of collection of Experimental materials

All the accessions, except G.E and PARENT (collected from Department of Plant and Environmental Biology (DPEB), University of Ghana), were obtained from the International Institute of Tropical Agriculture (IITA) Germplasm Resources Information Centre, Ibadan, Nigeria.

3.3 Site Description and Experimental Design

The field study was carried out at the Department of Plant and Environmental Biology (DPEB), School of Biological Sciences, University of Ghana, Legon. The experiment was designed in pot with dimension 3.20 m³. A total of 187 pots were arranged in three lines of sixty-three rows. Spacing used was 0.8 meters between lines and 0.5 meters between rows. Two cowpea seeds per accession were planted per hole in each pot at a depth of 3 cm to 4 cm. The experiment was carried out in March for over three (3) to seven (7) months in pots.

Table 3.1: List of cowpea accessions used for the study

Plant genotype	Country of Origin	Plant genotype	Country of Origin
W.1	USA	W.33	Paraguay
W.2	Tanzania	W.34	India
W.3	USA	W.35	Turkey
W.4	Tanzania	W.37	Ghana
W.5	South Africa	W.38	USA
W.6	South Africa	W.39	USA
W.7	Philippines	W.40	Nigeria
W.8	Uganda	W.41	Nigeria
W.9	Uganda	W.42	Nigeria
W.10	Tanzania	W.43	Nigeria
W.11	USA	W.44	Nigeria
W.12	Nigeria	W.45	Nigeria
W.13	USA	W.46	Nigeria
W.14	South Africa	W.47	Nigeria
W.15	South Africa	W.48	Nigeria
W.16	USA	W.49	Nigeria
W.17	Uganda	W.50	USA
W.18	India	W.51	Nigeria
W.19	Guatemala	W.52	Nigeria
W.20	Puerto Rico	W.53	Nigeria
W.21	Nigeria	W.54	USA
W.22	Nigeria	W.55	Puerto Rico
W.23	Nigeria	W.56	Nigeria
W.24	Nigeria	W.57	Turkey
W.25	Nigeria	W.58	USA
W.26	USA	W.59	South Africa
W.27	USA	W.60	Puerto Rico
W.28	India	W.61	India
W.29	Nigeria	W.62	Nigeria
W.30	Nigeria	W.63	India
W.31	USA	W.64	Nigeria
W.32	Hungary	W.65	Nigeria

W = Wild relative

Table 3.1 contn'd

Plant genotype	Country of Origin	Plant genotype	Country of Origin
W.66	Nigeria	C.98	Uganda
W.67	Nigeria	C.99	Zaire
W.68	Nigeria	C.100	Tanzania
W.69	Niger	C.101	Nigeria
W.70	Nigeria	C.102	Guinea
W.71	Nigeria	C.103	Chad
W.72	Nigeria	C.104	Mali
W.73	Nigeria	C.105	Uganda
W.74	Niger	C.106	Benin
W.75	USA	C.107	Botswana
W.76	South Africa	C.108	Botswana
W.77	USA	C.109	Cameroon
W.78	USA	C.110	Cameroon
W.79	USA	C.111	Cameroon
W.80	Hungary	C.112	Nigeria
W.81	USA	C.113	Cote d'Ivoire
W.82	USA	C.114	Tanzania Central African
W.83	USA	C.115	Republic
W.84	USA	C.116	Nigeria
W.85	Nigeria	C.117	Malawi
W.86	USA	C.118	Tanzania
W.87	USA	C.119	Nigeria
W.88	USA	C.120	Lesotho
W.89	USA	C.121	Guinea
W.90	USA	C.122	Nigeria
W.93	USA	C.123	Ethiopia
W.94	USA	C.124	Niger
W.95	USA	C.125	Niger
PARNT	DPEB	C.126	Nigeria
G.E	DPEB	C.127	Uganda
C.96	Nigeria	C.128	Tanzania
C.97	Tanzania	C.129	Nigeria

W = wild relative; G.E = Golden eye C = Cultivated type

Table 3.1 contn'd

Plant genotype	Country of Origin	Plant genotype	Country of Origin
C.130	Uganda	C.160	Egypt
C.131	Nigeria	C.161	Malawi
C.132	Chad	C.162	Nigeria
C.133	Botswana	C.163	Nigeria
C.134	Malawi	C.164	Nigeria
C.135	Liberia	C.165	Nigeria
C.136	Nigeria	C.166	Nigeria
C.137	Nigeria	C.167	Niger
C.138	Chad	C.168	Zaire
C.139	Nigeria	C.169	Tanzania
C.140	Malawi	C.170	Tanzania
C.141	Mali	C.171	Nigeria
C.142	Malawi	C.172	Senegal
C.143	Burkina Faso	C.173	Mali
C.144	Malawi	C.174	Republic of the Congo
C.145	Malawi	C.175	Senegal
C.146	Benin	C.176	Botswana
C.147	Nigeria	C.177	Botswana
C.148	Niger	C.178	Botswana
C.149	Nigeria	C.179	Tanzania
C.150	Uganda	C.180	Nigeria
C.151	Ghana	C.181	Botswana
C.152	South Africa	C.182	Zaire
C.153	Tanzania	C.183	Zaire
C.154	Nigeria	C.184	Nigeria
C.155	Nigeria	C.185	Cote d'Ivoire
C.156	Nigeria	C.186	Mali
C.157	Niger	C.187	Tanzania
C.158	Mali	C.188	Chad
C.159	Nigeria		

C = Cultivated type

3.4 Phenotyping

Data on morphological and agronomic traits were collected based on the Cowpea descriptor by the International Board for Plant Genetic Resources Institute (IBPGRI). A total number of thirty-two phenotypic traits were assessed. The traits examined were grouped into vegetative, reproductive and seed quality traits.

3.4.1 Vegetative traits

The vegetative traits recorded were: days to 50% germination, days to first leaf stage, leaf texture, leaf colour, chlorophyll content, terminal leaflet shape, growth habit, growth pattern, twinning tendency, plant pigmentation, plant hairiness and V-marking on leaflet.

3.4.2 Reproductive traits

The traits scored were: days to flowering, number of flowers per plant, flower colour, raceme position, number of pods per peduncle, days to first matured pod, mean peduncle length per plant, mean pod length per plant, number of pods per plant, mean pod pigmentation, pod colour, pod wall thickness and pod curvature.

3.4.3 Seed characters

Mean number of seeds per pod, twenty-mean seed weight per plant, mean seed yield per plant, mean seed abortion rate, seed shape, seed coat colour and seed coat pattern were scored.

3.4.4 Determination of chlorophyll content (Spectrophotometry)

Chlorophyll content was measured using leaf samples from fourth to fifth leaves stage of four to six weeks old plants. The chlorophyll concentration in the leaves was recorded using spectroradiometer and recorded in mg/liters. The leaves were scanned to estimate the chlorophyll

concentrations by the use of image processing algorithm using Canon scanner having a resolution of 300 pixels per ppi (inch) and colour depth of 24 bit. This measures leaf absorbance of infra-red light and red light at approximately 940 nm and 650 nm respectively (Parry *et al.*, 2014).

3.4.5 Amino acid analysis of seed quality traits

Total number of nineteen (19) amino acids were analyzed. These were: B-Threonine, DL-Beta-phenyl-Alanine, Glutamine, Iso-Leucine, L-Aspartic Acid, L-Histidine, L-Methionine, L-Threonine, L-Tyrosine, Trans-4-Hydroxyl-Proline, DL-Alpha-Alanine, DL-Proline, Glycine, L-Asparagine, L-Cysteine, L-Lysine, L-Serine, L-Tryptophan and L-Valine.

Sample Preparation

Twenty (20) seeds (108 out of the 187) from each cowpea accession were pulverized because 108 accessions out of the 187 flowered and produced seeds. 1.25 g of the pulverized cowpea seeds of each of the accessions was weighed into beakers. Ethanol extracts were prepared from 10ml of 100% ethanol after 24 hours. The samples were filtered into 1.5ml McCartney bijou glass bottles for further analysis at the Ghana Standard Authority (GSA), precisely at the Pesticide Residue Laboratory.

3.5 Genotyping

Leaf sample collection, DNA extraction and SNPs Genotyping by sequencing (GBS).

Leaf samples from the first trifoliate leaves of two to three weeks old plants per accession were collected and shipped to the LGC Limited for genotyping and isolation of genomic DNA. Leaf collection was done by using plant sample collection kits tool from Laboratory of the Government Chemist (LGC) Limited, a British Company in United Kingdom (UK) (Tinkler *et al.*, 1998). Forty-

six (46) SNPs markers were used for the study. The sequences for the 46 SNPs markers with their respective alleles and chromosome positions are presented in Table 3.2.

3.6 Data Analysis

3.6.1 Morpho-agronomic traits and Seed quality traits

The software Stata/MP version 13 was used to perform descriptive statistics analysis on morpho-agronomic traits and amino acids. Pearson correlation analysis and principal component analysis were also performed on morpho-quantitative traits.

Table 3.2: List of 46 cowpea SNPs markers used with their respective alleles, chromosome position and sequence

Marker names	Alleles	Chromosome	Position	Sequence
1107_518	G/A	1	0	AGCCAATAGCTACAA[A/G]TTTTGTTCGTTC
18_107	C/T	1	5	CACAAAACCTCCCAAA[T/C]CCAGTTCCAAGATT
14164_1877	T/A	1	5	GTTTTTATGAATGAA[A/T]KYTAGTATGTAAGT
4980_497	C/T	1	5	ACCATTCCGTGCCCT[T/C]CTTGATGTTGGTCT
12929_463	G/A	1	5	TTTTGACCTTATTTT[C/A/G]TATAAATGGATTTG
9815_2051	C/T	1	13	ATTGAAGACAGAGTT[T/C]CCTGAGCTTCTTTT
8777_825	T/A	1	14	TAGGATATTTTGACA[A/T]GTTATGTATCCGAT
642_527	C/T	1	14	TGTGACCTGTGTGAC[T/C]CTTTCCAAATCGTT
8306_119	G/C	1	15	CGAAAACCGGTGTTT[C/G]TGAAGGTGGATCAA
6804_755	G/T	1	17	TCTTGTCGGTTAACT[T/G]GGTCATAGTTTATG
16494_1773	C/T	1	21	GCCTCTTTGAGCACA[T/C]GTTCTACACAAGGC
5074_629	C/T	1	21	ATAATAAGATGTTTC[T/C]CATTTTAAATGTTCA
14542_452	G/C	1	21	CAATGAGGACCACGT[C/G]GCTATTATAAAGGA
3787_812	C/T	1	21	TCTTACTCATGTTCAT[T/C]ACCAAAGCCATCAC
1181_710	G/A	1	22	ATCAAGAATTACAGG[A/G]AAGCCTGAAGAGCA
5553_147	C/T	1	22	TCTTGTTTGTGACAA[T/C]GGAACAGGAATGGT
13281_572	G/A	1	23	TACATGAGCGARCTC[A/G]ACATCAACCTCGTC
13772_1075	G/C	1	23	GAGGGTGATCATAGC[C/G]AGCCGGGGTCCAGA
2535_666	C/A	1	24	CCGATTCCCTGCTTT[A/C]TTAGTTAATGATTA
5084_519	G/C	1	24	TCTGGGTGTTTTT[CAG/C/G]AACTTCYGMGGAGC
11367_1228	G/C	1	24	TAAATAATTTTATCT[C/G]TTTCGAACCTCTCT
15779_1173	G/C	1	24	CAAGAGAAGGTTGCT[C/G]TGGTACTGTGAGGT
571_592	G/A	1	24	TCAGCAAGCTTGAAA[A/G]ATTGCTCTCTTTTG
7205_420	G/A	1	24	GGAAGAGTTTCTGAG[A/G]TCTCATTGGATGGC
8770_1480	G/T	1	27	AAATAATAGAAGCTT[T/G]TACAATGTGTCCCA
1426_521	C/T	1	28	CTTTTATTTTGCCCCA[T/C]GTAACAGATACACT
1545_161	C/T	1	28	TGGCAAGTACACCCT[T/C]GGTTACAAGACCGT
13947_415	T/A	1	30	CTTGTTACCTGTCAC[A/T]GAGACCTTGTTCTC
9521_957	T/A	1	30	CCWACTAGTGGCAAC[A/T]TGCAGCCAGATAGT
15451_698	G/T	1	30	AGATAAAAGGAGAGT[T/G]ACCCAAGCACTGAT
6796_936	C/T	1	30	TGAATTACTTACATG[T/C]GCTGAGCAGGTCC
25_592	T/A	1	33	TCTGTTTCATAGTTT[A/T]GCCAATTATAATTG
5240_1403	G/T	1	33	GTATGTTGTGAATTT[T/G]ACAGTAAATATTTT
12882_709	G/A	1	35	CTAACCCCTAGTCCTA[A/G]TATCAGTCTAAGTA
5069_298	T/A	1	36	AAACATGGCAGTGAT[A/T]TGGGAGGAAAAGAC
14929_258	C/T	1	36	CGACAAGTCCGAGGT[T/C]GCAGATCGCGTCAT
17149_508	C/T	1	36	GTAACTGATATACC[T/C]CCCTTGTAGACATG
3841_598	T/A	1	36	AGCATTCTSTTTCCA[A/T]GTAAAAATATTATG
5149_220	G/C	1	36	TCTTCAAGTGGAAGA[C/G]AAAATCGAATACTA
967_118	G/C	1	36	GAACCTCTTCTTCCTC[C/G]ATCACTCCACGCCA
10269_488	C/A	1	37	GATTTCTATAGGATT[A/C]GATTGCCGTCCAAT
15152_845	G/A	1	37	TGATTGAACCATAGA[A/G]CTCAGAGTGTTGTA
12526_795	C/T	1	37	GTAAAGGTTACTATA[T/C]ATTGCATGGAGATC
6904_1061	G/C	1	38	AGACTGTGTTGTATT[C/G]CYTGTTTCATTCCG
1204_901	G/C	1	38	ATTGTATCCTATTAT[C/G]CAGAGTGCTGTAGA
2077_348	C/T	1	38	ACTTCTGCTGTATCC[T/C]AATCCATCAGACCC

3.6.2 Population Structure Analysis

Data set generated from SNPs genotyping (genotype data) were used to analyze for the population genetic structure. The software *STRUCTURE* Harvester (Earl and von Holdt, 2012), was used to analyze for the optimum population structure ('K' value), i.e. $K=2$. This was done using 10 iterations per simulation and 10000 burn-in for both the Inferred Ancestry Model and the Allele frequency model correlated among the populations. The K value was evaluated based on the plateau criterion suggested by Pritchard *et al.* (2007), using Wilcoxon model and the Delta K (ΔK) technique (Rosenberg *et al.*, 2001; Evanno *et al.*, 2005). This was in turn used to estimate the inferred ancestry of individuals ('Q' matrix), (Pritchard *et al.*, 2010; Tamil, 2011). The software *STRUCTURE* version 3.2.2 was used to generate the population genetic structure, (i.e. the 'Q' matrix). Structure plots (i.e. bar, data and triangular plots) as well as histogram distribution of F_{ST} were deduced by the *CLUMP* software using *DISTRUCT* to illustrate clear genetic differentiation among individuals in the sub-population.

3.6.3 Genetic Diversity Analysis

Genotypic data set generated from single nucleotide polymorphisms (SNPs) genotyping was used for the analysis. The software *POPGENE* 1.30 was used for analysis of the following: Nei's genetic diversity, likelihood ratio test for Hardy Weinberg equilibrium, F-statistics and gene flow at each locus from raw data to determine variability within the sampled population.

3.6.4 Estimation of Genetic distance

The software Graphical genotype (*GGT*) 2.0 was used to generate the dendrograms using the unweighted pair group method with arithmetic mean (UPGMA) Jaccard cluster method. Linkage disequilibrium decay plot was also constructed by using *GGT* 2.0 software. It is a simple

agglomerative (bottom-up) hierarchical clustering method. It is an important tool in understanding how various traits came about in living things. The software has the facility of combining morphological traits and SNPs markers' data. Graph of linkage disequilibrium decay was also generated using this software.

3.6.5 Estimation of Pairwise linkage disequilibrium (LD) and marker-trait association (MTA).

Data generated from SNPs genotyping was used to analyze for the pairwise linkage disequilibrium and linkage disequilibrium decay; and marker-trait associations using the software *TASSEL* 2.1.

CHAPTER FOUR

4.0 RESULTS

4.1 Frequency distribution of morpho-agronomical qualitative traits

The frequency distribution of 18 morpho-agronomic qualitative traits measured on 187 cowpea genotypes by their phenotypic classes are presented in Table 4.1.

Plant pigmentation

Plant pigmentation showed seven different phenotypic classes. The overall population distribution frequency ranged from 1.07 % (*intermediate*) to 66.84 % (*non pigmented*). The frequency distribution for the wild relatives ranged from 1.08 % (*intermediate*) to 70.97 % (*non pigmented*) while that for the cultivated types ranged between 1.06 % (*intermediate*) and 62.77 % (*non pigmented*).

Plant hairiness

Three phenotypic classes were detected. Frequency distribution for overall population ranged from 4.81 % (*pubescent to hirsute*) to 74.19 % (*glabrescent*). Frequency distribution based on accession type ranged from 9.68 % (*pubescent to hirsute*) to 74.19 % (*glabrescent*) for the wild relatives while that for the cultivated types ranged from 0.00 % (*short appressed hairs and pubescent to hirsute*) to 100 % (*glabrescent*).

Growth habit

Seven different phenotypic classes were recorded for growth habit. The overall population frequency for the phenotypic classes varied between 1.07 % in accessions with *intermediate bush* and 42.25 % in accessions with *erect* growth habits. Frequency distribution based on accession type varied from 2.15 % in *intermediate* to 22.58 % in *semi-erect* growth habits for wild relatives

and 0.00 % in accessions with *acute erect*, *intermediate* and *semi-prostrate* growth habit to 69.15 % in accessions with *erect* growth habit for the cultivated types.

Growth pattern

The overall population frequency distribution for the two classes was 2.14 % for *determinate* and 97.86 % for *indeterminate* growth patterns. Frequency distribution for wild relatives was 3.23 % (*determinate*) and 96.77 % (*indeterminate*) while that of the cultivated types was 1.06 % for *determinate* and 98.94% for *indeterminate* growth pattern.

Twinning tendency

Four different phenotypic classes were detected. Frequency distribution for the overall population varied from 14.44 % (*intermediate*) to 39.57 % (*pronounced*). Frequency distribution based on accession type varied between 16.13 % (*slight and intermediate*) and 45.16 % (*pronounced*) for the wild relatives while that for the cultivated types varied from 12.77 % (*intermediate*) to 34.04 % (*pronounced*).

Leaf colour

There were four different phenotypic classes observed. The overall population frequency distribution ranged from 2.14 % (*variegated*) to 44.39 % (*dark green*). Frequency distribution based on accession type ranged from 3.23 % (*variegated*) to 39.78 % (*dark green*) for the wild relatives and 1.06 % (*variegated*) to 48.94 % (*dark green*) for the cultivated types.

Terminal leaflet shape

Six different phenotypic classes were observed. The frequency distribution for overall population varied between 3.74 % (*lanceolate*) and 33.16 % (*sub-globose*). Frequency distribution based on accession type ranged from 0.00 % (*globose*) to 37.63 % (*hastate*) for the wild relatives and that for the cultivated types was 0.00 % (*linear and lanceolate*) to 51.06 % (*sub-globose*).

Leaf texture

Three phenotypic classes were observed. The frequency distribution for overall population ranged between 30.48 % (*membranous*) and 36.90 % (*intermediate*). Frequency distribution based on accession type ranged from 31.18 % (*intermediate*) to 35.48 % (*membranous*) for the wild relatives, while that for the cultivated type was 25.53 % (*membranous*) to 42.55 % (*intermediate*).

V-marking on leaflet

Two phenotypic classes were observed. Frequency distribution for overall population ranged between 4.28 % (*absent*) and 95.72 % (*present*). Frequency distribution for the wild relatives ranged between 8.60 % (*absent*) and 91.40 % (*present*) while that for the cultivated type was 0.00 % (*absent*) and 100 % (*present*).

Table 4.1: Frequency distribution of morpho-agronomic qualitative traits.

Trait	Phenotypic class	Frequency (%)		
		Wild relatives	Cultivated types	Overall population
Plant pigmentation	Not pigmented	70.97	62.77	66.84
	Very slight	9.68	9.57	9.63
	Moderate at the base and tips of petiole	8.60	19.15	13.90
	Intermediate	1.08	1.06	1.07
	Extensive	5.38	5.32	15.35
	Solid	4.30	2.13	3.21
Plant hairiness	Glabrescent	74.19	100	87.17
	Short appressed hairs	16.13	0	8.02
	Pubescent to hirsute	9.68	0	4.81
Growth habit	Acute erect	7.53	0	3.74
	Erect	15.05	69.15	42.25
	Semi-erect	22.58	28.72	25.67
	Intermediate	2.15	0	1.07
	Semi-prostrate	18.28	0	9.09
	Prostrate	12.90	1.06	6.95
	Climbing	21.51	1.06	11.23
Growth pattern	Determinate	3.23	1.06	2.14
	Indeterminate	96.77	98.94	97.86
Twinning tendency	None	22.58	25.53	24.06
	Slight	16.13	27.66	21.93
	Intermediate	16.13	12.77	14.44
	Pronounced	45.16	34.04	39.57
Leaf colour	Pale green	19.35	9.57	14.44
	Intermediate green	37.63	40.43	39.04
	Dark green	39.78	48.94	44.39
	Variegated	3.23	1.06	2.14
Terminal leaflet shape	Globose	0	35.11	17.65
	Sub-globose	15.05	51.06	33.16
	Sub-hastate	36.56	10.64	23.53
	Hastate	37.63	3.19	20.32
	Linear	3.23	0	1.60
	Lanceolate	7.53	0	3.74

Table 4.1 cont'd

Trait	Phenotypic class	Frequency (%)		
		Wild relatives	Cultivated types	Overall population
Leaf texture	Cariaceous	33.33	31.91	32.62
	Intermediate	31.18	42.55	36.90
	Membranous	35.48	25.53	30.48
V-marking on leaflet	Absent	8.60	0	4.28
	Present	91.40	100	95.72
Flower colour	Deep purple	60.00	35.71	42.86
	Light purple	17.14	41.67	34.45
	Cream	2.86	10.71	8.40
	Purplish-white	2.86	4.76	4.20
	White	0	3.57	2.52
	Purplish cream	0	2.38	1.68
	Mauve-pink	8.57	1.19	3.36
	Yellow	8.57	0	2.52
Raceme position	Mostly above canopy	37.14	47.62	44.54
	In upper canopy	57.14	21.43	31.93
	Throughout canopy	5.72	30.95	23.53
Main pod pigmentation	Not pigmented	88.57	77.38	80.67
	Splashes of pigment	0	10.71	7.56
	Uniformly pigmented	11.43	11.91	11.77
Pod colour	Brown	5.71	30.95	23.53
	Flesh	2.86	33.34	24.37
	Dark brown mottled	5.71	10.71	9.24
	Dark purple	2.86	2.38	2.52
	Dark brown	25.72	9.52	14.29
	Light brown	0	9.52	6.72
	Brown mottled	0	3.58	2.52
	Dark green	45.72	0	13.45
	Black	5.71	0	1.68
	Forest green	5.71	0	1.68
Pod wall thickness	Thin	0	36.90	26.05
	Intermediate	2.86	47.62	34.45
	Thick	97.14	15.48	39.50

Table 4.1 cont'd

Trait	Phenotypic class	Frequency (%)		
		Wild relatives	Cultivated types	Overall population
Pod curvature	Straight	88.57	64.29	71.43
	Slightly curved	11.43	30.95	25.21
	Curved	0	1.19	0.84
	Coiled	0	3.57	2.52
Seed shape	Kidney	8.57	14.29	12.61
	Ovoid	25.71	44.05	38.66
	Crowder	2.86	1.19	1.67
	Globose	2.86	10.71	8.40
	Rhomboid	60.00	29.76	38.66
Seed coat colour	Red	2.86	8.33	6.73
	Dark brown mottled	42.85	9.52	19.34
	Brown mottled	0	8.33	11.76
	Cream	20.00	11.90	8.40
	Flesh	0	16.67	11.76
	Brick red	2.86	4.76	4.20
	Brown	0	16.67	11.76
	Black	8.57	4.76	5.88
	Dark purple	0	2.38	1.68
	Dirty-white	2.86	7.14	5.88
	Purple-brown mottled	0	5.95	4.20
	Red and cream	0	2.38	1.68
	Dark green mottled	11.42	1.19	4.20
	Black mottled	2.86	0	0.84
	Dark green	2.86	0	0.84
	Green	2.86	0	0.84
Seed coat pattern	Solid	89.60	38.10	56.30
	Small eye	10.40	36.90	26.05
	Whippoorwill	0	4.76	3.36
	Holstein	0	15.48	10.92
	Watson	0	3.57	2.52
	Golden	0	1.19	0.84

Flower colour

Eight different phenotypic classes were detected. The overall population frequency distribution ranged between 1.68 % (*purplish-cream*) and 42.86 % (*deep purple*). Frequency distribution ranged from 0.00 % (*white* and *purplish-cream*) to 60.00 % (*deep purple*) for the wild relatives while that for the cultivated types ranged from 0.00 % (*yellow*) to 41.67 % (*light purple*).

Raceme position

Three different phenotypic classes were observed. The overall population frequency distribution varied from 23.53 % (*throughout canopy*) to 44.54 % (*mostly above canopy*). Frequency distribution for the wild relatives varied from 5.72 % (*throughout canopy*) to 57.14 % (*in upper canopy*) while that for the cultivated types was 21.43 % (*in upper canopy*) to 47.62 % (*mostly above canopy*).

Main pod pigmentation

Three phenotypic classes were detected for this trait. Overall population frequency distribution varied between 7.56 % (*splashes of pigment*) and 80.67 % (*non pigmented*). Frequency distribution for the wild relatives varied from 0.00% (*splashes of pigment*) to 88.57% (*non pigmented*) while that for the cultivated types was 10.71% (*splashes of pigment*) to 77.38% (*non pigmented*).

Pod colour

There were ten different phenotypic classes. The overall population frequency distribution varied between 1.68 % (*black*) and 24.37 % (*flesh*). Frequency distribution ranged between 0.00 % (*light brown* and *brown mottled*) and 45.72 % (*dark green*) for the wild relatives, while that for the cultivated types was 0.00 % (*dark green* and *black*) and 33.34 % (*flesh*).

Pod wall thickness

Three different phenotypic classes were observed. The overall population frequency distribution was between 26.05 % (*thin*) and 39.50 % (*thick*). Frequency distribution ranged from 0.00 % (*thin*) to 97.14 % (*thick*) for the wild relatives while that of the cultivated types ranged between 15.48 % (*thick*) and 47.62 % (*intermediate*) in this trait.

Pod curvature

Four different phenotypic classes were detected for this trait. Frequency distribution for overall population ranged from 0.84 % (*curved*) to 71.43 % (*straight*). Frequency distribution for wild relatives ranged from 0.00 % (*curved* and *coiled*) to 88.57 % (*straight*) while that of the cultivated type was 1.19 % (*curved*) to 64.29 % (*straight*).

Seed shape

There were five different phenotypic classes observed in this trait. The overall frequency distribution ranged between 1.67 % (*crowder*) and 38.66 % (*ovoid* and *rhomboid*). Frequency distribution ranged from 2.86 % (*crowder* and *globose*) to 60.00 % (*rhomboid*) for the wild relatives, and 1.19 % (*crowder*) to 44.05 % (*ovoid*) for the cultivated types.

Seed coat colour

A total of sixteen different phenotypic classes were observed. The frequency distribution for overall population varied between 0.84 % (*black mottled*, *dark green* and *green*) and 19.34 % (*dark brown mottled*). Frequency distribution for wild relatives ranged from 0.00 % (*brown mottled*, *flesh*, *brown*, *dark purple*, *purple-brown mottled* and *red & cream*) to 42.85 % (*dark brown mottled*), while that of the cultivated types ranged between 0.00 % (*black mottled*, *dark green* and *green*) and 16.67 % (*flesh* and *brown*).

Seed coat pattern

There were six different phenotypic classes observed. The overall population frequency distribution varied from 0.84 % (*golden*) to 56.30 % (*solid*). Frequency distribution varied between 0.00 % (*Whippoorwill*, *Holstein*, *Watson* and *golden*) and 89.60 % (*solid*) for the wild relatives, while that for the cultivated types ranged between 1.19 % (*golden*) and 38.10 % (*solid*).

4.2 Distribution of cowpea morpho-agronomic quantitative traits

Results for means and their standard errors for the morpho-agronomic traits are shown in Table 4.2.

Mean days to germination

Mean days to germination for the overall cowpea population ranged between 2.0 and 41.0 days with a mean of 3.93 ± 0.26 days. Mean days to germination for the cultivated types ranged between 2.0 and 12.0 days with a mean of 3.18 ± 0.09 days while that for the wild relatives was 3.0 and 41.0 days with a mean of 5.79 ± 0.81 days.

Mean days to first leaf stage

Mean number of days to first leaf stage was 12.40 ± 0.24 days ranging from 10.0 to 47.0 days for the total population. In the cultivated types, mean days to first leaf stage was 12.01 ± 0.13 days and ranged from 10.0 to 18.0 days while that of the wild relatives was 10 to 47 days with a mean of 13.35 ± 0.74 days.

Table 4.2: Means and their standard errors for 14 morpho-agronomic quantitative traits.

Trait	Mean and (standard error)		
	Wild relatives	Cultivated types	Overall
Mean days to germination	5.79 (0.81)	3.18 (0.09)	3.93 (0.26)
Mean days to first leaf stage	13.35 (0.74)	12.01(0.13)	12.40 (0.24)
Mean chlorophyll content (mg/l)	1.29 (0.04)	1.50 (0.02)	1.44 (0.02)
Mean days to flowering	76.50 (4.27)	61.70 (1.99)	65.97 (1.97)
Mean number of flowers per plant	11.62 (1.38)	7.87 (0.49)	8.95 (0.55)
Mean peduncle length per plant (cm)	14.41 (0.75)	12.98 (0.55)	13.39 (0.45)
Mean number of pods per peduncle	2.00 (0.00)	1.96 (0.02)	1.97 (0.01)
Mean days to first matured pod	93.09 (4.27)	77.36 (1.98)	81.86 (1.97)
Mean number of pods per plant	9.74 (1.36)	6.02 (0.47)	7.09 (0.54)
Mean pod length per plant (cm)	8.44 (0.30)	12.78 (0.28)	11.53 (0.28)
Mean number of seeds per pod	10.36 (0.34)	9.66 (0.31)	9.86 (0.24)
Mean number of seeds per plant	104.62 (15.24)	56.42 (4.22)	70.31 (5.65)
Mean 20-seed weight (g)	0.6021 (0.08)	1.9596 (0.52)	1.5580(0.07)
Mean seed abortion rate (%)	1.59 (0.11)	2.36 (0.09)	2.14 (0.08)

Mean chlorophyll content

Mean chlorophyll content ranged from 0.33 to 1.90 mg/liters with a mean content of 1.44 ± 0.02 mg/liters across the overall cowpea population. In the wild relatives mean chlorophyll content ranged between 0.33 and 1.77 mg/liters with a mean of 1.29 ± 0.04 mg/liters while that for the cultivated types ranged between 1.04 and 1.90 mg/liters with mean of 1.50 ± 0.02 mg/liters.

Mean days to flowering

Mean days to flowering recorded for the total cowpea population was 65.97 ± 1.97 and ranged from 29.0 to 143 days. Mean days to flowering for the cultivated types ranged from 29.0 to 130.0 with a mean of 61.70 ± 1.99 while that for the wild relatives ranged between 38.0 and 143.0 days with a mean of 76.50 ± 4.27 days.

Mean number of flowers per plant

An overall population mean of 8.95 ± 0.55 ranging between 2.0 and 43.0 flowers was observed. Mean number of flowers for the wild relatives ranged from 2 to 43 with a mean of 11.62 ± 1.38 while that for the cultivated types was 2.0 to 28.0 with a mean of 7.87 ± 0.49 .

Mean peduncle length per plant

Mean peduncle length per plant varied between 3.0 cm and 23.9 cm for the overall cowpea germplasm with a mean of 13.39 ± 0.45 cm. In the wild relatives mean peduncle length per plant varied from 4.4 to 23.4 with a mean length of 14.41 ± 0.75 cm while that for the cultivated types was 3 cm to 23.9 cm with a mean of 12.98 ± 0.55 cm.

Mean number of pod per peduncle

The overall population mean recorded for this trait was 1.97 ± 0.01 ranging between 1.0 and 2.0 pods. Mean number of pod per peduncle for the wild relatives was 2.0 pods per peduncle with a mean of 2.0 ± 0.00 while that for the cultivated types ranged between 1.0 and 2.0 with a mean of 1.96 ± 0.02 .

Mean days to first matured pod

Mean days to first pod maturation for the overall cowpea population ranged from 45 to 159 days with a mean of 81.86 ± 1.97 . In the cultivated types mean days to first matured pod ranged between 45.0 and 145.0 with a mean of 77.36 ± 1.98 while that for the wild relatives was 53.0 and 159 with a mean of 93.0 ± 4.27 .

Mean number of pods per plant

Mean number of pods per plant for the overall population ranged between 1.0 and 40.0 with a mean of 7.09 ± 0.54 . In the wild relatives, number of pods per plant ranged from 1.0 to 40.0 with a mean of 9.74 ± 1.36 while that of the cultivated types was between 1.0 and 25.0 with a mean of 6.02 ± 0.47 .

Mean pod length per plant

Mean pod length per plant varied between 5.2 cm and 18.3 cm in the entire cowpea germplasm with a mean of 11.53 ± 0.28 cm. This trait ranged from 6.7 cm to 18.3 cm with a mean of 12.78 ± 0.28 cm in the cultivated types, and 5.2 cm to 14.7 cm with a mean of 8.44 ± 0.30 cm for the wild relatives.

Mean number of seeds per pod

Mean number of seeds per pod ranged from 4.0 to 18.0 with a mean of 9.86 ± 0.24 in the overall cowpea population. Accessions from wild relatives recorded a mean of 10.36 ± 0.34 and ranged between 5.8 and 13.8 seeds while that for the cultivated types was 9.66 ± 0.31 and ranged from 4.0 to 18.0 seeds.

Mean 20-seed weight (g)

Mean 20-seed weight ranged from 0.3112 g to 3.0241 g with a mean of 1.5580 ± 0.07 g across the overall cowpea population. Mean 20-seed weight for the wild relatives and the cultivated types

ranged from 0.3112 g to 2.7206 g with a mean of 0.6021 ± 0.08 g, and 0.3589 g to 3.0241 g with a mean of 1.9596 ± 0.52 g respectively.

Mean number of seeds per plant

The mean number of seeds per plant ranged from 8.0 to 479 with a mean of 70.31 ± 5.65 for the entire cowpea population. In the wild relatives mean number of seeds per plant ranged between 11.0 and 479 with a mean of 104.62 ± 15.24 while that for the cultivated types was 8.0 and 210 seeds with a mean of 56.42 ± 4.22 .

Mean seed abortion rate

Mean seed abortion rate of 2.14 ± 0.08 was recorded for the total cowpea population and varied between 0.0 and 5.0 seeds. Mean seed abortion rate varied from 0.0 to 3.0 with a mean of 1.59 ± 0.11 in the wild relatives while that for the cultivated types ranged between 0.0 and 5.0 with a mean of 2.36 ± 0.09 .

4.3 Amino acid analysis of seed quality traits.

The concentrations of the 19 amino acids in the cowpea accessions recorded is presented in Table 4.3.

B-Threonine

The concentration of B-Threonine content ranged from 12.04×10^{-5} ppm to 485.79×10^{-5} ppm in the overall cowpea germplasm with a mean of $(46.65 \pm 5.52) \times 10^{-5}$ ppm. The concentration of this trait for the wild relatives ranged between 12.04×10^{-5} ppm and 113.76×10^{-5} ppm with a mean of $(52.51 \pm 3.85) \times 10^{-5}$ ppm while that for the cultivated types ranged between 16.72×10^{-5} ppm and 485.79×10^{-5} ppm with a mean of $(43,369.33 \pm 8044.69) \times 10^{-5}$ ppm.

Table 4.3: Concentrations of 19 amino acids in the cowpea accessions.

Amino acid	Mean and (standard error) (x10 ⁻⁵) ppm		
	Wild relatives	Cultivated types	Overall
B-Threonine*	52.51 (3.85)	43,369.33 (8044.69)	46.65 (5.52)
DL-Alpha-Alanine	194.22 (64.10)	465,739.30 (6406.07)	362.77 (48.75)
DL-Beta_phenyl-Alanin*	340.86 (105.60)	1,840,778.00 (3742.80)	339.79 (262.36)
D-Proline	312.63 (62.15)	201,552.70 (4184.90)	240.96 (35.38)
Glutamine	34.45 (5.63)	32,882.83 (5190.03)	33.57 (3.94)
Glycine	76.41 (5.78)	48,022.50 (3396.22)	57.85 (3.32)
Iso-Leucine*	589.17 (132.18)	129,082.70 (2952.21)	288.99 (54.26)
L-Asparagine	773.96 (88.37)	1,422,056.00 (1934.50)	1,209.72 (135.84)
L-Aspartic Acid	199.73 (77.29)	115,366.20 (9588.56)	144.72 (27.42)
L-Cysteine	nd	nd	nd
L-Histidine*	441.98 (67.32)	822,493.70 (1190.50)	691.30 (84.59)
L-Lysine*	33.57 (4.53)	28,009.00 (3756.57)	30.03 (2.95)
L-Methionine*	17.52 (5.36)	18,266.33 (5169.38)	18.21 (3.89)
L-Serine	65.66 (3.47)	40,960.33 (2524.18)	49.46 (2.40)
L-Threonine*	63.87 (3.94)	52,443.67 (4006.77)	56.49 (3.03)
L-Tryptophan*	21,623.03 (5299.45)	3,953,909.00 (7143.39)	33,483.57 (516.31)
L-Tyrosine	198.65 (29.51)	170,256.30 (1914.91)	178.22 (15.91)
L-Valine*	558.59 (47.33)	492,365.70 (3168.28)	514.97 (26.74)
Trans-4-Hydroxyl-Proline	373.95 (66.87)	1028,05.30 (2257.64)	197.34 (30.45)

*Essential amino acid

DL-Alpha-Alanine

The concentration of this amino acid for the overall cowpea germplasm ranged from 0.29×10^{-5} ppm to 2646.13×10^{-5} ppm with a mean of $(362.77 \pm 48.75) \times 10^{-5}$ ppm. This amino acid recorded a mean of $(194.22 \pm 64.10) \times 10^{-5}$ ppm and $(1840778.00 \pm 3742.80) \times 10^{-5}$ ppm for the wild and the cultivated types ranging from 0.82×10^{-5} ppm to 1464.63×10^{-5} ppm and 0.0029×10^{-5} ppm to 2646.13×10^{-5} ppm respectively.

DL- Beta_ phenyl-Alanin

It was observed that the value of this amino acid ranged between 27.10×10^{-5} ppm and 18491.41×10^{-5} ppm for both the overall cowpea population and the cultivated types with a mean of $(339.79 \pm 262.36) \times 10^{-5}$ ppm and $(1840778.00 \pm 3742.80) \times 10^{-5}$ ppm respectively. Mean concentration for the wild relatives was $(340.86 \pm 105.60) \times 10^{-5}$ ppm and ranged between 27.57×10^{-5} ppm and 3256.20×10^{-5} ppm.

D-Proline

The concentration of this amino acid ranged from 6.15×10^{-5} ppm to 1978.18×10^{-5} ppm for the overall cowpea population and the cultivated species with a mean of $(240.96 \pm 35.38) \times 10^{-5}$ ppm and $(201552.70 \pm 4184.90) \times 10^{-5}$ ppm respectively. The value of this amino acid for the wild relatives varied between 61.15×10^{-5} ppm and 1665.75×10^{-5} ppm with a mean of $(312.63 \pm 62.15) \times 10^{-5}$ ppm.

Glutamine

Glutamine concentration ranged from 9.52×10^{-5} ppm to 278.834×10^{-5} ppm for both the overall population and the cultivated types with a mean of $(33.57 \pm 3.94) \times 10^{-5}$ ppm and $(32882.83 \pm 5190.03) \times 10^{-5}$ ppm respectively. The value of this amino acid for the wild relatives

ranged between 10.79×10^{-5} ppm and 190.35×10^{-5} ppm with a mean of $(34.45 \pm 5.63) \times 10^{-5}$ ppm.

Glutamine was recorded across the entire cowpea germplasm.

Glycine

Glycine content ranged from 7.65×10^{-5} ppm to 150.44×10^{-5} ppm with a mean of $(57.85 \pm 3.32) \times 10^{-5}$ ppm. The concentration for the cultivated type varied between 7.78×10^{-5} ppm and 119.53×10^{-5} ppm with a mean of $(48022.50 \pm 3396.22) \times 10^{-5}$ ppm while that for the wild relatives ranged from 7.65×10^{-5} ppm to 150.44×10^{-5} ppm with a mean of $(76.41 \pm 5.78) \times 10^{-5}$ ppm.

Iso-Leucine

It was observed that Iso-Leucine content ranged from 17.53×10^{-5} ppm to 3378.18×10^{-5} ppm with a mean of $(288.99 \pm 54.26) \times 10^{-5}$ ppm in the overall cowpea germplasm that were assessed. The value of this amino acid for the wild relatives ranged from 25.48×10^{-5} ppm to 3378.18×10^{-5} ppm with a mean of $(589.17 \pm 132.18) \times 10^{-5}$ ppm while that for the cultivated type varied between 17.53×10^{-5} ppm and 837.96×10^{-5} ppm with a mean of $(129082.70 \pm 2952.21) \times 10^{-5}$ ppm. Fifty-seven (57) accessions, representing 52.78% of the total cowpea genotypes analyzed recorded 0.0 ppm of this amino acid.

L-Asparagine

The concentration of this trait ranged from 53.58×10^{-5} ppm to 8268.21×10^{-5} ppm with a mean of $(1209.72 \pm 135.84) \times 10^{-5}$ ppm throughout the overall cowpea population. The content of L-Asparagine ranged from 60.02×10^{-5} ppm to 2195.23×10^{-5} ppm with a mean of $(773.96 \pm 88.37) \times 10^{-5}$ ppm for the wild relatives while that for the cultivated types was 53.58×10^{-5} ppm to 8268.21×10^{-5} ppm with a mean of $(1422056.00 \pm 1934.50) \times 10^{-5}$ ppm.

L-Aspartic acid

The concentration of L-Aspartic acid varied between 15.25×10^{-5} ppm to 2482.40×10^{-5} ppm with a mean of $(144.72 \pm 27.42) \times 10^{-5}$ ppm within the overall cowpea population. The content of this amino acid for the wild relatives ranged from 37.66×10^{-5} ppm to 2482.40×10^{-5} ppm with a mean of $(199.73 \pm 77.29) \times 10^{-5}$ ppm but that of the cultivated types was 15.25×10^{-5} ppm to 454.56×10^{-5} ppm with a mean of $(115366.20 \pm 9588.56) \times 10^{-5}$ ppm. Aspartic acid was noticed in all the cowpea genotypes analyzed.

L-Cysteine

The concentration of this amino acid was beyond detection in all the various cowpea germplasm that were assessed.

L-Histidine

L-Histidine content ranged from 36.86×10^{-5} ppm to 6175.69×10^{-5} ppm throughout the cowpea genotypes with a mean of $(691.30 \pm 84.59) \times 10^{-5}$ ppm. The highest value of 473.39×10^{-5} ppm and the least value of 62.40×10^{-5} ppm with a mean of $(441.98 \pm 67.32) \times 10^{-5}$ ppm was recorded for the wild relatives while that of the cultivated ones was $(822493.70 \pm 1190.50) \times 10^{-5}$ ppm and ranged between 36.86×10^{-5} ppm to 6175.69×10^{-5} ppm. L-Histidine was also noticed in all the cowpea genotypes analyzed.

L-Lysine

The concentration of this amino acid ranged between 12.57×10^{-5} ppm and 212.04×10^{-5} ppm with a mean of $(30.03 \pm 2.95) \times 10^{-5}$ ppm for the overall population. The concentration of L-Lysine for the wild relatives ranged from 15.76×10^{-3} ppm to 140.30×10^{-5} ppm with a mean of $(33.57 \pm 4.53) \times 10^{-5}$ ppm while that for the cultivated species was 12.57×10^{-5} ppm to 212.04×10^{-5} ppm with a

mean of $(28009.00 \pm 3756.57) \times 10^{-5}$ ppm. This amino acid was detected in all the cowpea accessions that were analyzed.

L-Methionine

It was observed that the content of L-Methionine in the entire cowpea germplasm was $(18.21 \pm 3.89) \times 10^{-5}$ ppm and varied between 1.12×10^{-5} ppm and 221.00×10^{-5} ppm. The value of this amino acid for the wild relatives varied between 1.12×10^{-5} ppm and 124.18×10^{-5} ppm with a mean of $(17.52 \pm 5.36) \times 10^{-5}$ ppm, while that for the cultivated types ranged between 0.28×10^{-5} ppm and 221.00×10^{-5} ppm with a mean of $(18266 \pm 5169.38) \times 10^{-5}$ ppm.

L-Serine

The concentration of L-Serine ranged from 6.38×10^{-5} ppm to 135.91×10^{-5} ppm with a mean of $(49.46 \pm 2.40) \times 10^{-5}$ ppm in the overall cowpea accessions. In the wild relatives the value of this trait varied between 30.26×10^{-5} ppm and 98.96×10^{-5} ppm with a mean of $(65.66 \pm 3.47) \times 10^{-5}$ ppm, but that for the cultivated types was $(40960.33 \pm 2524.18) \times 10^{-5}$ ppm and ranged between 6.38×10^{-5} ppm and 135.91×10^{-5} ppm.

L-Threonine

It was observed that the value of this amino acid varied between 7.47×10^{-5} ppm and 320.14×10^{-5} ppm with a mean of $(56.49 \pm 3.03) \times 10^{-5}$ ppm throughout the total population. The concentration of this amino acid in the wild relatives ranged from 23.46×10^{-5} ppm to 122.52×10^{-5} ppm with a mean of $(63.87 \pm 3.94) \times 10^{-5}$ ppm while that for the cultivated ones was 7.47×10^{-5} ppm to 320.14×10^{-5} ppm with a mean of $(52443.67 \pm 4006.77) \times 10^{-5}$ ppm. L-Threonine was detected in all the cowpea varieties that were analysed.

L-Tryptophan

The concentration of L-Tryptophan for the overall cowpea germplasm ranged from 0.104×10^{-5} ppm to 259843.40×10^{-5} ppm with a mean of $(33483.57 \pm 516.31) \times 10^{-5}$ ppm. The content of this amino acid in the wild relatives varied between 2079.65×10^{-5} ppm and 135248.80×10^{-5} ppm with a mean of $(21623.03 \pm 5299.45) \times 10^{-5}$ ppm but that for the cultivated types ranged from 0.104×10^{-5} ppm to 259843.40×10^{-5} ppm with a mean of $(3953909.00 \pm 7143.39) \times 10^{-5}$ ppm.

L-Tyrosine

The content of L-Tyrosine across the entire cowpea genotypes studied ranged between 6.61×10^{-5} ppm to 751.94×10^{-5} ppm with a mean of $(178.22 \pm 15.91) \times 10^{-5}$ ppm. The concentration of this trait for the wild relatives was $(198.65 \pm 29.51) \times 10^{-5}$ ppm and ranged from 77.97×10^{-5} ppm to 705.72×10^{-5} ppm while that for the cultivated ones was $(170256.30 \pm 1914.91) \times 10^{-5}$ ppm and ranged from 6.61×10^{-5} ppm to 751.94×10^{-5} ppm. L-Tyrosine was noticed in all the cowpea genotypes.

L-Valine

L-Valine content ranged from 14.25×10^{-5} ppm to 1318.61×10^{-5} ppm with a mean of $(514.97 \pm 26.74) \times 10^{-5}$ ppm throughout the total cowpea germplasm. The concentration of this trait for the wild relatives was $(558.59 \pm 47.33) \times 10^{-5}$ ppm and varied between 192.09×10^{-5} ppm and 1313.93×10^{-5} ppm while that for the cultivated types was $(492365.70 \pm 3168.28) \times 10^{-5}$ ppm and varied between 14.25×10^{-5} ppm to 1318.61×10^{-5} ppm. L-Valine was noticed in all the cowpea genotypes analyzed.

Trans-4-Hydroxyl-Proline

It was observed that the concentration of Trans-4-Hydroxyl-Proline ranged between 8.91×10^{-5} ppm to 1660.40×10^{-5} ppm in the entire cowpea germplasm with a mean of $(197.34 \pm 30.45) \times 10^{-5}$ ppm.

ppm. The value of this trait for the wild relatives ranged from 45.98×10^{-5} ppm to 1660.40×10^{-5} ppm with mean concentration of $(373.95 \pm 66.87) \times 10^{-5}$ ppm while that for the cultivated types was 621.39×10^{-5} ppm to 621.39×10^{-5} ppm with mean range of $(102805.30 \pm 2257.64) \times 10^{-5}$ ppm. Fifty-six (56) plants representing 51.85% of the total cowpea genotypes analyzed recorded 0.0ppm for this amino acid.

4.4 Distribution of morphological quantitative traits in the cowpea population by their phenotypic classes.

Results for distribution of 14 quantitative traits by their phenotypic classes are presented in Tables 4.4, 4.5 and 4.6 respectively.

4.4.1 Vegetative

Mean days to germination

Growth habit: The mean days to germination varied between 3.00 ± 0.00 in accessions with *intermediate* growth habit and 7.62 ± 1.14 in those with *prostrate* growth habit.

Growth pattern: Accessions that had *indeterminate* growth pattern scored a mean of 4.63 ± 0.31 days to germination while 5.5 ± 1.4 days was recorded for those with *determinate* growth pattern.

Plant pigmentation: Mean days to germination for the different phenotypic classes for plant pigmentation ranged from 3.80 ± 0.51 in accessions that had *extensive pigmentation* to 9.00 ± 5.99 for those with *intermediate pigmentation*.

Plant hairiness: Three phenotypic classes were detected with mean days to germination ranging from 4.54 ± 0.33 in plant genotypes that had *glabrescent* hairiness to 6.22 ± 1.44 for those that had *pubescent to hirsute*.

Twinning tendency: Four phenotypic classes were observed for this trait. The mean days to germination ranged from 3.68 ± 0.95 in genotypes that had *pronounced* twinning tendency to 6.70 ± 1.57 in genotypes that had *intermediate* tendency.

Leaf colour: Mean days to germination ranged from 4.25 ± 1.25 in accessions that had *variegated* leaf colour to 5.22 ± 0.64 in those with *intermediate green* colour

Terminal leaflet shape: Mean days to germination for this trait ranged from 3.03 ± 0.03 days in accessions that had *globose* leaflet shape to 9.00 ± 2.76 days in those with *lanceolate* terminal leaflet shape.

Leaf texture: Mean days to germination for leaf texture ranged between 3.87 ± 0.21 days in genotypes that had *intermediate* leaf texture and 5.74 ± 0.78 in those with *cariaceous* leaf texture.

V-marking on leaflet: Accessions with this trait *present* scored a mean of 4.51 ± 0.30 while those with *no V-marking* recorded 7.75 ± 2.22 days.

Flower colour: Eight phenotypic classes were observed. Mean days to germination for flower colour ranged from 3.0 ± 0.00 days in accessions that had *cream, white, creamy purple and mauve-pink* to 5.6 ± 2.36 in those with *purplish white* flower colour.

Raceme position: Mean days to germination varied from 3.04 ± 0.04 in accessions that had raceme position *throughout canopy* to 5.05 ± 0.72 days in those that had raceme position *in upper canopy*.

Main pod pigmentation: Genotypes that had *splashes of pigment* had the lowest mean of 2.89 ± 0.11 while those with *no pod pigmentation* recorded the highest mean of 4.11 ± 0.32 days.

Pod colour: A total of ten phenotypic classes were observed. Accessions that had *light brown* pod colour scored the lowest mean of 3.0 ± 0.00 . However, accessions that had *dark purple* pod colour scored the highest mean of 8.67 ± 3.56 .

Pod wall thickness: Mean days to germination for this trait ranged from 3.06 ± 0.04 in accessions that had *thin* pod wall thickness to 5.02 ± 0.61 in accessions that had *thick* pod wall thickness.

Pod curvature: Accessions with *coiled* pod curvature germinated fastest with mean days of 3.0 ± 0.00 while those that had *straight* pod curvature germinated later with mean days to germination of 4.14 ± 0.35 .

Seed shape: Mean days to germination for this trait ranged from 3.10 ± 0.10 days in accessions that had *globose* seed shape to 5.50 ± 2.50 days in *crowder* phenotypes.

Seed coat colour: Sixteen phenotypic classes were observed. Accessions with the following seed coat colour (*cream, brick red, dark purple, red and cream, dark green mottled, black mottled and green*) germinated first with mean concentration of 3.0 ± 0.00 while those with *dark brown mottled* recorded a mean of 5.48 ± 1.04 days to germination.

Seed coat pattern: Mean days to germination for seed coat pattern ranged from 2.75 ± 0.25 in plant genotypes that had *Whippoorwill* seed coat pattern to 4.45 ± 0.20 in genotypes that had *solid* seed coat pattern.

Mean days to first leaf stage

Growth habit: The mean number of days to first leaf stage varied between 12.00 ± 0.00 in accessions that had *intermediate* growth habit and 14.0 ± 0.91 in those that had *prostrate* growth habit.

Growth pattern: A mean of 12.74 ± 0.27 days to first leaf stage was recorded for plant genotypes that had *indeterminate* growth pattern while 16.25 ± 4.03 days was recorded for genotypes that had *determinate* growth pattern.

Plant pigmentation: Mean days to first leaf stage for the different phenotypic classes of plant pigmentation ranged from 11.6 ± 0.40 (*extensive*) pigmentation to 17.00 ± 0.50 (*intermediate*) pigmentation.

Plant hairiness: Three phenotypic classes were detected with a mean days to first leaf stage ranging from 12.07 ± 0.64 in plant genotypes that had *short appressed hairs* to 14.11 ± 1.05 in genotypes with *pubescent to hirsute*.

Twinning tendency: Four phenotypic classes were observed for this trait with mean days to first leaf stage ranging from 12.27 ± 0.33 in genotypes that had *slight* twinning tendency to 14.52 ± 1.45 in genotypes that had *intermediate* twinning tendency.

Leaf colour: Mean days to first leaf stage ranged from 12.29 ± 0.30 in genotypes that had *dark green* leaf colour to 15.5 ± 4.19 in those that had *variegated* leaves.

Terminal leaflet shape: Mean days to first leaf stage for this trait ranged from 11.73 ± 0.18 in accessions that had *globose* to 16.57 ± 2.36 in those that had *lanceolate* terminal leaflet shape.

Leaf texture: Plant genotypes that had *intermediate* leaf texture recorded a least mean of 12.10 ± 0.17 days while those with *cariaceous* leaf texture recorded a highest mean of 13.98 ± 0.73 .

V-marking on leaflet: Accessions with this trait *present* scored a least mean of 12.73 ± 0.27 while those with *no V-marking* scored a highest mean of 7.75 ± 2.22

Flower colour: Eight phenotypic classes were observed. Accessions with *white and mauve-pink* flower colour recorded a least mean of 11.0 ± 0.58 and 11.0 ± 0.41 days respectively. However, accessions with *purplish white* flower colour recorded a highest mean of 14.20 ± 1.74 .

Raceme position: Mean of 11.75 ± 0.19 days to first leaf stage was recorded for plant genotypes that had raceme position *throughout canopy* while 13.37 ± 0.63 was recorded for those *in upper canopy*.

Main pod pigmentation: The mean days to first leaf stage for this trait ranged from 11.79 ± 0.29 in accessions that had *uniformly* pigmented pod to 12.51 ± 0.29 in those with *no pod pigmentation*.

Pod colour: Ten phenotypic classes were observed. Accessions that had *forest green* pod colour recorded a lowest mean of 10.0 ± 0.00 while those that had *dark purple* pod colour recorded the highest mean of 16.33 ± 0.77 .

Pod wall thickness: Mean days to first leaf stage for this trait ranged from 11.68 ± 0.19 in accessions that had *thin* pod wall thickness to 12.98 ± 0.55 in those that had *thick* pod wall thickness.

Pod curvature: Accessions that had *slightly curved* pod curvature developed leaf stage first with a mean of 11.87 ± 0.22 while those that had *curved* pod curvature developed late with a mean of 13.0 ± 0.00 .

Seed shape: Mean days to first leaf stage for this trait ranged from 12.0 ± 0.37 in accessions that had *globose* seed shape to 13.50 ± 0.71 (*Crowder*).

Seed coat colour: Sixteen phenotypic classes were observed. Accessions that had *dark green* seed coat colour developed leaf stage first with mean of 10.0 ± 0.00 days while those that had *black* coat colour recorded a mean of 13.56 ± 1.24 .

Seed coat pattern: Mean days to first leaf stage for this trait ranged from 11.0 ± 0.00 in accessions that had *golden* seed coat pattern to 13.0 ± 0.99 in those that had *Watson* seed coat pattern

Table 4.4: Distribution of cowpea vegetative quantitative traits by phenotypic classes.

Trait	Phenotypic class	Vegetative quantitative traits		
		Mean days to germination	Mean days to first leaf stage	Mean chlorophyll content
Growth habit	Acute erect	4.86 (1.55)	12 (1.19)	1.54 (0.07)
	Erect	3.78 (0.27)	12.52 (0.29)	1.45 (0.02)
	Semi-erect	4.58 (0.84)	12.82 (0.65)	1.39 (0.03)
	Intermediate	3.0 (0.00)	12.0 (0.00)	1.25 (0.37)
	Semi-prostrate	4.88 (0.59)	12.47 (0.44)	1.22 (0.07)
	Prostrate	7.62 (1.14)	14.0 (0.91)	1.27 (0.07)
	Climbing	6.14 (1.11)	13.0 (1.02)	1.19 (0.05)
Growth pattern	Determinate	5.5 (1.45)	16.25 (4.03)	1.39 (0.16)
	Indeterminate	4.63 (0.31)	12.74 (0.27)	1.38 (0.02)
Plant pigmentation	Not pigmented	4.96 (0.42)	13.08 (0.40)	1.38 (0.02)
	Very slight	3.83 (0.40)	12.06 (0.33)	1.34 (0.09)
	Moderate at the base and tips of petiole	3.58 (0.36)	12.15 (0.32)	1.39 (0.05)
	Intermediate	9.00 (5.99)	17.00 (0.50)	1.57 (0.03)
	Extensive	3.80 (0.51)	11.60 (0.40)	1.37 (0.07)
	Solid	5.33 (1.94)	13.17 (1.25)	1.37 (0.11)
Plant hairiness	Glabrescent	4.54 (0.33)	12.82 (0.31)	1.40 (0.02)
	Short appressed hairs	4.93 (0.85)	12.07 (0.64)	1.22 (0.07)
	Pubescent to hirsute	6.22 (1.44)	14.11 (1.05)	1.26 (0.06)
Twinning tendency	None	5.42 (0.55)	13.6 (0.54)	1.36 (0.04)
	Slight	4.22 (0.44)	12.27 (0.33)	1.45 (0.03)
	Intermediate	6.70 (1.57)	14.52 (1.45)	1.33 (0.06)
	Pronounced	3.68 (0.95)	12.03 (0.22)	1.36 (0.03)
Leaf colour	Pale green	4.33 (0.51)	12.48 (0.38)	1.30 (0.04)
	Intermediate green	5.22 (0.64)	13.40 (0.56)	1.36 (0.03)
	Dark green	4.28 (0.34)	12.29 (0.30)	1.44 (0.03)
	Variegated	4.25 (1.25)	15.5 (4.19)	0.98 (0.12)
Terminal leaflet shape	Globose	3.03 (0.03)	11.73 (0.18)	1.53 (0.02)
	Sub-globose	3.68 (0.24)	12.19 (0.22)	1.43 (0.03)
	Sub-hastate	4.39 (0.45)	12.45 (0.39)	1.30 (0.04)
	Hastate	7.03 (1.11)	14.5 (1.08)	1.26 (0.04)
	Linear	6.33 (1.20)	13.0 (1.53)	1.24 (0.17)
	Lanceolate	9.0 (2.76)	16.57 (2.36)	1.38 (0.06)

Table 4.4 cont'd

Trait	Phenotypic class	Vegetative quantitative traits		
		Mean days to germination	Mean days to first leaf stage	Mean chlorophyll content
Leaf texture	Cariaceous	5.74 (0.78)	13.98 (0.73)	1.31 (0.03)
	Intermediate	3.87 (0.21)	12.10 (0.17)	1.38 (0.03)
	Membranous	4.44 (0.44)	12.44 (0.34)	1.43 (0.03)
V-marking on leaflet	Absent	7.75 (2.22)	14.88 (2.06)	1.30 (0.08)
	Present	4.51 (0.30)	12.73 (0.27)	1.38 (0.02)
Flower colour	Deep purple	4.51 (0.53)	12.96 (0.47)	1.42 (0.04)
	Light purple	3.37 (0.18)	11.83 (0.19)	1.45 (0.03)
	Cream	3.0 (0.00)	12.0 (0.40)	1.49 (0.05)
	Purplish white	5.6 (2.36)	14.2 (1.74)	1.45 (0.11)
	White	3.0 (0.00)	11.0 (0.58)	1.43 (0.03)
	Purplish cream	3.0 (0.00)	12.0 (1.00)	1.61 (0.09)
	Mauve-pink	3.0 (0.00)	11.0 (0.41)	1.36 (0.08)
	Yellow	5.0 (1.53)	11.67 (1.20)	1.17 (0.09)
Raceme position	Mostly above canopy	3.60 (0.23)	12.0 (0.22)	1.43 (0.03)
	In upper canopy	5.05 (0.72)	13.37 (0.63)	1.37 (0.03)
	Throughout canopy	3.04 (0.04)	11.75 (0.19)	1.51 (0.03)
Main pod pigmentation	Not pigmented	4.11 (0.32)	12.51 (0.29)	1.42 (0.02)
	Splashes of pigment	2.89 (0.11)	11.89 (0.48)	1.43 (0.06)
	Uniformly pigmented	3.36 (0.36)	11.79 (0.29)	1.46 (0.03)
Pod colour	Brown	3.39 (0.25)	12.21 (0.22)	1.49 (0.02)
	Flesh	3.31 (0.19)	12.10 (0.21)	1.53 (0.03)
	Dark brown mottled	4.09 (1.09)	12.91 (5.84)	1.42 (0.06)
	Dark purple	8.67 (3.56)	16.33 (0.77)	1.52 (0.14)
	Dark brown	4.71 (0.84)	12.29 (0.37)	1.39 (0.07)
	Light brown	3.0 (0.00)	11.75 (0.37)	1.53 (0.07)
	Brown mottled	3.33 (0.33)	12.33 (0.88)	1.37 (0.09)
	Dark green	4.63 (0.89)	12.75 (0.75)	1.22 (0.07)
	Black	5.5 (2.50)	12.5 (1.50)	1.23 (0.12)
	Forest green	3.5 (0.50)	10.0 (0.00)	1.11 (0.03)
Pod wall thickness	Thin	3.06 (0.04)	11.68 (0.19)	1.47 (0.03)
	Intermediate	3.34 (0.18)	12.22 (0.18)	1.52 (0.03)
	Thick	5.02 (0.61)	12.98 (0.55)	1.33 (0.04)

Table 4.4 cont'd

Vegetative quantitative traits				
Trait	Phenotypic class	Mean days to germination	Mean days to 1 st leaf stage	Mean chlorophyll content
Pod curvature	Straight	4.14 (0.35)	12.56 (0.32)	1.41 (0.02)
	Slightly curved	3.43 (0.24)	11.87 (0.22)	1.46 (0.04)
	Curved	4.0 (0.00)	13.0 (0.00)	1.58 (0.00)
	Coiled	3.0 (0.00)	12.0 (1.00)	1.59 (0.09)
Seed shape	Kidney	4.47 (0.60)	12.87 (0.81)	1.48 (0.06)
	Ovoid	3.26 (0.13)	12.15 (0.18)	1.00 (0.03)
	Crowder	5.50 (2.50)	13.5 (0.71)	1.32 (0.21)
	Globose	3.10 (0.10)	12.0 (0.37)	1.46 (0.03)
	Rhomboid	4.54 (0.56)	12.48 (0.25)	1.42 (0.04)
Seed coat colour	Red	3.63 (0.03)	12.25 (0.53)	1.49 (0.04)
	Dark brown mottled	5.48 (1.04)	13.48 (0.97)	1.38 (0.06)
	Brown mottled	3.57 (0.36)	12.0 (0.38)	1.36 (0.05)
	Cream	3.0 (0.00)	11.8 (0.39)	1.51 (0.04)
	Flesh	3.21 (0.15)	11.86 (0.28)	1.54 (0.05)
	Brick red	3.0 (0.00)	12.2 (0.66)	1.32 (0.09)
	Brown	3.36 (0.36)	11.79 (0.37)	1.44 (0.04)
	Black	5.43 (1.74)	13.56 (1.24)	1.37 (0.08)
	Dark purple	3.0 (0.00)	12.5 (0.50)	1.42 (0.30)
	Dirty-white	4.23 (1.27)	13.0 (0.90)	1.43 (0.08)
	Purple-brown mottled	4.0 (1.00)	12.2 (0.58)	1.49 (0.08)
	Red and cream	3.0 (0.00)	10.5 (0.50)	1.58 (0.13)
	Dark green mottled	3.0 (0.00)	12.0 (0.71)	1.31 (0.04)
	Black mottled	3.0 (0.00)	11.0 (0.00)	1.72 (0.00)
	Dark green	4.0 (0.00)	10.0 (0.00)	1.54 (0.00)
	Green	3.0 (0.00)	11.0 (0.00)	1.35 (0.00)
Seed coat pattern	Solid	4.45 (0.20)	12.63 (0.40)	1.37 (0.03)
	Small eye	3.45 (0.23)	12.23 (0.20)	1.49 (0.03)
	Whippoorwill	2.75 (0.25)	12.0 (0.92)	0.58 (0.12)
	Holstein	3.08 (0.08)	11.53 (0.29)	1.53 (0.03)
	Watson	3.0 (0.00)	13.0 (0.99)	1.44 (0.06)
	Golden	3.0 (0.00)	11.0 (0.00)	1.81 (0.00)

Mean chlorophyll content

Growth habit: Plant genotypes that had *climbing* growth habit recorded the least chlorophyll content with a mean of 1.19 ± 0.05 while those that had *acute-erect* growth habit recorded the highest value 1.54 ± 0.07 .

Growth pattern: Mean chlorophyll concentration of 1.38 ± 0.02 was recorded for plant genotypes that had *indeterminate* growth pattern while 1.39 ± 0.16 was recorded for genotypes that had *determinate* growth pattern.

Plant pigmentation: Mean chlorophyll content for the different phenotypic classes of plant pigmentation ranged from 1.34 ± 0.09 in genotypes that had *very slight* pigmentation to 1.57 ± 0.03 in those that had pigment *moderately at the base and tips of petiole*.

Plant hairiness: Three phenotypic classes were detected with mean chlorophyll concentration ranging from 1.22 ± 0.07 in plant genotypes that had *short appressed hairs* to 1.40 ± 0.02 in those that had *glabrescent* hairiness.

Twinning tendency: Mean chlorophyll content for the different phenotypic classes of twinning tendency ranged from 1.33 ± 0.06 in genotypes that had *intermediate* twinning tendency to 1.45 ± 0.03 in genotypes that had *slight* tendency.

Leaf colour: Mean chlorophyll content ranged from 0.98 ± 0.12 in accessions that had *variegated* leaf colour to 1.44 ± 0.03 in those with *dark green* colour.

Terminal leaflet shape: Mean chlorophyll content for this trait ranged from 1.24 ± 0.17 in accessions that had *linear* leaflet shape to 1.53 ± 0.02 in those that had *globose* terminal leaflet shape.

Leaf texture: Plant genotypes that had *cariaceous* leaf texture recorded a least mean of 1.31 ± 0.03 while those that had *membranous* leaf texture recorded a highest mean of 1.43 ± 0.03 .

V-marking on leaflet: Accessions with this trait *present* recorded a mean of 1.38 ± 0.02 while those with *no V-marking* recorded 1.30 ± 0.08 .

Flower colour: Eight phenotypic classes were observed. Accessions that had *yellow* flower colour recorded a least chlorophyll concentration of 1.17 ± 0.09 while those that had *creamy purple* flower colour recorded a highest mean of 1.61 ± 0.09 .

Raceme position: Genotypes that had raceme position *in upper canopy* recorded a least mean of 1.37 ± 0.03 while those that had raceme position *throughout canopy* recorded a highest mean of 1.51 ± 0.03 .

Main pod pigmentation: Plant genotypes that had *uniformly pigmented* pods recorded a highest mean of 1.46 ± 0.03 . Genotypes that had *no pod pigmentation* recorded a least mean of 4.11 ± 0.32 .

Pod colour: A total of ten phenotypic classes were observed. Accessions that had *green* pod colour recorded a least mean of 1.11 ± 0.03 while those that had *flesh* and *light brown* pod colours recorded highest means of 1.53 ± 0.03 and 1.53 ± 0.07 respectively.

Pod wall thickness: Mean chlorophyll content for this trait ranged from 1.33 ± 0.04 in accessions that had *thick* pod wall thickness to 1.52 ± 0.03 in those that had *intermediate* pod wall thickness.

Pod curvature: Accessions with *coiled* pod curvature recorded a highest mean chlorophyll content of 1.59 ± 0.09 mg/l while those that had *straight* pod curvature recorded a least mean of 1.41 ± 0.02 mg/l in this trait.

Seed shape: Mean chlorophyll content for this trait ranged from 1.00 ± 0.03 mg/l in accessions that had *ovoid* seed shape to 1.48 ± 0.06 mg/l (*kidney*).

Seed coat colour: Sixteen phenotypic classes were observed. The mean chlorophyll content for this trait varied between 1.31 ± 0.04 mg/l (*dark green mottled*) to 1.72 ± 0.00 mg/l (*black mottled*).

Seed coat pattern: Plant genotypes that had *whippoorwill* seed coat pattern recorded a least mean chlorophyll content of (0.58 ± 0.12) mg/l while those that had *golden* seed coat pattern recorded a highest mean of (1.81 ± 0.00) mg/l.

4.4.2 Reproductive

Mean days to flowering and Days to first matured pod

Growth habit: The mean days to flowering for this trait varied between 46.0 ± 0.00 (*prostrate*) and 86.0 ± 8.42 (*climbing*), and 62.0 ± 0.00 (*prostrate*) and 101.82 ± 8.4 (*climbing*) for days to first matured pod respectively.

Growth pattern: Mean days to flowering ranged from 65.99 ± 1.99 days for plant genotypes that had *indeterminate* growth pattern to 66.0 ± 16.00 days for genotypes that had *determinate* growth pattern. Days to first matured pod was 81.82 ± 2.00 (*indeterminate*) to 81.50 ± 15 (*determinate*).

Plant pigmentation: Mean days to flowering and days to first matured pod for the different phenotypic classes of plant pigmentation ranged from 58.0 ± 12.00 and 74.0 ± 2.00 (*solid*) to 68.84 ± 2.59 and 84.32 ± 0.50 (*no pigment*) respectively.

Plant hairiness: Three phenotypic classes were detected with a mean days to flowering and first matured pod ranging from 65.32 ± 2.02 and 80.83 ± 2.00 in plant genotypes that had *glabrescent* hairiness to 81.0 ± 10.35 and 105.75 ± 9.14 with those that had *short appressed hairs* respectively.

Twinning tendency: Four phenotypic classes were observed for these traits. The mean days to flowering and pod maturation ranged from 63.24 ± 3.05 and 78.96 ± 2.99 in genotypes that had *no twinning tendency* to 73.35 ± 7.45 and 87.88 ± 7.34 in genotypes that had *intermediate* twinning tendency respectively.

Leaf colour: Mean days to flowering and pod maturation ranged from 63.92 ± 3.04 and 79.53 ± 3.03 in accessions that had *dark green* leaf colour to 90.0 ± 0.00 and 106.0 ± 0.00 for those that had *variegated* leaf respectively.

Terminal leaflet shape: The mean concentration for days to flowering and days to first matured pod varied from 59.57 ± 2.81 and 75.58 ± 2.84 (*globose*) to 143.0 ± 0.00 and 159.0 ± 0.00 (*lanceolate*) respectively.

Leaf texture: Plant genotypes that had *intermediate* leaf texture recorded the least mean of 58.76 ± 2.68 and 74.51 ± 2.67 for days to flowering and days to first matured pod respectively. Genotypes with *cariaceous* leaf texture flowered and matured late with a mean of 70.86 ± 3.95 and 87.36 ± 4.03 respectively.

V-marking on leaflet: Accessions with this trait *present* flowered and matured with a least mean of 65.15 ± 1.89 and 80.91 ± 1.73 while those with *no V-marking* recorded a highest mean of 98.0 ± 22.55 and 113.0 ± 13.32 days respectively.

Flower colour: Eight phenotypic classes were observed. Accessions that had *white* flower colour flowered and matured first with means of 55.67 ± 2.90 and 71.0 ± 2.24 respectively, while those that had *yellow* flower colour recorded the highest mean of 77.67 ± 2.60 and 92.33 ± 2.90 days respectively.

Raceme position: Genotypes with raceme position *above canopy* flowered and matured earlier with a mean of 61.49 ± 2.53 and 77.53 ± 2.57 days while those that had raceme position *in upper canopy* flowered and matured late with a mean of 74.14 ± 4.17 and 89.59 ± 4.21 days respectively.

Main pod pigmentation: Plant genotypes that had *splashes of pigment* flowered and matured with a least mean of 58.89 ± 2.92 and 74.56 ± 2.86 . Genotypes that had *uniformly pigmented* pods scored the highest mean of 67.43 ± 5.06 and 82.71 ± 5.17 days respectively.

Pod colour: A total of ten phenotypic classes were observed. Accessions that had *brown* pod colour flowered and matured with least mean of 57.14 ± 3.91 and 73.86 ± 3.89 . Accessions that had *brown mottled* pod colour flowered with the highest mean of 83.33 ± 8.67 .

Pod wall thickness: Mean days to flowering and pod maturation for this trait ranged from 60.49 ± 2.71 and 76.05 ± 2.69 in accessions that had *intermediate* pod wall thickness to 73.11 ± 3.85 and 89.40 ± 3.64 days in accessions that had *thick* pod wall thickness respectively.

Pod curvature: Accessions that had *coiled* pod curvature flowered and matured with a least mean of 60.67 ± 9.53 and 76.33 ± 9.39 respectively while those that had *straight* pod curvature flowered with mean range of 66.33 ± 2.44 .

Seed shape: Mean days to flowering and pod maturation for these traits ranged from 59.9 ± 5.43 and 74.60 ± 5.28 in accessions that had *globose* seed shape to 79.00 ± 6.00 and 95.00 ± 7.99 (Crowder) respectively. Accessions that had kidney seed shape recorded a highest mean of 68.27 ± 4.51 and 84.20 ± 4.50 respectively.

Seed coat colour: Sixteen phenotypic classes were observed. The mean days to flowering and pod maturation for these traits ranged from 48.38 ± 1.52 and 64.25 ± 1.56 in accessions that had *red* seed coat colour to 95.20 ± 7.81 and 108.80 ± 10.3 in those that had *dark green mottled* coat colour respectively.

Seed coat pattern: Plant genotypes that had *Whippoorwill* seed coat pattern flowered and matured earlier with a mean of 51.0 ± 8.45 and 67.25 ± 8.49 while those that had *golden* seed coat pattern flowered and matured later with a mean of 90.0 ± 0.00 and 105.0 ± 0.00 respectively.

Mean number of flowers per plant, number of pod per peduncle and number of pods per plant

Growth habit: Mean number of flowers per plant, number of pods per peduncle and number of pods per plant varied from 4.50 ± 0.49 (*acute erect*) to 11.76 ± 1.46 (*semi-erect*) flowers per plant, 1.50 ± 0.50 (*acute erect*) to 2.00 ± 0.00 (*prostrate*) pods per peduncle and 3.0 ± 1.00 (*acute erect*) to 9.76 ± 1.42 (*semi-erect*) pods per plant respectively. Plant genotypes that had intermediate growth habit was beyond detection in all the above traits analysed.

Growth pattern: A mean of 8.92 ± 0.56 flowers per plant, 1.67 ± 0.05 pods per peduncle and 7.09 ± 0.54 pods per plant were recorded for plant genotypes that had *indeterminate* growth pattern while 11.50 ± 5.50 flowers per plant, 1.50 ± 0.05 pods per peduncle and 9.50 ± 6.50 were recorded for genotypes that had *determinate* growth pattern respectively.

Plant pigmentation: Mean number of flowers per plant, pods per peduncle and pods per plant for the different phenotypic classes of plant pigmentation ranged from 7.77 ± 0.46 (*not pigmented*) to 20.0 ± 8.00 (*intermediate*), 1.50 ± 0.50 (*intermediate and solid*) to 1.86 ± 0.28 (*extensive*), and 6.00 ± 0.46 (*not pigmented*) to 18.0 ± 7.00 (*intermediate*) respectively.

Plant hairiness: Three phenotypic classes were detected with means ranging from 8.83 ± 0.57 in plant genotypes that had *glabrescent* hairiness to 11.50 ± 2.50 with *pubescent to hirsute* for number of flowers per plant, 1.50 ± 0.50 (*pubescent to hirsute*) to 2.25 ± 0.25 (*short appressed hairs*) for number of pods per peduncle and 6.99 ± 0.56 (*glabrescent*) to 11.0 ± 5.00 (*short appressed hairs*) for number of pods per plant respectively.

Twinning tendency: Four phenotypic classes were observed for this trait with means ranging from 5.96 ± 0.50 in genotypes that had *slight* twinning tendency to 11.10 ± 1.00 in genotypes that had *pronounced* tendency for number of flowers per plant, 1.35 ± 0.10 (*slight*) to 1.94 ± 0.07

(*pronounced*) for number of pods per peduncle and 4.0 ± 0.50 (slight) to 9.21 ± 0.97 (*pronounced*) for number of pods per plant respectively.

Leaf colour: Mean number of flowers per plant, ranged from 5.93 ± 0.68 (*pale green*) to 10.02 ± 0.82 (*intermediate*). Plant genotypes that had *variegated* leaf colour recorded a least mean of 1.00 ± 0.00 pods per peduncle while those that had *intermediate green* recorded 1.71 ± 0.08 in all the four phenotypic classes. Accessions that had *pale green* leaf colour recorded the least mean of 4.29 ± 0.73 pods per plant while those that had *intermediate green* leaf colour recorded the highest mean of 4.33 ± 0.51 respectively.

Terminal leaflet shape: Mean flowers per plant for this trait ranged from 2.0 ± 0.00 (*lanceolate*) to 14.0 ± 3.0 (*linear*) terminal leaflet shape. The mean number of pods per peduncle ranged between 1.0 ± 0.00 (*linear*) and 1.82 ± 0.14 (*sub-hastate*). The mean number of pods per plant for this trait ranged from 1.0 ± 0.00 (*lanceolate*) to 12.50 ± 2.50 (*linear*) terminal leaflet shape.

Leaf texture: The mean number of flowers and number of pods per plant varied from 8.53 ± 0.86 and 6.58 ± 0.85 in plant genotypes that had *membranous* leaf texture to 9.31 ± 1.23 and 7.44 ± 1.20 in genotypes with *cariacious* leaf texture respectively. Mean number of pods per peduncle for this trait varied between 1.56 ± 0.09 (*cariacious*) and 1.76 ± 0.11 in genotypes that had *membranous* leaf texture respectively.

V-marking on leaflet: Accessions with this trait *present* recorded a mean of 8.94 ± 0.54 flowers per plant, 1.67 ± 0.05 flowers per peduncle and 7.09 ± 0.54 pods per plant while those that had *no V-marking* recorded 10.00 ± 4.36 , 1.67 ± 0.33 and 8.67 ± 4.09 respectively.

Flower colour: Eight phenotypic classes were observed. Accessions that had *cream* flower colour recorded a least means of 5.56 ± 0.47 flowers per plant, 1.33 ± 0.17 pods per peduncle and 3.67 ± 0.62 pods per plant respectively. Accessions that had *yellow* flower colour recorded highest mean of

15.00±1.99 and 13.67±1.90 flowers per plant and pods per plant respectively while 2.25±0.26 (*mauve-pink*) was recorded for number of flowers per peduncle

Raceme position: Genotypes with raceme position *throughout canopy* recorded a least mean of 8.11±0.92 flowers per plant, 1.52±0.10 pods per peduncle and 6.22±0.92 pods per plant. Highest mean of 9.26±1.01 flowers per plant was recorded for genotypes that had raceme position *mostly above canopy* while 1.73±1.26 pods per peduncle and 7.65±0.74 pods per plant were recorded for genotypes that had raceme position *in upper canopy* respectively.

Main pod pigmentation: Accessions that had *splashes of pigment* recorded a least mean of 5.78±0.57 flowers per plant, 1.56±0.18 pods per peduncle and 4.11±0.63 pods per plant. Accessions that had *no pod pigmentation* recorded a highest mean of 9.67±0.66 flowers per plant and 7.78±0.65 pods per plant while those that had *uniformly pigmented* pods recorded a highest mean of 1.93±0.13 pods per peduncle.

Pod colour: A total of ten phenotypic classes were observed. The means for the different phenotypic classes ranged from 4.67±1.33 and 3.00±1.15 in accessions that had *dark purple* pod colour to 28.50±14.50 (*green*) and 26.5±13.50 (*green*) for number of flowers and pods per plant respectively. Mean number of pods per peduncle for this trait varied between 1.0±0.00 in accessions that had *brown mottled* to 2.50±0.50 in those that had *dark green* pod colour.

Pod wall thickness: The mean number of flowers per plant and number of pods per plant varied from 7.13±0.77 and 5.32±0.76 in plant genotypes that had *thin* pod wall to 10.60±1.06 and 8.77±1.03 in genotypes with *thick* pod wall respectively. Mean number of pods per peduncle for this trait varied between 1.51±0.08 (*intermediate*) and 1.89±0.87 in genotypes that had *thick* pod wall.

Seed shape: The mean number of flowers and number of pods per plant varied from 7.11 ± 0.53 and 5.04 ± 0.55 in plant genotypes that had *ovoid* seed shape to 14.50 ± 2.50 and 12.50 ± 2.50 in genotypes that had *crowder* seed shape respectively. Mean number of pods per peduncle for this trait varied between 1.50 ± 0.50 (*crowder*) and 1.74 ± 0.10 (*rhomboid*).

Seed coat colour: A total of ten phenotypic classes were observed. The mean recorded for the different phenotypic classes ranged from 3.50 ± 1.50 and 2.50 ± 1.51 (*dark purple*) to 25.00 ± 0.00 and 23.00 ± 0.00 (*dark green*) for number of flowers and pods per plant respectively. Mean of 1.86 ± 0.10 pods per peduncle was recorded for accessions that had *flesh* seed coat colour. Apart from the following three seed coat colours (i.e. *cream*, *flesh* and *brick red*), the remaining phenotypic classes of this trait recorded a maximum mean value of 2.00 ± 0.00 pods per peduncle.

Seed coat pattern: The mean number of flowers per plant and number of pods per plant varied from 5.33 ± 1.33 and 3.67 ± 1.66 in plant genotypes that had *Watson* seed coat pattern to 10.0 ± 1.48 and 7.85 ± 1.49 in genotypes that had *Holstein* seed coat pattern respectively. Mean number of pods per peduncle for this trait varied between 1.0 ± 0.00 (*golden*) to 1.75 ± 0.07 in genotypes that had *solid* seed coat pattern.

Table 4.5: Distribution of cowpea reproductive quantitative traits by phenotypic classes

Trait	Phenotypic class	Reproductive quantitative traits			
		Mean and (standard error)			
		Mean days to flowering	Mean peduncle length/plant	Mean number of flowers per plant	Mean No of pod per peduncle
Growth habit	Acute erect	78.0 (20.00)	11.45 (3.75)	4.50 (0.49)	1.50 (0.50)
	Erect	64.63 (2.50)	13.14 (0.61)	7.61 (0.05)	1.54 (0.10)
	Semi-erect	60.61 (3.00)	13.62 (0.90)	11.76 (1.46)	1.82 (0.10)
	Intermediate	nd	nd	nd	nd
	Semi-prostrate	74.4 (9.37)	15.15 (1.32)	8.00 (2.28)	1.80 (0.20)
	Prostrate	46.0 (0.00)	9.70 (0.00)	5.0 (0.00)	2.0 (0.00)
	Climbing	86.0 (8.42)	13.35 (0.60)	10.18 (1.16)	1.91 (0.17)
Growth pattern	Determinate	66.0 (16.00)	8.05 (1.75)	11.5 (5.50)	1.50 (0.50)
	Indeterminate	65.99 (1.99)	13.44 (0.46)	8.92 (0.56)	1.67 (0.05)
Plant pigmentation	Not pigmented	68.84 (2.59)	13.28 (0.60)	7.77 (0.46)	1.64 (0.07)
	Very slight	63.5 (6.36)	12.29 (1.83)	12.0 (3.73)	1.80 (0.20)
	Moderate at the base and tips of petiole	59.91 (4.10)	12.95 (0.96)	9.59 (1.14)	1.68 (0.12)
	Intermediate	65.0 (2.20)	19.85 (0.66)	20.0 (8.00)	1.50 (0.50)
	Extensive	61.14 (7.83)	15.2 (1.32)	12.14 (3.34)	1.86 (0.26)
	Solid	58.0 (12.00)	12.75 (2.35)	9.0 (3.00)	1.50 (0.50)
Plant hairiness	Glabrescent	65.32 (2.02)	13.22 (0.47)	8.83 (0.57)	1.65 (0.05)
	Short appressed hairs	81.0 (10.35)	18.08 (1.93)	11.5 (2.5)	2.25 (0.25)
	Pubescent to hirsute	73.5 (8.50)	10.95 (1.15)	11.5 (5.50)	1.5 (0.50)
Twinning tendency	None	63.24 (3.05)	11.64 (0.16)	7.8 (0.71)	1.48 (0.12)
	Slight	65.65 (4.39)	12.27 (0.88)	5.96 (0.50)	1.35 (0.10)
	Intermediate	73.35 (7.45)	13.39 (1.22)	8.23 (1.52)	1.53 (0.12)
	Pronounced	65.06 (9.28)	14.64 (0.69)	11.10 (1.00)	1.94 (0.07)
Leaf colour	Pale green	74.93 (6.86)	10.63 (1.06)	5.93 (0.68)	1.43 (0.14)
	Intermediate green	65.18 (2.64)	13.66 (0.74)	10.02 (0.82)	1.71 (0.08)
	Dark green	63.92 (3.04)	13.62 (0.64)	8.79 (0.91)	1.70 (0.08)
	Variegated	90.0 (0.00)	22.0 (0.00)	9.0 (0.00)	1.00 (0.00)
Terminal leaflet shape	Globose	59.57 (2.81)	12.58 (0.36)	8.54 (2.81)	1.54 (0.10)
	Sub-globose	60.0 (2.40)	14.15 (0.72)	9.21 (0.96)	1.66 (0.08)
	Sub-hastate	77.04 (4.16)	12.83 (0.83)	8.65 (0.97)	1.83 (0.14)
	Hastate	89.57 (9.67)	12.81 (2.08)	9.29 (1.02)	1.71 (0.18)
	Linear	75.5 (2.50)	9.10 (0.80)	14.0 (3.0)	2.00 (0.00)
	Lanceolate	143.0 (0.00)	14.50 (0.00)	2.0 (0.00)	1.0 (0.00)

Table 4.5 cont'd

Trait	Phenotypic class	Reproductive quantitative traits			
		Mean and (standard error)			
		Mean days to flowering	Mean peduncle length/plant	Mean number of flowers per plant	Mean No of pod per peduncle
Leaf texture	Cariaceous	70.86 (3.95)	13.54 (0.84)	9.31 (1.23)	1.56 (0.09)
	Intermediate	58.76 (2.68)	13.15 (0.78)	9.04 (0.81)	1.69 (0.26)
	Membranous	70.17 (3.41)	13.40 (0.74)	8.53 (0.86)	1.75 (0.11)
V-marking	Absent	98.0 (22.55)	10.90 (1.86)	10.00 (4.36)	1.67 (0.33)
	Present	65.15 (1.89)	13.41 (0.46)	8.94 (0.56)	1.67 (0.05)
Flower colour	Deep purple	70.48 (3.66)	13.49 (0.68)	8.72 (0.72)	1.68 (0.08)
	Light purple	60.61 (2.49)	13.13 (2.48)	9.05 (3.80)	1.66 (0.29)
	Cream	64.33 (5.88)	12.46 (1.54)	5.56 (0.47)	1.33 (0.17)
	Purplish-white	61.00 (8.22)	14.52 (3.10)	10.00 (2.24)	1.80 (0.20)
	White	55.67 (2.90)	14.37 (1.98)	11.67 (3.18)	1.67 (0.33)
	Purplish-cream	60.5 (12.50)	11.30 (5.90)	10.00 (4.99)	1.5 (0.50)
	Mauve-pink	76.75 (11.2)	17.68 (2.72)	10.50 (2.02)	2.25 (0.25)
	Yellow	77.67 (2.60)	9.33 (0.52)	15.00 (1.99)	1.67 (0.33)
Raceme position	Mostly above canopy	61.49 (2.53)	13.96 (1.17)	9.26 (1.01)	1.70 (0.12)
	In upper canopy	74.14 (4.17)	13.35 (0.70)	9.16 (0.71)	1.73 (1.26)
	Throughout canopy	63.67 (3.17)	12.15 (0.83)	8.11 (0.92)	1.52 (0.10)
Main pod pigmentation	Not pigmented	66.46 (2.31)	13.67 (0.49)	9.67 (0.66)	1.64 (0.06)
	Splashes of pigment	58.89 (2.92)	10.52 (1.26)	5.78 (0.57)	1.56 (0.18)
	Uniformly pigmented	67.43 (5.06)	12.99 (1.54)	6.57 (0.61)	1.93 (0.13)
Pod colour	Brown	57.14 (3.91)	13.61 (1.06)	8.14 (0.90)	1.54 (0.10)
	Flesh	65.66 (2.87)	13.77 (0.86)	8.72 (0.81)	1.52 (0.09)
	Dark brown mottled	67.09 (4.93)	11.11 (1.40)	6.82 (0.78)	1.82 (0.18)
	Dark purple	76.0 (33.51)	13.2 (2.21)	4.67 (1.33)	1.33 (0.33)
	Dark brown	73.65 (6.55)	13.45 (1.13)	8.94 (1.08)	1.76 (0.11)
	Light brown	64.88 (4.24)	11.16 (1.65)	6.00 (0.68)	1.75 (0.15)
	Brown mottled	83.33 (8.67)	13.77 (2.46)	8.00 (0.58)	1.00 (0.00)
	Dark green	74.19 (5.35)	14.63 (1.21)	11.38 (1.67)	2.00 (0.18)
	Black	77.5 (11.57)	9.05 (0.75)	17.00 (0.00)	1.50 (0.50)
	Forest green	58.00 (5.00)	18.0 (4.60)	28.50 (14.50)	2.50 (0.50)
Pod wall thickness	Thin	62.77 (3.09)	12.05 (1.02)	7.13 (0.77)	1.52 (0.09)
	Intermediate	60.49 (2.71)	13.79 (0.75)	8.49 (4.95)	1.51 (0.08)
	Thick	73.11 (3.85)	13.84 (0.64)	10.60 (1.06)	1.89 (0.87)

Table 4.5 cont'd

Trait	Phenotypic class	Reproductive quantitative traits			
		Mean and (standard error)			
		Mean days to flowering	Mean peduncle length/plant	Mean No of flowers per plant	Mean No of pod per peduncle
Pod curvature	Straight	66.33 (2.44)	13.82 (0.53)	9.65 (0.70)	1.71 (0.06)
	Slightly curved	66.03 (3.45)	12.49 (0.92)	7.50 (0.75)	1.57 (0.10)
	Curved	61.00 (0.00)	5.50 (0.00)	9.00 (0.00)	2.00 (0.00)
	Coiled	60.67 (9.53)	11.43 (1.67)	4.33 (0.66)	1.33 (0.33)
Seed shape	Kidney	68.27 (4.51)	13.57 (1.38)	7.80 (1.36)	1.67 (0.13)
	Ovoid	66.61 (2.95)	12.92 (0.70)	7.11 (0.53)	1.61 (0.08)
	Crowder	79.00 (6.00)	12.75 (4.45)	14.50 (2.50)	1.50 (0.50)
	Globose	59.9 (5.43)	13.01 (1.35)	10.20 (1.58)	1.60 (0.16)
	Rhomboid	65.59 (3.67)	13.83 (0.76)	10.70 (1.11)	1.74 (0.10)
Seed coat colour	Red	48.38 (1.52)	14.86 (1.89)	6.88 (0.87)	2.00 (0.00)
	Dark brown mottled	74.83 (5.73)	14.00 (0.89)	8.43 (0.93)	2.00 (0.00)
	Brown mottled	61.57 (3.26)	13.97 (1.58)	11.43 (3.00)	2.00 (0.00)
	Cream	62.70 (5.53)	12.97 (1.38)	7.60 (1.28)	1.90 (0.10)
	Flesh	59.36 (4.12)	12.23 (1.08)	8.71 (1.53)	1.86 (0.10)
	Brick red	66.00 (6.90)	12.54 (3.17)	7.20 (1.02)	2.00 (0.00)
	Brown	58.43 (3.49)	13.24 (1.60)	7.43 (0.80)	2.00 (0.00)
	Black	79.57 (7.73)	10.80 (1.93)	9.29 (1.64)	2.00 (0.00)
	Dark purple	94.0 (13.00)	16.70 (6.90)	3.50 (1.50)	2.00 (0.00)
	Dirty-white	62.14 (7.80)	13.13 (1.23)	10.57(2.83)	2.00 (0.00)
	Purple-brown mottled	55.40 (7.22)	10.94 (0.69)	8.0 (1.00)	2.00 (0.00)
	Red and cream	62.00 (11.0)	11.20 (5.80)	11.50 (6.50)	2.00 (0.00)
	Dark green mottled	95.20 (7.81)	15.88 (1.91)	11.80 (2.08)	2.00 (0.00)
	Black mottled	86.00 (0.00)	19.50 (0.00)	10.00 (0.00)	2.00 (0.00)
	Dark green	61.00 (0.00)	17.40 (0.00)	25.00 (0.00)	2.00 (0.00)
	Green	82.00 (0.00)	9.80 (0.00)	17.00 (0.00)	2.00 (0.00)
Seed coat pattern	Solid	69.13 (2.90)	13.91 (0.64)	9.99 (0.86)	1.75 (0.07)
	Small eye	63.10 (3.06)	12.80 (0.85)	7.13 (0.52)	1.58 (0.09)
	Whippoorwill	51.0 (8.45)	14.18 (1.26)	5.75 (0.23)	1.50 (0.29)
	Holstein	59.92 (5.01)	12.85 (1.13)	10.0 (1.48)	1.62 (0.14)
	Watson	67.0 (3.79)	9.53 (2.59)	5.33 (1.33)	1.33 (0.33)
	Golden	90.0 (0.00)	8.50 (0.00)	8.0 (0.00)	1.00 (0.00)

Table 4.5 cont'd

Trait	Phenotypic class	Reproductive quantitative traits		
		Mean and (standard error)		
		Mean days to 1 st matured pod	Mean No of pods per plant	Mean pod length per plant
Growth habit	Acute erect	93.0 (21.00)	3.0 (1.00)	8.10 (0.70)
	Erect	80.06 (2.45)	5.82 (0.52)	12.76 (0.35)
	Semi-erect	76.52 (3.04)	9.76 (1.42)	11.12 (0.46)
	Intermediate	nd	nd	nd
	Semi-prostrate	95.0 (10.69)	6.40 (2.40)	7.78 (0.36)
	Prostrate	62.0 (0.00)	4.0 (0.00)	9.50 (0.00)
	Climbing	101.82 (8.4)	8.36 (1.31)	7.82 (0.61)
Growth pattern	Determinate	81.5 (15.50)	9.5 (6.50)	11.75 (2.95)
	Indeterminate	81.82 (2.00)	7.09 (0.54)	11.51 (0.23)
Plant pigmentation	Not pigmented	84.32 (0.50)	6.0 (0.46)	11.31 (0.37)
	Very slight	81.70 (7.28)	9.8 (3.62)	12.46 (1.01)
	Moderate at the base and tips of petiole	75.68 (4.10)	7.55 (1.07)	11.82 (0.63)
	Intermediate	81.5 (22.50)	18.0 (7.00)	10.85 (1.95)
	Extensive	77.0 (7.99)	10.86 (3.41)	11.13 (1.22)
	Solid	74.0 (2.00)	7.0 (3.00)	12.85 (1.51)
Plant hairiness	Glabrescent	80.83 (2.00)	6.99 (0.56)	11.69 (0.29)
	Short appressed hairs	105.75(9.14)	9.0 (3.03)	8.45 (0.40)
	Pubescent to hirsute	88.5 (8.50)	11.0 (5.00)	7.95 (0.85)
Twinning tendency	None	78.96 (2.99)	6.08 (0.70)	12.43 (0.63)
	Slight	81.48 (4.37)	4.0 (0.50)	12.51 (0.65)
	Intermediate	87.88 (7.34)	6.53 (1.46)	12.13 (0.62)
	Pronounced	81.35 (2.89)	9.21 (0.97)	10.43 (0.43)
Leaf colour	Pale green	89.21 (6.64)	4.29 (0.73)	10.56 (0.88)
	Intermediate green	81.67 (2.74)	7.98 (0.81)	11.49 (0.50)
	Dark green	79.53 (3.03)	7.09 (0.89)	11.73 (0.37)
	Variegated	106.0 (0.00)	7.0 (0.00)	14.5 (0.00)
Terminal leaflet shape	Globose	75.58 (2.84)	6.75 (0.91)	13.31 (0.46)
	Sub-globose	75.98 (2.44)	7.21 (0.93)	11.98 (0.39)
	Sub-hastate	92.26 (4.17)	7.22 (0.99)	9.66 (0.53)
	Hastate	105.71 (9.52)	7.0 (1.45)	7.64 (0.74)
	Linear	90.0 (2.99)	12.5 (2.50)	5.55 (0.25)
	Lanceolate	159.0 (0.00)	1.0 (0.00)	10.20 (0.00)

Table 4.5 cont'd

Trait	Phenotypic class	Reproductive quantitative traits		
		Mean and (standard error)		
		Mean days to first ^t matured pod	Mean no of pods per plant	Mean pod length per plant
Leaf texture	Cariaceous	87.36 (4.03)	7.44 (1.20)	11.19 (0.54)
	Intermediate	74.51 (2.67)	7.31 (0.80)	12.29 (0.45)
	Membranous	85.39 (3.35)	6.58 (0.85)	10.87 (0.49)
V-marking	Absent	113 (13.32)	8.67 (4.09)	7.10 (1.56)
	Present	80.91 (1.73)	7.09 (0.54)	11.63 (0.29)
Flower colour	Deep purple	85.96 (3.62)	6.94 (0.68)	11.38 (0.41)
	Light purple	77.22 (2.66)	7.15 (1.16)	12.08 (0.48)
	Cream	79.11 (5.85)	3.67 (0.62)	11.84 (1.13)
	Purplish-white	76.80 (8.42)	8.60 (2.56)	11.06 (1.61)
	White	71.0 (2.24)	9.67 (3.18)	14.87 (1.09)
	Purplish-cream	76.0 (12.99)	7.50 (4.50)	11.35 (1.35)
	Mauve-pink	92.5 (11.33)	8.25 (2.56)	8.45 (0.64)
	Yellow	92.33 (2.90)	13.67 (1.9)	6.63 (1.09)
Raceme position	Mostly above canopy	77.53 (2.57)	7.23 (0.98)	11.99 (0.40)
	In upper canopy	89.59 (4.21)	7.65 (0.74)	9.82 (0.51)
	Throughout canopy	79.56 (3.27)	6.22 (0.92)	12.90 (0.48)
Main pod pigmentation	Not pigmented	82.37 (2.32)	7.78 (0.65)	11.56 (0.33)
	Splashes of pigment	74.56 (2.86)	4.11 (0.63)	12.09 (1.03)
	Uniformly pigmented	82.71 (5.07)	4.71 (0.64)	10.87 (0.72)
Pod colour	Brown	73.86 (3.89)	6.32 (0.84)	11.52 (0.51)
	Flesh	81.10 (2.87)	6.76 (1.00)	13.85 (0.08)
	Dark brown mottled	83.00 (4.97)	5.00 (0.86)	11.36 (0.10)
	Dark purple	91.67 (3.36)	3.00 (1.15)	10.50 (0.40)
	Dark brown	89.29 (6.50)	7.65 (1.10)	10.48 (0.65)
	Light brown	80.88 (4.22)	4.13 (0.69)	14.01 (0.89)
	Brown mottled	98.33 (8.67)	6.33 (0.33)	12.33 (0.79)
	Dark green	91.63 (5.37)	9.00 (1.67)	7.91 (0.32)
	Black	92.00 (5.00)	15.5 (0.50)	7.30 (1.50)
	Forest green	74.50 (4.49)	26.5 (13.5)	8.65 (1.15)
Pod wall thickness	Thin	78.48 (3.09)	5.32 (0.76)	12.36 (0.46)
	Intermediate	76.05 (2.69)	6.59 (0.75)	13.41 (0.41)
	Thick	89.40 (3.64)	8.77 (1.03)	9.21 (0.34)

Table 4.5 cont'd

Trait	Phenotypic class	Reproductive quantitative traits		
		Mean and (standard error)		
		Mean days to first matured pod	Mean No of pods per plant	Mean pod length per plant
Pod curvature	Straight	82.38 (2.45)	7.81 (0.68)	11.16 (0.33)
	Slightly curved	81.5 (3.43)	5.63 (0.78)	12.27 (0.59)
	Curved	77.0 (0.00)	6.00 (0.00)	10.20 (0.00)
	Coiled	76.33 (9.39)	2.67 (0.88)	13.27 (1.36)
Seed shape	Kidney	84.20 (4.50)	5.87 (1.19)	13.11 (0.77)
	Ovoid	82.26 (2.87)	5.04 (0.55)	12.04 (0.10)
	Crowder	95.00 (7.99)	12.50 (2.50)	7.80 (2.00)
	Globose	74.60 (5.28)	8.90 (1.66)	12.49 (0.78)
	Rhomboid	81.96 (3.75)	8.98 (1.07)	10.33 (0.38)
Seed coat colour	Red	64.25 (1.56)	6.75 (0.65)	12.36 (0.87)
	Dark brown mottled	89.96 (5.75)	6.83 (3.20)	9.83 (0.64)
	Brown mottled	79.86 (4.25)	9.50 (2.91)	10.53 (0.85)
	Cream	78.20 (5.47)	6.30 (1.42)	13.23 (0.78)
	Flesh	75.07 (4.15)	6.86 (1.49)	13.48 (0.67)
	Brick red	82.40 (6.68)	5.40 (1.17)	12.56 (1.99)
	Brown	74.21 (3.46)	5.71 (0.84)	12.49 (0.76)
	Black	95.86 (7.67)	7.00 (1.93)	9.79 (1.34)
	Dark purple	109.0 (3.60)	2.50 (1.51)	9.50 (1.00)
	Dirty-white	78.00 (8.08)	7.57 (2.52)	11.46 (0.88)
	Purple-brown mottled	71.20 (7.13)	6.40 (0.75)	13.78 (0.79)
	Red and cream	77.5 (11.55)	9.50 (6.50)	14.00 (1.30)
	Dark green mottled	108.8 (10.3)	9.60 (2.31)	9.22 (0.41)
	Black mottled	104.0 (0.00)	8.00 (0.00)	8.40 (0.00)
	Dark green	77.00 (0.00)	23.00 (0.00)	7.20 (0.00)
	Green	97.00 (0.00)	16.00 (0.00)	8.80 (0.00)
Seed coat pattern	Solid	85.10 (2.91)	8.13 (0.84)	10.14 (0.75)
	Small eye	78.90 (3.03)	5.35 (0.51)	13.56 (0.36)
	Whippoorwill	67.25 (8.49)	4.25 (1.11)	11.75 (1.26)
	Holstein	75.62 (5.09)	7.85 (1.49)	12.52 (0.64)
	Watson	82.67(3.53)	3.67 (1.66)	15.20 (0.93)
	Golden	105.0 (0.00)	6.0 (0.00)	11.20 (0.00)

4.4.3 Yield component

Average seed per pod and 20-seed weight (g)

Growth habit: The mean seed per pod ranged from 8.0 ± 0.00 (*prostrate*) to 10.25 ± 0.25 (*acute-erect*), and 0.3361 ± 0.01 g (*acute erect*) to 1.9719 ± 0.00 g (*prostrate*) for 20-seed weight respectively. Plant genotypes that had *intermediate* growth habit was beyond detection in all the above traits analyzed.

Growth pattern: Least means of 9.79 ± 0.25 average seed per pod and 1.5521 ± 0.07 seed weight were recorded for plant genotypes that had *indeterminate* growth pattern while accessions that had *determinate* growth pattern recorded highest means of 10.9 ± 1.10 average seed per pod and 1.6149 ± 1.10 g seed weight.

Plant pigmentation: Mean seed per pod and 20-seed weight for the different phenotypic classes of plant pigmentation ranged from 7.70 ± 1.20 (*solid*) to 9.86 ± 0.57 (*moderately at the base and tips of petiole*) and 1.19 ± 0.16 (*intermediate*) to 2.15 ± 0.64 (*solid*) respectively.

Plant hairiness: Three phenotypic classes were detected with a mean ranged from 9.74 ± 0.26 in plant genotypes that had *glabrescent* hairiness to 11.45 ± 1.65 (*pubescent to hirsute*) for average seed per pod and 0.4272 ± 8.20 g (*pubescent to hirsute*) to 1.6107 ± 0.07 g (*glabrescent*) for seed weight.

Twinning tendency: Four different phenotypic classes were observed for this trait with a mean ranged from 9.42 ± 0.63 in genotypes that had *slight* twinning tendency to 10.08 ± 0.59 in genotypes that had *no twinning* tendency for average seed per pod and 1.2682 ± 0.12 g (*pronounced*) to 1.9061 ± 0.11 g (*intermediate*) for 20 seed weight respectively.

Leaf colour: Mean seed per pod ranged from 7.50 ± 0.00 (*variegated*) to 9.95 ± 0.80 (*pale green*).

Plant genotypes that had *intermediate green* leaf colour recorded a least mean of 1.4625 ± 0.11 g

seed weight while those that had *variegated* leaf colour recorded highest mean of 2.0019 ± 0.00 g seed weight in all the four phenotypic classes.

Terminal leaflet shape: Mean seed per pod for this trait ranged from 6.15 ± 0.35 in accessions that had *linear* terminal leaflet shape to 13.0 ± 0.00 in those with *lanceolate* terminal leaflet shape. A mean of 0.4826 ± 0.16 g (*linear*) to 1.9678 ± 0.10 g (*globose*) was recorded for seed weight.

Leaf texture: Mean seed per pod and 20-seed weight varied from 9.26 ± 0.40 and 1.3595 ± 0.14 g in plant genotypes that had *membranous* leaf texture to 10.07 ± 0.36 and 1.6831 ± 0.09 g in genotypes with *intermediate* leaf texture respectively.

V-marking on leaflet: Accessions with this trait *present* recorded a mean of 9.85 ± 0.25 average seed per pod and 1.58 ± 0.07 g seed weight while those with *no V-marking* recorded 8.43 ± 2.29 and 0.6657 ± 0.21 g for average seed per pod and 20-seed weight respectively.

Flower colour: Eight phenotypic classes were observed. Mean average seed per pod for this trait ranged from 5.95 ± 1.95 (*creamy-purple*) to 11.17 ± 1.10 (*white*) and seed weight was 0.4914 ± 0.09 g (*yellow*) to 2.4105 ± 0.41 g (*creamy-purple*),

Raceme position: Genotypes with raceme position *in upper canopy* recorded a least mean of 9.62 ± 0.44 average seed per pod and 1.1392 ± 0.14 g seed weight. for genotypes that had raceme position *throughout canopy*. Genotypes that had raceme position *throughout canopy* recorded the highest mean of 10.14 ± 0.50 average seed and 1.9225 ± 0.09 g seed weight for this trait.

Main pod pigmentation: Mean seed per pod for this trait ranged from 9.62 ± 0.26 in accessions that had *no pod pigmentation* to 11.2 ± 1.35 (*splashes of pigment*) while that of 20 seed weight was 1.3790 ± 0.21 g (*uniformly pigmented*) to 1.8062 ± 0.11 g (*splashes of pigment*).

Pod colour: A total of ten phenotypic classes were observed. Mean seed per pod recorded for this trait ranged from 7.80 ± 2.00 (*black*) to 12.43 ± 1.62 (*light brown*) and that of seed weight was 0.3483 ± 7.07 g (*green*) to 2.1549 ± 0.45 g (*brown mottled*),

Pod wall thickness: Mean seed per pod and seed weight for the different phenotypic classes of pod wall thickness ranged from 9.29 ± 0.58 (*thin*) to 10.04 ± 0.45 (*intermediate*) and 0.9222 ± 0.43 g (*thick*) to 1.9813 ± 0.47 g (*intermediate*) respectively.

Seed shape: Mean seed per pod varied from 8.84 ± 0.79 (*globose*) to 10.48 ± 0.45 (*ovoid*) while that of seed weight was 1.3353 ± 0.13 g (*rhomboid*) to 1.7769 ± 0.20 g (*kidney*).

Seed coat colour: A total of sixteen phenotypic classes were observed. Mean seed per pod for this trait ranged between 6.70 ± 2.70 (*red and cream*) and 11.38 ± 0.37 (*dark green mottled*) while that of seed weight was between 0.3406 ± 0.00 g (*dark green*) and 2.4528 ± 0.26 g (*purple brown mottled*).

Seed coat pattern: Mean seed per pod for this trait varied from 8.80 ± 0.74 (*whippoorwill*) to 10.76 ± 0.57 (*small eyed*) while seed weight was 1.2083 ± 0.10 g (*solid*) to 3.0102 ± 0.00 g (*golden*).

Average seed yield per plant and seed abortion rate

Growth habit: The mean seed yield per plant and seed abortion rate varied between 31.50 ± 10.50 (*acute erect*) and 97.06 ± 15.94 (*semi-erect*), and between 0.20 ± 0.20 (*semi-prostrate*) and 1.00 ± 0.00 % (*prostrate*) respectively.

Growth pattern: Relatively least means of 69.73 ± 5.75 seed yield and 0.84 ± 0.06 % seed abortion rate were recorded for plant genotypes that had *indeterminate* growth pattern while accessions that had *determinate* growth pattern recorded highest means of 94.50 ± 5.50 seed yield and 0.50 ± 0.50 % seed abortion rate.

Plant pigmentation: Mean seed yield per plant and seed abortion rate for the different phenotypic classes of plant pigmentation ranged from 57.50 ± 3.10 (*solid*) to 162.50 ± 4.7 (*intermediate*), and 0.50 ± 0.50 (*solid*) to 0.95 ± 0.12 (*moderately at the base and tips of petiole*) respectively.

Plant hairiness: Three different phenotypic classes were detected with a mean ranged from 68.43 ± 5.87 (*glabrescent*) to 112.0 ± 38.92 (*pubescent to hirsute*) for seed yield and 0.00 ± 0.00 % (*pubescent to hirsute*) to 0.86 ± 0.06 % (*glabrescent*) for seed abortion rate respectively.

Twinning tendency: Four phenotypic classes were observed for this trait with a mean ranged from 37.48 ± 5.12 (*slight*) to 91.83 ± 10.62 (*pronounced*) for seed yield and 0.75 ± 0.09 % (*pronounced*) to 1.0 ± 0.15 % (*intermediate*) for seed abortion rate respectively.

Leaf colour: Mean seed yield per plant ranged from 42.71 ± 7.04 (*pale green*) to 78.45 ± 7.41 . Accessions that had *variegated* leaf colour recorded a least mean of 0.00 ± 0.00 % seed abortion rate while those that had *intermediate green* leaf colour recorded highest mean of 0.88 ± 0.10 % for this trait.

Terminal leaflet shape: A mean ranged from 13.00 ± 0.00 (*lanceolate*) to 79.50 ± 14.50 (*linear*) was recorded for seed yield per plant while a mean ranged from 0.00 ± 0.00 % (*lanceolate*) to 1.00 ± 0.12 % (*globose*) for seed abortion rate was recorded for of this trait.

Leaf texture: Mean seed yield per plant and seed abortion rate for this trait varied between 66.78 ± 9.14 (*membranous*) to 72.39 ± 13.47 in genotypes that had *cariaceous* leaf texture and 0.64 ± 0.11 % (*cariaceous*) to 1.02 ± 0.09 % (*intermediate*) respectively.

V-marking on leaflet: Accessions with this trait *present* recorded a mean of 70.49 ± 5.83 seed yield and 0.85 ± 0.05 % seed abortion rate while those with *no V-marking* recorded 57.33 ± 23.69 and 0.33 ± 0.33 % respectively.

Flower colour: Mean seed yield per plant ranged from 38.0 ± 5.41 (*cream*) to 103.33 ± 25.26 (*yellow*) and seed abortion rate was 0.33 ± 0.33 % (*yellow*) to 1.00 ± 0.41 % (*white-purple* and *mauve-pink*).

Raceme position: Genotypes with raceme position *in upper canopy* recorded a least mean of 0.76 ± 0.09 abortion rate while 62.93 ± 10.54 mean seed yield was recorded for genotypes that had raceme position *throughout canopy*. Genotypes that had raceme position *throughout canopy* recorded the highest mean of 0.96 ± 0.13 % abortion rate, and those that had raceme position *mostly above canopy* recorded the highest mean of 71.68 ± 10.80 seed yield for this trait.

Main pod pigmentation: Mean seed per pod recorded for this trait ranged from 42.22 ± 7.50 (*splashes of pigment*) to 76.18 ± 6.97 (*not pigmented*) seed yield and 0.81 ± 0.07 % (*not pigmented*) to 1.11 ± 0.20 % (*splashes of pigment*) seed abortion rate.

Pod colour: A total of ten phenotypic classes were observed. Mean seed yield per plant recorded for this trait ranged from 28.67 ± 10.61 (*dark purple*) to 304.0 ± 7.50 (*green*) while seed abortion rate was 1.50 ± 0.50 % (*black and green*) to 4.00 ± 0.58 % (*brown mottled*).

Pod wall thickness: Mean seed yield and seed abortion rate for the different phenotypic classes of pod wall thickness ranged from 46.45 ± 6.08 (*thin*) to 91.26 ± 12.50 (*thick*) and 1.83 ± 0.12 % (*thick*) to 2.55 ± 0.15 % (*thin*) respectively.

Seed shape: Mean seed yield recorded for this trait ranged from 53.35 ± 5.42 (*ovoid*) to 110.0 ± 16.00 (*crowder*) while 2.00 ± 0.13 % (*rhomboid*) to 2.50 ± 0.50 % (*crowder*) was recorded for abortion rate.

Seed coat colour: A total of sixteen phenotypic classes were observed. Mean seed yield per plant and seed abortion rate recorded for this trait ranged from 15.0 ± 5.00 (*dark purple*) to 221.0 ± 0.00 (*dark green*) and 1.00 ± 0.00 % (*green*) to 3.50 ± 0.50 % (*dark purple*) respectively.

Seed coat pattern: Six different phenotypic classes were observed. Mean seed yield per plant varied between 39.50 ± 10.94 (*whippoorwill*) and 80.58 ± 9.13 (*solid*) while seed abortion rate was 0.00 ± 0.00 % (*golden*) to 2.53 ± 0.24 % (*Holstein*).

Table 4.6: Distribution of cowpea yield component quantitative traits by phenotypic classes.

Trait	Phenotypic class	Yield component quantitative traits			
		Mean and (standard error)			
		Mean average seed per pod	Mean 20-seed weight (g)	Mean seed yield per plant	Mean seed abortion rate
Growth habit	Acute erect	10.25 (0.25)	0.3361 (0.01)	31.50 (10.5)	0.50 (0.49)
	Erect	9.81 (0.37)	1.8662 (0.08)	56.72 (5.50)	0.97 (0.08)
	Semi-erect	9.81 (0.41)	1.5035 (0.13)	97.06 (15.94)	0.76 (0.12)
	Intermediate	nd	nd	nd	nd
	Semi-prostrate	10.92 (1.09)	0.6142 (0.16)	66.60 (24.36)	0.2 (0.20)
	Prostrate	8.00 (0.00)	1.9719 (0.00)	32.00 (0.00)	1.0 (0.00)
	Climbing	9.45 (0.60)	0.4625 (0.07)	80.91 (10.04)	0.64 (0.15)
Growth pattern	Determinate	10.90 (1.10)	1.6149 (1.10)	94.50 (5.50)	0.5 (0.50)
	Indeterminate	9.79 (0.25)	1.5521 (0.07)	69.73 (5.75)	0.84 (0.06)
Plant pigmentation	Not pigmented	9.95 (0.32)	1.5605 (0.10)	58.50 (4.47)	0.82 (0.08)
	Very slight	10.61 (0.70)	1.5314 (0.24)	107.30 (4.36)	0.70 (0.21)
	Moderate at the base and tips of petiole	9.86(0.57)	1.6101 (0.14)	76.77 (11.24)	0.95 (0.12)
	Intermediate	9.45 (1.25)	1.1942 (0.16)	162.5 (4.750)	1.50 (0.50)
	Extensive	8.89 (1.04)	1.2592 (0.24)	96.71 (6.44)	0.71 (0.19)
	Solid	7.69 (1.20)	2.1528 (0.64)	57.50 (3.15)	0.50 (0.50)
Plant hairiness	Glabrescent	9.74 (0.26)	1.6107 (0.07)	68.43 (5.87)	0.86 (0.06)
	Short appressed hairs	11.13 (0.52)	0.5098 (0.17)	97.00 (3.04)	0.75 (0.25)
	Pubescent to hirsute	11.45 (1.65)	0.4272 (8.20)	112.00 (3.89)	0.00 (0.00)
Twinning tendency	None	10.08 (0.59)	1.8565 (0.15)	61.92 (7.15)	0.88 (0.12)
	Slight	9.42 (0.63)	1.9061 (0.11)	37.48 (5.12)	0.87 (0.11)
	Intermediate	9.71 (0.74)	1.5015 (0.15)	60.18 (12.97)	1.00 (0.15)
	Pronounced	9.90 (0.31)	1.2682 (0.12)	91.83 (10.62)	0.75 (0.09)
Leaf colour	Pale green	9.95 (0.80)	1.5078 (0.22)	42.71 (7.04)	0.79 (0.19)
	Intermediate green	9.86 (0.37)	1.4625 (0.11)	78.45 (7.41)	0.88 (0.10)
	Dark green	9.78 (0.37)	1.6406 (0.10)	70.08 (10.24)	0.83 (0.08)
	Variegated	7.50 (0.00)	2.0019 (0.00)	52.00 (0.00)	0.00 (0.00)
Terminal leaflet shape	Globose	10.34 (0.54)	1.9678 (0.10)	66.86 (12.64)	1.0 (0.12)
	Sub-globose	9.81 (0.35)	1.7014 (0.10)	71.25 (10.27)	0.86 (0.09)
	Sub-hastate	9.76 (0.50)	1.1113 (0.16)	72.04 (10.87)	0.70 (0.12)
	Hastate	8.51 (0.88)	0.5417 (0.12)	73.86 (13.70)	0.71 (0.29)
	Linear	6.15 (0.35)	0.4826 (0.16)	79.50 (14.50)	0.50 (0.50)
	Lanceolate	13.00 (0.00)	1.0321 (0.00)	13.00 (0.00)	0.00 (0.00)

Table 4.6 cont'd

Trait	Phenotypic class	Yield component quantitative traits			
		Mean and (standard error)			
		Mean average seed per pod	Mean 20- seed weight (g)	Mean seed yield per plant	Mean seed abortion rate
Leaf texture	Cariaceous	10.05 (0.51)	1.5846 (0.01)	72.39 (13.47)	0.64 (0.11)
	Intermediate	10.07 (0.36)	1.6831 (0.09)	71.07 (7.33)	1.02 (0.09)
	Membranous	9.26 (0.40)	1.3595 (0.14)	66.78 (9.14)	0.81 (0.09)
V- marking	Absent	8.43 (2.29)	0.6657 (0.21)	57.33 (23.69)	0.33 (0.33)
	Present	9.85 (0.25)	1.5765 (0.07)	70.49 (5.83)	0.85 (0.05)
Flower colour	Deep purple	10.32 (0.36)	1.4789 (0.12)	72.26 (7.20)	0.80 (0.09)
	Light purple	9.62 (0.43)	1.6658 (0.10)	69.34 (12.85)	0.90 (0.09)
	Cream	8.76 (0.95)	1.7602 (0.19)	38.00 (5.41)	0.89 (0.11)
	Purplish-white	9.74 (0.75)	1.6331 (0.32)	68.20 (10.6)	1.0 (0.44)
	White	11.17 (1.10)	1.8299 (0.24)	101.67 (24.18)	0.67 (0.33)
	Purplish-cream	5.95 (1.95)	2.4105 (0.41)	53.00 (4.1)	0.50 (0.50)
	Mauve-pink	10.73 (1.18)	0.9102 (0.39)	87.00 (27.39)	1.0 (0.41)
	Yellow	7.37 (1.24)	0.4914 (0.09)	103.33 (25.26)	0.33 (0.33)
Raceme position	Mostly above canopy	9.78 (0.37)	1.6541 (0.10)	71.68 (10.80)	0.83 (0.09)
	In upper canopy	9.63 (0.44)	1.1392 (0.14)	73.24 (6.89)	0.76 (0.09)
	Throughout canopy	10.14 (0.50)	1.9225 (0.09)	62.93 (10.54)	0.96 (0.13)
Main pod pigmenta tion	Not pigmented	9.62 (0.26)	1.5549 (0.08)	76.18 (6.97)	0.81 (0.07)
	Splashes of pigment	11.20 (1.35)	1.8062 (0.11)	42.22 (7.50)	1.11 (0.20)
	Uniformly pigmented	10.24 (0.70)	1.3790 (0.21)	47.64 (8.53)	0.86 (0.18)
Pod colour	Brown	8.89 (0.40)	1.7471 (0.11)	56.32 (16.49)	2.29 (0.13)
	Flesh	9.98 (0.49)	2.0541 (0.10)	63.10 (8.18)	2.07 (0.19)
	Dark brown mottled	10.35 (0.81)	1.6169 (0.20)	54.27 (11.10)	2.45 (0.16)
	Dark purple	10.33 (1.45)	1.6199 (0.36)	28.67 (10.61)	1.67 (0.33)
	Dark brown	9.24 (0.54)	1.3204 (0.22)	74.53 (13.25)	2.06 (0.28)
	Light brown	12.44 (1.62)	1.9413 (0.07)	47.25 (0.24)	2.38 (0.26)
	Brown mottled	9.97 (1.71)	2.1549 (0.45)	63.00 (8.02)	4.00 (0.58)
	Dark green	10.21 (0.53)	0.4982 (0.08)	99.00 (16.74)	1.63 (0.15)
	Black	7.80 (2.00)	0.5766 (0.67)	122.5 (28.50)	1.50 (0.50)
	Forest green	11.00 (1.10)	0.3483 (7.07)	304.00 (75.0)	1.50 (0.50)
Pod wall thickness	Thin	9.29 (0.58)	1.962 (0.08)	46.45 (6.08)	2.55 (0.15)
	Intermediate	10.04 (0.45)	1.9813 (0.47)	64.20 (6.80)	2.17 (0.16)
	Thick	10.02 (0.33)	0.9222 (0.43)	91.26 (12.50)	1.83 (0.12)

Table 4.6 cont'd

Trait	Phenotypic class	Yield component quantitative traits			
		Mean and (standard error)			
		Mean average seed per pod	Mean 20-seed weight (g)	Mean seed yield per plant	Mean seed abortion rate
Pod curvature	Straight	9.55 (0.28)	1.4319 (0.09)	76.45 (7.70)	2.14 (0.10)
	Slightly curved	10.42 (0.52)	1.8936 (0.11)	57.00 (6.83)	2.17 (0.17)
	Curved	9.30 (0.00)	1.9518 (0.00)	56.00 (0.00)	2.00 (0.00)
	Coiled	12.10 (0.10)	1.6417 (0.19)	32.33 (10.65)	1.67 (0.33)
Seed shape	Kidney	9.85 (0.46)	1.7769 (0.20)	58.93 (12.93)	2.13 (0.24)
	Ovoid	10.48 (0.45)	1.6882 (0.11)	53.35 (5.42)	2.24 (0.14)
	Crowder	9.20 (3.40)	1.3511 (0.71)	110.00 (16.0)	2.50 (0.50)
	Globose	8.84 (0.79)	1.696 (0.16)	73.80 (13.35)	2.20 (0.25)
	Rhomboid	9.43 (0.35)	1.3353 (0.13)	88.37 (11.95)	2.00 (0.13)
Seed coat colour	Red	9.38 (0.81)	2.1175 (0.21)	42.25 (4.01)	2.63 (0.26)
	Dark brown mottled	10.42 (0.46)	1.0517 (0.17)	75.17 (10.31)	1.59 (0.14)
	Brown mottled	9.56 (0.73)	1.2207 (0.24)	95.50 (33.27)	1.93 (0.22)
	Cream	10.20 (1.51)	1.9323 (0.13)	59.00 (8.33)	2.30 (0.33)
	Flesh	10.59 (0.98)	1.9439 (0.10)	64.00 (12.05)	2.57 90.25)
	Brick red	10.02 (2.03)	1.4382 (0.33)	60.60 (18.31)	2.40 (0.24)
	Brown	8.86 (1.03)	1.8031 (0.13)	49.86 (7.79)	2.29 (0.19)
	Black	9.64 (0.69)	1.4176 (0.28)	63.14 (16.51)	2.14 (0.26)
	Dark purple	10.00 (0.00)	2.1103 (0.31)	15.00 (5.00)	3.50 (0.50)
	Dirty-white	8.56 (0.84)	1.8913 (0.27)	70.57 (26.97)	1.86 (0.26_
	Purple-brown mottled	10.24 (1.17)	2.4528 (0.26)	71.80 (14.0)	2.40 (0.81)
	Red and cream	6.70 (2.70)	2.1495 (0.13)	81.00 (69.0)	3.00 (1.00)
	Dark green mottled	11.38 (0.37)	0.5505 (0.21)	106.80 (25.40)	1.60 (0.24)
	Black mottled	10.30 (0.00)	0.6613 (0.00)	77.00 (0.00)	2.00 (0.00)
	Dark green	8.40 (0.00)	0.3406 (0.00)	221.00 (0.00)	2.00 (0.00)
	Green	9.80 (0.00)	0.5092 (0.00)	151.00 (0.00)	1.00 (0.00)
Seed coat pattern	Solid	9.58 (0.28)	1.2083 (0.10)	80.58 (9.13)	2.05 (0.11)
	Small eye	10.76 (0.57)	2.0119 (0.08)	54.97 (5.94)	2.23 (0.15)
	Whippoorwill	8.80 0.74)	2.0926 (0.08)	39.50 (10.94)	2.25 (0.25)
	Holstein	8.93 (0.70)	1.8918 (0.11)	69.23 (12.76)	2.54 (0.24)
	Watson	10.60 (2.11)	2.0340 (0.58)	42.67 (20.20)	2.0 (0.00)
	Golden	12.00 (0.000)	3.0102 (0.00)	72.00 (0.00)	0.0 (0.00)

4.5 Pearson's correlation among 14 morpho-agronomic phenotypic traits in cowpea genotypes

Pearson's Pairwise correlation coefficients for 14 morpho-agronomic traits measured on cowpea genotypes showing the total number of significant correlations are presented in Table 4.7. This comprised 51 significant pairwise correlation coefficients among the morpho-agronomic traits.

Table 4.7: Pearson pairwise correlation coefficients among the 14 morpho-agronomic traits

	Days to germination	Days 1st leaf stage	Chlorophyll content	Days to flowering	No of flowers/plant	Mean ped. length/plt	No of pods/peduncle	Dys 1st matd pod	No of pods/plant	Mean pod length/plt	Average seed/pod	20 Seed weight (g)	Seed yield/plt	Seed abortion rate
Days to germination	1													
Days to 1st leaf stage	0.91***	1												
Chlorophyll content	-0.21**	-0.06ns	1											
Days to flowering	0.28***	0.16*	0.30ns	1										
No of flowers/plant	-0.08ns	0.28***	-0.16ns	-0.25**	1									
Mean peduncle length	-0.31ns	-0.27ns	0.31**	0.02ns	0.23**	1								
No of pods/peduncle	-0.05ns	-0.12ns	-0.15*	-0.09ns	0.42ns	0.23**	1							
Days to 1st matd pod	0.29***	0.27**	0.30ns	0.99***	-0.22**	0.05ns	-0.09**	1						
No of pods/plant	-0.06ns	-0.20ns	-0.18*	-0.23**	0.91***	-0.03ns	0.44ns	-0.20*	1					
Mean pod length/plt	-0.23**	0.08ns	0.36***	-0.24**	0.07ns	-0.01ns	0.01*	-0.26**	0.05ns	1				
Average seed/pod	0.13ns	0.16ns	0.02ns	-0.11ns	0.03ns	0.15*	0.15**	-0.13ns	0.04ns	0.25**	1			
20 Seed weight (g)	-0.26**	0.19*	0.21***	-0.03**	-0.11**	-0.16ns	-0.16ns	0.03***	-0.15***	0.68***	0.11ns	1		
Seed yield/plant	-0.09ns	-0.21*	-0.17**	-0.19*	0.90***	0.06**	0.44ns	-0.44ns	0.95***	0.14ns	0.19**	-0.14***	1	
Seed abortion rate	-0.08**	-0.10ns	-0.13ns	-0.13**	-0.19*	0.02ns	0.00*	-0.15**	-0.20ns	0.11*	0.05ns	0.14***	-0.19*	1

* $p \leq 0.05$; ** $p \leq 0.01$; *** $p \leq 0.001$; ns = not significant

4.6 Principal Component Analysis for cowpea quantitative traits

4.6.1 Phenotypic quantitative traits

The results of the principal component analysis for cowpea morphological quantitative traits are presented in Table 4.8. The scree plot (Figure 4.1) showed that the first three principal components were the most important. The first principal component (PC1) explained 24.90 % variability within the cowpea genotypes. The second principal component (PC2) accounted for 22.42 % while the third one (PC3) accounted for 11.09 %. The first three principal components altogether explained 58.42 % of the phenotypic variability. Comparative analysis revealed that the first principal component (PC1) correlated positively with days to germination, days to first leaf stage, number of flowers per plant, mean peduncle length per plant, number of pod per peduncle, number of pod per plant, average seed per pod and seed yield per plant. The second principal component (PC2) was also positively correlated with days to germination, days to first leaf stage, days to flowering, number of pod per peduncle, days to first matured pod and average seed per pod; and negatively correlated with the remaining traits. The third principal component (PC3) positively correlated with all the traits except days to flowering, number of pod per peduncle, days to first matured pod and seed abortion rate. PC1, PC2 and PC3 recorded a mean values of 0.0361, 0.0229 and 0.0137 respectively. PCA values above their respective means were significant. A score plot of PC1 against PC2 revealed one cluster with several outliers of the genotypes of both wild and cultivated species. (Figure 4.2).

Table 4.8: Eigenvectors of first three principal components for morphological quantitative traits

	Eigenvectors		
Trait	PC1	PC2	PC3
Days to germination	0.1421	0.3713	0.4517
Days to first leaf stage	0.0540	0.3470	0.5296
Chlorophyll content	-0.2057	-0.1871	0.0882
Days to flowering	-0.0668	0.4651	-0.1402
Number of flowers/plant	0.4884	-0.1612	0.0209
Mean peduncle length	0.1496	-0.1176	0.0821
Number of pods/peduncle	0.0289	0.1080	-0.1877
Days to first pod maturation	0.0516	0.4632	-0.1450
Number of pods per plant	0.4905	-0.1580	0.0177
Mean pod length per plant	-0.2164	-0.2587	0.4191
Average seed per pod	0.0442	0.0488	0.4052
50 seed weight/grams	-0.3018	-0.2724	0.2805
Seed yield per plant	0.4939	-0.1309	0.0664
Seed abortion rate	-0.2031	-0.1968	-0.0365
Mean	0.0361	0.0229	0.0137
Eigenvalue	3.48657	3.13837	1.55322
Proportion (%)	24.90	22.42	11.09
%Cumulative	24.90	47.32	58.42

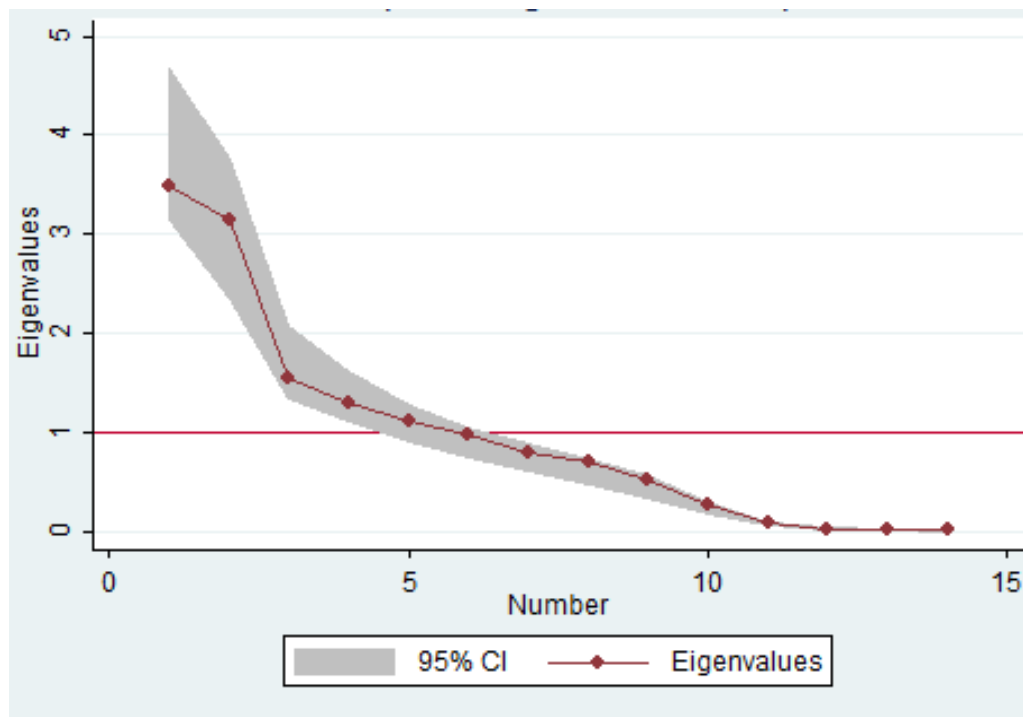


Figure 4.1: Scree plot of eigenvalues of cowpea accessions for morphological quantitative traits. CI = confidence interval

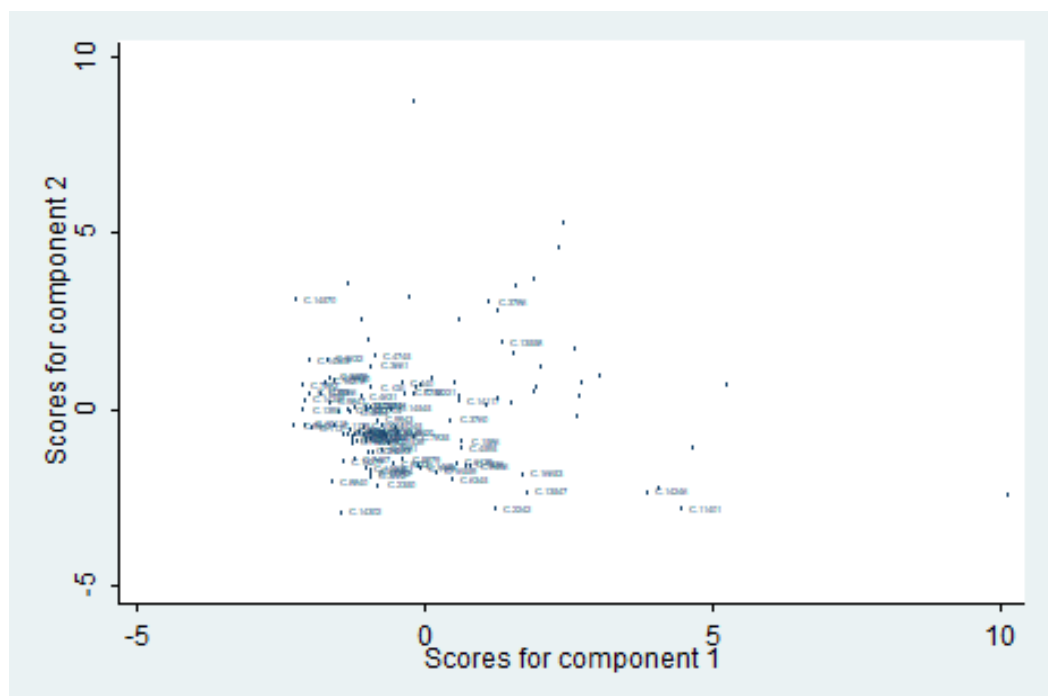


Figure 4.2: Score plot of PC1 and PC2 of cowpea accessions for morphological quantitative traits.

4.6.2 Amino Acids

Results for the principal component analysis for amino acids is presented in Table 4.9. The scree plot (Figure 4.3) showed that the first four principal components were very informative. The first principal component (PC1) explained 20.49 % variability within the cowpea germplasm while the second, third and fourth principal components accounted for 14.47 %, 9.54 % and 7.65 % respectively. The first four principal components altogether explained 52.16 % of the phenotypic variability. Comparatively, it was observed that the first principal component (PC1) correlated positively with all the amino acids and negatively with DL-Beta_phenyl-Alanine and L-Tryptophan. The second principal component correlated positively with B-Threonine, DL-Alpha-Alanine, DL-Beta_phenyl-Alanine, D-Proline, L-Asparagine, L-Histidine, L-Tryptophan, L-Tyrosine and L-Valine, and negatively correlated with the remaining traits. The third principal component also correlated positively with DL-Alpha-Alanine, Glutamine, L-Asparagine, L-Histidine, L-Lysine, L-Tryptophan, L-Tyrosine and L-Valine, and negatively with the remaining amino acids. The fourth principal component also correlated positively with DL-Alpha-Alanine, Glycine, Iso-Leucine, L-Aspartic Acid, L-Histidine, L-Methionine, L-Tryptophan, L-Tyrosine, L-Valine and Trans-4-Hydroxyl-Proline, but negatively with the remaining traits. PC1, PC2, PC3 and PC4 recorded a mean values of 0.1936, 0.1113, 0.0571 and 0.0146 respectively. A score plot of PC1 against PC2 also revealed one cluster with several outliers of the genotypes of both wild and cultivated types. (Figure 4.4).

Table 4.9: Principal Component Analysis of cowpea genotypes using Amino acids

	Eigenvectors			
Trait	PC1	PC2	PC3	PC4
B-Threonine	0.2950	0.0901	-0.1141	-0.3429
DL-Alpha-Alanine	0.0266	0.3464	0.1274	0.0440
DL-Beta_phenyl-Alanine	-0.0204	0.4435	-0.0315	-0.0798
D-Proline	0.2270	0.2193	-0.2040	-0.4308
Glutamine	0.1760	-0.0971	0.6379	-0.1788
Glycine	0.2756	-0.0241	-0.1277	0.0638
Iso-Leucine	0.4093	-0.1093	-0.1282	0.2417
L-Asparagine	0.0509	0.4235	0.0573	-0.1415
L-Aspartic Acid	0.0940	-0.0356	-0.1162	0.0051
L-Histidine	0.0477	0.5175	0.0648	0.0322
L-Lysine	0.1852	-0.1201	0.6178	-0.1593
L-Methionine	0.3049	-0.0243	-0.0268	0.0329
L-Serine	0.3407	-0.0264	-0.1216	-0.0922
L-Threonine	0.3172	-0.0038	-0.0253	-0.0624
L-Tryptophan	-0.0034	0.3115	0.0824	0.3987
L-Tyrosine	0.1173	0.1092	0.1444	0.5491
L-Valine	0.2519	0.1178	0.1492	0.1827
Trans-4-Hydroxyl-Proline	0.3886	-0.1351	-0.1408	0.2005
Mean	0.1936	0.1113	0.0571	0.0146
Eigenvalue	3.68886	2.60436	1.71786	1.37696
Proportion (%)	20.49	14.47	0.0954	0.0765
%Cumulative	20.49	34.96	0.4451	0.5216

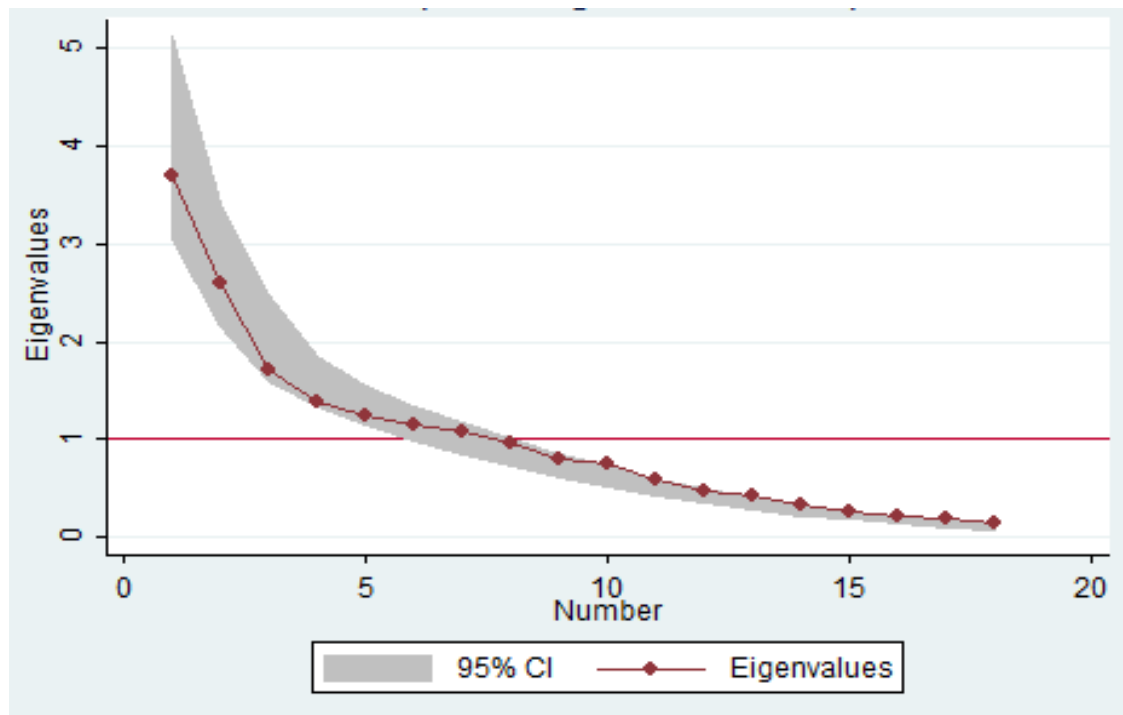


Figure 4.3: Scree plot of eigenvalues of cowpea accessions for amino acids. CI = confidence interval

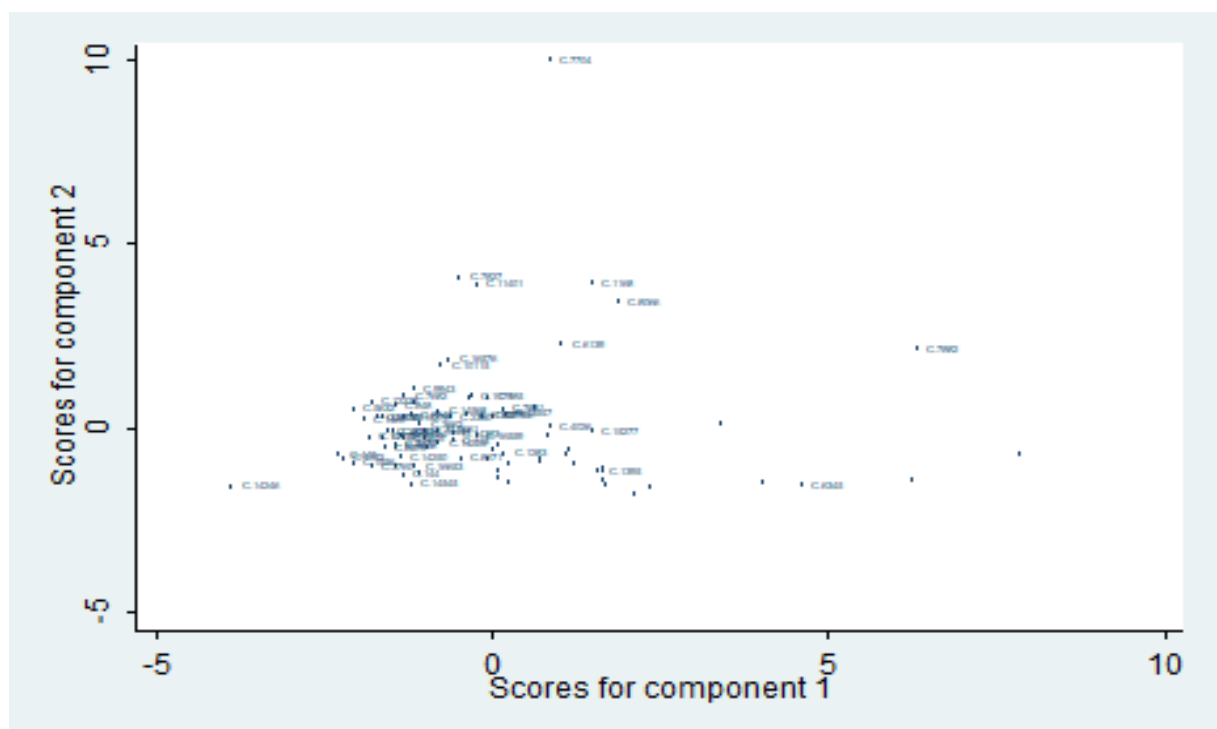


Figure 4.4: Score plot of PC1 and PC2 of cowpea accessions for amino acids.

4.7 Genetic Diversity in cowpea population

4.7.1 Nei's Genetic Diversity

Nei's genetic variation for cowpea population at 46 SNPs loci is shown in Table 4.10. Forty-three (43) polymorphic loci, representing 93.48% were observed. Genetic diversity in the overall cowpea population varied between 0.0110 at gene locus *18_107* and 0.5000 at gene loci *13281_572* and *1426_521* with mean diversity of 0.3001 ± 0.1750 . Diversity in the wild relatives ranged between 0.0126 at gene locus *7205_420* and 0.4998 at gene locus *1426_521* with mean diversity of 0.2016 ± 0.1787 . Thirty-nine (39) polymorphic loci, representing 84.78% were observed. Nei's genetic diversity in the cultivated species ranged from 0.0215 at gene locus *18_107* to 0.4998 at gene locus *1426_521* with mean diversity of 0.2744 ± 0.1665 . Forty-three (43) polymorphic loci, representing 93.48% were observed.

Table 4.10: Nei's Genetic Diversity Indices for cowpea population at 46 SNPs loci.

Locus	Nei's Diversity		
	Wild Relatives	Cultivated Types	Overall
<i>1107_518</i>	0.0582	0.0823	0.0740
<i>18_107</i>	0.0000	0.0215	0.0110
<i>14164_187</i>	0.0256	0.2405	0.1511
<i>4980_497</i>	0.4849	0.3723	0.4420
<i>12929_463</i>	0.0000	0.3376	0.2449
<i>9815_2051</i>	0.0877	0.4745	0.4481
<i>8777_825</i>	0.2000	0.1919	0.1954
<i>642_527</i>	0.3750	0.1919	0.3222
<i>8306_119</i>	0.0220	0.4930	0.3537
<i>6804_755</i>	0.3750	0.1007	0.4303
<i>16494_177</i>	0.0454	0.2248	0.1442
<i>5074_629</i>	0.3478	0.4431	0.4998
<i>14542_452</i>	0.1487	0.4055	0.3162
<i>3787_812</i>	0.3675	0.4149	0.3944
<i>1181_710</i>	0.0220	0.2963	0.1765
<i>5553_147</i>	0.1284	0.4818	0.3634
<i>13281_572</i>	0.2700	0.2778	0.5000
<i>13772_107</i>	0.3501	0.3122	0.4981
<i>2535_666</i>	0.0000	0.0425	0.0282
<i>5084_519</i>	0.3803	0.2873	0.3217
<i>11367_1228</i>	0.4200	0.4639	0.4505
<i>15779_1173</i>	0.2558	0.2988	0.4995
<i>571_592</i>	0.2340	0.4313	0.3510
<i>7205_420</i>	0.0126	0.0631	0.0401
<i>8770_1480</i>	0.3153	0.4121	0.4985

Table 4.10 Contn'd

Locus	Nei's Diversity		
	Wild Relatives	Cultivated Types	Overall
<i>1426_521</i>	0.4998	0.4998	0.5000
<i>1545_161</i>	0.0000	0.0000	0.0000
<i>13947_415</i>	0.1562	0.2753	0.2220
<i>9521_957</i>	0.0351	0.3013	0.2137
<i>15451_698</i>	0.2423	0.4902	0.4186
<i>6796_936</i>	0.0000	0.0000	0.0000
<i>25_592</i>	0.4974	0.2849	0.4268
<i>5240_1403</i>	0.0000	0.0000	0.0000
<i>12882_709</i>	0.0000	0.1653	0.1446
<i>5069_298</i>	0.1782	0.1028	0.1413
<i>14929_258</i>	0.4998	0.4359	0.4875
<i>17149_508</i>	0.4048	0.4882	0.4977
<i>3841_598</i>	0.2294	0.1017	0.4944
<i>5149_220</i>	0.4082	0.3187	0.4696
<i>967_118</i>	0.0588	0.1435	0.1087
<i>10269_488</i>	0.4951	0.4998	0.4982
<i>15152_845</i>	0.0345	0.0832	0.0649
<i>12526_795</i>	0.0523	0.4980	0.4039
<i>6904_1061</i>	0.3807	0.1113	0.2132
<i>1204_901</i>	0.4664	0.0631	0.2654
<i>2077_348</i>	0.1244	0.3958	0.4804
Mean	0.2106	0.2744	0.3001
Standard deviation	0.1787	0.1665	0.1750
No. of polymorphic loci	39	43	43
% of polymorphic loci	84.78%	93.48%	93.48%

4.7.2 Likelihood Ratio (G-square) test for Hardy Weinberg equilibrium

Table 4.11 shows the likelihood ratio test for Hardy Weinberg equilibrium for cowpea genotypes at 43 SNPs loci in sub-divided population. The likelihood ratio varied from 22.1160 at gene locus 2535_666 to 246.1419 at gene locus 2077_384 across the overall population. G-square value in the wild relatives ranged from 6.7959 at gene locus 1107_518 to 125.7508 at gene locus 4980_497 while that of the cultivated types was between 0.0146 and 128.6293 at gene locus 8306_119. A total of 43 polymorphic SNPs loci were observed.

Table 4.11: Likelihood Ratio test (G-square test) for Hardy Weinberg equilibrium for cowpea genotypes at 46 loci

Locus	G-square		Overall
	Wild Relatives	Cultivated Types	
1107_518	6.7959	34.0625	37.6083
18_107	***	12.4190	13.7667
14164_187	12.0609	76.2707	97.7412
4980_497	125.7508	105.0534	235.5800
12929_463	***	97.8406	115.8456
9815_2051	17.9151	125.1510	209.7313
8777_825	34.5839	64.5105	94.7563
642_527	7.3335	64.5105	91.5384
8306_119	12.3748	128.6295	198.1638
6804_755s	36.2434	40.1215	151.1975
16494_177	20.1487	72.5468	99.2469
5074_629	35.0163	99.4570	157.0736
14542_452	18.3454	110.5645	131.2866
3787_812	66.2243	87.2954	152.9891
1181_710	12.3748	89.8797	118.8773
5553_147	44.7105	121.1219	194.4315
13281_572	77.7862	82.1186	246.3727
13772_107	72.5951	92.4017	223.7701
2535_666	***	20.4216	22.1160
5084_519	54.4250	86.0313	140.6741
11367_1228	45.5793	123.1306	163.9716
15779_1173	61.7994	89.4784	236.5329
571_592	44.6943	111.8575	158.1338
7205_420	0.0000	27.5342	25.3887
8770_1480	35.4773	113.0644	179.0865

*** = Monomorphic locus.

Table 4.11 Contr'n'd

Locus	G-square		
	Wild Relatives	Cultivated Types	Overall
<i>1426_521</i>	55.1243	125.7305	174.1083
<i>1545_161</i>	***	***	***
<i>13947_415</i>	32.3490	52.0416	85.6909
<i>9521_957</i>	11.4191	70.7712	91.0613
<i>15451_698</i>	64.4880	128.1106	209.4103
<i>6796_936</i>	***	***	***
<i>25_592</i>	49.4177	86.4112	148.9489
<i>5240_1403</i>	***	***	***
<i>12882_709</i>	***	27.8768	29.1107
<i>5069_298</i>	59.7536	39.9005	99.8910
<i>14929_258</i>	70.3653	0.0146	30.7843
<i>17149_508</i>	43.6837	113.9898	166.0149
<i>3841_598</i>	45.1877	40.0116	218.0125
<i>5149_220</i>	43.2625	83.1794	160.2109
<i>967_118</i>	19.0757	50.2332	69.8468
<i>10269_488</i>	107.0185	128.5038	231.9763
<i>15152_845</i>	11.4548	33.9758	44.8291
<i>12526_795</i>	15.2031	111.5442	192.8996
<i>6904_1061</i>	49.9279	33.2091	90.5438
<i>1204_901</i>	55.1601	27.5342	108.2992
<i>2077_348</i>	45.1317	108.6477	246.1419

***= Monomorphic locus.

4.7.3 F-Statistics and Gene flow in the cowpea genotypes

Table 4.12 shows the F-Statistics and Gene flow of 43 loci of cowpea genotypes.

The level of observed heterozygosity ranged from 0.0111 at gene locus *9815_2051* to 0.6901 at gene locus *14929_258*. The frequency of cross pollination (C) ranged from 0.0177 at gene loci *3787_812* to 2.6284 at gene locus *14929_258*. The Wrights fixation index for inbreeding (F_{IS}) ranged from -0.4488 at gene locus *14929_258* to 1.0000 at gene loci *18_107*, *14164_187*, *498_497*, *12929_463*, *8306_119*, *16494_177*, *1181_710*, *5553_147*, *13281_572*, *2535_666*, *5084_519*, *15451_698*, *12882_709*, *5069_298*, *967_118*, *15152_845* and *2077_348*. The coefficient of inbreeding at different levels within populations (F_{IT}) ranged from -0.3949 at gene locus *14929_258* to 1.0000 at gene loci *18_107* and *14164_187*. A mean of 0.0242, 0.0805, 0.9143 and 0.8935 were recorded for observed heterozygosity, frequency of cross pollination, F_{IS} and F_{IT} respectively. The Degree of genetic differentiation (F_{ST}) ranged from 0.0001 at gene locus *8777_825* to 0.6668 at gene locus *3841_598* with a mean of 0.1952. Gene flow (N_m) ranged from 0.1249 at gene locus *3841_598* to 1000.00 at gene locus *8777_825* with a mean of 1.0309.

Table 4.12: F-Statistics and Gene flow of 46 SNPs loci of cowpea genotypes

Locus	Obs Het	F_{IS}	F_{IT}	F_{ST}	N_m	C
1107_518	0.0070	0.8578	0.8578	0.0012	207.5288	0.0766
18_107	0.0000	1.0000	1.0000	0.0055	45.5000	0.0000
14164_187	0.0000	1.0000	1.0000	0.0570	4.1381	0.0000
4980_497	0.0000	1.0000	1.0000	0.0310	7.8019	0.0000
12929_463	0.0000	1.0000	1.0000	0.1205	1.8250	0.0000
9815_2051	0.0111	0.9591	0.9740	0.3637	0.4373	0.0209
8777_825	0.0122	0.9281	0.9281	0.0001	1000.0000	0.0373
642_527	0.0183	0.7795	0.8724	0.4213	0.3434	0.1239
8306_119	0.0000	1.0000	1.0000	0.2640	0.6971	0.0000
6804_755	0.0267	0.8499	0.9257	0.5051	0.2449	0.0811
16494_177	0.0000	1.0000	1.0000	0.0398	6.0373	0.0000
5074_629	0.0347	0.8981	0.9185	0.1998	1.0009	0.0537
14542_452	0.0187	0.9204	0.9258	0.0684	3.4045	0.0414
3787_812	0.0135	0.9652	0.9653	0.0033	74.9050	0.0177
1181_710	0.0000	1.0000	1.0000	0.0830	2.7616	0.0000
5553_147	0.0000	1.0000	1.0000	0.1558	1.3550	0.0000
13281_572	0.0000	1.0000	1.0000	0.4522	0.3029	0.0000
13772_107	0.0113	0.9640	0.9762	0.3371	0.4917	0.0183
2535_666	0.0000	1.0000	1.0000	0.0110	22.5000	0.0000
5084_519	0.0000	1.0000	1.0000	0.0098	25.1849	0.0000
11367_1228	0.0140	0.9547	0.9550	0.0048	51.3611	0.0232
15779_1173	0.0108	0.9612	0.9785	0.4449	0.3119	0.0198
571_592	0.0172	0.9469	0.9494	0.0461	5.1724	0.0273
7205_420	0.0058	0.8327	0.8342	0.0090	27.3918	0.0913

Nm = Gene flow; C= Frequency of cross pollination.

Table 4.12 Contn'd

Locus	Obs Het	F_{IS}	F_{IT}	F_{ST}	N_m	C
8770_1480	0.0139	0.9461	0.9604	0.2661	0.6893	0.0277
1426_521	0.0205	0.9464	0.9464	0.0004	622.2742	0.0275
1545_161	0.0000	****	****	0.0000	****	****
13947_415	0.0347	0.8416	0.8439	0.0144	17.0808	0.0860
9521_957	0.0135	0.9354	0.9403	0.0765	3.0178	0.0334
15451_698	0.0000	1.0000	1.0000	0.1024	2.1913	0.0000
6796_936	0.0000	****	****	0.0000	****	****
25_592	0.0268	0.9087	0.9219	0.1446	1.4788	0.0478
5240_1403	0.0000	****	****	0.0000	****	****
12882_709	0.0000	1.0000	1.0000	0.0476	5.0000	0.0000
5069_298	0.0000	1.0000	1.0000	0.0070	35.3940	0.0000
14929_258	0.6901	-0.4488	-0.3949	0.0372	6.4712	2.6284
17149_508	0.0274	0.9266	0.9331	0.0889	2.5634	0.0381
3841_598	0.0167	0.8959	0.9653	0.6668	0.1249	0.0549
5149_220	0.0211	0.9291	0.9480	0.2676	0.6842	0.0368
967_118	0.0000	1.0000	1.0000	0.0110	22.4312	0.0000
10269_488	0.0109	0.9779	0.9779	0.0015	67.0941	0.0112
15152_845	0.0000	1.0000	1.0000	0.0057	43.7292	0.0000
12526_795	0.0160	0.9418	0.9602	0.3167	0.5394	0.0300
6904_1061	0.0074	0.9781	0.9797	0.0729	3.1801	0.0111
1204_901	0.0137	0.9301	0.9425	0.1773	1.1603	0.0362
2077_348	0.0000	1.0000	1.0000	0.4569	0.2971	0.0000
Mean	0.0242	0.8935	0.9143	0.1952	1.0309	0.0805
Standard deviation	0.1009					

Nm = Gene flow; C = Frequency of cross pollination; *** = Monomorphic locus.

4.8 Analysis of genetic distance

Dendrogram of UPGMA cluster showing genetic relationship and distance among 46 SNPs loci is shown in Figure 5.

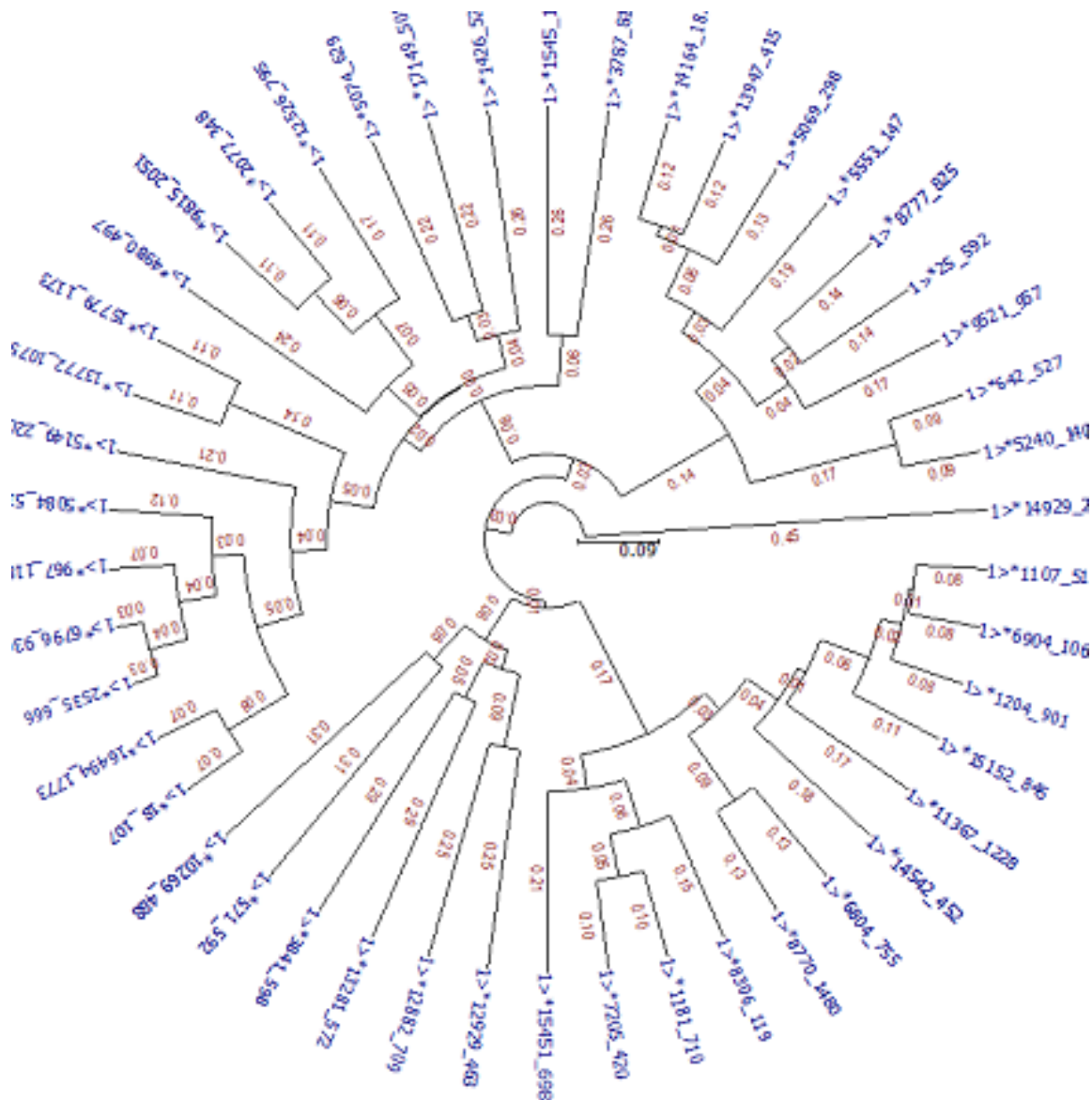


Figure 4.5: Dendrogram of UPGMA cluster showing genetic relationship and distance among 46 SNPs loci

Dendrogram constructed from a combination of morphological and SNPs markers' data showing genetic relationship and distance among 46 SNPs loci is presented in Figure 4.6. The measure of dissimilarity ranged between 0.00 and 0.26. Two clusters were formed. Forty-six (46) cowpea genotypes constituted the minor cluster while the remaining genotypes (141) constituted the major cluster.

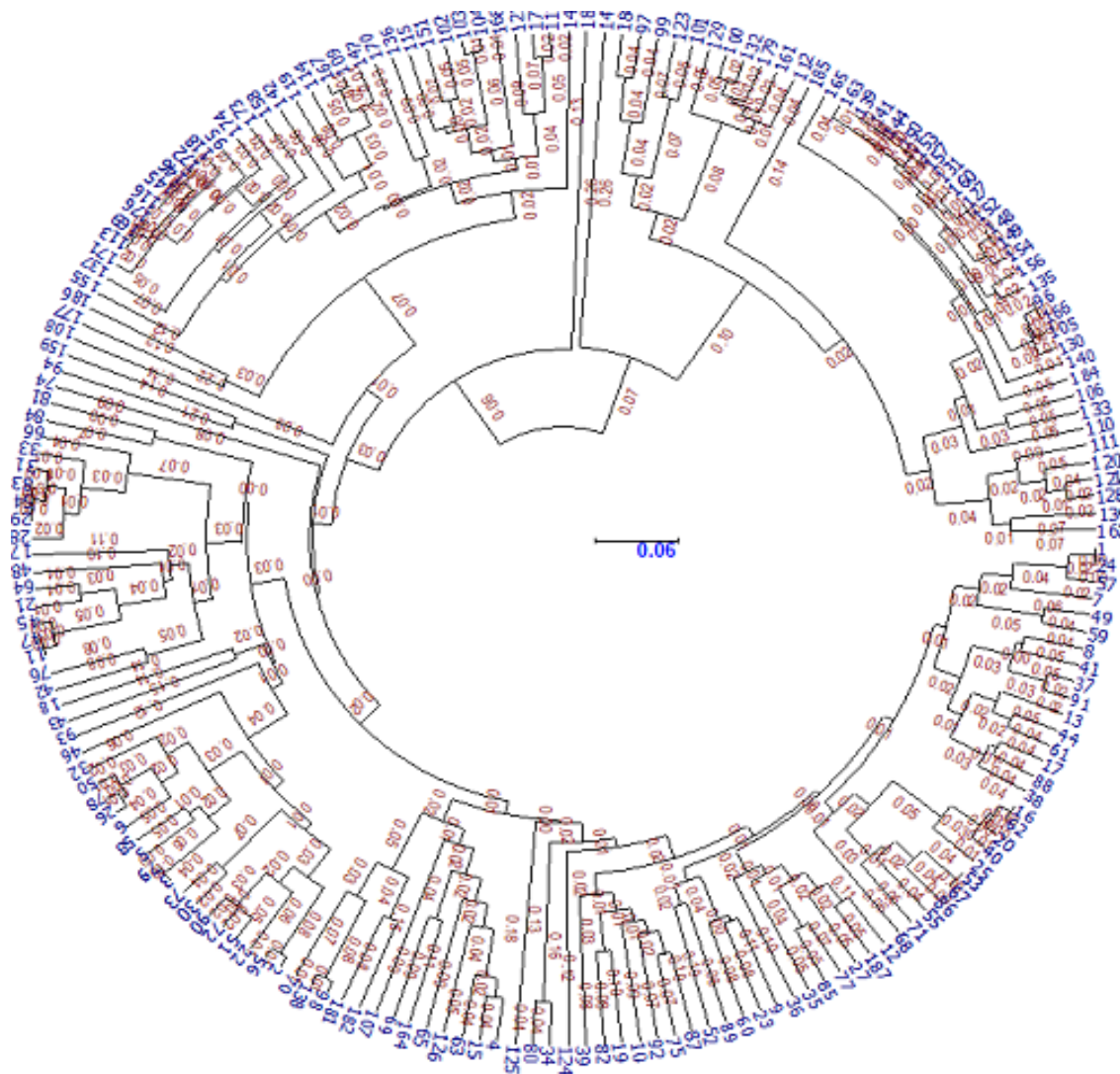


Figure 4.6: Dendrogram of UPGMA cluster showing genetic relationship and distance among 187 cowpea accessions.

4.9 Population structure Analysis

4.9.1: The optimum K value and Delta K (ΔK) analysis

The optimum K value obtained based on Wilcoxon approach and the ΔK method is presented in Figure 4.7. The optimum K value obtained was K=2 which correspond with the optimum value while Delta K (ΔK) method gave a maximum of 393.513. The graph represents two substructure plots generated by means of *CLUMP* software using *DISTRUCT* presented in Figure 4.8.

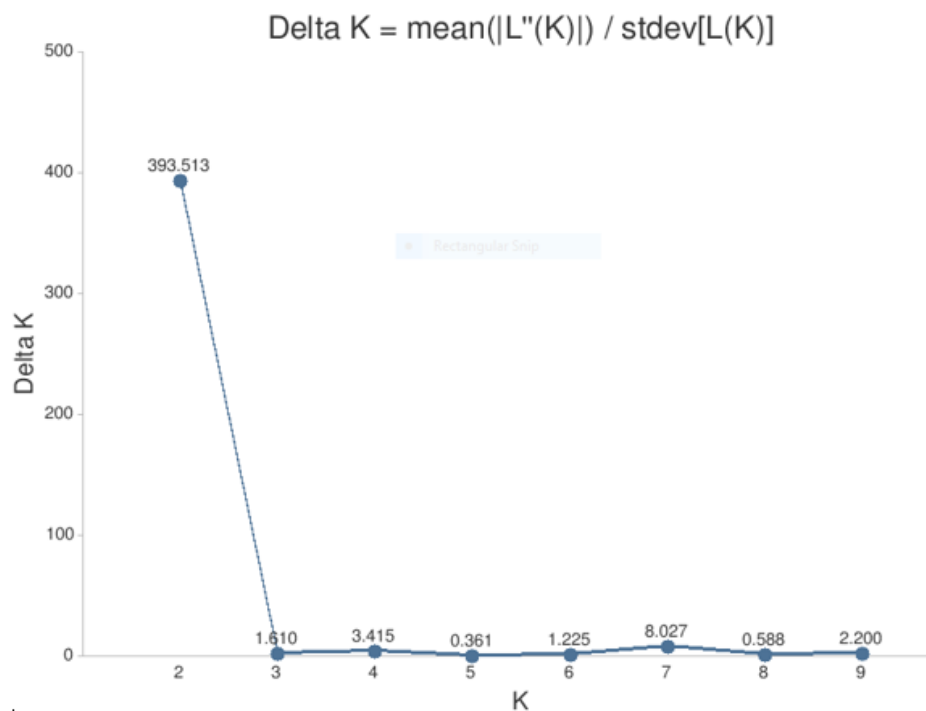
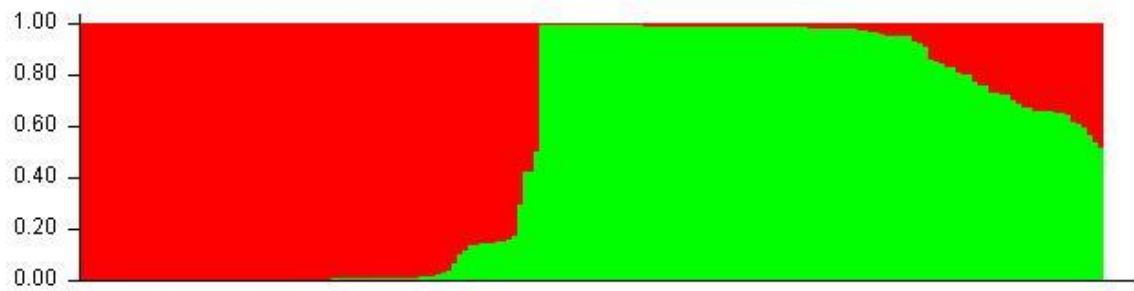


Figure 4.7: Graph of ΔK analysis showing the maximum K value.

Figure 4.8: *DISTRUCT* plot of two cowpea population groups



Population differentiation as a result of changes in allelic frequencies caused by non-random mating, selection, genetic drift, gene flow and localised adaptation. Cluster 1= Red; Cluster 2= Green.

4.9.2 Clustering the cowpea population

Figure 4.9 shows a Triangular *DISTRUCT* plot of cowpea accessions constructed from genotype data. The diagram revealed two clustered populations. This was in relation to the inferred ancestry generated from the population.

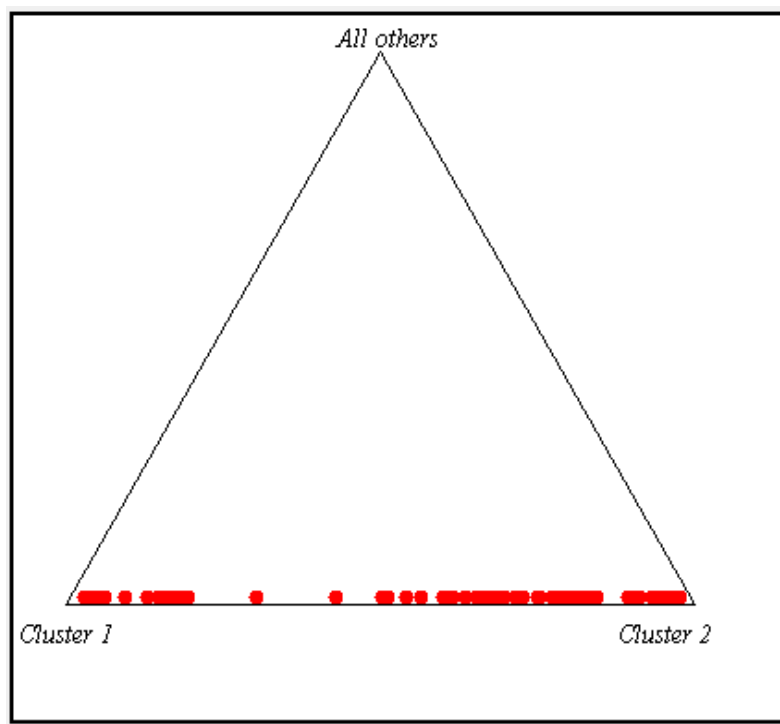


Figure 4.9: Triangular *DISTRUCT* plot showing number of clusters in the cowpea population.

4.9.3 Membership of accessions in the inferred ancestry clusters

Table 4.13 gives a summary of proportion of membership of accessions in each of the inferred clusters. Proportion of membership for cluster one was 0.551 (55.08%) and that for cluster two was 0.449 (44.92%). Probability of membership for Q1 ranged from 0.511 (W.89) to 0.996 (C.98) and that for Q2 ranged from 0.574 (PARENT) to 0.997 (W.84).

Table 4.13: Proportion of membership of accessions in the inferred ancestry cluster

Inferred clusters	Frequency of membership	Probability range
Cluster 1 (Q1)	103 (0.551)	0.511 – 0.996
Cluster 2 (Q2)	84 (0.449)	0.574 – 0.997

4.9.4 Mean F_{ST} values for the two clusters

The mean value for genetic differentiation (F_{ST}) for the two clusters are presented in Table 4.14. The mean F_{ST} values for cluster one was 0.064 and that for cluster 2 was 0.048. Distribution of genetic differentiation (F_{ST}) for the Q1 and Q2 are represented in Figures 10a and 10b respectively.

Table 4.14: Mean F_{ST} value for the inferred ancestry cluster

Inferred ancestry clusters	Proportion of membership
1	0.064
2	0.048

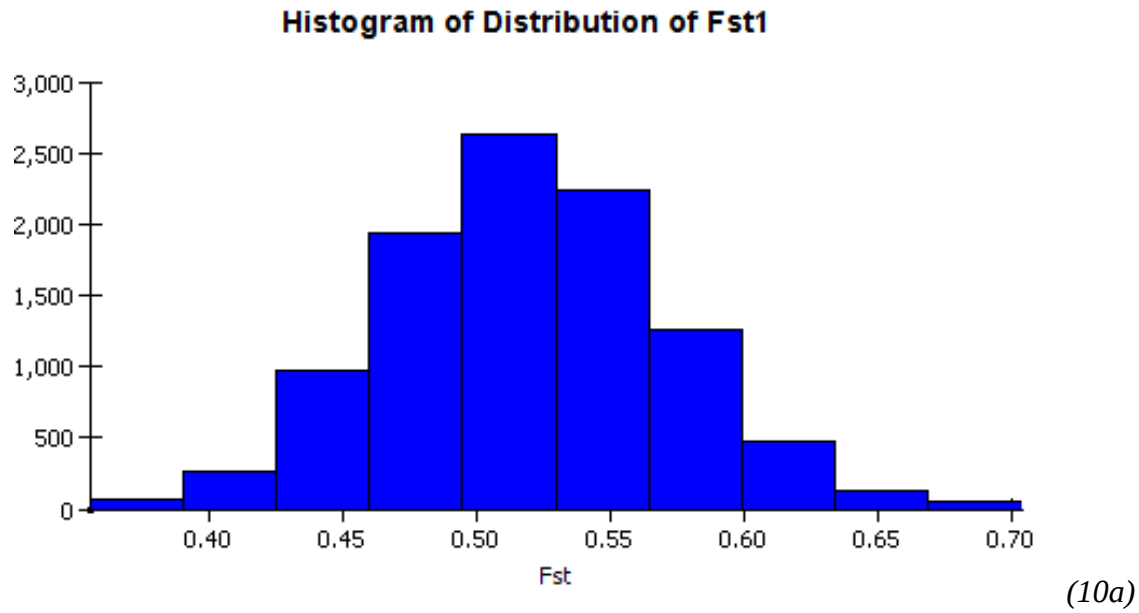


Figure 4.10a: Histogram distribution of degree of genetic differentiation (F_{ST}) of cowpea population in sub-population one

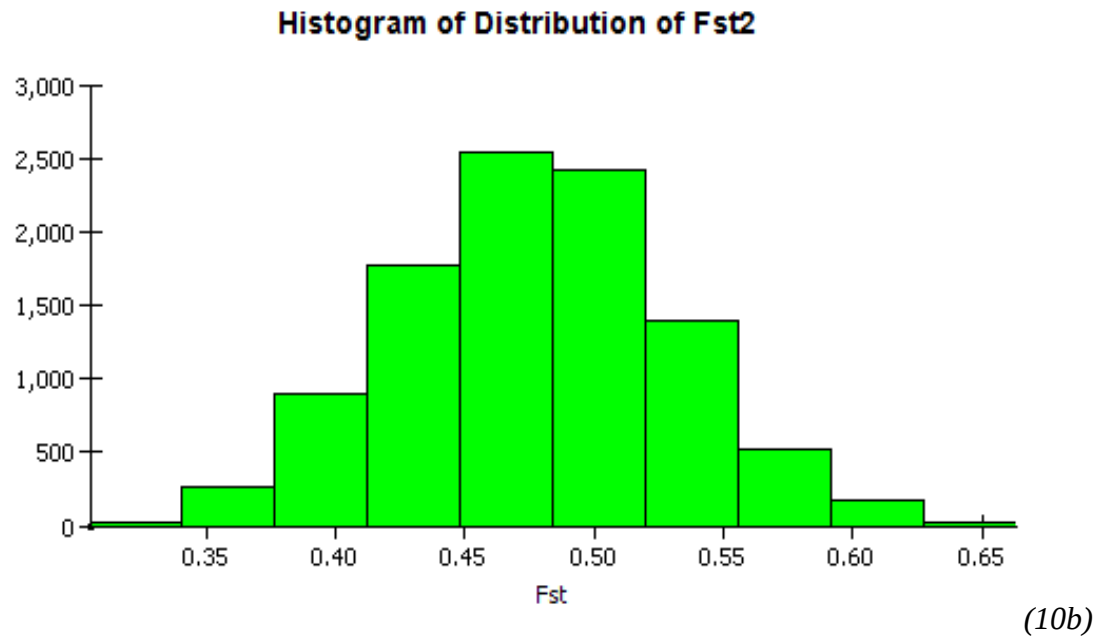


Figure 4.10b: Histogram distribution of degree of genetic differentiation (F_{ST}) of cowpea population in sub-population two

4.9.5 Net Nucleotide Distance (Divergence in allele frequency) among populations, calculated from point estimates of P.

Results for net nucleotide distance (Divergence in allele frequency) among the two clusters are presented in Table 4.15. The distance observed between the two clusters was 0.2093.

Table 4.15: Net Nucleotide distance (Divergence in allele frequency), calculated from point estimates of P

	Cluster 1	Cluster 2
Cluster 1	-----	0.2093
Cluster 2	0.2093	-----

4.10 Linkage disequilibrium (LD)

4.10.1 Pair-wise linkage disequilibrium (LD)

Estimate of Intra chromosomal linkage disequilibrium (LD) for SNPs loci at the entire genome in the cowpea accessions are shown in Table 4.16. At the threshold level of $r^2 \geq 0.1$, 12.64% (120/949) of SNPs loci showed significant LD ($p \leq 0.05$). At a threshold level of $r^2 \geq 0.05$, 15.38% (146/949) of the SNPs loci showed significant LD ($p \leq 0.05$).

Table 4.16: Estimate of Intra chromosomal linkage disequilibrium for SNPs loci on chromosome one of the cowpea accessions.

Parameters	Threshold level	
	$r^2 \geq 0.1$	$r^2 \geq 0.05$
Sample size	187	187
Intra-chromosomal LD% (LD / non LD)	12.64% (120/949)	15.38% (146/949)

4.10.2 Intra chromosomal linkage disequilibrium (LD) blocks

Size of intra chromosomal linkage disequilibrium block estimate for SNPs loci in the entire genome of the cowpea accessions at significant level of $r^2 \geq 0.1$ and $p < 0.05$ is shown in Table 4.17. The largest LD block was 25.0 bp between markers *6904_1061* and *9815_2051* at correlation co-efficient (measure of variability between the two loci r^2) of 0.10 and the homogenized difference between the coupling and repulsion gamete frequencies at two the two marker loci (D') of 0.89.

Table 4.17: Size of intra-chromosomal linkage disequilibrium blocks in cowpea loci at $r^2 \geq 0.1$

Locus 1	Locus 2	Distance (bp)	r^2	D'	Chromosome
6804_755	4980_497	12.0	0.26	0.62	1
6804_755	9815_2051	4.0	0.25	0.89	1
5074_629	8777_825	7.0	0.11	0.36	1
16494_1773	9815_2051	8.0	0.11	0.41	1
3787_812	6804_755	4.0	0.13	0.52	1
16494_1773	14542_452	0.0	0.27	1.0	1
1181_710	8306_119	7.0	0.22	0.78	1
11367_1228	9815_2051	11.0	0.31	0.77	1
11367_1228	6804_755	7.0	0.30	0.67	1
2535_666	14164_1877	19.0	0.13	1.0	1
2535_666	16494_1773	3.0	0.13	1.0	1
8770_1480	4980_497	22.0	0.27	0.58	1
8770_1480	8306_119	12.0	0.15	0.64	1
8770_1480	6804_755	10.0	0.26	0.73	1
8770_1480	1181_710	5.0	0.13	1.0	1
9521_957	8777_825	16.0	0.22	0.54	1
9521_957	5074_629	9.0	0.15	0.44	1
15451_698	8306_119	15.0	0.14	0.43	1
15451_698	14542_452	9.0	0.11	0.48	1
15451_698	1181_710	8.0	0.16	0.76	1
13947_415	15451_698	0.0	0.22	0.91	1
25_592	9815_2051	20.0	0.11	0.61	1
25_592	8777_825	19.0	0.14	0.67	1
14929_258	8777_825	22.0	0.11	0.88	1
14929_258	15779_1173	12.0	0.12	0.46	1
12526_795	14164_1877	32.0	0.10	0.69	1
12526_795	6804_755	20.0	0.15	0.81	1
12526_795	5074_629	16.0	0.17	0.55	1
12526_795	11367_1228	13.0	0.13	0.55	1
12526_795	14929_258	1.0	0.11	0.41	1
15152_845	3787_812	16.0	0.10	0.56	1
6904_1061	9815_2051	25.0	0.10	0.89	1
6904_1061	6804_755	21.0	0.17	0.73	1
1204_901	5084_519	14.0	0.17	0.78	1
1204_901	25_592	5.0	0.10	0.49	1
1204_901	5069_298	2.0	0.12	0.46	1
2077_348	6804_755	21.0	0.30	0.82	1
2077_348	5074_629	17.0	0.12	0.36	1
2077_348	11367_1228	14.0	0.37	0.71	1
2077_348	12526_795	1.0	0.14	0.48	1
2077_348	6904_1061	0.0	0.13	0.82	1
1204_901	8777_825	24.0	0.10	0.32	1
6904_1061	1204_901	0.0	0.16	0.44	1

4.10.3 Linkage disequilibrium decay

Genome-wide linkage disequilibrium decay was evaluated by plotting a graph of r^2 values of LD against genetic distance which revealed partial decay (Figure 4.11). The level of dissimilarity measure ranged between 0.0 and 0.75 and map distance of 0.0 and 38.75 cM.

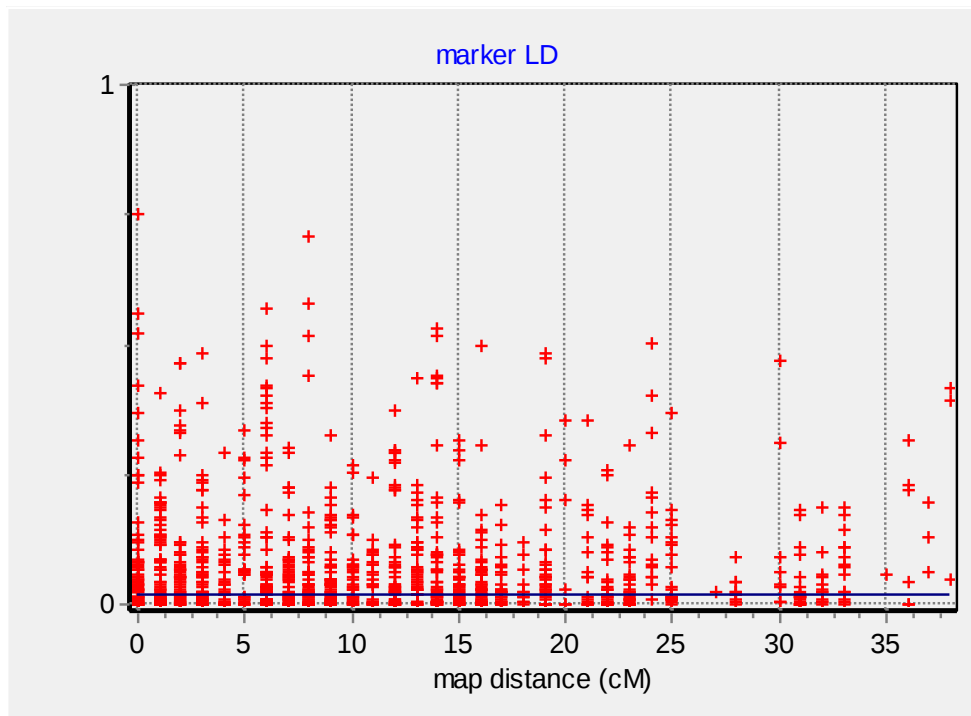


Figure 4.11: Scatterplot of r^2 values of linkage disequilibrium against population genetic distance.

4.11 Marker-trait association (MTA) Analysis

Genome-wide association of SNPs markers associated with 14 phenotypic quantitative traits in cowpea accessions grouped under vegetative traits; reproductive traits; yield component and seed quality traits are shown in Tables 4.18, 4.19 and 4.20 respectively.

4.11.1 Vegetative traits

Five (5) out of the total number of 46 SNPs markers were found to be associated with three (3) phenotypic vegetative characters: days to germination, Days to first leaf stage and Days to first leaf stage. Five marker-trait associations were identified. GLM revealed three marker-trait associations while MLM gave four associations.

Table 4.18: SNPs markers associated with vegetative traits in cowpea accessions

Trait	SNPs marker/ Locus name	R ² values of GLM results	R ² values of MLM results	Position on chromosome (cM)	Chromo- some
Days to germination	13281_572	-	0.03*	23	1
Days to first leaf stage	25_592	0.05*	0.05**	33	1
	17149_508	0.04*	0.05*	36	1
Chlorophyll content	642_527	0.06*	-	14	1
	967_118	-	0.03*	36	1

GLM = general linear model; MLM = mixed linear model; R² = phenotypic variation expressed by the SNP; ***P ≤ 0.001; **P ≤ 0.01; *P ≤ 0.05.

4.11.2 Reproductive traits

Thirty-one (31) out of the 43 SNPs markers were found to be associated with seven (7) reproductive traits. Seventy-nine (79) significant marker-trait associations were identified (Table 4.19). MLM revealed 34 marker-trait associations while GLM gave 62 associations.

Table 4.19: SNPs markers associated with reproductive traits in cowpea accessions

Trait	SNPs marker/ Locus name	R ² values of GLM results	R ² values of MLM results	Position on chromosome (cM)	Chromo -some
Days to flowering	9815_2051	-	0.06*	13	1
	642_527	0.11**	0.15**	14	1
	16494_1773	0.04*	0.05*	21	1
	3787_812	0.06**	-	21	1
	13772_1075	-	0.07*	23	1
	13281_572	0.03*	-	23	1
	11367_1228	0.11***	0.10**	24	1
	571_592	0.09**	0.09**	24	1
	8770_1480	0.08**	0.10**	27	1
	1426_521	-	0.08*	28	1
	14929_258	0.06*	-	36	1
	5149_220	0.11***	0.10**	36	1
	3841_598	-	0.08**	36	1
	10269_488	0.08**	0.09**	37	1
	1204_901	0.09**	0.08*	38	1
Number of flowers per plant	12929_463	0.11**	0.12***	5	1
	4980_497	-	0.06**	5	1
	14164_1877	0.04*	-	5	1
	9815_2051	0.07*	0.06*	13	1
	642_527	0.08*	0.09*	14	1
	8777_825	0.06*	0.37***	14	1
	16494_1773	0.04*	-	21	1
	5553_147	-	0.05*	22	1
	13772_1075	0.09**	0.07**	23	1
	15779_1173	0.07**	-	24	1
	571_592	0.08*	0.06*	24	1
	2535_666	0.05*	0.05*	24	1
	5084_519	0.05*	-	24	1
	8770_1480	0.31*	0.35**	27	1
	1426_521	0.06*	0.05**	28	1
	1204_901	0.06*	0.07*	38	1
Mean peduncle length / plant	4980_497	0.04*	-	5	1
	5069_298	-	0.04*	36	1
Number of pods per peduncle	4980_497	0.03*	-	5	1
	8306_119	-	0.04*	15	1
	9815_2051	0.07**	0.05*	13	1
	13281_572	0.04*	-	23	1
	13772_1075	0.07**	0.06**	23	1

GLM = general linear model; MLM = mixed linear model; R² = phenotypic variation expressed by the SNP; ***P ≤ 0.001; **P ≤ 0.01; *P ≤ 0.05.

Table 4.19 contn'd

Trait	SNPs marker/ Locus name	R ² values of GLM results	R ² values of MLM results	Chromoso me position	Chromo -some
Days to first matured pod	642_527	0.11**	0.14**	14	1
	16494_1773	0.04*	-	21	1
	3787_812	0.05**	-	21	1
	13772_1075	-	0.08*	23	1
	13281_572	0.03*	-	23	1
	11367_1228	0.11***	0.10**	24	1
	571_592	0.09**	0.09**	24	1
	8770_1480	0.09**	0.10**	27	1
	1426_521	-	0.06*	28	1
	14929_258	0.06*	-	36	1
	5149_220	0.11***	0.09**	36	1
	3841_598	-	0.09**	36	1
	10269_488	0.08**	0.10**	37	1
	1204_901	-	0.08*	38	1
Number of pods per plant	12929_463	-	0.10***	5	1
	14164_1877	0.03*	-	5	1
	9815_2051	0.07*	0.06*	13	1
	642_527	0.08*	0.07**	14	1
	8777_825	0.06*	-	14	1
	16494_1773	0.04*	0.05*	21	1
	5553_147	-	0.04*	22	1
	13772_1075	0.09**	-	23	1
	15779_1173	0.07**	0.09*	24	1
	2535_666	0.06**	0.06**	24	1
	5084_519	0.05**	-	24	1
	571_592	-	0.10**	24	1
	1426_521	0.06*	-	28	1
	15451_698	0.04*	-	30	1
	1204_901	0.06*	0.07*	38	1
Mean pod length per plant	642_527	0.15**	-	14	1
	8777_825	0.08**	-	14	1
	8306_119	-	0.05*	15	1
	14542_452	0.05**	0.04*	21	1
	1181_710	0.04**	-	22	1
	7205_420	-	0.47**	23	1
	13281_572	0.05***	-	24	1
	5084_519	0.03*	0.02**	24	1
	8770_1480	0.05**	0.03**	27	1
	13947_415	0.07***	0.07**	30	1
	15451_698	0.09***	-	30	1
	9521_957	0.06**	0.06*	30	1

GLM=general linear model; MLM = mixed linear model; R² = phenotypic variation expressed by the SNP; ***P ≤ 0.001; **P ≤ 0.01; *P ≤ 0.05

4.11.3 Seed yield component

Twenty-eight (28) SNPs markers were found to be associated with four (4) seed yield component traits in the cowpea accessions. Thirty-four (34) significant marker-trait associations were observed. GLM revealed thirty (30) marker-trait associations while MLM gave nineteen (19) associations.

Table 4.20: SNPs markers associated with yield component traits in cowpea accessions

Trait	SNPs marker/ Locus name	R ² values of GLM results	R ² values of MLM results	Chromosome position	Chromo- some
Average number of seeds per pod	14542_452	0.09**	0.06*	21	1
	3787_812	-	0.04*	21	1
	5074_629	0.07**	0.06**	21	1
	571_592	0.06*	-	24	1
	12882_709	0.10*	0.09*	35	1
20 seed weight per plant/g	1107_518	0.05**	-	0	1
	642_527	0.19***	0.18**	14	1
	8777_825	0.03*	0.02*	14	1
	8306_119	0.02*	0.03*	15	1
	6804_755	0.03*	-	17	1
	1181_710	0.03**	0.03*	22	1
	13281_572	0.06***	0.05**	23	1
	13772_1075	0.08***	-	23	1
	11367_1228	0.05**	-	24	1
	5084_519	0.05**	0.04*	24	1
	8770_1480	0.05**	0.03*	27	1
	13947_415	0.03*	-	30	1
	15451_698	0.05**	0.04*	30	1
	9521_957	0.09***	0.08**	30	1
	25_592	0.03*	-	33	1
	14929_258	0.05**	0.03**	36	1
	967_118	0.07***	-	36	1
	5149_220	-	0.07*	36	1
	2077_348	0.02*	-	38	1
Seed yield per plant	4980_497	-	0.06**	5	1
	642_527	0.09**	-	14	1
	3787_812	-	0.02***	21	1
	13772_1075	0.06*	-	23	1
	15779-1173	0.05*	-	24	1
	5084_519	0.04*	-	24	1
	17149_508	0.06*	-	36	1
Seed abortion rate	8306_119	0.08**	0.07*	15	1
	5084_519	0.07**	-	24	1
	12526_795	0.05**	0.04*	37	1

GLM = general linear model; MLM = mixed linear model; R² = phenotypic variation expressed by the SNP; ***P ≤ 0.001; **P ≤ 0.01; *P ≤ 0.05

4.11.4 Seed quality traits (Amino acids)

Sixteen (16) out of the nineteen (19) amino acids that were assessed revealed significant genome-wide association with the SNPs markers as shown in Table 4.21. Seven (7) out of these were essential amino acids. These comprised: Iso-Leucine, L-Histidine, L-Lysine, L-Methionine, L-Tryptophan, L-Threonine and L-Valine. Three of the amino acids; B-Threonine, L-Cysteine and Trans-4-Hydroxyl-L-Proline had no marker-trait associations. Twenty-one (21) out of the 43 SNPs markers were found to be associated with the amino acids analyzed. Thirty-six (36) marker-trait associations were identified. GLM revealed 35 while MLM gave 16 associations.

Table 4.21: SNPs markers association with seed quality traits (amino acids) in cowpea accessions

Trait	Marker name	R ² values of GLM results	R ² values of MLM results	Chromosome position	Chromosome
DL-Alpha Alanine	9815_2051	0.08**	0.09*	13	1
	25_592	0.06*	-	33	1
	3841_598	0.09**	0.09**	36	1
DL-Beta_phenyl-Alanine	18_107	0.08**	-	5	1
	15451_698	0.06**	-	30	1
D-Proline	1107_518	0.09**	0.14***	0	1
	3787_812	0.05*	0.07**	21	1
	15451_698	0.05*	-	30	1
Glutamine	2077_348	0.04*	-	38	1
Glycine	642_527	0.07**	-	14	1
Iso-Leucine	1107_518	0.08**	0.07**	0	1
	642_527	0.07**	0.05**	14	1
	3841_598	0.06*	-	36	1
L-Asparagine	16494_1773	0.07**	-	21	1
	14929_258	0.06*	-	36	1
L-aspartic acid	5074_629	0.09**	-	21	1
	13947_415	0.08**	-	30	1
	967_118	-	0.08**	36	1
	6904_1061	-	0.15***	38	1
L-Histidine	1107_518	0.08**	0.10***	0	1
	9815_2051	0.09**	0.14**	13	1
	8306_119	0.09***	0.09**	15	1
L-Lysine	2077_348	0.05*	-	38	1
L-Methionine	5553_147	0.04*	0.03**	22	1
L-Tryptophan	9815_2051	0.08**	0.09**	13	1
	8306_119	0.05*	-	15	1
L-Threonine	3787_812	0.06*	-	21	1
	1107_518	0.04*	0.09**	0	1
L-Serine	8306_119	0.03*	-	15	1
	14929_258	0.08**	-	36	1
	3841_598	0.08**	0.11**	36	1
	17149_508	-	0.37***	36	1
	10269_488	0.06**	-	37	1
	12526_795	0.05**	-	37	1
L-Tyrosine	8306_119	0.04*	-	15	1
	15451_698	0.04*	-	30	1
L-Valine	9815_2051	0.08**	-	13	1
	2535_666	0.05*	-	24	1

MLM = mixed linear model; GLM = general linear model; R² = phenotypic variation expressed by the SNP; ***P ≤ 0.001; **P ≤ 0.01; *P ≤ 0.05

CHAPTER FIVE

5.0 DISCUSSION

5.1 Morpho-agronomic variability and association

Morphological markers include monogenic biological traits that are highly heritable with essentially constant expression over a range of climatic conditions. They serve as useful markers for the selection of desirable quantitative traits in a breeding program. (Acquaah, 2012).

Pigmentation is one of the most important morphological markers used by cowpea breeders and geneticists in germplasm characterization as well as selection in breeding programs. The results of genetic linkage studies in cowpea revealed that pigmentation is under Mendelian inheritance (Asante and Laing 1991). In the present study, pigmentation was assessed under plant pigmentation and main pod pigmentation. Seven different phenotypic classes of plant pigmentation and three classes of pod pigmentation were observed in the 187 cowpea accessions studied. Generally accessions that had *no pigmentation* were more frequent. This was in agreement with the results reported by Lazaridi *et al.* (2017) who reported seven different forms of plant pigmentation with the most frequent being *absence of pigmentation*. In a similar study by Asare *et al.* (2011) and Zoryeku (2019) five and four different classes of plant pigmentation respectively, were reported. In both cases absence of pigmentation recorded the lowest frequency. These disparities between their findings and those in the present study may be attributed to differences in accession types and the sizes of the population studied.

Growth habit: Seven different phenotypic classes of growth habit were observed for the cowpea accessions in the overall population. Growth habit is useful in deciding on the planting distance (Egbadzor *et al.*, 2014) as *erect* lines would need closer planting than *semi-erect*. This is also useful

in choosing the planting system required for the variety. The *prostrate*, *climbers* and *erect* cowpea genotypes would be required in diverse planting systems such as intercropping or sole cropping reported by Hall *et al.* (1997). Plant erection determines the amount of sunlight captured by the plant and ease of harvesting. In the present study most of the cultivated accessions showed *erect* growth habit while most of the wild relatives exhibited *climbing* or *prostrate* growth habit.

Twinning tendency: In a similar study by Cobbinah *et al.* (2011), accessions with *slight* twinning tendency ranked highest in the overall cowpea population. This is at variance with the results of the present study where *pronounced* twinning tendency ranked highest. This disparity may also be attributed to differences in size of populations and accessions studied.

Terminal leaflet shape: Six different classes were observed. In the present study, the most frequent terminal leaflet shape types observed in the total cowpea population were *sub-globose* and *sub-hastate* with very slight differences between the leaves. Most accessions from the wild relatives had *sub-hastate* while the cultivated ones had *sub-globose* terminal leaflet shape. Similar results were reported by Egbadzor *et al.* (2014).

Raceme position: The wild accessions had longer, erect peduncles with raceme position *mostly above canopy*. The cultivated types usually had short peduncles with raceme position *mostly within and throughout canopy*. Accessions that had longer peduncles produced more seeds than those that had short peduncles in agreement with report made by Bennett-Lartey and Ofori (1999); Cobbinah *et al.* (2011) and Egbadzor *et al.* (2014). For instance, in this study, genotype W.24 which recorded the longest peduncle length of 27.4 cm produced 40 pods and 479 seeds representing the highest number of pods per plant and seed yield per plant respectively. Long peduncle length and raceme position mostly above canopy could serve as desirable traits which may facilitate easy harvesting in cowpea.

Diverse variation was observed in flower colour. Eight different phenotypic classes were observed. According to Kehinde *et al.* (1997) and Omoigui *et al.* (2006), several morpho-agronomic traits in cowpea including flower colour, pod pigmentation and coat pattern are linked. In the present study accessions with *deep purple* and *light purple* flower colours ranked high across the overall population. In a similar study by Cobbinah *et al.* (2011), accessions with *purple* flowers ranked highest. The association of flower colour to other morphological and agronomic traits could help in the selection of desirable economic traits.

Five different phenotypic classes of Seed shape were observed. In the current study some members of the cultivated showed either *rhomboid* or *ovoid* seed shape which produced low number of pods and number of seeds per pod. This was in contrast with the results reported by Egbadzor *et al.* (2014) where accessions with *kidney* shaped seeds normally produced few pods or seeds compared to *rhomboid* types. However, accession W.24 from the wild relative which had *rhomboid* seed shape produced 40 pods and 479 seeds for the highest pod and seed per plant respectively in agreement with Egbadzor *et al.* (2014). The inconsistency could be due to the type of germplasm used for the study.

Seed coat colour: Consumer preference in cowpea is highly influenced by the seed coat colour (Mustapha, 2008). According to Timko and Singh (2008), even though highly improved and quality grain yield are the main objectives of cowpea breeding programs, grain colour is highly valued by consumers. Variability was observed in seed coat colour and seed coat pattern in the overall cowpea population. Some accessions from the cultivated types were observed to have two or more different colours, in agreement with Egbadzor *et al.* (2014) indicating variability within the accessions.

Days to germination: Good yield can be traced from germination data. Farmers are mostly particular about the germination rate of their crops. As a result, they resort to the use of viable seeds for better germination. In the present study, accessions from the cultivated types germinated early, ranged between 2.0 and 12.0 days while that for the wild relatives germinated late, ranged between 3.0 and 41 days. Delayed germination in plant development within the accessions could be due to the fact that the gene for expression of normal germination could have switched on late due to lack of nutrition for the developing embryo. Delayed cell division in the embryo could also be part of the wild behaviour. Accessions from the wild relatives had small seed size with tough seed coat structure which could have also caused the delayed days to germination.

Days to flowering: In the current study there was a high variation in number of days to flowering ranging between 29 days and 143 days after planting. After this date, there were still some accessions that had not flowered. This was in agreement with report made by Timko and Singh (2008) and Egbadzor *et al.* (2014) who attributed it to photoperiodic sensitivity which delayed the flowering period. However, it can be concluded that the population comprised very early maturing genotypes as well as late maturing ones. It could also be accounted for by differences in photoperiodic response between the accessions.

5.2 Amino acid analysis (seed quality trait).

The basic components of protein are amino acids. Cowpea contains high levels of amino acids which are important for metabolic activities. These fall into two groups: non-essential and essential amino acids. In the present research, all the cowpea germplasm analyzed showed the presence of both non-essential and essential amino acids except L-Cysteine, a non-essential amino acid, which was beyond detection in all the accessions studied, 52.78 % and 51.85 % of the accessions analysed recorded 0.0 ppm for Iso-Leucine and Trans-4-Hydroxyl-Proline respectively. Relatively low

concentrations of amino acids were recorded in the total cowpea population which was in agreement with report made by Zoryeku (2019). However, this was in contrast to the results reported by Aremu *et al.* (2006) on amino acid profiles of cowpea varieties who recorded high contents of this trait. L-Tryptophan recorded the highest amino acid content in this study while L-Methionine recorded the lowest. This was in agreement with results reported by Ukpene and Imade (2015) who also analyzed amino acid contents of some selected cowpea accessions. However, in a similar study by Elharadallou *et al.* (2015), L-Methionine was the amino acid with the highest content in the overall population. The disparity could be due to differences in amino acid concentrations in the accession type as well as differences in laboratory protocols.

5.3 Genetic diversity among cowpea accessions

Genetic variation refers to the degree of genetic differences in DNA or RNA sequence or alleles of genes in the genepool of a population. In this study, mean Nei's genetic diversity for the total cowpea population was 93.48 % with 43 polymorphic loci. The mean fixation index for coefficient of inbreeding (F_{IS}) values were positive at all the loci except for one (-0.4488 at gene locus 14929_258). Positive F_{IS} values signifies heterozygote deficiencies which implies deviation from Hardy-Weinberg equilibrium law resulting from non-random mating and other genetic factors (Gehring and Lindhart, 1992; Asante *et al.*, 2003). In the present study the mean value for genetic differentiation (F_{ST}) was 0.1952 signifying high level of homozygosity which may be attributed to non-random mating since cowpea is self-pollinated crop. Previous study by Asante *et al.* (2003) revealed genetic differentiation (F_{ST}) value of 0.075 compared with 0.1952 obtained in the present study. This implies higher level of differentiation or higher levels of homozygosity in the population studied emanating from the cultivated types. In the present work, there was significant

level of gene flow (N_m) linking the genotypes. The overall gene flow (N_m) estimate among genotypes was 1.0309 indicating adequate gene flow to prevent localized differentiation.

5.4 Population structure analysis

To utilize germplasm efficiently, it is advisable to determine the diversity and relatedness between the accessions before introducing them for breeding purposes (Qin *et al.*, 2016). In this study, population structure analysis by the *STRUTURE* software grouped the overall cowpea accessions into two gene pools. This was in accordance with previously reported research by Xiong *et al.* (2016) who worked with landraces of cowpea. He observed two different genepools that corresponded to genepools belonging to regions of West Africa and Eastern Africa respectively. However, the Principal component analysis (PCA) grouped the population into one major cluster with several outliers. In a similar study by Zoryeku (2019), four clusters were observed while PCA analysis of amino acids grouped the overall cowpea population into two principal components.

5.5 Pair-wise linkage disequilibrium (LD) and linkage disequilibrium decay

Different statistical models have been proposed for the evaluation of LD (Hedrick, 1987). However, r^2 and D' are the most frequently used measures in association mapping analysis at two different loci (Stich and Melchinger, 2010). In the present study, evaluation of intra-chromosomal LD showed that, at a threshold of $r^2 \geq 0.1$, 12.64 % of SNPs loci showed significant LD ($p \leq 0.05$). At a threshold of $r^2 \geq 0.05$, 15.38 % of the SNPs loci showed significant LD ($p \leq 0.05$). Previous reports made by Khushboo *et al.* (2017) revealed a very low intra-chromosomal LD of 7.47 % (26/348) and 4.59 % (16/348) of SSR loci at $r^2 \geq 0.05$ and $r^2 \geq 0.1$ respectively. The difference in the levels of LD can be attributed to several factors such as selection, genetic drift, mutation and other genetic factors. The size of intra chromosomal linkage disequilibrium block for SNPs loci at

the entire genome of the cowpea accession was estimated with the longest LD block of 25.0 bp, (equivalent to 2.5×10^{-5} cM) between markers *6904_1061* and *9815_2051* on chromosome one at correlation co-efficient measure of variability between the two loci (r^2) of 0.10 and the homogenized difference between the coupling and repulsion gamete frequencies at two different loci (D') of 0.89. In a similar research by Khushboo *et al.* (2017), a very long LD block of 104.6 cM, (equivalent to 104600000 bp) was observed between markers NAU-1167 and BLN-3259 on chromosome 3. The wide difference between the LD blocks can be attributed to the distribution of markers on only one chromosome as well as the type of SNPs markers used for the study.

The rate at which linkage disequilibrium (LD) decreases in outcrossing species is much faster than inbred species due to reduced effective recombination in inbred species, i.e. homozygosity result in increased LD while heterozygosity results in decreased LD (Flint-Garcia *et al.*, 2005; Gómez *et al.*, 2011). The level of disparity measure ranged between 0.0 and 0.75 within map distance of 0.0 to 38.75 cM. In the current study there was partial linkage disequilibrium decay (Figure 4.11). This can be attributed to the fact that linkage disequilibrium decay in the studied population at the various SNP loci had either just started or still undergoing decay. Previous research revealed genome-wide linkage disequilibrium decay within map distance of 9 to 10 cM (Khushboo *et al.*, 2017).

5.6 Association mapping and marker-trait association of cowpea accessions

Knowledge of association mapping serves as useful information in germplasm resource management to promote the success of breeding programs (Roldán-Ruiz *et al.*, 2001; Ali *et al.*, 2008). Association mapping has been identified to be an essential technique for dissecting important quantitative traits. It aims at identifying specific significant markers associated with phenotypic traits. A number of studies have been conducted with association analysis to find

significant molecular markers associated with cowpea quantitative traits including aphid resistance, salt tolerance, agronomic traits of dry beans and plant growth habit. In the present study, the following marker-trait associations were identified: Number of flowers per plant was found to be associated with three markers, *12929_463*, *4980_497* and *14164_1877* at 5 cM map distance. Mean peduncle length per plant and number of pods per peduncle were associated with one marker, *4980_497* at 5 cM map distance. Number of pods per plant was associated with two markers, *12929_463* and *14164_1877* at 5 cM map distance. Twenty-seed weight per plant was associated with one marker, *1107_518* at 0 cM map distance. Seed yield per plant was associated with one marker, *4980_497* at 5 cM map distance. DL-Beta-phenyl-Alanine was associated with *18_107* at 5 cM map distance and D-Proline, Iso-Lucine, L-Histidine and L-Serine were associated with one marker, *1107_518* at 0 cM map distance (Appendix 8). These were recorded for distances between 0 and 10 cM signifying very close and strong associations. Significant overlapping single nucleotide polymorphism markers (SNPs) were found between the morphological reproductive, yield component and the contents of amino acids. Results of the present study is in agreement with reports made by previous researchers. In a similar study, Ravelombola (2017) performed association analysis for salt tolerance in cowpea genotypes at germination stage and seedling stage to identify SNPs markers associated with these trait. High level of variability was observed in the salt tolerance among the cowpea genotypes. Three SNPs markers were observed to be associated with salt tolerance at germination stage, seven markers at seedling stage and four for both germination and seedling stages. Agarwal (2014) also in a similar work on association analysis of agronomic traits of dry beans identified significant markers associated with phenotypic traits. The following SNPs marker: 9, 9, 11 and 13 were found to be associated with plant height, 100-seed weight, maturity and seed yield respectively. A SNP-based association analysis by Ravelombola

et al. (2017) for plant growth habit in cowpea germplasm also revealed ten (10) significant SNPs markers which were strongly associated with the cowpea growth habit. The disparity in the number of SNPs markers obtained in the present study and that of the previous studies could be due to the total number of SNPs markers used for the study.

CHAPTER SIX

6.0 CONCLUSIONS AND RECOMMENDATIONS

6.1 Conclusions

A wide variability was observed in the cowpea accessions for both the morpho-agronomic and amino acid compounds studied. Significant pairwise correlations were observed among morpho-agronomic as well as amino acid traits.

Analysis of seed quality traits (amino acids) revealed considerably high levels of L-Tryptophan content and low levels of L-Methionine.

The mean Nei's genetic diversity observed was 0.3001 ± 0.18 for the overall cowpea population, 0.2106 ± 0.18 for the wild and 0.2744 ± 0.17 for the cultivated. Mean observed heterozygosity was 0.0242. Mean fixation index of coefficient of inbreeding (F_{IS}) was 0.8935. Mean coefficient of inbreeding at different levels (F_{IT}) was 0.9143. Mean degree of genetic differentiation (F_{ST}) was 0.1952. Mean gene flow (N_m) was 1.00 and frequency of cross pollination (F_C) was 0.0805.

Population structure analysis grouped the total cowpea accessions into two subpopulations, based on their inferred ancestry values.

Intra chromosomal linkage disequilibrium estimate for SNPs loci revealed 12.64% and 15.38% at the threshold level of $r^2 \geq 0.1$ and $r^2 \geq 0.05$ respectively. The largest LD block observed was 25.0 bp between markers 6904_1061 and 9815_2051 at correlation co-efficient measure of variability between two loci (r^2) of 0.10 and the difference between the gamete frequencies at two different loci (D') of 0.89.

Partial linkage disequilibrium (LD) decay was observed, signifying low levels of recombination frequencies in the total cowpea population.

The following cowpea accessions were observed to be of economic importance based on the:

(a) Vegetative, reproductive and yield components:

C.111 for days to germination; W.31, C.99, C.158 and C.178 for days to flowering; W.14, W.24, W.31, W.32 and C.109 for number of flowers per plant; W.31, C.99, C.105, C.158 and C.178 for days to first matured pod; W.14, W.24 W.31, W.32, C.109 and C.159 for number of pods per plant; C.101, C.121, C.148 and C.184 for average seed per pod; W.82, G.E, C.98, C.125, C.126, C.152, C.157, C.178 and C.188 for seed weight; W.14, W.24, W.31, W.32 and C.109 for seed yield per plant, and PARENT, G.E and C.125 for seed abortion rate.

(b) seed quality trait (amino acid content)

C.109 (L-Tryptophan), C.158 (DL-Beta phenyl-Alanin and L-Histidine), C.163 (L-Asparagine and L-Serine), W.31 (Iso-Leucine and Glycine), C.113 (DL-Alpha-Alanine), W.29 (L-Aspartic Acid), C.137 (D-Proline and B-Threonine), W.25 (Trans-4-Hydroxyl-Proline), C.159 (L-Valine and L-Threonine), C.102 (L-Tyrosine), C.150 (Glutamine), C.100 (L-Methionine), C.150 (L-Lysine).

Significant marker-trait associations were identified with very high potential for exploitation in marker-assisted breeding for the important traits in cowpea.

(i) Number of flowers per plant associated with SNP markers *12929_463*, *4980_497* and *14164_1877* at 5 cM map distance.

(ii) Mean peduncle length per plant associated with SNP marker *4980_497* at 5 cM.

- (iii) Number of pods per peduncle associated with SNP marker *4980_497* at 5 cM.
- (iv) Number of pods per plant associated with SNP markers *12929_463* and *14164_1877* at 5 cM map distance.
- (v) 20 seed weight per plant associated with SNP marker *1107_518* at 0 cM map distance.
- (vi) Seed yield per plant associated with SNP marker *4980_497* at 5 cM map distance.
- (vii) DL-Beta_phenyl_Alanine associated with SNP marker *18_107* at 5 cM map distance.
- (viii) D-Proline, Iso-Lucine, L-Histidine and L-Serine associated with SNP marker *1107_518* at 0 cM.

6.2 Recommendations

The accessions with superior morpho-agronomic and seed quality traits should be incorporated into cowpea breeding programs in the University of Ghana.

The single nucleotide polymorphisms (SNPs) markers identified must be validated and used for cowpea germplasm characterization through collaborative effort between the Department of Plant and Environmental Biology and the Department of Crop Science.

The SNPs markers associated with economic agronomic traits must be validated for cowpea improvement programs.

In subsequent studies more SNPs markers possibly covering more chromosomes may be investigated.

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APPENDICES

Appendix 1: Morpho-agronomic qualitative traits of Cowpea genotypes

Plant genotype	Plant pigmentation	Plant hairiness	Growth habit	Growth pattern	Twinning tendency
W.01	Extensive	Glabrescent	Semi-erect	Indeterminate	Pronounced
W.02	None	Short appressed hair	Prostrate	Indeterminate	None
W.03	None	Glabrescent	Semi-erect	Indeterminate	Intermediate
W.04	Intermediate	Glabrescent	Semi-erect	Indeterminate	Intermediate
W.05	None	Glabrescent	Climbing	Indeterminate	Intermediate
W.06	None	Short appressed hair	Climbing	Indeterminate	Pronounced
W.07	None	Glabrescent	Climbing	Indeterminate	Intermediate
W.08	None	Glabrescent	Climbing	Indeterminate	Pronounced
W.09	None	Glabrescent	Erect	Indeterminate	Pronounced
W.10	None	Short appressed hair	Erect	Indeterminate	Pronounced
W.11	None	Glabrescent	Prostrate	Indeterminate	Intermediate
W.12	None	Glabrescent	Prostrate	Indeterminate	None
W.13	None	Glabrescent	Erect	Indeterminate	Intermediate
W.14	Extensive	Glabrescent	Semi-erect	Indeterminate	Pronounced
W.15	None	Glabrescent	Semi-erect	Indeterminate	Pronounced
W.16	None	Pubescent	Erect	Determinate	None
W.17	None	Glabrescent	Prostrate	Indeterminate	Intermediate
W.18	None	Glabrescent	Prostrate	Indeterminate	None
W.19	None	Glabrescent	Acute-erect	Indeterminate	None
W.20	None	Glabrescent	Climbing	Indeterminate	Pronounced
W.21	None	Glabrescent	Climbing	Indeterminate	Intermediate
W.22	Extensive	Glabrescent	Climbing	Indeterminate	Intermediate
W.23	None	Glabrescent	Climbing	Indeterminate	None
W.24	V. slight	Glabrescent	Semi-erect	Indeterminate	Pronounced
W.25	None	Glabrescent	Climbing	Indeterminate	Pronounced
W.26	None	Glabrescent	Climbing	Indeterminate	Pronounced
W.27	None	Glabrescent	Climbing	Indeterminate	Pronounced
W.28	None	Glabrescent	Climbing	Indeterminate	Pronounced
W.29	None	Glabrescent	Climbing	Indeterminate	Pronounced
W.30	Moderate	Glabrescent	Erect	Indeterminate	Pronounced
W.31	Extensive	Glabrescent	Semi-erect	Indeterminate	Pronounced
W.32	Moderate	Glabrescent	Semi-erect	Indeterminate	Pronounced

W. = Wild relative; C. = Cultivated type

Appendix 1 contn'd

Plant genotype	Plant pigmentation	Plant hairiness	Growth habit	Growth pattern	Twinning tendency
W.33	None	Glabrescent	Semi-prostrate	Indeterminate	Pronounced
W.34	V. slight	Glabrescent	Climbing	Indeterminate	Pronounced
W.35	None	Short appressed hair	Semi-erect	Indeterminate	Pronounced
W.37	Moderate	Pubescent	Climbing	Indeterminate	Pronounced
W.38	None	Short appressed hair	Semi-prostrate	Indeterminate	Intermediate
W.39	None	Pubescent	Climbing	Indeterminate	Pronounced
W.40	Solid	Short appressed hair	Semi-prostrate	Indeterminate	None
W.41	None	Glabrescent	Climbing	Indeterminate	Pronounced
W.42	None	Glabrescent	Prostrate	Indeterminate	None
W.43	V. slight	Glabrescent	Semi-prostrate	Indeterminate	Pronounced
W.44	None	Glabrescent	Semi-erect	Indeterminate	Intermediate
W.45	Extensive	Glabrescent	Erect	Indeterminate	None
W.46	None	Glabrescent	Erect	Determinate	None
W.47	V. slight	Pubescent	Semi-prostrate	Indeterminate	Slight
W.48	None	Short appressed hair	Semi-prostrate	Indeterminate	Slight
W.49	None	Glabrescent	Semi-erect	Indeterminate	Pronounced
W.50	None	Glabrescent	Semi-erect	Indeterminate	Pronounced
W.51	V. slight	Short appressed hair	Semi-prostrate	Indeterminate	Pronounced
W.52	None	Glabrescent	Semi-erect	Indeterminate	None
W.53	None	Glabrescent	Acute-erect	Indeterminate	Pronounced
W.54	None	Glabrescent	Acute-erect	Indeterminate	Pronounced
W.55	None	Short appressed hair	Semi-prostrate	Indeterminate	Pronounced
W.56	None	Glabrescent	Prostrate	Indeterminate	Slight
W.57	None	Glabrescent	Semi-prostrate	Indeterminate	Slight
W.58	None	Glabrescent	Erect	Indeterminate	Intermediate
W.59	None	Glabrescent	Prostrate	Indeterminate	Slight
W.60	V. slight	Short appressed hair	Semi-prostrate	Indeterminate	Pronounced
W.61	None	Short appressed hair	Semi-prostrate	Indeterminate	None
W.62	Moderate	Glabrescent	Semi-erect	Indeterminate	Intermediate
W.63	V. slight	Short appressed hair	Climbing	Indeterminate	Pronounced
W.64	V. slight	Glabrescent	Semi-prostrate	Indeterminate	Pronounced
W.65	None	Glabrescent	Semi-prostrate	Indeterminate	None

W. = Wild relative; C. = Cultivated type

Appendix 1 contn'd

Plant genotype	Plant pigmentation	Plant hairiness	Growth habit	Growth pattern	Twinning tendency
W.66	None	Glabrescent	Semi-prostrate	Indeterminate	Slight
W.67	None	Pubescent	Semi-prostrate	Indeterminate	Slight
W.68	None	Pubescent	Semi-erect	Indeterminate	None
W.69	None	Glabrescent	Climbing	Indeterminate	Pronounced
		Short appressed			
W.70	None	hair	Prostrate	Indeterminate	None
W.71	None	Glabrescent	Erect	Indeterminate	Pronounced
W.72	None	Pubescent	Semi-prostrate	Indeterminate	None
W.73	None	Pubescent	Prostrate	Indeterminate	None
W.74	None	Glabrescent	Semi-prostrate	Indeterminate	Slight
W.75	None	Glabrescent	Acute-erect	Indeterminate	Slight
W.76	None	Glabrescent	Semi-erect	Indeterminate	Slight
W.77	None	Glabrescent	Semi-prostrate	Indeterminate	Pronounced
W.78	Solid	Glabrescent	Semi-erect	Indeterminate	Pronounced
W.79	Solid	Glabrescent	Semi-erect	Indeterminate	Pronounced
W.80	V. slight	Glabrescent	Acute-erect	Indeterminate	Pronounced
W.81	None	Glabrescent	Acute-erect	Indeterminate	Slight
W.82	None	Glabrescent	Semi-erect	Determinate	None
W.83	Moderate	Glabrescent	Semi-prostrate	Indeterminate	Slight
W.84	Moderate	Glabrescent	Acute-erect	Indeterminate	Slight
W.85	Solid	Glabrescent	Erect	Indeterminate	Slight
W.86	None	Glabrescent	Erect	Indeterminate	Slight
		Short appressed			
W.87	None	hair	Climbing	Indeterminate	Pronounced
W.88	Moderate	Glabrescent	Semi-erect	Indeterminate	Pronounced
W.89	Moderate	Glabrescent	Erect	Indeterminate	Pronounced
W.90	None	Glabrescent	Erect	Indeterminate	Intermediate
		Short appressed			
W.93	None	hair	Prostrate	Indeterminate	None
W.94	None	Pubescent	Erect	Indeterminate	None
W.95	None	Glabrescent	Semi-erect	Indeterminate	Intermediate
PARENT	None	Glabrescent	Prostrate	Indeterminate	None
G. E	V. slight	Glabrescent	Erect	Indeterminate	Slight
C.96	Moderate	Glabrescent	Erect	Indeterminate	Intermediate
C.97	None	Glabrescent	Erect	Indeterminate	Pronounced

Appendix 1 contn'd

Plant genotype	Plant pigmentation	Plant hairiness	Growth habit	Growth pattern	Twinning tendency
C.98	Slight	Glabrescent	Erect	Indeterminate	Pronounced
C.99	Moderate	Glabrescent	Erect	Indeterminate	None
C.100	Slight	Glabrescent	Semi-erect	Indeterminate	Slight
C.101	Moderate	Glabrescent	Erect	Indeterminate	Slight
C.102	Moderate	Glabrescent	Erect	Indeterminate	None
C.103	V. slight	Glabrescent	Erect	Indeterminate	None
C.104	Moderate	Glabrescent	Erect	Indeterminate	Intermediate
C.105	V. slight	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.106	V. slight	Glabrescent	Erect	Indeterminate	Slight
C.107	None	Glabrescent	Erect	Indeterminate	None
C.108	Extensive	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.109	Intermediate	Glabrescent	Erect	Indeterminate	Intermediate
C.110	Moderate	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.111	Moderate	Glabrescent	Erect	Indeterminate	Intermediate
C.112	Extensive	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.113	Moderate	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.114	None	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.115	None	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.116	Moderate	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.117	None	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.118	None	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.119	V. slight	Glabrescent	Erect	Indeterminate	Intermediate
C.120	None	Glabrescent	Erect	Indeterminate	Slight
C.121	None	Glabrescent	Erect	Indeterminate	Intermediate
C.122	Extensive	Glabrescent	Erect	Indeterminate	Slight
C.123	None	Glabrescent	Erect	Indeterminate	Intermediate
C.124	None	Glabrescent	Erect	Indeterminate	Pronounced
C.125	None	Glabrescent	Erect	Indeterminate	Slight
C.126	None	Glabrescent	Erect	Indeterminate	None
C.127	None	Glabrescent	Erect	Indeterminate	Slight
C.128	None	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.129	None	Glabrescent	Erect	Indeterminate	Slight

C = Cultivated type

Appendix 1 contn'd

Plant genotype	Plant pigmentation	Plant hairiness	Growth habit	Growth pattern	Twinning tendency
C.130	None	Glabrescent	Erect	Indeterminate	Pronounced
C.131	None	Glabrescent	Erect	Indeterminate	Pronounced
C.132	None	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.133	Moderate	Glabrescent	Erect	Indeterminate	Intermediate
C.134	None	Glabrescent	Erect	Indeterminate	None
C.135	None	Glabrescent	Erect	Indeterminate	Pronounced
C.136	Moderate	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.137	None	Glabrescent	Semi-erect	Indeterminate	Slight
C.138	None	Glabrescent	Semi-erect	Indeterminate	Slight
C.139	None	Glabrescent	Erect	Indeterminate	Slight
C.140	None	Glabrescent	Erect	Indeterminate	None
C.141	V. slight	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.142	None	Glabrescent	Erect	Indeterminate	None
C.143	None	Glabrescent	Erect	Indeterminate	None
C.144	None	Glabrescent	Erect	Indeterminate	None
C.145	None	Glabrescent	Erect	Indeterminate	None
C.146	None	Glabrescent	Prostrate	Indeterminate	None
C.147	None	Glabrescent	Erect	Indeterminate	None
C.148	None	Glabrescent	Erect	Indeterminate	None
C.149	None	Glabrescent	Semi-erect	Indeterminate	Slight
C.150	None	Glabrescent	Semi-erect	Indeterminate	Slight
C.151	None	Glabrescent	Erect	Indeterminate	None
C.152	None	Glabrescent	Erect	Indeterminate	None
C.153	None	Glabrescent	Erect	Indeterminate	Pronounced
C.154	None	Glabrescent	Erect	Indeterminate	None
C.155	V. slight	Glabrescent	Erect	Indeterminate	None
C.156	None	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.157	Moderate	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.158	Moderate	Glabrescent	Erect	Indeterminate	Intermediate
C.159	Moderate	Glabrescent	Erect	Indeterminate	None
C.160	Moderate	Glabrescent	Erect	Indeterminate	None
C.161	None	Glabrescent	Erect	Indeterminate	None

C = Cultivated type

Appendix 1 contn'd

Plant genotype	Plant pigmentation	Plant hairiness	Growth habit	Growth pattern	Twinning tendency
C.162	None	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.163	None	Glabrescent	Erect	Indeterminate	Slight
C.164	Moderate	Glabrescent	Erect	Indeterminate	Intermediate
C.165	None	Glabrescent	Erect	Indeterminate	None
C.166	None	Glabrescent	Climbing	Indeterminate	Pronounced
C.167	Extensive	Glabrescent	Erect	Indeterminate	None
C.168	None	Glabrescent	Erect	Indeterminate	None
C.169	None	Glabrescent	Erect	Indeterminate	Pronounced
C.170	None	Glabrescent	Erect	Indeterminate	Pronounced
C.171	None	Glabrescent	Erect	Indeterminate	Slight
C.172	Moderate	Glabrescent	Erect	Indeterminate	Slight
C.173	None	Glabrescent	Erect	Indeterminate	Slight
C.174	Extensive	Glabrescent	Erect	Indeterminate	Slight
C.175	None	Glabrescent	Erect	Indeterminate	Intermediate
C.176	none	Glabrescent	Erect	Indeterminate	Slight
C.177	none	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.178	none	Glabrescent	Erect	Indeterminate	Slight
C.179	none	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.180	none	Glabrescent	Semi-erect	Indeterminate	Slight
C.181	none	Glabrescent	Erect	Indeterminate	Slight
C.182	V. slight	Glabrescent	Erect	Indeterminate	Slight
C.183	None	Glabrescent	Erect	Indeterminate	Slight
C.184	V. slight	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.185	None	Glabrescent	Erect	Indeterminate	Slight
C.186	Moderate	Glabrescent	Erect	Indeterminate	Intermediate
C.187	None	Glabrescent	Semi-erect	Indeterminate	Pronounced
C.188	None	Glabrescent	Erect	Indeterminate	Pronounced

C = Cultivated type

Appendix 1 contn'd

Plant			Terminal	
genotype	Leaf colour	Leaf texture	leaflet shape	V-markings
W.01	Dark green	Intermediate	Hastate	Absent
W.02	Dark green	Membranous	Hastate	Present
W.03	Dark green	Intermediate	Linear	Present
W.04	Dark green	Membranous	Hastate	Present
W.05	Dark green	Cariaceous	Lanceolate	Absent
W.06	Intermediate green	Intermediate	Sub-hastate	Present
W.07	Dark green	Intermediate	Hastate	Present
W.08	Dark green	Membranous	Sub-globose	Present
W.09	Dark green	Membranous	Sub-hastate	Present
W.10	Intermediate green	Intermediate	Sub-globose	Present
W.11	Intermediate green	Membranous	Sub-hastate	Present
W.12	Pale green	Cariaceous	Hastate	Present
W.13	Pale green	Membranous	Hastate	Present
W.14	Intermediate green	Membranous	Sub-globose	Present
W.15	Dark green	Membranous	Sub-hastate	Present
W.16	Dark green	Intermediate	Sub-hastate	Present
W.17	Intermediate green	Cariaceous	Lanceolate	Absent
W.18	Dark green	Intermediate	Lanceolate	Absent
W.19	Intermediate green	Cariaceous	Hastate	Present
W.20	Dark green	Membranous	Sub-hastate	Present
W.21	Dark green	Membranous	Hastate	Present
W.22	Dark green	Intermediate	Sub-hastate	Present
W.23	Intermediate green	Membranous	Sub-hastate	Present
W.24	Dark green	Cariaceous	Sub-globose	Present
W.25	Intermediate green	Membranous	Hastate	Present
W.26	Intermediate green	Intermediate	Linear	Absent
W.27	Pale green	Cariaceous	Linear	Absent
W.28	Intermediate green	Intermediate	Sub-globose	Present
W.29	Intermediate green	Cariaceous	Hastate	Present
W.30	Dark green	Membranous	Sub-hastate	Present
W.31	Dark green	Intermediate	Sub-globose	Present
W.32	Dark green	Membranous	Sub-globose	Present

W = Wild relative

Appendix 1 contn'd

Plant		Terminal		
genotype	Leaf colour	Leaf texture	leaflet shape	V-markings
W.33	Intermediate green	Cariaceous	Sub-globose	Present
W.34	Intermediate green	Cariaceous	Lanceolate	Absent
W.35	Dark green	Membranous	Sub-hastate	Present
W.37	Dark green	Intermediate	Sub-hastate	Present
W.38	Dark green	Intermediate	Hastate	Present
W.39	Intermediate green	Intermediate	Hastate	Present
W.40	Pale green	Intermediate	Sub-globose	Present
W.41	Dark green	Intermediate	Hastate	Present
W.42	Dark green	Cariaceous	Hastate	Present
W.43	Intermediate green	Intermediate	Sub-hastate	Present
W.44	Intermediate green	Cariaceous	Hastate	Present
W.45	Dark green	Intermediate	Sub-hastate	Present
W.46	Variegated	Cariaceous	Hastate	Present
W.47	Intermediate green	Cariaceous	Sub-hastate	Present
W.48	Intermediate green	Cariaceous	Sub-hastate	Present
W.49	Intermediate green	Membranous	Sub-globose	Present
W.50	Intermediate green	Membranous	Sub-hastate	Present
W.51	Intermediate green	Cariaceous	Sub-globose	Present
W.52	Variegated	Cariaceous	Hastate	Present
W.53	Intermediate green	Membranous	Sub-hastate	Present
W.54	Intermediate green	Membranous	Hastate	Present
W.55	Dark green	Cariaceous	Sub-hastate	Present
W.56	Intermediate green	Cariaceous	Sub-hastate	Present
W.57	Dark green	Cariaceous	Hastate	Present
W.58	Pale green	Membranous	Sub-globose	Present
W.59	Intermediate green	Cariaceous	Sub-hastate	Present
W.60	Intermediate green	Cariaceous	Sub-hastate	Present
W.61	Variegated	Membranous	Sub-hastate	Present
W.62	Intermediate green	Cariaceous	Sub-globose	Present
W.63	Dark green	Intermediate	Sub-hastate	Present
W.64	Dark green	Intermediate	Hastate	Present
W.65	Dark green	Membranous	Hastate	Present

W = Wild relative

Appendix 1 contn'd

Plant		Terminal		
genotype	Leaf colour	Leaf texture	leaflet shape	V-markings
W.66	Intermediate green	Membranous	Hastate	Present
W.67	Pale green	Intermediate	Hastate	Present
W.68	Intermediate green	Membranous	Lanceolate	Present
W.69	Pale green	Cariaceous	Hastate	Absent
W.70	Intermediate green	Cariaceous	Hastate	Present
W.71	Pale green	Cariaceous	Sub-hastate	Present
W.72	Dark green	Membranous	Sub-hastate	Present
W.73	Pale green	Intermediate	Sub-hastate	Present
W.74	Dark green	Membranous	Hastate	Present
W.75	Dark green	Membranous	Hastate	Present
W.76	Pale green	Cariaceous	Hastate	Present
W.77	Pale green	Cariaceous	Sub-hastate	Present
W.78	Pale green	Cariaceous	Sub-hastate	Present
W.79	Pale green	Intermediate	Hastate	Present
W.80	Pale green	Membranous	Hastate	Present
W.81	Intermediate green	Membranous	Sub-hastate	Present
W.82	Pale green	Intermediate	Sub-globose	Present
W.83	Intermediate green	Intermediate	Sub-hastate	Present
W.84	Dark green	Membranous	Hastate	Present
W.85	Pale green	Cariaceous	Hastate	Present
W.86	Intermediate green	Cariaceous	Hastate	Present
W.87	Dark green	Membranous	Lanceolate	Present
W.88	Pale green	Cariaceous	Hastate	Present
W.89	Intermediate green	Intermediate	Sub-hastate	Present
W.90	Dark green	Membranous	Sub-hastate	Present
W.93	Intermediate green	Intermediate	Sub-hastate	Present
W.94	Dark green	Membranous	Lanceolate	Present
W.95	Pale green	Intermediate	Sub-hastate	Present
PARENT	Dark green	Intermediate	Hastate	Present
G. E	Dark green	Membranous	Globose	Present
C.96	Dark green	Intermediate	Globose	Present
C.97	Intermediate green	Intermediate	Sub-globose	Present

W = Wild relative; G. E = Golden eye; C = Cultivated type

Appendix 1 contn'd

Plant		Terminal		
genotype	Leaf colour	Leaf texture	leaflet shape	V-markings
C.98	Dark green	Membranous	Globose	Present
C.99	Dark green	Membranous	Sub-globose	Present
C.100	Intermediate green	Intermediate	Globose	Present
C.101	Dark green	Intermediate	Globose	Present
C.102	Dark green	Intermediate	Globose	Present
C.103	Dark green	Intermediate	Globose	Present
C.104	Dark green	Intermediate	Globose	Present
C.105	Intermediate green	Intermediate	Globose	Present
C.106	Dark green	Membranous	Globose	Present
C.107	Intermediate green	Intermediate	Sub-globose	Present
C.108	Dark green	Intermediate	Globose	Present
C.109	Intermediate green	Intermediate	Sub-globose	Present
C.110	Dark green	Membranous	Globose	Present
C.111	Dark green	Intermediate	Sub-globose	Present
C.112	Dark green	Intermediate	Globose	Present
C.113	Dark green	Intermediate	Globose	Present
C.114	Intermediate green	Membranous	Globose	Present
C.115	Intermediate green	Membranous	Globose	Present
C.116	Dark green	Membranous	Globose	Present
C.117	Dark green	Cariaceous	Sub-globose	Present
C.118	Intermediate green	Cariaceous	Sub-globose	Present
C.119	Dark green	Membranous	Sub-globose	Present
C.120	Intermediate green	Intermediate	Sub-globose	Present
C.121	Dark green	Cariaceous	Globose	Present
C.122	Dark green	Membranous	Globose	Present
C.123	Intermediate green	Cariaceous	Sub-globose	Present
C.124	Dark green	Intermediate	Sub-globose	Present
C.125	Intermediate green	Cariaceous	Sub-globose	Present
C.126	Dark green	Intermediate	Globose	Present
C.127	Dark green	Intermediate	Sub-globose	Present
C.128	Dark green	Cariaceous	Sub-globose	Present

C = Cultivated type

Appendix 1 contn'd

Plant			Terminal leaflet	V-
genotype	Leaf colour	Leaf texture	shape	markings
C.129	Dark green	Cariaceous	Globose	Present
C.130	Dark green	Membranous	Sub-globose	Present
C.131	Dark green	Cariaceous	Sub-globose	Present
C.132	Dark green	Intermediate	Globose	Present
C.133	Pale green	Membranous	Globose	Present
C.134	Intermediate green	Membranous	Sub-globose	Present
C.135	Intermediate green	Intermediate	Sub-globose	Present
C.136	Intermediate green	Intermediate	Sub-globose	Present
C.137	Dark green	Cariaceous	Globose	Present
C.138	Dark green	Intermediate	Sub-globose	Present
C.139	Pale green	Intermediate	Sub-globose	Present
C.140	Dark green	Cariaceous	Globose	Present
C.141	Intermediate green	Intermediate	Sub-globose	Present
C.142	Dark green	Intermediate	Sub-globose	Present
C.143	Intermediate green	Intermediate	Globose	Present
C.144	Dark green	Membranous	Sub-globose	Present
C.145	Pale green	Intermediate	Sub-globose	Present
C.146	Dark green	Intermediate	Sub-hastate	Present
C.147	Intermediate green	Cariaceous	Hastate	Present
C.148	Intermediate green	Cariaceous	Sub-globose	Present
C.149	Dark green	Membranous	Sub-hastate	Present
C.150	Dark green	Membranous	Sub-globose	Present
C.151	Intermediate green	Cariaceous	Sub-globose	Present
C.152	Dark green	Cariaceous	Sub-globose	Present
C.153	Intermediate green	Intermediate	Sub-globose	Present
C.154	Intermediate green	Cariaceous	Sub-globose	Present
C.155	Intermediate green	Cariaceous	Sub-globose	Present
C.156	Dark green	Membranous	Sub-globose	Present
C.157	Dark green	Cariaceous	Sub-globose	Present
C.158	Dark green	Membranous	Sub-globose	Present
C.159	Pale green	Intermediate	Globose	Present
C.160	Intermediate green	Cariaceous	Sub-hastate	Present

C = Cultivated type

Appendix 1 contn'd

Plant genotype	Leaf colour	Leaf texture	Terminal leaflet shape	V-markings
C.161	Pale green	Intermediate	Sub-hastate	Present
C.162	Intermediate green	Intermediate	Sub-hastate	Present
C.163	Pale green	Intermediate	Sub-hastate	Present
C.164	Intermediate green	Membranous	Sub-hastate	Present
C.165	Intermediate green	Cariaceous	Sub-hastate	Present
C.166	Intermediate green	Cariaceous	Hastate	Present
C.167	Intermediate green	Cariaceous	Sub-hastate	Present
C.168	Intermediate green	Cariaceous	Hastate	Present
C.169	Pale green	Cariaceous	Sub-globose	Present
C.170	Intermediate green	Cariaceous	Globose	Present
C.171	Intermediate green	Membranous	Sub-globose	Present
C.172	Pale green	Intermediate	Globose	Present
C.173	Pale green	Intermediate	Sub-globose	Present
C.174	Dark green	Intermediate	Sub-globose	Present
C.175	Intermediate green	Cariaceous	Sub-globose	Present
C.176	Intermediate green	Intermediate	Sub-globose	Present
C.177	Intermediate green	Cariaceous	Globose	Present
C.178	Dark green	Intermediate	Sub-globose	Present
C.179	Intermediate green	Intermediate	Sub-globose	Present
C.180	Dark green	Intermediate	Sub-globose	Present
C.181	Dark green	Membranous	Sub-globose	Present
C.182	Dark green	Membranous	Sub-globose	Present
C.183	Dark green	Membranous	Sub-globose	Present
C.184	Intermediate green	Cariaceous	Sub-globose	Present
C.185	Variegated	Cariaceous	Sub-hastate	Present
C.186	Dark green	Membranous	Globose	Present
C.187	Intermediate green	Cariaceous	Globose	Present
C.188	Intermediate green	Cariaceous	Globose	Present

Appendix 1 contn'd

Plant genotype	Flower colour	Raceme position	Main pod pigmentation	Pod colour
W.04	Deep purple	In upper canopy	Not pigmented	Dark brown
W.05	Deep purple	In upper canopy	Not pigmented	Dark brown
W.08	Deep purple	Mostly above canopy	Not pigmented Uniformly	Flesh
W.10	Deep purple	Mostly above canopy	pigmented	Dark green
W.14	Light purple	Mostly above canopy	Not pigmented	Dark green
W.15	Mauve/pink	In upper canopy	Not pigmented	Dark green
W.16	Yellow	In upper canopy	Not pigmented	Black
W.20	Deep purple	In upper canopy	Not pigmented	Dark brown Dark brown
W.23	Deep purple	In upper canopy	Not pigmented	mottled
W.24	Light purple	Mostly above canopy	Not pigmented	Forest green
W.25	Cream	In upper canopy	Not pigmented	Dark green
W.26	Yellow	In upper canopy	Not pigmented	Black
W.27	Yellow	In upper canopy	Not pigmented	Dark brown
W.28	Mauve/pink Whitish-	Mostly above canopy	Not pigmented	Forest green
W.29	purple	In upper canopy	Not pigmented	Dark green
W.30	Deep purple	In upper canopy	Not pigmented	Dark green
W.31	Deep purple	Mostly above canopy	Not pigmented	Dark brown
W.32	Deep purple	Mostly above canopy	Not pigmented	Dark green
W.33	Deep purple	Mostly above canopy	Not pigmented	Dark green
W.35	Deep purple	In upper canopy	Not pigmented Uniformly	Dark brown
W.41	Light purple	In upper canopy	pigmented	Brown
W.49	Deep purple	Mostly above canopy	Not pigmented	Dark green
W.51	Light purple	Mostly above canopy	Not pigmented Uniformly	Dark green Dark brown
W.53	Light purple	In upper canopy	pigmented	mottled
W.58	Deep purple	Mostly above canopy	Not pigmented	Dark green
W.60	Mauve/pink	Below upper canopy	Not pigmented	Dark green
W.62	Deep purple	Mostly above canopy	Not pigmented	Dark green
W.72	Deep purple	In upper canopy	Not pigmented Uniformly	Dark brown
W.77	Deep purple	In upper canopy	pigmented	Brown
W.81	Deep purple	In upper canopy	Not pigmented	Dark green
W.82	Deep purple	Mostly above canopy	Not pigmented	Dark brown

Appendix 1 contn'd

Plant genotype	Flower colour	Raceme position	Main pod pigmentation	Pod colour
W.88	Deep purple	In upper canopy	Not pigmented	Dark green
W.89	Light purple	Below upper canopy	Not pigmented	Dark green
W.90	Deep purple	In upper canopy	Not pigmented	Dark brown
PARENT	Deep purple	In upper canopy	Not pigmented	Dark brown
G. E	Cream	Below upper canopy	Not pigmented	Flesh
C.96	Deep purple	Below upper canopy	Not pigmented	Brown
C.97	Light purple	Mostly above canopy	Not pigmented	Flesh
C.98	Deep purple	Below upper canopy	Not pigmented	Flesh
C.99	Cream	In upper canopy	Not pigmented	Brown
C.100	Light purple	Below upper canopy	Not pigmented	Brown
C.101	Deep purple	In upper canopy	Not pigmented	Light brown
C.102	Light purple	In upper canopy	Not pigmented	Flesh
			Uniformly	Dark brown
C.103	Deep purple	Below upper canopy	pigmented	mottled
C.104	Deep purple	Below upper canopy	Not pigmented	Brown
C.105	Light purple	Below upper canopy	Not pigmented	Brown
C.106	Light purple	Below upper canopy	Not pigmented	Flesh
C.107	Whitish-purple	Mostly above canopy	Not pigmented	Flesh
C.108	Whitish-purple	In upper canopy	Not pigmented	Flesh
C.109	Deep purple	Mostly above canopy	Not pigmented	Flesh
			Splashes of	
C.111	Deep purple	Mostly above canopy	pigment	Dark purple
C.112	Cream	Below upper canopy	Not pigmented	Flesh
			Uniformly	Dark brown
C.113	Deep purple	Below upper canopy	pigmented	mottled
C.114	Light purple	Below upper canopy	Not pigmented	Flesh
			Uniformly	Dark brown
C.115	Deep purple	In upper canopy	pigmented	mottled
			Splashes of	Dark brown
C.116	White	Below upper canopy	pigment	mottled
C.117	Whitish-purple	In upper canopy	Not pigmented	Dark brown
C.119	Cream	Mostly above canopy	Not pigmented	Flesh
C.120	Light purple	Mostly above canopy	Not pigmented	Brown
			Splashes of	
C.121	Deep purple	Below upper canopy	pigment	Light brown
C.122	Cream	Below upper canopy	Not pigmented	Flesh
C.123	Light purple	Mostly above canopy	Not pigmented	Brown

Appendix 1 contn'd

Plant genotype	Flower colour	Raceme position	Main pod pigmentation	Pod colour
C.124	Whitish-purple	Mostly above canopy	Not pigmented	Flesh
C.125	Deep purple	Mostly above canopy	Not pigmented	Flesh
C.126	Deep purple	Below upper canopy	Not pigmented	Flesh
C.127	Light purple	Mostly above canopy	Not pigmented	Flesh
C.128	Light purple	Mostly above canopy	Splashes of pigment Uniformly pigmented	Dark brown mottled Dark brown mottled
C.130	Deep purple	Mostly above canopy	pigmented	mottled
C.131	Light purple	Mostly above canopy	Not pigmented	Brown
C.133	Deep purple	Below upper canopy	Not pigmented	Flesh
C.135	Light purple	Mostly above canopy	Not pigmented	Dark brown
C.136	Light purple	Mostly above canopy	Not pigmented	Brown
C.137	Cream	Below upper canopy	Not pigmented	Dark brown
C.138	Deep purple	Mostly above canopy	Not pigmented	Flesh
C.139	Light purple	Mostly above canopy	Not pigmented Uniformly pigmented	Brown Brown
C.141	Deep purple	Mostly above canopy	pigmented	Brown
C.142	Deep purple	Mostly above canopy	Not pigmented	Light brown
C.143	Light purple	Below upper canopy	Not pigmented	Brown
C.144	Light purple	Mostly above canopy	Not pigmented	Brown
C.145	Deep purple	Mostly above canopy	Not pigmented Uniformly pigmented	Brown mottled Brown
C.146	Cream	In upper canopy	pigmented	Brown
C.148	Light purple	Mostly above canopy	Not pigmented	Flesh
C.149	Deep purple	Mostly above canopy	Not pigmented	Flesh
C.150	Creamy-ppl	Mostly above canopy	Not pigmented	Light brown
C.151	Deep purple	Mostly above canopy	Not pigmented	Flesh
C.152	Deep purple	Mostly above canopy	Not pigmented Splashes of pigment	Brown Dark brown mottled
C.153	Deep purple	In upper canopy	pigment	mottled
C.154	Deep purple	Mostly above canopy	Not pigmented	Flesh
C.155	Light purple	Mostly above canopy	Not pigmented	Brown
C.156	Light purple	In upper canopy	Not pigmented	Dark brown

C = Cultivated type

Appendix 1 contn'd

Plant genotype	Flower colour	Raceme position	Main pod pigmentation	Pod colour
C.157	Creamy-purple	In upper canopy	Not pigmented Uniformly	Flesh
C.158	Light purple	Mostly above canopy	pigmented	Brown
C.159	White	Below upper canopy	Not pigmented	Brown mottled
C.160	Deep purple	In upper canopy	Not pigmented Splashes of	Brown Dark brown
C.161	Light purple	In upper canopy	pigment	mottled
C.162	Mauve/pink	In upper canopy	Not pigmented	Dark brown
C.163	Deep purple	In upper canopy	Not pigmented	Flesh
C.164	White	In upper canopy	Not pigmented	Flesh
C.165	Light purple	Below upper canopy	Not pigmented	Flesh
C.166	Deep purple	In upper canopy	Not pigmented Uniformly	Dark brown
C.167	Light purple	In upper canopy	pigmented Splashes of	Brown Dark brown
C.168	Light purple	In upper canopy	pigment Splashes of	mottled
C.169	Light purple	Mostly above canopy	pigment Splashes of	Light brown
C.170	Light purple	Below upper canopy	pigment	Light brown
C.171	Light purple	Mostly above canopy	Not pigmented Uniformly	Flesh
C.172	Light purple	Below upper canopy	pigmented	Dark purple
C.173	Deep purple	Mostly above canopy	Not pigmented	Brown
C.174	Light purple	Mostly above canopy	Not pigmented	Brown
C.175	Light purple	Mostly above canopy	Not pigmented	Light brown
C.176	Light purple	Mostly above canopy	Not pigmented	Brown
C.177	Light purple	Below upper canopy	Not pigmented	Brown
C.178	Deep purple	Mostly above canopy	Not pigmented	Brown mottled
C.181	Light purple	Mostly above canopy	Not pigmented	Flesh
C.183	Light purple	Mostly above canopy	Not pigmented Uniformly	Brown
C.184	Cream	Mostly above canopy	pigmented	Light brown
C.185	Deep purple	Mostly above canopy	Not pigmented	Brown
C.186	Cream	Below upper canopy	Not pigmented	Dark brown
C.187	Deep purple	Below upper canopy	Not pigmented	Brown
C.188	Light purple	Below upper canopy	Not pigmented	Dark brown

C = Cultivated type

Appendix 1 contn'd

Plant genotype	Pod wall Thickness	Pod curvature	Seed shape	Seed coat colour	Seed coat pattern
C.04	Thick	Straight	Kidney	Dark brown mottled	Solid
C.05	Thick	Straight	Rhomboid	Dark brown mottled	Solid
C.08	Intermediate	slightly curved	Rhomboid	Black mottled	Solid
C.10	Thick	Straight	Rhomboid	Dark green mottled	Solid
C.14	Thick	Straight	Rhomboid	Dark green	Solid
C.15	Thick	slightly curved	Ovoid	Dark brown mottled	Solid
C.16	Thick	Straight	Globose	Green	Solid
C.20	Thick	Straight	Ovoid	Brick red	Solid
C.23	Thick	Straight	Rhomboid	Dark brown mottled	Solid
C.24	Thick	Straight	Rhomboid	Brown mottled	Solid
C.25	Thick	slightly curved	Ovoid	Dark brown mottled	Solid
C.26	Thick	slightly curved	Crowder	Black	Solid
C.27	Thick	Straight	Ovoid	Dark brown mottled	Solid
C.28	Thick	Straight	Rhomboid	Brown mottled	Solid
C.29	Thick	Straight	Rhomboid	Black	Solid
C.30	Thick	Straight	Rhomboid	Dark green mottled	Solid
C.31	Thick	Straight	Rhomboid	Dark brown mottled	Solid
C.32	Thick	Straight	Kidney	Dirty white	Solid
C.33	Thick	Straight	Rhomboid	Brown mottled	Solid
C.35	Thick	Straight	Rhomboid	Dark brown mottled	Solid
C.41	Thick	Straight	Rhomboid	Brown mottled	Solid
C.49	Thick	Straight	Ovoid	Brown mottled	Solid
C.51	Thick	Straight	Rhomboid	Brown mottled	Solid
C.53	Thick	Straight	Kidney	Dark brown mottled	Solid
C.58	Thick	Straight	Ovoid	Dark green mottled	Solid
C.60	Thick	Straight	Ovoid	Black	Solid
C.62	Thick	Straight	Rhomboid	Dark brown mottled	Solid
C.72	Thick	Straight	Rhomboid	Dark brown mottled	Solid
C.77	Thick	Straight	Ovoid	Brown mottled	Solid
C.81	Thick	Straight	Rhomboid	Dark brown mottled	Solid
C.82	Thick	Straight	Rhomboid	Red	Solid

C = Cultivated type

Appendix 1 contn'd

Plant genotype	Pod wall Thickness	Pod curvature	Seed shape	Seed coat colour	Seed coat pattern
W.88	Thick	Straight	Ovoid	Dark brown mottled	Solid
W.89	Thick	Straight	Rhomboid	Dark green mottled	Solid
W.90	Thick	Straight	Rhomboid	Dark brown mottled	Solid
PARENT	Thick	Straight	Rhomboid	Dark brown mottled	Solid
G. E	Intermediate	slightly curved	Kidney	Cream	Golden
C.96	Thin	Coiled	Ovoid	Red	Solid
C.97	Intermediate	Straight	Ovoid	Dark brown mottled	small eye
C.98	Thin	Straight	Ovoid	Brown mottled	small eye
C.99	Intermediate	Straight	Ovoid	Cream	Whippoorwill
C.100	Intermediate	Straight	Rhomboid	Flesh	small eye
C.101	Intermediate	Straight	Ovoid	Brick red	small eye
C.102	Intermediate	Straight	Globose	Brown	small eye
C.103	Thin	slightly curved	Kidney	Flesh	Whippoorwill
C.104	Thin	Curved	Kidney	Dark brown mottled	small eye
C.105	Intermediate	Straight	Rhomboid	Dark brown mottled	Holstein
C.106	Intermediate	slightly curved	Rhomboid	Flesh	small eye
C.107	Intermediate	slightly curved	Ovoid	Dirty white	Holstein
C.108	Thin	slightly curved	Globose	Cream	Holstein
C.109	Intermediate	Straight	Rhomboid	Brown mottled	Solid
C.111	Thick	Straight	Rhomboid	Dark brown mottled	Whippoorwill
C.112	Intermediate	Straight	Kidney	Cream	small eye
C.113	Thin	slightly curved	Ovoid	Brown mottled	small eye
C.114	Thick	Straight	Ovoid	Flesh	small eye
C.115	Thick	Straight	Crowder	Black	Solid
C.116	Intermediate	Straight	Globose	Cream	Holstein
C.117	Thick	Straight	Ovoid	Dark purple	Solid
C.119	Intermediate	slightly curved	Globose	Dark brown mottled	Solid
C.120	Thick	slightly curved	Rhomboid	Black	Solid
C.121	Thin	Straight	Ovoid	Flesh	small eye
C.122	Intermediate	Straight	Globose	Dirty white	Holstein
C.123	Intermediate	Straight	Ovoid	Flesh	small eye

W = Wild relative; G. E = Golden eye; C = Cultivated type

Appendix 1 contn'd

Plant genotype	Pod wall Thickness	Pod curvature	Seed shape	Seed coat colour	Seed coat pattern
C.123	Intermediate	Straight	Ovoid	Flesh	small eye
C.124	Thin	Straight	Ovoid	Cream	Holstein
				Purple brown	
C.125	Intermediate	slightly curved	Ovoid	mottled	small eye
				Purple brown	
C.126	Intermediate	Straight	Ovoid	mottled	small eye
C.127	Intermediate	Straight	Kidney	Brown	small eye
C.128	Thick	Straight	Rhomboid	Brown mottled	small eye
C.130	Intermediate	Straight	Ovoid	Red	small eye
C.131	Intermediate	Straight	Rhomboid	Brown	Solid
C.133	Intermediate	Straight	Ovoid	Dirty white	Holstein
C.135	Intermediate	Straight	Globose	Flesh	small eye
C.136	Thin	Straight	Rhomboid	Dirty white	Holstein
C.137	Thin	Straight	Kidney	Cream	Holstein
				Dark brown	
C.138	Intermediate	Coiled	Rhomboid	mottled	small eye
C.139	Thin	slightly curved	Rhomboid	Brown	Solid
C.141	Thin	Straight	Kidney	Flesh	Solid
C.142	Intermediate	slightly curved	Ovoid	Flesh	Solid
C.143	Thick	Straight	Ovoid	Brown	Solid
C.144	Thin	slightly curved	Rhomboid	Flesh	Solid
C.145	Intermediate	Straight	Ovoid	Brown mottled	Solid
C.146	Thick	slightly curved	Ovoid	Red	Solid
C.148	Intermediate	slightly curved	Ovoid	Flesh	small eye
C.149	Intermediate	Straight	Rhomboid	Black	Solid
C.150	Thin	Straight	Rhomboid	Red & cream	Holstein
				Purple brown	
C.151	Intermediate	Straight	Ovoid	mottled	small eye
C.152	Thin	Straight	Rhomboid	Red	Solid
				Dark brown	
C.153	Intermediate	slightly curved	Rhomboid	mottled	Watson
C.154	Thin	Straight	Globose	Flesh	small eye
C.155	Intermediate	Straight	Rhomboid	Brown	small eye
C.156	Thick	slightly curved	Kidney	Red	Solid

C = Cultivated type

Appendix 1 contn'd

Plant genotype	Pod wall Thickness	Pod curvature	Seed shape	Seed coat colour	Seed coat pattern
C.157	Thin	Straight	Rhomboid	Dirty white	Holstein
C.158	Thin	Straight	Ovoid	Brown	Solid
C.159	Thin	slightly curved	Ovoid	Cream	Holstein
C.160	Intermediate	Straight	Ovoid	Dirty white	Whippoorwill
C.161	Intermediate	slightly curved	Ovoid	Brown mottled	Watson
C.162	Thick	Straight	Ovoid	Brown Purple brown	small eye
C.163	Thin	slightly curved	Kidney	mottled	small eye
C.164	Thin	slightly curved	Rhomboid	Red & cream	Holstein
C.165	Thin	slightly curved	Ovoid	Brown Dark green	Solid
C.166	Thick	Straight	Rhomboid	mottled	Solid
C.167	Thick	Straight	Rhomboid	Brown	Solid
C.168	Thin	Straight	Ovoid	Brick red	Solid
C.169	Intermediate	slightly curved	Globose	Flesh	small eye
C.170	Thick	Coiled	Ovoid	Brick red	Solid
C.171	Thin	slightly curved	Kidney	Brown	Solid
C.172	Thin	slightly curved	Rhomboid	Brown	Solid
C.173	Thin	slightly curved	Ovoid	Dark purple	small eye
C.174	Thin	Straight	Ovoid	Red	Solid
C.175	Intermediate	Straight	Ovoid	Brown	Solid
C.176	Intermediate	Straight	Ovoid	Brown mottled	Watson
C.177	Intermediate	Straight	Ovoid	Flesh Purple brown	Solid
C.178	Intermediate	Straight	Rhomboid	mottled	Solid
C.181	Thin	Straight	Ovoid	Black	Solid
C.183	Intermediate	Straight	Rhomboid	Red	Solid
C.184	Thin	Straight	Ovoid	Cream	small eye
C.185	Intermediate	slightly curved	Kidney	Brick red	Solid
C.186	Thin	Straight	Rhomboid	Cream	small eye
C.187	Intermediate	Straight	Globose	Brown Dark brown	small eye
C.188	Thin	Straight	Kidney	mottled	small eye

C = Cultivated type

Appendix 2: Final amino acid concentrations (x10-3ppm) for the seed quality traits.

Plant genotype	B-Threonine*	DL-Alpha-Alanine	DL-Beta_phenyl-Alanin*	D-Proline	Glutamine	Glycine
W.04	0.50443	0	0.85971	3.58785	0.33672	0.78656
W.08	0.60078	1.15927	3.11958	2.47497	0.34192	1.09388
W.10	0.85197	0	2.91538	1.66148	0.22058	1.09867
W.14	0.68893	2.22455	2.68564	2.57727	0.29298	1.37246
W.15	0.63604	1.46536	1.3792	1.59441	0.33302	0.96879
W.16	0.33929	1.75339	6.23005	2.79205	0.24351	0.67526
W.20	0.63754	1.57727	32.5621	3.45982	0.21542	1.08273
W.23	0.69361	0	8.89487	1.67226	0.23532	0.81758
W.24	0.63687	0.79264	3.03021	1.16732	0.35073	1.22449
W.25	0.77183	0	3.22397	2.25086	0.61721	0.35629
W.26	0.68193	0.09276	6.09655	2.08933	1.90352	0.91736
W.28	0.5271	0.92249	5.81634	1.76844	0.25744	0.75226
W.29	0.41744	0.73912	6.23137	4.81384	0.35889	0.67962
W.30	0.40839	0	1.44523	16.6575	0.25324	0.53642
W.31	1.13765	5.20101	5.13297	7.9665	0.61697	1.50441
W.32	0.5868	0.06709	1.78248	2.68392	0.15451	0.84851
W.33	0.52483	0	1.52232	7.19717	0.29744	0.58353
W.35	0.37603	0.08855	0.61498	11.8061	0.24535	0.85347
W.41	0.41159	0.08878	2.14938	2.53151	0.21923	0.94764
W.51	0.71906	0.04745	0.57822	2.37235	0.33023	0.66103
W.53	0.40647	0.16354	0.2799	1.61029	0.38714	0.95559
W.58	0.81314	0.12254	0.30209	2.0157	0.16448	0.6295
W.60	0.33367	0.06141	1.1953	1.95153	0.32349	0.47952
W.62	0.43035	0.08164	0.27576	1.55264	0.19246	0.81066
W.72	0.34611	14.6463	0.28262	0.72684	0.24348	0.8096
W.77	0.5397	2.99503	1.01743	0.72619	0.10789	0.36676
W.81	0.1204	2.46634	0.40199	1.00874	0.18127	0.07648

Appendix 2 contn'd

Plant genotype	B-Threonine*	DL-Alpha-Alanine	DL-Beta-phenyl-Alanin*	D-Proline	Glutamine	Glycine
W.82	0.25554	7.34059	0.40202	0.74764	0.1666	0.70239
W.88	0.32719	3.42794	0.63782	0.61148	0.48176	0.35425
W.89	0.24083	0.00824	0.28327	1.86015	0.41433	0.30571
C.96	0.42797	0.44286	2.13358	2.38286	0.17385	0.76982
C.97	0.4198	0.00285	0.27335	1.29494	0.30389	0.44508
C.98	0.54165	0	7.24407	0.75329	0.20004	0.71904
C.99	0.22658	6.8613	9.1997	0.98031	0.26235	0.42319
C.100	0.52551	3.11212	6.16896	2.06666	0.46288	0.76884
C.101	0.22838	9.13909	6.10235	0.69616	0.29051	0.4885
C.102	0.32445	2.39034	13.2563	3.14978	0.35609	0.64765
C.103	0.3904	3.15126	17.7186	2.36384	0.4534	0.17224
C.104	0.22222	0.79359	4.07773	1.45122	0.20827	0.48336
C.105	0.38604	2.0715	4.59541	1.58019	0.32731	0.22397
C.106	0.29464	16.4522	15.3021	1.2981	0.18412	0.71367
C.107	0.31386	12.674	4.31927	0.97836	0.19273	0.4342
C.108	0.32814	9.06263	3.25124	0.94314	0.23976	0.68166
C.109	0.26739	3.39155	15.7081	1.45899	0.31757	0.60315
C.111	0.47772	0.41547	9.55542	1.51873	0.25482	1.08386
C.112	0.22035	15.3072	24.3006	4.69065	0.34261	0
C.113	0.1912	26.4613	2.61584	1.18976	0.31739	0.47805
C.114	0.35576	1.21257	5.88324	2.86337	0.4809	0.35716
C.115	0.42071	6.69502	7.1841	3.43166	0.35702	0.32457
C.116	0.20511	1.74835	4.41188	1.72944	0.28335	0.13174
C.117	0.22161	2.4633	12.2833	0.72042	0.13508	0.6882
C.120	0.23614	6.57293	3.27228	0.06149	0.1157	0.44756
C.121	0.25286	4.62602	30.9281	1.22692	0.20002	0.07929
C.122	0.23651	1.79923	12.8687	1.29288	0.14732	0.31483

*Essential amino acid; W = Wild relative; C = Cultivated type

Appendix 2 contn'd

Plant genotype	B-Threonine*	DL-Alpha-Alanine	DL-Beta_phenyl-Alanin*	D-Proline	Glutamine	Glycine
C.123	0.32968	1.75023	24.2099	1.34697	0.18041	0.38213
C.124	0.32728	2.32832	23.0419	0.77191	0.63132	0.52161
C.125	0.28131	2.39074	22.8487	0.85713	0.10524	0.13387
C.126	0.3484	1.06178	14.8674	0.47559	0.13505	0.27979
C.127	0.42698	4.90716	16.0922	1.08327	0.1609	0.77428
C.128	0.19871	1.03764	9.49424	1.05267	0.1065	0.3669
C.130	0.28723	3.00752	15.5526	1.22559	0.51559	0.69696
C.131	0.16723	1.216	12.2184	0.62844	0.14287	0.61016
C.133	0.57112	0.03914	4.1722	0.79225	0.3003	0.49573
C.135	0.17074	1.7802	3.82787	0.61808	0.14046	0.71054
C.136	0.77484	2.75078	41.6362	0.80696	0.32306	1.19526
C.137	4.85794	8.12819	8.59497	19.7818	0.53708	0.56145
C.138	0.17133	1.68768	47.9036	0.66892	0.13757	0.69461
C.139	0.34628	0.81356	25.5531	1.94352	0.20057	0.4936
C.141	0.2224	6.86549	7.6878	1.72282	0.10386	0.35798
C.142	0.54329	2.30339	78.4062	0.48324	0.15171	0.47971
C.143	0.19031	5.16629	57.8148	1.21183	0.20712	0.1468
C.145	0.23091	6.98591	31.0976	0.37583	0.68743	0.70659
C.146	0.42544	3.88416	2.65352	0.95985	0.72228	0.85434
C.148	0.33371	0.28274	89.7815	1.05296	0.16116	0.11454
C.149	0.52508	8.36423	8.34711	1.49872	1.16473	0.49196
C.150	0.38588	5.11293	8.50666	1.37489	2.78834	0.64691
C.151	0.32282	4.93173	4.40289	2.05547	0.1361	0.1585
C.152	1.76876	13.6552	68.7954	2.30072	0.2973	0.57853
C.153	0.23227	0.05679	7.65488	0.57425	0.14489	0.61212
C.154	0.28276	11.4727	21.9447	4.8934	0.1271	0.20856
C.155	0.29731	1.5275	20.0086	0.60021	0.32689	0.09724

*Essential amino acid; C = Cultivated type

Appendix 2 contn'd

Plant genotype	B-Threonine*	DL-Alpha-Alanine	DL-Beta_phenyl-Alanine*	D-Proline	Glutamine	Glycine
C.156	0.19924	1.62559	nd	0.11123	0.24342	0.07783
C.157	0.24537	0.94921	25.2628	0.09646	0.1445	0.49788
C.158	0.47652	11.9814	184.914	16.9395	0.12281	0.9942
C.159	0.69279	5.39589	nd	12.8739	0.63424	1.03285
C.160	0.30282	2.9068	nd	1.08953	0.25666	1.08324
C.161	0.51574	9.18735	nd	1.03186	0.18528	0.89994
C.162	0.30022	0.60016	0.27312	1.26682	0.09749	0.34921
C.163	0.39666	4.43887	nd	2.74069	0.18754	0.88741
C.164	0.31478	0.02263	nd	0.75583	0.64226	0.6641
C.167	0.41509	4.05205	nd	1.50395	0.10166	0.29595
C.168	1.35842	7.81628	0.27158	1.10406	0.14727	0.44165
C.169	0.46611	5.3443	nd	0.6087	0.22288	1.16969
C.170	0.42758	0.13144	nd	0.81008	0.16499	0.3012
C.171	0.37735	0.19839	nd	2.28421	0.18495	0.5809
C.172	0.53083	12.5773	nd	0.74955	0.30364	0.52964
C.174	0.47685	2.91312	nd	1.05899	0.2263	0.24023
C.175	0.26891	4.32202	nd	0.70953	0.13354	0.57345
C.176	0.36998	5.04847	0.27111	0.60673	1.40893	0.1584
C.177	0	1.23718	0.27198	0	0.0952	0
C.178	0.18561	2.74105	nd	2.5133	0.11185	0.77439
C.181	0.56318	5.65906	0.27137	1.14794	0.21799	0.6247
C.183	0.42953	0.28845	0.27181	4.30136	0.12314	0.24974
C.184	0.66307	6.80764	0.271	1.36982	0.11564	1.076
C.185	0.45162	5.50164	0.2712	3.08355	0.13374	0.80952
C.186	0.3241	0.06304	0.27178	1.67868	0.14085	0.45011
C.187	0.4626	0.44522	nd	2.27071	0.25456	0.80439
C.188	0.53197	1.98596	nd	0.21567	0.2042	0.67243

*Essential amino acid; C = Cultivated type; nd= Not detected

Appendix 2 contn'd

Plant genotype	Iso-Leucine*	L-Asparagine	L-Aspartic Acid	L-Cysteine	L-Histidine*	L-Lysine*
W.04	4.25811	9.71885	1.54017	0	2.02334	0.35397
W.08	9.35294	3.08026	1.77766	0	1.27692	0.31418
W.10	2.6895	5.22957	1.71268	0	1.64459	0.19962
W.14	3.38542	8.22308	0.69915	0	2.3441	0.27251
W.15	1.68567	10.4812	0.59358	0	3.89344	0.33323
W.16	9.10167	1.70106	1.22019	0	1.26287	0.22148
W.20	15.9006	11.9953	4.18386	0	14.7339	0.21589
W.23	2.56959	9.9899	1.79905	0	13.6404	0.26285
W.24	8.70774	7.16377	0.4683	0	4.75926	0.34933
W.25	23.0491	13.4659	2.41766	0	9.64991	0.71693
W.26	5.40103	20.5477	2.05784	0	2.59831	1.40303
W.28	1.12738	8.9206	0.64635	0	8.1638	0.27597
W.29	7.83357	0.60017	24.824	0	0.93906	0.33372
W.30	7.98507	9.03632	1.42585	0	1.98711	0.22204
W.31	33.7818	4.23281	1.26041	0	4.98935	0.45063
W.32	5.29161	6.69035	1.34031	0	1.18987	0.27645
W.33	1.57848	3.40751	1.1116	0	1.38783	0.36244
W.35	1.27437	11.613	0.38385	0	2.30745	0.27557
W.41	0	7.51179	1.35953	0	4.78786	0.21778
W.51	0.66025	6.99794	0.50631	0	3.07788	0.32002
W.53	12.5671	21.9523	0.70191	0	5.29718	0.24052
W.58	0	4.29242	1.72255	0	0.62404	0.2746
W.60	1.3294	3.62233	0.95711	0	1.38274	0.30409
W.62	0	6.75397	0.40928	0	3.8442	0.17998
W.72	6.45853	12.9604	1.08848	0	3.5992	0.18428
W.77	0.60314	7.72873	1.4944	0	1.55181	0.23091
W.81	3.02093	2.23938	0.90924	0	2.55067	0.15763

*Essential amino acid; W = Wild relative

Appendix 2 contn'd

Plant genotype	Iso- Leucine*	L- Asparagine	L-Aspartic Acid	L-Cysteine	L- Histidine*	L- Lysine*
W.82	0.25476	6.84018	0.82333	0	4.90668	0.19431
W.88	7.50757	5.39704	1.21707	0	10.8564	0.91593
W.89	5.27223	3.11721	0.37663	0	7.40396	0.15789
C.96	2.98457	20.2836	0.20842	0	8.17072	0.18826
C.97	0.451	4.8104	0.41633	0	1.18787	0.28121
C.98	1.27229	14.0027	1.13326	0	6.26046	0.17334
C.99	0.80828	4.12741	1.5369	0	10.1081	0.25168
C.100	8.37963	5.97084	0.73039	0	2.20675	0.37494
C.101	1.64458	8.58941	0.31682	0	2.41383	0.21876
C.102	5.31776	5.94954	0.80194	0	6.50414	0.22774
C.103	6.72028	8.66581	0.90242	0	4.54929	0.34355
C.104	0.17531	4.41819	0.93057	0	2.09382	0.18932
C.105	2.39732	0.97514	0.59075	0	4.17483	0.33285
C.106	0.55907	6.14601	0.6962	0	1.40439	0.15107
C.107	0	4.41788	0.88779	0	8.33962	0.18809
C.108	5.25816	5.06138	3.71839	0	12.9583	0.19979
C.109	0	34.9656	1.78269	0	25.1216	0.24925
C.111	0.31442	12.1629	1.55581	0	19.6326	0.22137
C.112	0	81.1385	1.41213	0	14.1479	0.35514
C.113	6.2033	58.2831	0.98406	0	16.5318	0.20625
C.114	0	15.6749	1.1745	0	6.36477	0.29703
C.115	0	7.40605	0.27857	0	2.46133	0.32868
C.116	4.26123	35.7986	1.23744	0	5.17336	0.25272
C.117	1.65182	9.16539	0.81941	0	2.32263	0.12949
C.120	0	8.05327	0.33357	0	6.45426	0.21037
C.121	3.51713	8.31914	1.1944	0	29.2629	0.21352
C.122	0	4.75597	0.69684	0	5.26568	0.25148

*Essential amino acid; C = Cultivated type

Appendix 2 contn'd

Plant genotype	Iso-Leucine*	L-Asparagine	L-Aspartic Acid	L-Cysteine	L-Histidine*	L-Lysine*
C.123	2.47303	18.6852	1.341	0	9.51334	0.21829
C.124	0	6.33818	0.81585	0	16.1747	0.12775
C.125	0	4.36148	0.85526	0	6.60596	0.14763
C.126	0.81406	8.37502	0.84598	0	18.6594	0.20283
C.127	2.47633	32.4272	1.63674	0	9.65792	0.20435
C.128	0	3.881	0.97076	0	3.47389	0.17079
C.130	5.49211	12.9122	1.07727	0	4.29407	0.29471
C.131	0	3.5801	0.67864	0	3.14183	0.19989
C.133	0	4.38015	0.90642	0	8.40771	0.33379
C.135	0	15.0139	0.93725	0	4.28439	0.13921
C.136	0	12.9705	1.40054	0	11.5424	0.13542
C.137	7.51699	19.8333	0.47862	0	10.1174	0.42343
C.138	0	6.04184	1.11615	0	3.26893	0.2686
C.139	0	34.1081	2.24271	0	13.3294	0.34106
C.141	0	28.1795	1.30347	0	6.15408	0.169
C.142	0	9.51999	0.87039	0	8.73243	0.15101
C.143	6.76091	2.40444	0.48857	0	1.20584	0.25603
C.145	0	5.6673	0.72634	0	2.5562	0.17881
C.146	0	6.54044	0.97613	0	2.37889	0.18145
C.148	0	2.86028	0.72765	0	3.96339	0.21383
C.149	0	7.05058	0.85483	0	6.01235	0.84715
C.150	0	4.95701	1.23712	0	11.7482	2.12037
C.151	0	6.15354	0.8918	0	10.9034	0.16846
C.152	0	20.2559	1.36161	0	15.48	0.22974
C.153	0	3.40841	0.70925	0	3.15748	0.14724
C.154	0	3.83035	1.11606	0	3.99086	0.21785
C.155	0	5.93508	0.94316	0	1.80332	0.20872

*Essential amino acid; C = Cultivated type

Appendix 2 contn'd

Plant genotype	Iso-Leucine*	L-Asparagine	L-Aspartic Acid	L-Cysteine	L-Histidine*	L-Lysine*
C.156	0	25.9124	1.3183	0	12.4335	0.15271
C.157	0	4.97587	4.5456	0	3.61778	0.24774
C.158	0	52.2852	2.55824	0	61.7569	0.20589
C.159	0	29.9052	1.8647	0	34.9365	0.41951
C.160	0	5.37833	1.80891	0	4.14353	0.2114
C.161	0	12.3381	1.65327	0	4.63199	0.17727
C.162	0	8.57863	1.2363	0	2.17469	0.18592
C.163	0	82.6821	2.87637	0	5.30246	0.28442
C.164	0	11.4068	1.50862	0	3.83721	0.14247
C.167	0	15.7643	0.43029	0	4.50422	0.19059
C.168	0	23.8945	1.53191	0	2.88146	0.1291
C.169	0	5.20569	0.76059	0	1.13066	0.20924
C.170	0	54.9654	0.7601	0	6.84082	0.15118
C.171	0	9.92104	3.65604	0	3.16358	0.19445
C.172	0	12.2015	1.5964	0	5.82535	0.26008
C.174	0	10.0399	0.9525	0	2.27079	0.1766
C.175	0	6.03096	0.72842	0	2.31452	0.1426
C.176	0	18.5633	1.02405	0	1.86787	0.23363
C.177	0	0.53584	0.15245	0	0.36862	0.12556
C.178	0	24.1771	1.26153	0	1.49641	0.1948
C.181	0	10.3025	1.30216	0	6.08657	0.16908
C.183	0	31.879	1.99956	0	3.746	0.15457
C.184	0	21.6256	1.76069	0	5.29206	0.21669
C.185	0	23.5104	1.77278	0	4.96171	0.22224
C.186	0	23.304	1.95681	0	5.52338	0.14593
C.187	0	45.3529	2.12997	0	9.36231	0.23636
C.188	0	8.36772	0.59623	0	2.95338	0.24001

*Essential amino acid; C = Cultivated type

Appendix 2 contn'd

Plant genotype	L-Methionine*	L-Serine	L-Threonine*	L-Tryptophan*	L-Tyrosine	L-Valine*	Trans-4-Hydroxy-L-Proline
W.04	0.07147	0.8084	0.64766	65.8145	1.42817	6.28669	3.29499
W.08	0.04023	0.90063	0.7153	54.7717	1.34504	5.889	6.96755
W.10	0.02784	0.88024	1.03652	43.9593	1.03998	8.24332	2.16538
W.14	0.18458	0.52377	0.88389	21.7437	1.67908	5.19979	2.67748
W.15	0.1394	0.83934	0.76881	72.4363	1.46541	3.91378	1.48229
W.16	0.20107	0.91537	0.48508	84.0577	1.82447	6.24478	6.7252
W.20	0	0.68293	0.59961	99.3452	4.09008	6.59204	11.5402
W.23	0.18781	0.73574	0.86708	120.85	0.92056	5.13122	2.09918
W.24	0	0.73122	0.7911	80.385	0.77969	2.3799	6.44668
W.25	1.24177	0.71346	0.85406	169.353	1.24655	13.1393	16.6064
W.26	0.5621	0.88821	0.81411	44.8615	1.21921	10.7526	4.1044
W.28	0	0.72065	0.62247	53.4014	0.80754	6.56137	1.07889
W.29	0.31413	0.77281	0.40375	249.534	0.79805	4.53104	5.82713
W.30	0.01116	0.52025	0.52592	63.6315	0.80763	2.24163	5.93442
W.31	0.82532	0.98956	1.22523	305.644	5.14076	10.9389	8.05043
W.32	0.34507	0.30828	0.68313	37.0077	0.86951	2.58959	4.02691
W.33	0.03578	0.63836	0.61548	20.7965	0.89194	5.82403	1.39728
W.35	0.02265	0.60287	0.5523	125.202	0.79706	2.31073	1.18531
W.41	0	0.71546	0.54766	140.159	2.46873	6.93219	0
W.51	0	0.48197	0.79233	133.057	1.57987	6.04724	0.76882
W.53	0	0.84352	0.55149	160.25	1.84182	3.41366	1.60745
W.58	0	0.90199	0.9469	58.2076	0.97242	2.34001	0
W.60	0.05592	0.30263	0.38208	96.4462	0.9076	6.40101	1.22087
W.62	0	0.68278	0.57918	241.222	1.0946	3.0979	6.15127
W.72	0.01278	0.48542	0.49468	689.714	3.70076	6.31537	4.8565
W.77	0.04133	0.50624	0.43555	408.006	1.68522	6.27386	0.70821
W.81	0	0.45889	0.23459	145.201	2.10352	5.3422	2.41882

*Essential amino acid; W = Wild relative

Appendix 2 contn'd

Plant genotype	L-Methionine*	L-Serine	L-Threonine*	L-Tryptophan*	L-Tyrosine	L-Valine*	Trans-4-Hydroxy-L-Proline
W.82	0.46701	0.46368	0.41503	1352.49	7.05724	4.72623	0.45982
W.88	0	0.53945	0.50753	266.695	5.41772	1.92086	5.59457
W.89	0	0.38671	0.39323	1007.52	0.85559	6.47782	0.52889
C.96	0.49521	0.51439	0.55901	1965.37	1.7559	1.62073	2.39306
C.97	0	0.07485	0.53173	290.961	0.14391	4.7625	3.22304
C.98	0.11389	0.23928	0.67795	48.0352	3.07961	5.14017	1.18043
C.99	0.51905	0.47017	0.33217	365.197	4.4465	4.61088	0.85106
C.100	2.20997	0.67086	2.15002	79.7413	1.09048	2.75976	6.21385
C.101	0.10855	0.36132	0.36081	329.377	3.19592	1.72957	1.44409
C.102	0	0.21372	0.43625	206.806	7.51941	1.56646	4.14012
C.103	1.27763	0.3845	0.27686	338.614	3.21964	11.3802	5.0387
C.104	0.00282	0.33645	0.3712	68.0611	2.06003	1.85823	0.40355
C.105	0.10139	0.38092	0.50132	162.214	2.65041	1.54611	1.98333
C.106	0.09811	0.28079	0.40838	37.3929	1.25633	5.20499	0.67533
C.107	0	0.41283	0.42829	291.38	4.74581	5.10357	0
C.108	0.19506	0.505	0.43754	784.576	1.31848	5.04576	4.00397
C.109	0.1361	0.36476	0.4364	2598.434	4.26123	10.0417	0
C.111	0	0.45529	0.62879	90.8366	1.39337	3.75267	0.50206
C.112	0.24317	0.62978	0.428	415.002	0.81813	5.98576	0
C.113	0.06458	0.43921	1.74617	275.434	1.04289	7.66802	4.67089
C.114	0	0.48627	0.41975	399.904	0.26307	6.00039	0.12148
C.115	0.027	0.08868	0.45479	97.5387	3.26996	1.48415	0
C.116	0	0.33613	1.10756	405.97	3.48486	6.32175	3.2972
C.117	0	0.27677	0.33292	1547.16	0.72751	4.19755	0.0891
C.120	0.26501	0.32375	0.38713	95.3864	1.39962	3.97089	0
C.121	0	0.38611	0.41038	202.304	5.2492	5.80993	2.99754
C.122	0.52276	0.34166	0.38349	249.626	2.26513	1.73575	0

*Essential amino acid; W = Wild relative; C = Cultivated type

Appendix 2 contn'd

Plant genotype	L-Methionine*	L-Serine	L-Threonine*	L-Tryptophan*	L-Tyrosine	L-Valine*	Trans-4-Hydroxy-L-Proline
C.123	0	0.47408	0.49611	114.361	2.05387	6.0891	0.72848
C.124	0	0.30634	0.44761	1007.94	0.32193	1.50543	0
C.125	0.30869	0.36195	0.37192	52.9908	1.97723	6.48742	0
C.126	0	0.35265	0.46031	402.834	1.4702	5.07389	0.85578
C.127	0.03097	0.3737	0.60252	227.913	0.46524	6.11282	2.03313
C.128	0	0.21388	0.34771	112.212	0.24379	4.32977	0
C.130	0.11467	0.56946	0.44633	115.463	2.16384	2.78413	4.16808
C.131	0	0.34228	0.29315	12.0645	1.91075	1.41051	0
C.133	0.06708	0.44366	0.69827	563.597	0.79665	5.15521	0
C.135	0.12162	0.4099	0.33589	737.642	1.10012	4.46057	0
C.136	0.70303	0.41218	0.83626	2063.42	3.67025	8.41415	0
C.137	1.43115	0.72733	0.6494	209.485	2.27072	6.30489	5.60142
C.138	0	0.53112	0.32259	680.092	1.50338	4.76873	0
C.139	0	0.39456	0.45858	751.828	2.1237	7.55871	0
C.141	1.0397	0.06375	0.36833	563.477	0.53746	4.73217	0
C.142	0	0.37858	0.65898	28.6272	1.04649	5.75663	0
C.143	0	0.62887	0.36455	806.52	0.90802	7.63514	5.06747
C.145	0	0.39514	0.40042	0.0108	1.26508	3.75844	0
C.146	0.32968	0.3881	0.5427	136.214	1.24336	4.96964	0
C.148	0	0.32413	0.43081	0	0.35225	4.9696	0
C.149	0.19387	0.56873	0.65343	381.318	3.40912	9.07672	0
C.150	0	0.40291	0.58188	346.524	2.24544	5.36706	0
C.151	0	0.35416	0.44176	504.902	0.25929	4.12659	0
C.152	0	1.26531	0.44439	1685.33	1.55149	9.23079	0
C.153	0	0.32789	0.42794	0	0.67067	3.92087	0
C.154	0.08786	0.43234	0.44235	0	0.68344	2.23996	0
C.155	0	0.12592	0.46485	7.63808	0.85812	4.31478	0

*Essential amino acid; C = Cultivated type

Appendix 2 contn'd

Plant genotype	L-Methionine*	L-Serine	L-Threonine*	L-Tryptophan*	L-Tyrosine	L-Valine*	Trans-4-Hydroxy-L-Proline
C.156	0.05486	0.34078	0.32609	0	0.58231	4.80951	0
C.157	0	0.35153	0.21648	3.68382	0.97531	8.42191	0
C.158	0	0.43743	0.6181	812.022	0.79383	4.23879	0
C.159	0.37434	0.6109	3.20143	0.02723	2.20221	13.1861	0
C.160	0.02202	0.63777	0.49045	0.02663	0.46518	6.32351	0
C.161	0	0.42364	0.62871	0.00104	0.41415	5.77013	0
C.162	0	0.36326	0.4852	0	0.14415	4.15893	0
C.163	0	1.35912	0.51022	0	3.195	6.95775	0
C.164	0	0.37988	0.49749	0	0.46262	2.03551	0
C.167	0	0.93173	0.59249	0	0.24231	2.93081	0
C.168	0.12275	0.97126	0.38811	0	0.83562	2.14993	0
C.169	0.04342	0.47418	0.59974	0	0.37605	4.31595	0
C.170	0.01835	0.49047	0.56945	0	0.34343	3.05398	0
C.171	0.04758	0.18427	0.51411	0.07818	0.59004	2.47474	0
C.172	0.02163	0.41133	0.68386	0	1.03388	2.02718	0
C.174	0	0.38078	0.56588	0	2.47094	9.02621	0
C.175	0	0.11118	0.40274	0	0.22853	3.62208	0
C.176	0	0.2989	0.52548	0	0.14655	3.71018	0
C.177	0	0	0.07474	0	0.06606	0.14254	0
C.178	0.01733	0.62488	0.45585	0	1.38338	2.0996	0
C.181	0	0.40847	0.69789	0	0.81067	7.96474	0
C.183	0	0.46867	0.57424	0	0.20581	5.672	0
C.184	0	0.49094	0.89804	0	0.30058	2.71283	
C.185	0.02828	0.51957	0.60899	0	0.94404	9.87718	0
C.186	0	0.54221	0.45887	0	0.14327	3.15266	0
C.187	0.20525	0.56756	0.55764	0.05454	1.40421	2.53242	0
C.188	0.02101	0.36258	0.63942	0	0.37378	4.89638	0

*Essential amino acid; C = Cultivated type

Appendix 3: Morpho-agronomic quantitative traits of cowpea genotypes

Plant genotype	Days to germination	Days to first leaf stage	Chlorophyll content	Days to flowering	Number of flowers /plant	Mean peduncle length /plant	Number of pods /peduncle
W.01	5	12	1.16	nd	nd	nd	nd
W.02	6	12	1.32	nd	nd	nd	nd
W.03	7	15	1.58	nd	nd	nd	nd
W.04	15	22	1.59	87	12	15.8	2
W.05	21	28	1.46	143	2	14.5	2
W.06	8	16	1.38	nd	nd	nd	nd
W.07	6	13	1.19	nd	nd	nd	nd
W.08	3	11	1.72	86	10	19.5	2
W.09	3	11	1.63	nd	nd	nd	nd
W.10	3	10	1.3	70	11	23.4	2
W.11	8	13	0.56	nd	nd	nd	nd
W.12	7	13	1.15	nd	nd	nd	nd
W.13	6	12	1.06	nd	nd	nd	nd
W.14	4	10	1.54	61	25	17.4	2
W.15	3	11	1.44	68	10	21.3	2
W.16	3	11	1.35	82	17	9.8	2
W.17	13	18	1.3	nd	nd	nd	nd
W.18	5	11	1.6	nd	nd	nd	nd
W.19	14	19	1.26	nd	nd	nd	nd
W.20	3	10	1.14	64	10	8.9	2
W.21	8	14	1.15	nd	nd	nd	nd
W.22	3	11	0.99	nd	nd	nd	nd
W.23	15	23	0.99	81	10	12.7	2
W.24	4	10	1.08	51	43	27.4	2
W.25	3	11	1.17	51	8	17.7	2
W.26	8	14	1.11	73	17	8.3	2
W.27	4	10	1.04	78	11	9.9	2
W.28	3	10	1.14	61	14	22.6	2
W.29	15	21	1.02	90	11	4.4	2
W.30	3	13	1.22	83	13	13.4	2
W.31	3	10	1.33	38	21	18	2
W.32	12	18	1.11	40	25	10.9	2

W = Wild relative

Appendix 3 contn'd

Plant genotype	Days to germination	Days to first leaf stage	Chlorophyll content	Days to flowering	Number of flowers /plant	Mean peduncle length /plant	Number of pods /peduncle
W.33	3	14	1.08	58	5	18.9	2
W.34	3	14	1.16	nd	nd	nd	nd
W.35	3	10	1.31	81	13	16.3	2
W.37	3	12	1.1	nd	nd	nd	nd
W.38	4	10	1.03	nd	nd	nd	nd
W.39	3	13	1.13	nd	nd	nd	nd
W.40	4	11	0.91	nd	nd	nd	nd
W.41	8	13	1.22	89	7	15.8	2
W.42	4	10	1.23	nd	nd	nd	nd
W.43	3	13	1.2	nd	nd	nd	nd
W.44	41	47	1.09	nd	nd	nd	nd
W.45	8	14	1.04	nd	nd	nd	nd
W.46	8	28	1.05	nd	nd	nd	nd
W.47	6	12	1.05	nd	nd	nd	nd
W.48	4	11	1.37	nd	nd	nd	nd
W.49	3	11	1.48	66	6	13.2	2
W.50	3	10	1.4	nd	nd	nd	nd
W.51	4	11	1.35	63	17	16.5	2
W.52	3	10	0.72	nd	nd	nd	nd
W.53	3	11	1.65	98	4	15.2	2
W.54	3	10	1.77	nd	nd	nd	nd
W.55	3	11	1.42	nd	nd	nd	nd
W.56	15	21	1.35	nd	nd	nd	nd
W.57	8	14	1.31	nd	nd	nd	nd
W.58	3	14	1.25	108	5	13.8	2
W.59	5	13	1.34	nd	nd	nd	nd
W.60	3	12	1.46	110	5	16.1	2
W.61	3	12	0.87	nd	nd	nd	nd
W.62	4	12	0.33	66	8	10.3	2
W.63	3	11	0.58	nd	nd	nd	nd
W.64	8	14	0.33	nd	nd	nd	nd
W.65	3	12	1.62	nd	nd	nd	nd

W = Wild relative; nd= Not detected

Appendix 3 contn'd

Plant genotype	Days to germination	Days to first leaf stage	Chlorophyll content	Days to flowering	Number of flowers /plant	Mean peduncle length /plant	Number of pods /peduncle
W.66	4	12	1.32	nd	nd	nd	nd
W.67	8	15	1.29	nd	nd	nd	nd
W.68	3	13	1.47	nd	nd	nd	nd
W.69	3	12	1.57	nd	nd	nd	nd
W.70	15	19	1.42	nd	nd	nd	nd
W.71	3	13	1.21	nd	nd	nd	nd
W.72	11	17	1.35	65	6	12.1	2
W.73	4	13	1.09	nd	nd	nd	nd
W.74	3	11	1.38	nd	nd	nd	nd
W.75	3	11	1.58	nd	nd	nd	nd
W.76	3	12	1.15	nd	nd	nd	nd
W.77	3	12	1.49	45	8	15.3	2
W.78	4	14	1.55	nd	nd	nd	nd
W.79	3	11	1.27	nd	nd	nd	nd
W.80	3	10	1.73	nd	nd	nd	nd
W.81	3	11	1.35	58	5	7.7	2
W.82	8	15	1.35	50	6	6.3	2
W.83	4	12	1.48	nd	nd	nd	nd
W.84	5	12	1.45	nd	nd	nd	nd
W.85	15	19	1.27	nd	nd	nd	nd
W.86	4	13	1.45	nd	nd	nd	nd
W.87	3	11	1.15	nd	nd	nd	nd
W.88	5	14	1.09	110	10	15.5	2
W.89	3	11	1.28	85	18	13.6	2
W.90	3	11	1.66	138	4	14.9	2
W.93	8	14	1.4	nd	nd	nd	nd
W.94	15	21	1.49	nd	nd	nd	nd
W.95	3	13	1.33	nd	nd	nd	nd
PARENT	6	12	1.32	82	9	16.3	2
G.E	3	11	1.81	90	8	8.5	2
C.96	3	11	1.6	47	5	14.3	2
C.97	3	13	1.47	57	5	23.3	2

W = Wild relative; G. E = Golden eye; C = Cultivated type; nd= Not detected

Appendix 3 contn'd

Plant genotype	Days to germination	Days to first leaf stage	Chlorophyll content	Days to flowering	Number of flowers /plant	Mean peduncle length /plant	Number of pods /peduncle
C.98	3	12	1.63	70	6	10.4	2
C.99	3	14	1.58	35	7	15.2	1
C.100	3	12	1.57	46	12	15.1	1
C.101	3	12	1.61	50	7	18	2
C.102	3	13	1.54	41	11	16.4	2
C.103	3	11	1.7	55	6	14.8	2
C.104	4	13	1.58	61	9	5.5	2
C.105	3	12	1.62	35	17	8.8	2
C.106	3	12	1.83	61	7	16.4	1
C.107	4	13	1.66	57	9	13.2	2
C.108	3	11	1.56	39	18	14.6	2
C.109	3	12	1.54	43	28	23.9	2
C.110	3	11	1.67	nd	nd	nd	nd
C.111	2	10	1.79	41	6	16.2	2
C.112	3	13	1.45	58	5	17.4	2
C.113	3	13	1.49	68	5	3.0	2
C.114	3	11	1.42	65	8	8.3	2
C.115	3	13	1.52	85	12	17.2	2
C.116	3	11	1.49	61	9	10.5	2
C.117	3	13	1.45	58	5	23.6	2
C.118	3	13	1.46	nd	nd	nd	nd
C.119	3	13	1.54	74	6	8.7	2
C.120	3	13	1.47	50	7	12.3	2
C.121	3	12	1.52	58	5	13.4	2
C.122	3	12	1.58	87	5	12.3	2
C.123	3	13	1.61	55	9	17.6	2
C.124	3	13	1.57	61	7	16.8	2
C.125	8	14	1.37	55	8	9.8	2
C.126	3	13	1.78	70	7	11.6	2
C.127	3	13	1.69	62	5	16.8	2
C.128	3	11	1.42	52	6	11.5	2
C.129	3	10	1.53	nd	nd	nd	nd

C = Cultivated type; nd= Not detected

Appendix 3 contn'd

Plant genotype	Days to germination	Days to first leaf stage	Chlorophyll content	Days to flowering	Number of flowers /plant	Mean peduncle length /plant	Number of pods /peduncle
C.130	3	11	1.41	40	6	12.3	2
C.131	3	11	1.45	41	11	19.2	2
C.132	3	11	1.46	nd	nd	nd	nd
C.133	3	11	1.38	89	5	9.8	2
C.134	12	18	1.63	nd	nd	nd	nd
C.135	3	11	1.41	41	7	14.8	2
C.136	3	11	1.54	41	11	18	2
C.137	3	10	1.51	82	3	7.9	2
C.138	3	11	1.74	79	3	11.5	2
C.139	3	10	1.59	55	3	3.4	2
C.140	3	10	1.35	nd	nd	nd	nd
C.141	3	11	1.49	50	7	3.8	2
C.142	3	11	1.9	86	10	10.2	2
C.143	3	11	1.57	53	10	11.8	2
C.144	3	11	1.6	58	2	8.9	1
C.145	4	14	1.23	55	7	16.8	2
C.146	3	13	1.44	46	5	9.7	2
C.147	3	13	1.27	nd	nd	nd	nd
C.148	5	13	1.31	95	5	10.1	2
C.149	3	11	1.65	59	8	12.4	2
C.150	3	11	1.7	73	5	5.4	2
C.151	3	11	1.48	56	11	12.6	2
C.152	3	13	1.41	50	12	22.8	2
C.153	3	14	1.51	60	8	14.3	2
C.154	4	14	1.52	58	15	10.7	2
C.155	8	15	1.42	61	7	7	2
C.156	3	13	1.51	49	7	16.5	2
C.157	3	13	1.51	48	15	17.2	2
C.158	3	10	1.44	38	5	19.3	2
C.159	3	12	1.37	55	8	15.6	2
C.160	3	13	1.25	73	4	10.5	2
C.161	3	11	1.33	68	4	5.4	2

C = Cultivated type; nd= Not detected

Appendix 3 contn'd

Plant genotype	Days to germination	Days to first leaf stage	Chlorophyll content	Days to flowering	Number of flowers /plant	Mean peduncle length /plant	Number of pods /peduncle
C.162	3	11	1.41	68	13	10.7	2
C.163	3	12	1.34	67	5	11.8	2
C.164	3	10	1.45	51	18	17	2
C.165	3	10	1.35	71	5	12.5	2
C.166	3	12	1.48	130	12	15.2	2
C.167	3	12	1.52	90	6	8.9	2
C.168	3	13	1.15	70	5	5.3	2
C.169	3	11	1.23	64	4	9.6	2
C.170	3	14	1.44	56	5	8.5	2
C.171	3	12	1.04	65	5	21	2
C.172	3	11	1.32	44	6	8.9	2
C.173	3	12	1.39	130	2	9.8	2
C.174	3	11	1.56	55	5	17.8	2
C.175	3	11	1.41	57	7	6.8	2
C.176	3	14	1.49	73	4	8.9	2
C.177	3	13	1.46	39	25	17.5	2
C.178	3	11	1.52	29	9	8.9	2
C.179	3	11	1.37	nd	nd	nd	nd
C.180	3	10	1.32	nd	nd	nd	nd
C.181	3	13	1.33	90	5	4.9	2
C.182	3	13	1.45	nd	nd	nd	nd
C.183	3	11	1.71	50	9	19.2	2
C.184	3	12	1.39	75	5	17.4	2
C.185	3	12	1.28	90	9	22	2
C.186	3	11	1.38	71	6	5.8	2
C.187	3	13	1.39	52	10	22.7	2
C.188	3	11	1.43	70	7	15.6	2

C = Cultivated type; nd= Not detected

Appendix 3 contn'd

Plant genotype	Days to first matured pod	Number of pods /plant	Mean pod length/ plant	Average seed/pod	20 seed weight /grams	Seed yield /plant	Seed abortion rate
W.01	nd	nd	nd	nd	nd	nd	nd
W.02	nd	nd	nd	nd	nd	nd	nd
W.03	nd	nd	nd	nd	nd	nd	nd
W.04	104	11	8.9	10.7	1.032	115	2
W.05	159	1	10.2	13	1.0321	13	1
W.06	nd	nd	nd	nd	nd	nd	nd
W.07	nd	nd	nd	nd	nd	nd	nd
W.08	104	8	8.4	10.3	0.6613	77	2
W.09	nd	nd	nd	nd	nd	nd	nd
W.10	85	8	9.1	12.5	0.3511	100	2
W.11	nd	nd	nd	nd	nd	nd	nd
W.12	nd	nd	nd	nd	nd	nd	nd
W.13	nd	nd	nd	nd	nd	nd	nd
W.14	77	23	7.2	8.4	0.3406	221	2
W.15	83	9	7.5	13.8	0.3205	125	1
W.16	97	16	8.8	9.8	0.5092	151	1
W.17	nd	nd	nd	nd	nd	nd	nd
W.18	nd	nd	nd	nd	nd	nd	nd
W.19	nd	nd	nd	nd	nd	nd	nd
W.20	81	9	9.8	9.5	0.3408	116	2
W.21	nd	nd	nd	nd	nd	nd	nd
W.22	nd	nd	nd	nd	nd	nd	nd
W.23	95	9	7.9	11	0.3561	99	2
W.24	67	40	9.8	12.1	0.3559	479	1
W.25	68	1	6.1	9.8	0.321	59	2
W.26	87	15	5.8	5.8	0.644	94	2
W.27	93	10	5.3	6.5	0.3211	65	2
W.28	76	13	7.5	9.9	0.3406	129	2
W.29	107	10	5.2	8.4	0.3521	88	1
W.30	97	12	8.9	11.4	0.3425	131	2
W.31	53	20	11.3	11.1	1.1001	225	1
W.32	56	20	10.3	10.8	0.5083	215	1

W = Wild relative; nd= Not detected

Appendix 3 contn'd

Plant genotype	Days to first matured pod	Number of pods /plant	Mean pod length/ plant	Average seed/pod	20 seed weight /grams	Seed yield /plant	Seed abortion rate
W.33	72	3	8.7	7.3	1.0001	25	1
W.34	nd	nd	nd	nd	nd	nd	nd
W.35	97	12	8.8	11	0.3521	127	2
W.37	nd	nd	nd	nd	nd	nd	nd
W.38	nd	nd	nd	nd	nd	nd	nd
W.39	nd	nd	nd	nd	nd	nd	nd
W.40	nd	nd	nd	nd	nd	nd	nd
W.41	105	6	9	9.4	0.3598	47	2
W.42	nd	nd	nd	nd	nd	nd	nd
W.43	nd	nd	nd	nd	nd	nd	nd
W.44	nd	nd	nd	nd	nd	nd	nd
W.45	nd	nd	nd	nd	nd	nd	nd
W.46	nd	nd	nd	nd	nd	nd	nd
W.47	nd	nd	nd	nd	nd	nd	nd
W.48	nd	nd	nd	nd	nd	nd	nd
W.49	82	5	7.1	7	0.3112	35	2
W.50	nd	nd	nd	nd	nd	nd	nd
W.51	115	15	7.3	10	0.3592	150	1
W.52	nd	nd	nd	nd	nd	nd	nd
W.53	114	2	8.8	10	0.3211	21	2
W.54	nd	nd	nd	nd	.nd	nd	nd
W.55	nd	nd	nd	nd	nd	nd	nd
W.56	nd	nd	nd	nd	nd	nd	nd
W.57	nd	nd	nd	nd	nd	nd	nd
W.58	115	2	8.8	11	0.3315	22	1
W.59	nd	nd	nd	nd	nd	nd	nd
W.60	126	1	8.6	11	1.0215	11	2
W.61	nd	nd	nd	nd	nd	nd	nd
W.62	83	7	9	12.7	0.3501	89	3
W.63	nd	nd	nd	nd	nd	nd	nd
W.64	nd	nd	nd	nd	nd	nd	nd
W.65	nd	nd	nd	nd	nd	nd	nd

W = Wild relative; nd= Not detected

Appendix 3 contn'd

Plant genotype	Days to first matured pod	Number of pods/plant	Mean pod length/plant	Average seed/pod	20 seed weight /grams	Seed yield /plant	Seed abortion rate
W.66	nd	nd	nd	nd	nd	nd	nd
W.67	nd	nd	nd	nd	nd	nd	nd
W.68	nd	nd	nd	nd	nd	nd	nd
W.69	nd	nd	nd	nd	nd	nd	nd
W.70	nd	nd	nd	nd	nd	nd	nd
W.71	nd	nd	nd	nd	nd	nd	nd
W.72	80	6	7.1	13.1	0.34511	73	1
W.73	nd	nd	nd	nd	nd	nd	nd
W.74	nd	nd	nd	nd	nd	nd	nd
W.75	nd	nd	nd	nd	nd	nd	nd
W.76	nd	nd	nd	nd	nd	nd	nd
W.77	61	6	6.2	13.3	0.3211	75	1
W.78	nd	nd	nd	nd	nd	nd	nd
W.79	nd	nd	nd	nd	nd	nd	nd
W.80	nd	nd	nd	nd	nd	nd	nd
W.81	72	4	7.4	10.5	0.3511	42	2
W.82	66	3	14.7	12	2.7206	38	3
W.83	nd	nd	nd	nd	nd	nd	nd
W.84	nd	nd	nd	nd	nd	nd	nd
W.85	nd	nd	nd	nd	nd	nd	nd
W.86	nd	nd	nd	nd	nd	nd	nd
W.87	nd	nd	nd	nd	nd	nd	nd
W.88	126	8	6.8	7	0.3421	93	1
W.89	102	16	8.5	11.7	1.3685	178	2
W.90	153	2	8.7	7	1.0211	14	1
W.93	nd	nd	nd	nd	nd	nd	nd
W.94	nd	nd	nd	nd	nd	nd	nd
W.95	nd	nd	nd	nd	nd	nd	nd
PARNT	97	8	8.9	10	0.6881	80	0
G.E	105	6	11.2	12	3.0102	72	0
C.96	62	4	15.5	12	1.2775	48	2
C.97	73	4	17.3	14	1.9722	56	1

W = Wild relative; G. E = Golden eye; C = Cultivated type; nd= Not detected

Appendix 3 contn'd

Plant genotype	Days to first matured pod	Number of pods/plant	Mean pod length/plant	Average seed/pod	20 seed weight /grams	Seed yield /plant	Seed abortion rate
C.98	86	4	14.4	6.5	2.8159	26	2
C.99	51	6	12	8.2	2.1112	49	2
C.100	62	10	11.3	8.9	1.4896	89	2
C.101	67	5	18.3	16.8	1.9016	86	3
C.102	58	10	14.4	7.8	1.9268	78	2
C.103	72	5	15.2	11	2.0886	58	3
C.104	77	6	10.2	9.3	1.9518	56	2
C.105	51	13	10.8	10.6	1.2245	138	2
C.106	76	5	16.8	11.3	2.4642	59	2
C.107	73	5	14.7	12.4	2.0436	68	1
C.108	55	18	12.3	8.2	1.8063	107	2
C.109	59	25	12.8	8.2	1.3564	210	2
C.110	nd	nd	nd	nd	nd	nd	nd
C.111	57	5	10	8	1.8793	43	2
C.112	73	4	17.3	11.5	1.6743	46	2
C.113	85	2	10.4	12.5	1.9991	25	3
C.114	81	5	12.8	10	1.9541	53	3
C.115	103	10	9.8	12.6	2.0581	126	3
C.116	76	7	16.5	10.9	1.6872	76	3
C.117	73	4	10.5	10	2.1413	20	4
C.118	nd	nd	nd	nd	nd	nd	nd
C.119	78	5	13.2	7	2.0424	35	2
C.120	67	6	14.8	11.7	1.9546	70	2
C.121	74	4	13	18	1.5918	34	4
C.122	105	3	10.9	6	2.0112	18	2
C.123	71	7	15.6	9.3	2.1416	65	4
C.124	76	6	12.6	9.7	1.822	58	4
C.125	71	5	14.5	12.6	2.609	63	0
C.126	85	6	15.4	10.8	2.6878	89	2
C.127	78	2	17.2	10.5	1.2724	21	2
C.128	67	4	10.6	8.3	1.9551	34	2
C.129	nd	nd	nd	nd	nd	nd	nd

C = Cultivated type; nd= Not detected

Appendix 3 contn'd

Plant genotype	Days to first matured pod	Number of pods/plant	Mean pod length/ plant	Average seed/pod	20 seed weight /grams	Seed yield /plant	Seed abortion rate
C.130	56	4	10.2	8.3	2.1152	33	2
C.131	57	10	10.1	7.9	1.6938	79	2
C.132	nd	nd	nd	nd	nd	nd	nd
C.133	104	3	14.9	7	2.0432	21	3
C.134	nd	nd	nd	nd	nd	nd	nd
C.135	56	7	11.3	5.8	1.0387	41	4
C.136	56	9	9.6	7.8	1.5188	70	2
C.137	98	1	9.6	9	1.8125	9	3
C.138	94	1	10.8	12	1.7268	12	1
C.139	71	2	7.3	5	1.9812	10	3
C.140	nd	nd	nd	nd	nd	nd	nd
C.141	65	5	14.1	7	1.8178	35	2
C.142	102	8	14.7	12.1	2.2911	97	2
C.143	68	8	13.8	9.9	2.2586	79	2
C.144	73	1	10.2	8	2.0112	8	3
C.145	71	6	13.4	9.3	1.9389	56	4
C.146	62	4	9.5	8	1.9719	32	3
C.147	nd	nd	nd	nd	nd	nd	nd
C.148	111	2	17.5	17	2.2981	34	2
C.149	76	6	12.6	7	1.8806	42	2
C.150	89	3	12.7	4	1.9981	12	2
C.151	72	9	14.4	12.8	2.457	115	3
C.152	67	8	14	8.4	3.0207	67	2
C.153	76	7	15.4	11.8	2.1258	82	2
C.154	74	12	15.5	8.6	1.9278	103	2
C.155	76	6	13	11.8	1.9541	65	2
C.156	65	5	14.3	8	2.2924	40	3
C.157	63	12	10	7.9	2.8228	94	2
C.158	53	2	13.4	9.5	1.4364	19	3
C.159	71	23	12.8	13.2	1.5018	189	3
C.160	89	1	9.8	8	2.2911	8	2
C.161	84	2	13.5	13.5	2.0538	31	2

C = Cultivated type; nd= Not detected

Appendix 3 contn'd

Plant genotype	Days to first matured pod	Number of pods /plant	Mean pod length/ plant	Average seed/pod	20 seed weight /grams	Seed yield /plant	Seed abortion rate
C.162	85	10	10.2	8.2	1.9581	83	2
C.163	83	5	13.8	7.6	1.4862	38	2
C.164	66	16	15.3	9.4	2.3008	150	4
C.165	87	5	13.4	7.2	2.1121	35	1
C.166	145	10	10.8	10.3	0.3589	103	1
C.167	105	5	8.4	5	0.5082	24	3
C.168	85	3	6.7	4	1.026	12	3
C.169	79	2	9.6	14	2.0158	31	2
C.170	73	3	13.5	12.3	1.9208	37	2
C.171	81	3	15.5	13	2.3718	39	4
C.172	59	3	11.3	10	1.9482	30	2
C.173	145	1	8.5	10	2.0792	10	3
C.174	71	3	10.5	12	1.3738	36	2
C.175	72	5	14.5	8	1.8256	38	2
C.176	88	2	16.7	6.5	1.9225	15	2
C.177	55	6	11.1	8.2	2.0836	79	1
C.178	45	7	10.8	7.4	3.0241	54	5
C.179	nd	nd	nd	nd	nd	nd	nd
C.180	nd	nd	nd	nd	nd	nd	nd
C.181	105	1	11.7	11	2.0121	11	3
C.182	nd	nd	nd	nd	nd	.nd	nd
C.183	65	7	10.2	6.3	2.1675	44	4
C.184	91	3	15.8	14.3	1.9855	43	2
C.185	106	7	14.5	7.5	2.0019	52	2
C.186	86	6	12.2	5	1.9121	51	2
C.187	68	9	12.4	10.3	1.9957	98	2
C.188	86	6	15.8	9.8	3.0121	67	2

C = Cultivated type; nd= Not detected

Appendix 4. Inferred ancestry of individuals (Q Matrix)

PLANT			PLANT		
GENOTYPE/ ACCESSION	CLUSTER 1 (Q1)	CLUSTER 2 (Q2)	GENOTYPE/ ACCESSION	CLUSTER 1 (Q1)	CLUSTER 2 (Q2)
C.96	0.99	0.01	W.01	0.006	0.994
C.97	0.993	0.007	W.02	0.006	0.994
C.98	0.996	0.004	W.03	0.008	0.992
C.99	0.991	0.009	W.04	0.601	0.399
C.100	0.993	0.007	W.05	0.018	0.982
C.101	0.962	0.038	W.06	0.069	0.931
C.102	0.995	0.005	W.07	0.007	0.993
C.103	0.993	0.007	W.08	0.006	0.994
C.104	0.994	0.006	W.09	0.008	0.992
C.105	0.995	0.005	W.10	0.008	0.992
C.106	0.728	0.272	W.11	0.007	0.993
C.108	0.992	0.008	W.12	0.008	0.992
C.109	0.996	0.004	W.13	0.501	0.499
C.110	0.982	0.018	W.14	0.022	0.978
C.111	0.988	0.012	W.15	0.007	0.993
C.112	0.993	0.007	W.16	0.006	0.994
C.113	0.993	0.007	W.17	0.007	0.993
C.114	0.73	0.27	W.18	0.168	0.832
C.115	0.825	0.175	W.19	0.007	0.993
C.116	0.995	0.005	W.20	0.006	0.994
C.117	0.857	0.143	W.21	0.116	0.884
C.118	0.994	0.006	W.22	0.005	0.995
C.119	0.993	0.007	W.23	0.164	0.836
C.121	0.99	0.01	W.24	0.011	0.989
C.122	0.995	0.005	W.25	0.009	0.991
C.123	0.959	0.041	W.26	0.008	0.992
C.124	0.994	0.006	W.27	0.009	0.991
C.125	0.666	0.334	W.28	0.136	0.864
C.126	0.661	0.339	W.29	0.01	0.99
C.127	0.987	0.013	W.30	0.768	0.232
C.128	0.659	0.341	W.31	0.804	0.196
C.129	0.776	0.224	W.32	0.991	0.009

C = Cultivated type

Appendix 4 contn'd

PLANT			PLANT		
GENOTYPE/ ACCESSION	CLUSTER 1 (Q1)	CLUSTER 2 (Q2)	GENOTYPE/ ACCESSION	CLUSTER 1 (Q1)	CLUSTER 2 (Q2)
C.130	0.648	0.352	W.33	0.006	0.994
C.131	0.984	0.016	W.34	0.008	0.992
C.132	0.995	0.005	W.35	0.146	0.854
C.133	0.993	0.007	W.37	0.027	0.973
C.134	0.985	0.015	W.38	0.007	0.993
C.135	0.992	0.008	W.39	0.143	0.857
C.136	0.984	0.016	W.40	0.007	0.993
C.137	0.989	0.011	W.41	0.008	0.992
C.138	0.99	0.01	W.42	0.008	0.992
C.139	0.676	0.324	W.43	0.012	0.988
C.140	0.763	0.237	W.44	0.01	0.99
C.141	0.995	0.005	W.45	0.614	0.386
C.142	0.729	0.271	W.46	0.007	0.993
C.143	0.987	0.013	W.47	0.028	0.972
C.144	0.722	0.278	W.48	0.006	0.994
C.145	0.564	0.436	W.49	0.005	0.995
C.146	0.964	0.036	W.50	0.171	0.829
C.147	0.957	0.043	W.51	0.007	0.993
C.148	0.99	0.01	W.52	0.006	0.994
C.149	0.982	0.018	W.53	0.005	0.995
C.150	0.974	0.026	W.54	0.006	0.994
C.151	0.657	0.343	W.55	0.007	0.993
C.152	0.991	0.009	W.56	0.007	0.993
C.153	0.91	0.09	W.57	0.007	0.993
C.154	0.99	0.01	W.58	0.007	0.993
C.155	0.986	0.014	W.59	0.007	0.993
C.156	0.983	0.017	W.60	0.007	0.993
C.157	0.988	0.012	W.61	0.009	0.991
C.158	0.996	0.004	W.62	0.006	0.994
C.159	0.993	0.007	W.63	0.007	0.993
C.160	0.917	0.083	W.64	0.007	0.993

C = Cultivated type

Appendix 4 contn'd

PLANT			PLANT		
GENOTYPE/ ACCESSION	CLUSTER 1 (Q1)	CLUSTER 2 (Q2)	GENOTYPE/ ACCESSION	CLUSTER 1 (Q1)	CLUSTER 2 (Q2)
C.161	0.818	0.812	W.65	0.005	0.995
C.162	0.972	0.028	W.66	0.538	0.462
C.163	0.849	0.151	W.67	0.012	0.988
C.164	0.977	0.023	W.68	0.156	0.844
C.165	0.953	0.047	W.69	0.011	0.989
C.166	0.971	0.029	W.70	0.007	0.993
C.167	0.674	0.326	W.71	0.807	0.193
C.168	0.993	0.007	W.72	0.007	0.993
C.169	0.992	0.008	W.73	0.007	0.993
C.170	0.986	0.014	W.74	0.007	0.993
C.171	0.86	0.14	W.75	0.098	0.902
C.172	0.832	0.168	W.76	0.006	0.994
C.173	0.662	0.338	W.77	0.007	0.993
C.174	0.991	0.009	W.78	0.005	0.995
C.175	0.966	0.034	W.79	0.006	0.994
C.176	0.996	0.004	W.80	0.006	0.994
C.177	0.986	0.014	W.81	0.014	0.986
C.178	0.613	0.387	W.82	0.694	0.306
C.179	0.993	0.007	W.83	0.005	0.995
C.180	0.66	0.34	W.84	0.003	0.997
C.181	0.42	0.58	W.85	0.152	0.848
C.182	0.992	0.008	W.86	0.147	0.853
C.183	0.99	0.01	W.87	0.006	0.994
C.184	0.992	0.008	W.88	0.934	0.066
C.185	0.991	0.009	W.89	0.511	0.489
C.186	0.995	0.005	W.90	0.298	0.702
C.187	0.991	0.009	w.93	0.038	0.962
C.188	0.988	0.012	w.94	0.012	0.988
C.120	0.99	0.01	w.95	0.004	0.996
G.E	0.698	0.302	c.107	0.99	0.01
PARENT	0.426	0.574			

Appendix 5: Minimum and maximum ranges of cowpea quantitative traits.

Appendix 5a: Morpho-agronomic traits

Trait	Wild Relatives		Cultivated Types		Overall Population	
	Min*	Max*	Min*	Max*	Min*	Max*
Days to germination	3.00	41.00	2.00	12.00	2.00	41.00
Days to first leaf stage	10.00	47.00	10.00	18.00	10.00	47.00
Chlorophyll content	0.33	1.77	1.04	1.90	0.33	1.90
Days to flowering	38.00	143.00	29.00	130.00	29.00	143.00
Number of flowers/plant	2.00	43.00	2.00	28.00	2.00	43.00
Mean peduncle length	4.40	23.40	3.00	23.90	0.30	23.90
Number of pods/peduncle	1.00	3.00	1.00	2.00	1.00	3.00
Days to first pod maturation	53.00	159.00	45.00	145.00	45.00	159.00
Number of pods per plant	1.00	40.00	1.00	25.00	1.00	40.00
Mean pod length per plant	5.20	14.70	6.70	18.30	5.20	18.30
Average seed per pod	5.80	13.80	4.00	18.00	4.00	18.00
50 seed weight/grams	0.3112.0	2.721.0	0.3589.0	3.024.0	0.3112.0	3.0241.0
Seed yield per plant	11.00	479.00	8.00	210.00	8.00	479.00
Seed abortion rate	0.00	1.00	0.00	2.00	0.00	2.00

(se)= standard error; Min* and Max* represents the minimum and maximum range for the trait

Appendix 5b: Biochemical traits (amino acids).

Amino acid	Types					
	Wild relatives		Cultivated types		Overall Population	
	(x 10 ⁻⁵)		(x 10 ⁻⁵)		(x 10 ⁻⁵)	
	Min*	Max*	Min*	Max*	Min*	Max*
B-Threonine	12.04	113.76	0	485.79	0	485.79
DL-Alpha-Alanine	0	1464.63	0	2646.13	0	2646.13
DL-Beta_phenyl-Alanin	27.57	3256.2	27.1	18491.41	27.1	18491.41
D-Proline	61.15	16657.5	0	1978.18	0	1978.18
Glutamine	10.79	190.35	9.52	278.83	9.52	278.83
Glycine	7.65	150.44	0	119.53	0	100008.3
Iso-Leucine	0	3378.18	0	837.96	0	3378.18
L-Asparagine	60.02	2195.23	53.58	8268.21	53.58	8268.21
L-Aspartic Acid	37.66	2482.40	15.24	454.56	15.24	2482.4
L-Cysteine	0	0	0	0	0	0
L-Histidine	62.4	1473.39	36.86	6175.69	36.86	6175.19
L-Lysine	15.76	140.3	12.56	212.04	12.56	212.04
L-Methionine	0	124.18	0	221.00	0	22.1
L-Serine	30.26	98.96	0	135.91	0	135.91
L-Threonine	23.46	122.52	7.47	320.14	7.47	320.14
L-Tryptophan	2079.65	135248.8	0	259843.4	0	259843.4
L-Tyrosine	77.97	705.72	6.61	751.94	6.61	100003.4
L-Valine	192.09	1313.93	14.25	1318.61	14.25	1318.61
Trans-4-Hydroxyl-Proline	0	1660.64	0	621.39	0	1666.05

Min* and Max* represents the minimum and maximum range for the trait

Appendix 6: Individual cowpea genotypes with maximum amino acid concentrations across the overall cowpea population.

Plant genotype	Country of origin	Amino acid	Concentration (x10⁻⁵)
C.109	Cameroon	L-Tryptophan*	259843.40
C.158	Mali	DL-Beta_phenyl-Alanin*	18491.41
C.163	Nigeria	L-Asparagine	8268.21
C.158	Mali	L-Histidine*	6175.69
W.31	USA	Iso-Leucine*	3378.18
C.113	Cote d'Ivoire	DL-Alpha-Alanine	2646.13
W.29	Nigeria	L-Aspartic Acid	2482.4
C.137	Nigeria	D-Proline	1978.18
W.25	Nigeria	Trans-4-Hydroxyl-Proline	1660.64
C.159	Nigeria	L-Valine*	1318.61
C.102	Guinea	L-Tyrosine	751.94
C.137	Nigeria	B-Threonine*	485.79
C.159	Nigeria	L-Threonine*	320.14
C.150	Uganda	Glutamine	278.83
C.100	Tanzania	L-Methionine*	221.00
C.150	Uganda	L-Lysine*	212.04
W.31	USA	Glycine	150.44
C.163	Nigeria	L-Serine	135.91

C = Cultivated species; W = Wild relatives; *Essential amino acid

Appendix 7: Individual cowpea genotypes with highest values for some quantitative traits.

Trait	Range of traits	Plant genotypes/ accessions
Days to germination	As early as 2 days after planting	C.111
Days to flowering	29-38 days	W.31, C.99, C.158, C.178
Number of flowers per plant	25-43	W.14, W.24, W.31, W.32, C.109
Days to first matured pod	45-55	W.31, C.99, C.105, C.158, C.178
Number of pods per plant	20-40	W.14, W.24, W.31, W.32, C.109, C.159
Average seed per pod	13-18	C.101, C.121, C.148, C.161, C.171, C.184
20 seed weight /grams	2.50-3.00	W.82, C.98, C.125, C.126, C.152, C.157, C.178, C.188, G.E,
Seed yield per plant	210-479 seeds	W.14, W.24, W.31, W.32, C.109
Seed abortion rate	0	G.E, PARENT, C.125,

C = cultivated species; W = Wild relatives

Appendix 8: List of SNPs markers identified to be closely associated with some cowpea quantitative traits.

Trait	Marker name	Alleles	Chromosome position (cM)	Sequence
Number of flowers	12929_463	G/A	5	TTTGTGACCTTATTTTC[A/G]TATAAATGGATTTG
per plant	4980_497	C/T	5	ACCATTCCTGCGCCCT[T/C]CTTGATGTTGGTCT
Mean peduncle length	14164_1877	T/A	5	GTTTTTATGAATGAA[A/T]KYTAGTATGTAAGT
Number of pods per peduncle	4980_497	C/T	5	ACCATTCCTGCGCCCT[T/C]CTTGATGTTGGTCT
Number of pods per plant	12929_463	G/A	5	TTTGTGACCTTATTTTC[A/G]TATAAATGGATTTG
	14164_1877	T/A	5	GTTTTTATGAATGAA[A/T]KYTAGTATGTAAGT
20-seed weight	1107_518	G/A	0	AGCCAATAGCTACAA[A/G]TTTTTGTTCTGTTC
Seed yield per plant	4980_497	C/T	5	ACCATTCCTGCGCCCT[T/C]CTTGATGTTGGTCT