PHENOTYPIC CHARACTERIZATION OF COWPEA (*VIGNA UNGUICULATA* (L) WALP) ACCESSIONS

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DEPARTMENT OF PLANT AND ENVIRONMENTAL BIOLOGY

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DECLARATION

I, Kingsley Smith Arthur, declare that this thesis herein presented to the University of Ghana, Legon for the award of Master of Philosophy in Botany is my own investigation and no such work has been presented by me or any other person for a degree at any other University or institution of higher education.

14th January, 2022

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ABSTRACT

Cowpea is indigenous to the African continent and is usually grown for its leaves and grain in different countries of the world. The objective of this study was to evaluate cowpea accessions using morphological descriptors and phytochemical analysis to identify cowpea accessions with a more specific traits that could be used by breeders. Phenotypic characterization of twenty-seven (27) cowpea accessions which consist of twenty-four (24) from the Department of Plant and Environmental Biology as test material and three (3) others, namely ‘Asontem’, ‘Wang Kae’ and ‘Kirkhouse’ which were used as checks, was undertaken. The cowpea population was evaluated based on agro-morphological traits (quantitative and qualitative) and phytochemical traits. STATA version 15.0 was used to carry out descriptive, multivariate analyses whiles ‘R’ software was used for genetic component analysis to determine the extent of variation. Phytochemical analysis was carried out to study the polyphenolic and amino acid contents of the cowpea seeds using standard methods and protocols. Polyphenolic compounds were determined using a spectrometer and amino acid contents were determined with assistance from Ghana Standard Authority.

In the morphological qualitative traits studied, erect cowpea plants showed the highest distribution for growth habit with frequencies of 91% in the test material and 84.17% in the entire population. The pale tan pod colour recorded the highest frequency of 62.58% in the entire population, similarly, the pale tan with frequencies 65.48% and 62.58% were the highest frequency in both control and test material respectively. The white seed coat colour had the highest frequency of 66.11%in the entire population as well. The chi-square test of association between qualitative traits showed 86 significant associations in the test materials, with growth habit having the

highest significant associations with leaf size ($\chi^2 = 220.84$, $P = 0.000$), whereas the control showed 78 significant associations. The overall population exhibited 86 significant associations, with growth habit having the highest positive significant association with terminal leaflet shape ($\chi^2 = 243.87$, $P = 0.000$). The phenolic compound had higher mean concentration in the controls than the test material, however higher mean concentration of amino acid was obatined in the test materials than in the control. A total of 145, 113 and 123 significant pairwise correlations were observed in the control, test materials, and entire population respectively for all quantitative traits. In the test material vanillic acid was highly correlated with gallic acid ($r = 1.00$) and p-coumaric acid ($r = 1.00$).

Principal component analysis showed that, the first seven principal components in the morphological traits accounted for a total variability of 84.00% in the control, while nine principal components explained 81.00% of the total variation in the test material. On the other hand the first five principal components in the phytochemical traits accounted for 100%, 100% and 83% of the total variation in the control, test materials and entire population respectively. The biplot showed that the relationships among accessions and morphological, phytochemical and all traits explained 33% and 51% of the total variance respectively. The cluster analysis for the morphological traits revealed five distinct clusters. Genotypes named Asontem, T3, T5, T22 were grouped in a single cluster and were characterized by least days to germination (3.58), highest mean number of branches (4.93), least mean number of leaves (41.26), highest mean number of nodes (9.83), least mean leaflet width (3.69), the highest mean days to first flowering, least mean number of pods per peduncle (2.81), least average pod width (0.80), highest mean number of pods per plant (49.50), the highest average number of seed per pod (15.97), highest mean days to first matured pod (42.01), highest mean

number of seeds per plants (795.75) compared to other clusters. These genotypes could be used as parents in genetic improvement programs aiming to increase yield. Biometrical analysis revealed that the phenotypic variance (σ^2 p) was higher than the genotypic variance (σ^2 g) regarding all morphological traits evaluated. The number of seeds per plant reported the highest genotypic (80841.20) and phenotypic (107162.90) variance while the lowest genotypic (0.09) and phenotypic (0.69) value was recorded by the days to germination and average seed thickness respectively. Low ($\leq 20\%$) heritability broad sense values were observed in all the morphological traits and ranged from 0.33% for days to germination to 0.99% for seed weight.

DEDICATION

This work is dedicated to my parents Mr. King Arthur and Madam Selina Sam, as well as my supervisor Professor Isaac Kwadwo Asante

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LIST OF ABBREVIATION

DTG = Days to germination

PTL = Petiole length

NB = Number of branches

NL = Number of leaves

NN= Number of nodes

NPPPD = Number of pod per peduncle

PH = Plant height

TLL = Terminal leaflet length

TLW = Terminal leaflet width

DFF = Days to first flowering

APDLN = Average pod length

APDWD = Average pod width

ANLPP = Average number of locules per pod

NSPPL = Number of seeds per plant

ANSPP = Average number of seeds per pod

DFMP = Days to first matured pod

NSAB = Number of seeds aborted

PA = Percentage abortion

ASDLT = Average seed length

ASDWT = Average seed width

ASDTH = Average seed thickness

SDWG = Seed weight per plant

Lhis = L-Histidine

Llys = L-Lysine

Isoleu = Iso-Leucine

Llue = L-Leucine

Lmet = L-Methionine

Lval = L-Valine

Ltryp = L-Tryptophan

Dlbp = D-L-B-Phenylalanine

Ltyr = L-Tyrosine

Lasp = L-Aspartic Acid

Lser = L-Serine

Lcyst = L-Cysteine

Gly = Glycine

Gal = Gallic Acid

Vani = Vanillic Acid

Pca = P-Coumeric Acid

Rut = Rutin

Que = Quercetin

% = Percentage

cm = Centimeter

mm = Millimeter

g = Grams

≥ = greater than or equal to

IBPGR = International Board for Plant Genetics and Resources

GSA = Ghana Standard Authority

ppb = Part per billion

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CHAPTER ONE

1.0 INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp.] is one of the most grown and consumed pea in West Africa as well as some other parts of the world. It is usually grown in semi-arid areas intercropped or in rotation with other plant crops (Menéndez *et al*., 1997). Cowpea is believed to be indigenous to West Africa, but is part of the daily food of about 110 million people worldwide (Osondu, 1997). It is widely grown and consumed in sub Saharan African countires like Ghana, Nigeria and Niger (Aryeetey, 1971; Bennett-Lartey and Ofori, 1999). Cowpea is mostly grown by peasant farmers and in most cases, these farmers intercrop cowpea with different cereal plant and leagumes such as maize, sorghum, rice, millet as well as other crops including vegetables and plantain. Cowpea is a general-purpose crop, which grown for food for man and animal and serving as an important commodity that generate revenue for farmers and those who trade the grain (Singh 2002; Langyintuo *et al.* 2003). Cowpea that are grown are classified into five (5) main groups based solely on pod, seed and ovule traits (Pasquet, 1999; 1998). Cowpea plays an essential part in the livelihood of great number of individual worldwide, more especially in the emerging economies. It provide them dietary protein that nutritionally balances low-protein tuber crop staples and cereals (Timko and Singh, 2008). The protein content in the foliage of the cowpea ranges from 15 to 21% and in crop residues; it is 6% to 8%, but the total seed protein content also ranges from 23% to 32% (Nielsen et al., 1997). Cowpea plant is also enriched with vitamin B and vitamin B9 needed during pregnancy to decrease birth defect in the brain and spine according to various researches; (Hall et al., 2003; Timko and Singh 2008). Generally, cowpea are purposely cultivated for their seeds but few individual also grow them for their green leafy vegetables and for animal feed in

Africa and for their fresh pods in eastern part of Asia (Boukar et al., 2015). In the cowpea plant, the seed, is the most essential part for human consumption. They are mostly harvested and preserved by drying and consumed when needed. Cowpea can be consumed by cooking or milled into product of flour and used in numerous delicacy (Ahenkora et al. 1998). Cowpea has the capacity to use its root tubers to fix atmospheric nitrogen. They also grow well on barren soils with low levels of phosphorus, more than 85% sand, and less than 0.2% organic matter (Singh, 2003). The crop is known to be a shade tolerant however, its ability to be used in mixed cropping with other crops helps to prevent buildup of weeds, insects and diseases. Globally, cowpea production has increased to about 230 M.P as reported by Singh, (2003), from a yearly average of about 1.2mmt in the 1970s to about 3.6mmt per annum. This rise in production can partially be attributed to the prolonged drought in the West Africa Sahelian zone that made several farmers in sub sarhan of Africa moved away from the production of other crops, to cowpea due to its drought tolerance ability (Duivenbooden et al. 2002). Research has suggested that cowpea is one of the most extensively grown crops in Africa and statistics goes a long way to confirmed that, about 90% of the world's cowpea grain production of 5.7 million tonnes is cultivated and harvested in Africa (FAOSTAT, 2008). Cowpea is among the most useful crops grown in the hot and semi-arid area of Africa where other crops may not grow due to drought, low soil fertility conditions and poor adaptation to heat. (Ehlers & Hall, 1997; Singh et al., 1999a; Hall, 2004). Five (5), out of the six (6) leading producers of cowpea in the world are found in Africa and they are Burkina Faso, Mali, Nigeria, Niger and Senegal (Fery 2002). Subsequently, improvement of seed quality constitutes a major objective of almost all breeding programs; and the presence of diverse source material has been associated with progress in plant breeding (Mangova and Rachovska, 2004). The development of cowpea varieties that has early ripeness, resistance to some important diseases and pests, and acceptable grain quality have significantly improved yield and acreage (Ehlers and Hall, 1997). Yield is a complex characteristic and is affected by several other significant characteristics that are influenced by environmental factors and polygenes. The total effect of plant breeding on genetic diversity has long been an issue in the evolutionary biology of cultivated plants (Simmonds, 1962). Programmes for cowpea breeding has recognised some germplasm which are beneficial in advancement of the crop, the discoveries includes identifying populations of wild Vigna in the Kalahari Desert that resists bruchid beetle in the cowoea storage (Mathodi, 1992). Selection of plants or crops that have desirable traits to develop new varieties depends mainly on genetic diversity. Genetic diversity is a significant component to the reduction of crop vulnerability by promoting long-term selection and gains in genetic enhancement and encourages judicious use of genetic resources (Barrett and Kidwell, 1998; Messmer *et al*., 1993). Understanding the genetic diversity in a germplasm is helpful for plant breeders as it supports their decision about choosing a parent genotype and is important for increasing the genetic base of the crop (Prasanthi et al., 2012). The valuation of diversity also enables effective sampling, particularly when the core samples are well developed, which allows for adequate management of the germplasm (Van Hintum et al., 2000). According to Mayes et al., (2009) Some accessions are evaluated primarily on the basis of morphological traits, which are based on few genes and may not necessarily reflect the actual variation in agronomic traits present in the crop. In order to select improved cowpeas varieties that are better adapted to a dry environment, morphological, physiological and phenological criteria could be used to aid in the selection (Blum, 1988).

Traditionally, diversity is valued by measuring the variation in phenotypic traits, starting with flowering, days to maturity, plant type, flower colour, seed type, seed colour, seed size, hilum colour, and quantitative morphological characteristics. However, this approach is often limited and the expression of quantitative characteristics which is subjected to strong environmental influences (Kameswara, 2004). To increasing the main components of the cowpea that affect yields, such as pods per plant, seed size, pod length and seeds per pod, will allow for an improvement in the cowpea's yield potential. Morphological variability of cowpea traits has been reported by various authors such as Patil and Baviskar (1987), Sardana et al. (2001), Mishra et al. (2002), Carnide et al. (2007). Knowing about morphological and phytochemical variations and their relationships among cowpeas genotypes can be helpful for breeders to develop appropriate breeding techniques and programs that result in the production of adaptable and productive varieties. The presence of genetic diversity among cowpea genotypes for the different minerals and protein is vital to improve its nutritional quality through breeding (Ng'uni et al. 2012; Shegro et al. 2012; Gerrano et al. 2015; 2017) towards contributing to food and nutritional security. According to Carnovale et al. (1990), the nutritional characteristics in cowpea and they found that the mean concentrations for Ca, Zn, P and K contents in grains were 37.00, 4.70, 430.00 and 125.00 mg 100 g^{-1}, respectively. Therefore, cowpea genotypes can be selected with desirable nutritional contents through characterisation of the available genetic resources.

1.1 JUSTIFICATION

Cowpea is one of the most important grain legumes in Sub-Saharan Africa. Ngalamu et al., (2011) reported that West Africa produces over 80 % of the quantity produced in Africa, with Nigeria, Niger and Burkina Faso as leading producers in the sub-region. Cowpea is a crop cultivated for it grain seeds, immature pods, fresh and dried leaves, as well as hay for livestock feed (Xu et al., 2009). The crop provides strong support to the livelihood of small-scale farmers through its contributions to their nutritional security, income generation and soil fertility enhancement. According to Boukar *et al*., (2016), about 6.5 million metric tons of cowpea are produced annually on about 14.5 million hectares worldwide. Generally, cowpea production and productivity is low due to insufficient availability of improved varieties and locally adapted cultivars (Ishiyaku et al., 2005), as a results cowpea farmers also have limited access to quality seeds of improved varieties for planting. Some progress has been made through conventional breeding at international and national research institutions in the last three decades (Ishiyaku et al., 2005). Despite all the previous efforts, there is still a big gap in cowpea improvement to identify the ideal varieties that have high yielding potential, high productivity and enhanced nutrition. Cowpea improvement could also benefit from modern breeding methods based on molecular genetic tools, also nutritional analysis of diverse cowpea genotypes on the basis of grain mineral elements and crude protein content is essential in the identification of potential parental genotypes. Improvement of nutritional quality of cowpea genotypes, however, requires information on the genetic variability that exists among available germplasm. The knowledge of genetic variability, heritability, genetic advance as well as correlation among yield and its associated traits in the advance breeding lines is a pre-requisite for selection and development of well-adapted cowpea varieties (Addisu and Shumet, 2015). The efficiency with which genotypic variability can be exploited by selection depends upon heritability, genetic advance and correlation among the individual traits (Bilgin et al., 2010). This present study, report on the characterization of more than 27 cowpea accession from the department of plant and environmental biology (DPEB) was done. The present study was to analyse the morphological and phytochemical traits of these cowpea accessions to assess their genetic diversity. This study may assist in the selection process of cowpea for cultivation based on their characteristic features and draw more attention to the variations that differentiate consumer-preferred cowpea grains from the others. Superior accessions which may be identified during the study can aslo be used as parent to enhance cowpea improvement programmes.

1.2 OBJECTIVES OF STUDY

1.2.1 Main objective

The main objective of this study is to evaluate 27 accessions of cowpea using morphological descriptors and phytochemical analysis to identify cowpea accessions with a more specific traits that could be used by breeders.

1.2.2 Specific objectives

The specific objectives of the study were to;

1. Determine agro-morphological characterization of cowpea genotypes
2. Evaluate the phytochemical contents of 27 cowpea accessions.
3. Determine association among the cowpea traits.

4. Estimate genotypic and phenotypic variances and broad-sense heritability of the morphological traits

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 TAXONOMY, ORIGIN AND DISTRIBUTION

Cowpea (*Vigna unguiculata* (L.) Walp) is a member of the kingdom plantae, division Magnoliophyta, class Magnoliopsida, order Fabales, family Fabaceae, subfamily Faboideae, genus Vigna and species unguiculata (Singh *et al*., 1993). The cowpea is an herbaceous plant, which grows well under high temperature and drought throughout all development stages and have an optimal growth temperature of around 28 ° C (Craufurd et al. 1997). There are two main cultivated groups of cowpea and they are: unguiculata and sesquipedalis (Xu *et al*., 2011). Unguiculata is the largest group of varieties and the most diverse of the grown subspecies. These varieties have different growth habit which range from semi-erect, erect, climbing to prostrate. However, growth habit of this variety also ranges from indeterminate to determinate in this cultivar. Cultivar group Sesquipedalis (variously known as “asparagus bean”, “yardlong bean”, “long bean” or “snake bean”) has over 16 ovules and seeds spaced within the pod. Current molecular studies have revealed that the cultivar group Sesquipedalis is a subspecies (Xu *et al*., 2012; 2010). Faris (1965) concluded that cowpea cultivars were domesticated from subspecies *dekindtiana* in West Africa, the only centre of cowpea diversity. The variation in West Africa cultivars of subspecies *unguiculata* included the entire flower, pod and testa colour. And the range of variation within species is greatest in Southern Africa (Marechal, 1978). However, greater diversity does not necessarily mean centre of origin since agriculture is known to have spread from the north to the south through migration. According to Simmonds, (1976) cowpea is now grown throughout most parts of the world. Its use is recorded in Jamaica as early as 1675. It has a documented use in Florida in 1700 and in North Carolina in 1714. The introduction and spread of cowpea into the new tropics from West Africa are alleged to have occurred along the slave trade route through the Spanish (Simmonds, 1976). The crop was first grown in southern United States in the early eighteenth century.

Cowpea is believed to be one of the primeval crop plants known to human (Mejia 2004) and one of the first food source for humans since the Neolithic era. (Summerfield, Huxley, and Steel, cited by Agyemang *et al.*, 2014). The exact genesis of cultivated cowpeas has been an issue of speculation for such a long time (Timko & Singh, 2008). As assessed by Asante (1996), the origin of cowpea is unknown but believed to have originated from West Africa particularly, due to its abundance of most wild and cultivated species. Few archaeological evidences have revealed a counter argument supporting that Africa, Asia, and South America as the origin of the crop (Doumbia, 2012). One view is that, the origin and domestication of the cowpea took place in Africa near Ethiopia and was subsequently developed mainly in the farms of the African savannah. (Duke, quoted by UC SAREP, 2017). Girei (2013) also notes that the origin and subsequent domestication of cowpea correlates with pearl millet and sorghum in Africa. The slave trade in West Africa resulted in the harvest reaching the southern United States in the early 18th century (Doumbia, 2012). Other evidence suggests that the Transvaal region in the Republic of South Africa was the center of speciation for cowpeas due to the presence of the most primitive wild species (Padulosi and Ng, cited by Doumbia, 2012).

Cowpea is grown extensively in 16 African countries, with the continent producing two-thirds of the world total (Winrock, cited by Agyeman *et al*., 2014). West Africa produces the most diverse cultivated cowpea in an area including southern Niger, the savanna region of Nigeria, Togo, northern Benin, the northwestern part of Cameroon and part of Burkina Faso (Doumbia, 2012). In Nigeria, cowpea is known to be cultivated mostly in the North West and North Central geo-political zones also substantial quantities are also grown in the other four geo-political zones identified in the country, (Davis, cited by Girei, 2013). In South America, Brazil is the only major country which grows cowpea. (Gomez, 2004). There are three recognized specific groups of cultivated cowpeas. Two of these are grown in Australia with most varieties grown for grain, forage and green manure and the other type, the yard-long bean, is a minor vegetable. (Imrie, cited by Mejia, 2004).

The origin of cowpea had been related to its morphological and cytological proof and data on the geographical distribution and cultural practices (Ng, 1995; Ng and Maréchal, 1985). It is most probable that cowpea was first introduced to Asia during the Neolithic period (Pant *et al*. 1982) and prior to the Christian era, since it has a Sanskrit name in writings dated to 150 BC (Ng and Maréchal 1985). Therefore, Asia is often considered a secondary domestication site for the crop. Cowpea is geographically distributed worldwide on a large scale throughout the western and central African, countries such as Nigeria, Mali, Niger, Burkina Faso, Tanzania, Senegal and Uganda. Outside Africa, India, Myanmar, Sri Lanka, Australia, the United States, Brazil, Bosnia and Herzegovina all have significant distribution.

2.2 MORPHOLOGY AND BIOLOGY OF COWPEA

Morphological variations in different cowpea accessions is very high. In terms of use, there are three main types: for grain, feed or dual purpose. Cowpea is an herbaceous pendulous, climbing bushy, prostrate, or semi-upright annual plant that can grow to 15cm-80cm tall. The leaves are alternately three-leaved with a petiole length of 5-25cm. The lateral leaflet is asymmetrical and opposite, while the middle leaflet is ovoid and symmetrical. The leaves show noteworthy differences in shape (linear, hasty, spherical, and lanceolate to ovate), size (6-16 x 4-11) and are typically dark green in colour. The stems are straight, smooth or slightly hairy and sometimes purple in colour.

The flowers come in alternate pairs that mostly have only two flowers on each inflorescence. These are self-pollinating, conspicuous, borne on short pedicels and the corollas may be white, pink, cream, pale, yellow, blue or purple. The flowers close at about midday after opening early in the morning. They wilt and collapse after blooming/ anthesis. Growth pattern is usually indeterminate under favorable conditions but can be determinate as well. The pods of the fruit vary in shape, size, texture and colour. They plant can be crescent-shaped, erect or coild. They are commonly slightly yellow when ripe, but ca be purple or brown in colour. Seeds may weigh 5-30 g/100 seeds and are relatively large (0.2-1.2 cm long) in size. They are variable in shape such Crowder, kidney, rhomboid, ovoid, and globose; and may also vary in size (IBPGR, 1983). The testa can be either smooth or wrinkled, green, white, buff, brown, red, black, blotched, speckled, eyed or mottled in color. The seed shape dpends on pod shape. The average pod length of the cowpea is between 8-22 cm and it contains 10-20 seeds per pod (Chevalier, 1944). Cowpea is a short day plant and many cowpea accessions show photoperiodic sensitivity to flower bud initiation and development, but others are day neutral (Ehlers and Hall 1996; Craufurd et al. 1997). In some genotypes, the degree of sensitivity to the photoperiod is changed by temperature (Wein and Summerfield 1980; Ehlers and Hall 1996). In West Africa, different levels of light sensitivity was selected in different climatic zones, so that pod ripening at a certain location coincides with the end of the rainy season, regardless of the planting date, which is often variable due to the variability at the beginning of the rainy season (Steele and Mehra 1980). These characteristics allows pods to be protected againts harm from pathogens and excessive moisture. Photoperiod sensitivity, when well done, can be vital to guarantee crop maturity before drought, after wet seasons or cold weather limits that could impair crop growth. Cultivated cowpeas can be classified into five cultivar groups depending chiefly on their seed characteristics and pod (Pursglove 1968; Pasquet 1999). Cultivar group Unguiculata is the largest and includes most medium- and large-seeded African grain and forage-type cowpeas. Members of cultivar group Biflora abound in India and categorized by their relatively small smooth seeds borne in short pods that are held erect until maturity. Cultivar group Textilis is a rather rare form of cowpea with enlongated peduncles that were used in Africa as a source of fiber. Cultivar group Melanophthalmus includes “blackeye pea”-type cowpea with large, fragile pods, and somewhat elongated seeds with wrinkled seed coats (Pasquet 1999). Cultivar group Sesquipedialis (known as “yardlong bean,” “long bean,” “Asparagus bean,” or “snake bean”) is commonly grown in Asia for production of its very long (40 to 100 cm) green pods that are used as “snap” beans. Regardless of the differences in the morphological characteristics seen among the different cultivar groups, there are no known hurdle to recombination between members of the different cultivar groups.

2.3 PRODUCTION AND PRODUCTION CONSTRAINTS OF COWPEA

Rachie and Rawal (1975) reported that bulk of world-wide production of cowpea is mainly in Africa which produces about 75% with Nigeria being the principal producer (58.6%), Burkina Faso (5.6%), Niger (2.4%) and Senegal (2.0%). According to the Food and Agriculture Organization of the United Nations FAO / UN (2012), the average cowpea yield in West Africa in 2012 was an estimated 483 kg/m, which is 50% below the estimated potential production yield. Cowpea production is grown on over 10 million hectares of land worldwide, more than 85% of which is in Africa (FAOSTAT, 2008). Asia, Middle East, Southern Europe, South USA and Central and South America are also known to be huge producers of cowpea (Singh *et al*., 2002).

In Ghana, the crop is usually cultivated under rainfed conditions predominantly in the savannah and transitional agro ecological zones, but the bulk of the grain is produced in the northern part of the country (CSIR-SARI, 2012). Cowpea yields in Ghana are among the lowest in the world, averaging 310 kg ha-1 (Ofosu-Budu et al., 2007) and efforts made to improve the production of the crop include the introduction of high yielding varieties (Addo-Quaye et al. 2011).

According to FAOSTAT (2017), cowpea was grown on an estimated 11 million ha in Africa in 2017 with most of production confined to West Africa (10.6 million ha), especially in Niger, Nigeria, Burkina Faso, Mali, and Senegal. More than 7.4 million tons of cowpeas are produced worldwide, with Africa producing nearly 5.2 million tons. Second to the most important pulse after pigeon pea, cowpea contributes to about 13% to 17% of food pulses for subsistence in the tropics. For good plant stand and high yields, seeds must be free of insects and diseases (Dauost *et al*., 1985). Planting preferably should be planned in relation to the maturity period of the variety such that the crop is harvested in bright dry weather. According to (SARI, 2012) early light sensitive types can be planted depending on the patterns of rainfall.

Cowpea cultivars with creeping growth habit are shade tolerant, and can be grown with maize, millet, and sorghum in mixed cropping system. This quality makes cowpea an essential component in the mixed cropping systems, more importantly in dry savanna areas. In these areas, dried stalks of cowpea are valuable animal feed and are sold to livestock farmers. Most cowpea varieties form root nodules freely. But recent studies in northern Ghana have shown that cowpea will fix more nitrogen when farmers inoculate the soil with rhizobia.

Cowpea production faces challenges and thus affects its productivity worldwide. According to (ICRISAT, 2013), the major constraints in Africa's high yield cowpea production are mainly infertile soil, diseases, drought and insect pest. The major challenge to growing cowpea in Ghana is insect pests and weeds such as Striga and Alectra. Insects and weeds can cause losses of 15 to 100%, depending on the level of infestation, drought, soil fertility, and the susceptibility or resistance of the variety. A few cowpea varieties are resistant to striga.

Many areas with a high population of insect infestation can lead to zero crop output when appropriate steps are not implemented (Asiwe *et al*, 2005). Aphid (*Acyrthosiphon pisum*) is one of the most destructive insect pest of cowpea plant. In large numbers, aphids can lead to a lot of losses and early infestation can result in enation mosaic virus (ICRISAT, 2013). The insect sucks sap from the cowpea plant and through this feeding habit spreads viral diseases.

2.4 COWPEA GERMPLASM CHARACTERIZATION

Germplasm characterization refers to recording of traits that are highly heritable. These heritable traits and their attributes identified in germplasm characterization are known as descriptors. These descriptors can either be quantitative or qualitative. Qualitative refers to descriptive traits, whereas quantitative refers to measured or numerical scoring of characteristics.

Cobbinah *et al.* (2011) studied approximately one hundred and thirty-four (134) accessions of cowpea which were collected from eight (8) topographical origins in Ghana. These accessions were grown at two (2) different locations, Bunso, a semi-deciduous forest and Pokuase, a coastal savanna to analyse their performance and to select the genotype with desirable agro-morphological characters for further improvement. By 1986, about a total of 35,000 accessions of more than crop types have been multiplied and characterized. Like any other crop, cowpea breeding programmes comprise important procedures. The first step involves, breeders collecting and evaluating germplasm to select parental lines or cultivars for crosses. A germplasm characterization is carried out for the following reasons: Classification of accessions into their natural groups, describe accessions and determine their characteristics, estimate the extent of the variation in the genebank collection, assess relationships between accessions or between features and between geographical groups of collections, monitor possible genetic changes in the germplasm collection and identifying duplicates in a collection.

2.5 COWPEA CHARACTER ASSOCIATION STUDIES

Correlation coefficients, is the measure of relationship that exist among different plant characters or traits, which facilitate selection. The degree of identified association between two characters is referred to as, the total phenotypic correlation. However, environmental correlation is the measure of ecological impact on the co-variation between the two traits being referred to. Correlation studies provide knowledge regarding association of traits among themselves and with economic traits on which indirect selection could be made for improvement. It helps to simultaneously select for more than one character of importance at a time. However, correlation is inadequate to elucidate the exact association between traits, as yield is dependent on many components characters. The relative magnitude of several traits is therefore more desirable to be considered in order for a stronger representation of yield components for effective breeding programs (Ajayi et al., 2014; Sadras et al., 2019). Moreover, significant correlations among a number of traits and seed yield of different genotypes of cowpea across numerous locations are valuable in planning an effective selection and breeding program for cowpea. According to Falconer (1993), the amount of relationship between two traits that is observed directly is the phenotypic value. Many works on cowpea have revealed significant variability and degree of association of traits among yield and yield contributing traits in cowpea (Adewale et al., 2010; Ajayi et al., 2014). According to Patil *et al*. (1989) grain yield was much strongly influenced by number of pods per plant, 100 seed weight, pod length and days to 50 % flowering. Siddique and Gupta (1991b) identified an extensive correlation of seed yield per plant with days to 50 % flowering and number of pods per plant. Oseni *et al*. (1992) found a strong positive relationship between seed yield and pods per plant, between number of days to 50% flowering and 100-seed weight; however, negative association occurred between days to 50% flowering and seed yield and between 100 seed weight; seed yield, days to maturing, 100-seed weight, and days to pod maturity and pod length were the significant factors adding to yield. Altinbas and Sepetoglu (1993) suggested that days to flowering had no influence on seed yield. On the contrary100 seed weight was associated with number of pods per plant and seeds per pod. According to Sawant (1994) seed yield was significantly and particularly corresponded with number of branches per plant, inflorescence per plant, pod per plant, pods length, seeds per pod, 100-seed weight and harvest index. Tamilselven and Das (1994) suggested that number of pods per plant and 100 seed weight must be utilized as a determination model in the progression of high yielding cowpea genotypes. In a review including three F_2 populations Birader *et al*. (1996) detailed that there was solid connection existed in pod weight per plant and seed yield, number of seeds per pod and pod length, number of pods per plant and number of clusters and pod weight per plant. Gowda (1996) revealed a positive and huge relationship between seed yield and number of pods per plant, number of seeds per pod and 100-seed weight and further reported a critical and negative relationship with 100-seed weight and number of seeds per plant. Singh and Singh (1997) showed that the number of seeds per pod and number of pods per plant made most vital direct contribution to seed yield in 45 accessions of cowpea. Venkatesan *et al*. (2003) observed that the number of branches per plant, number of pods per cluster, number of pods per plant and pod yield were highly associated with seed yield at the genotypic and phenotypic levels when he considered the association and path analysis studies in 20 genotypes of cowpea. The extent of genotypic relationship was higher than that of phenotypic relationship.

2.6 PHYTOCHEMICAL AND NUTRITIONAL CHARACTERIZATION OF COWPEA

2.6.1 Phytochemical characterization

2.6.1.1. Polyphenolic compound

According to Mtolo, *et al*. (2017), Awika, and Duodu (2016), Phenolic compounds are the most important group of bioactive compounds in cowpea, are concentrated in the seed coat and have the potential to protect the body against chronic diseases. According to Pandey & Rizvi (2009), polyphenolic compounds are secondary plant metabolites which are usually used in defense against ultraviolet rays and aggression by plant pathogens. These phenolic compounds are responsible for most of the colouration, flavor, bitterness, odor and oxidative stability observed in diverse cowpea seeds (Pandey and Rizvi, 2009). The most vital phenolic compounds identified to be in cowpea are the flavonoids and phenolic acids (Awika, & Duodu 2016, and Zhao, *et al*., 2014). Important polyphenolic compounds which are predominant in cowpea include trans-ferulic acid, trands-p-courmaric and the derivatives of flavonoids (Pandey & Rizvi, 2009). Nassourou et al., (2016) stated that flavonoids are also have an essential role in plant protection. Epidemiological studies have revealed the consumption of phenolic antioxidants-rich foods protect humans against chronic non-communicable diseases such as cancer, ageing, diabetes, and cardiovascular disease, again they also act as scavengers of radicals, reducing agents, and metal ion chelators (Zhao, *et al*., 2014). According to Kapravelou et al. (2015), cowpea seeds have some beneficial health effects related to their antioxidant, hypoglycaemic, hypolipidaemic, and antihypertensive properties. Phenolic content composition and bioactive properties of cowpea may vary greatly depending on the cultivar or variety.

2.6.1.2 Amino acids

Amino acids are the building blocks of proteins and, based on their synthesis, are divided into essential and non-essential amino acids in humans. The essential amino acids are only synthesized by plants, while non-essential amino acids are synthesized by both plants and humans. The essential amino acids must be ingested from external sources in animal or vegetable food. Legumes are the most important staple food worldwide. Research has shown that their seeds contain the following nutritional content; Carbohydrates and proteins (Auestad & Fulgoni, 2015; Burch et al., 2007; Millward et al., 2008; Tessari et al., 2016).

Essential amino acids are those that are very important to build proteins in humans and animals, but cannot be synthesized by these organisms themselves. For this reason essential amino acids must be provided in the diet. In humans, there are nine essential amino acids, these are; histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan and valine. Non-essential simply means our bodies produce these amino acids, and must not necessary to be added to the food we eat. These are examples of non-essential amino acids; alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, proline, serine and tyrosine.

The legumes most commonly used worldwide are beans, chickpeas, lentils, peas, broad beans, soybeans (Guillon & Champ, 2002).

2.6.2 Nutrition

Cowpea (*Vigna unguiculate* (L.) Walp.) is a widespread food crop in the tropics and sub-Saharan regions that is used as human food because of its nutritional value (Alidu *et al.*, 2020). According to Addo-Quaye et al., (2011) cowpea seeds serve as a good source protein (19-35%) and an essential source of carbohydrate (50-60%). Quaye *et al*. (2009) reported that, cowpea may contains substantial quantity of micronutrients such as, iron, calcium, zinc and vitamin A. The high quantities of Ca, Mg, K, and Zn in the leaves and stems have also been identified, suggesting that they could used as a mineral source for animals and soil improvers to improve fertility and increase crop yield and also used as supplement (Alidu *et al.*, 2020). Anele et al., (2010) reveal in their study that the haulms of cowpea could be used to support milk production in lactating dairy cattle and the growth of animals. The chemical constitution of cowpea and its nutritional properties vary greatly between different variety (Giami, 2005; Rangel et al., 2004). Hence, they are a very important components of cowpea improvement. Therefore an evaluation of their nutritional-physiological properties is very important for a good use of newly developed cowpea varieties for human and / or animal nutrition (Giami, 2005).

2.7 GENETIC VARIABILITY AND HERITABILITY OF COWPEA

As with all crops, the likelihood of improvement in cowpea depends on the amount of genetic variability. Studies initiated by Johanssen (1909) and East (1916) have resulted in the division of total variability into genetic and environmental components. In all cases, both heritable and non-heritable factors influence variation in segregating populations, while variation in pure line is solely due to the environment (Johanssen, 1909). These heritable genetic characteristics vary among cowpea in diverse manner.

According to Inuwa et al. (2012) and Gerrano et al. (2015), the existence of wide-ranging genetic variability is essential to effective selection for traits of interest in a plant breeding improvement program.

According to Amoatey (1987), variability studies in seed colour, pod length, number of seed per pod have been conducted in some cowpea accessions in Ghana. In cultivated plants, the adaptability of the genotypes varies due to their genetic differences. As an expression of yield and other quantitative characteristics, the environmental conditions have a significant influence. Previous studies performed by Comstock and Robinson (1952), Athwal and Singh (1966) and Mital et al. (1969), all revealed that the evaluation of genotypes under several environmental conditions provided an interesting information on the relative magnitude of phenotypic and genotypic variability and the extent of genetic advance. Robinson et al., (1949), Grafius, (1959), and Nikell and Grafius, (1969) paid more emphasis on the improvement of crop yield by studying the variability and heritability of yield and yield contributing components of crops. Asante (1991) also studied variability in pigmentation of immature pod tip, flower bud tip and sepal, seed coat colour and eye pattern, flower colour and paleness in chlorophyll. Spillman (1913) noticed that all varieties having coffee-colour or white or cream-colour seed had white flowers and devoid of anthocyanin in stem and leaves. Grafius (1964), observed that the major yield components in cowpea in the accessions he studied were; number of seeds per pod, number of pods per plant and 100g seed weight. He further noted that any change in yield is as a results of change in any one or more of the component listed.

The heritability score of a trait shows the effectiveness of selecting the trait based on phenotypic expression. In almost all cases, quantitative traits are determined by a larger number of genes and are further influenced by the environment, some of the observed values of which are inheritable.

2.8 THE ROLE OF CLUSTER ANALYSIS AND PRINCIPAL COMPONENT ANALYSIS IN VARIABILITY STUDY

Morphological traits have been used comprehensively to establish phylogenetic relationships between and within species. Again, they have been used to study variability and correlated traits in different accessions of cowpeas. Environmental factors has a strong influence on morphological traits that may result in varied relationship pattern outlines (Smith & Smith 1989, Selvi et al. 2003), but they are nevertheless a good source of selecting materials. (Magloire 2005). Quantitative and qualitative traits have been used by many researchers for various purposes in cowpeas and related plants (Pasquet 1993, Obute 2001). Some multivariate statistical tools that have been used extensively include principal component analysis (PCA), and the cluster analysis (CA), these techniques identify plant traits that characterise the distinctness among selected genotypes.

Principal component analysis is used to analyze multivariate data and generate new sets of variables that are linear combinations of the original variables (Zagrodzki et al., 1995). The fundamental idea of Principal Component Analysis (PCA) is to reduce the dimensionality of a data set that consists of a large number of interrelated variables and at the same time, an attempt is made to preserve as much as possible of the variation present in the data set. This is achieved by converting it into a new set of variables, the Principal Components (PC), which are not correlated and are arranged in such a way that the first variables retain most of the variation that is present in all of the original variables (Jolliffe, 2002).

The Principal Component Analysis (PCA) has been used to partition observed agronomic variations in genotypes of many crops such as rubber (Omokhafe and Alika, 2000), rice (Nassir, 2002), and sesame (Mponda *et al.*, 1997). Principal component analysis is an adaptive data analysis technique which is effectively used to visualize the similarity and difference between the genotypes and helps in identifying the quantitative characters contributing maximum towards genetic divergence (Jindal et al., 2018, Ringnér 2008).

The use of cluster analysis as an effective tool in classifiying cowpea accessions with similar characteristics cannot be over emphasized, as it has now become very widespread in research studies (Sabater 2004, Vural & Karasu 2007). Furthermore, analysis of phylogenetic tree has most distinguished afford to classify the different clusters by the dendrogram construction for identifying the greater variability, which is more useful to the trait of interest for future crop plant breeding enhancement

Cluster analysis and Principal component analysis could be used to evaluate the degree of morphological variability betweem cowpea accessions and also to know the exact relationships between yield and yield component of these accessions. Hence, these will be useful tool for breeders for breeding purposes.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 SOURCES AND COLLECTION OF COWPEA ACCESSIONS

Seeds of accessions of cowpea were collected from Department of Plant and Environmental Biology (DPEB), University of Ghana. The cowpea germplasm had been collected, separated according to seed colour, assigned accession numbers and put under cold storage. Twenty-seven (27) cowpea accessions were selected from the germplasm for the study, out of which three were used as controls (Asontem, Kirk House and Wang Kae) and the remaining 24, the test materials. These cowpea accessions were evaluated for various agro-morphological and phytochemical characteristics of interest to plant breeders and growers. A list of the 27 cowpea accessions showing their origin is shown in Table 1.

Table 1: cowpea accessions used for the research

Accessions	**Sources**	**Accessions**	**Sources**
Asontem	*SARI*	T 12	*DPEB*
Kirk House	*SARI*	T 13	*DPEB*
Wang Kae	*SARI*	T 14	*DPEB*
T 1	*DPEB*	T 15	*DPEB*
T 2	*DPEB*	T 16	*DPEB*
T 3	*DPEB*	T 17	*DPEB*
T 4	*DPEB*	T 18	*DPEB*
T 5	*DPEB*	T 19	*DPEB*
T 6	*DPEB*	T 20	*DPEB*
T 7	*DPEB*	T 21	*DPEB*
T 8	*DPEB*	T 22	*DPEB*
T 9	*DPEB*	T 23	*DPEB*
T 10	*DPEB*	T 24	*DPEB*
T11	*DPEB*		

3.2 EXPERIMENTAL SITE

The experimental field was the Experimental farm of the West Africa Centre for Crop Improvement (WACCI), University of Ghana, Legon,

3.3 EXPERIMENTAL DESIGN

The experimental design used for the field experiment was a randomised complete block design (RCBD) with three (3) replications. Each accession was represented by 30 plants. The spacing between and within rows was maintained at 50 cm X 50 cm. One seed was planted per a hole.

3.4 CULTURAL PRACTICES

Plants were watered two times a day and weeding was done with cutlass every 2 weeks. No fertilizer was applied because the WACCI field was used. Cowpea plants were sprayed against insect pests using an insecticide called "*Attack*" at a rate of 600 mls/ha at 14, 28, and 42 days after sowing

3.5. MORPHOLOGICAL CHARACTERIZATION

Agro-morphological data on the plants were recorded after 6 weeks of planting. Cowpea Descriptor by International Board of Plant Genetic Resources (IBPGR) (1983) was used in collecting both quantitative and qualitative data on the following traits.

Thirty–nine (39) morphological triats (qualitative and quantitative) were scored comprising 16 qualitative and 23 quantitative traits. The sixteen (16) qualitative traits analysed were, growth pattern, growth habit, twinning tendency, attachment of pods to peduncle, flower colour, plant pigmentation, pod pigmentation, pod shape, pod thickness, terminal leaflet shape, leaflet markings, leaflet size, leaflet size, leaf colour, seed colour and plant hairiness.

The twenty-three (23) quantitative traits were studied. These comprised; plant height, days to germination, number of branches, number of nodes per main stem, number of leaves, petiole length, days to first flowering, days to pods maturity, pod length, pod width, leaflet length, leaflet width, seed length, seed width, seed thickness, number of seeds aborted, percentage seed abortion, pods per peduncle, locules per pod, seeds per pod, pods per plant, 100 seed weight, number of seed per plant and peduncle length.

3.5.1 Qualitative data

Qualitative characters were scored based on visual evaluation in accordance with the cowpea descriptor and with the aid of banana colour chat, where colours were involved. The qualitative traits were scored by using relevant scales as shown in Table 2.

Table 2: Qualitative traits measured in 27 cowpea (*Vigna unguiculata*) accessions.

Traits	Score Code
Growth habit	1=Acute erect, 2=Erect, 3=Semi-erect, 4=Intermediate, 5=Semi–prostrate, 6=Prostrate, 7=Climbing
Growth pattern	1=Determinate, 2=Indeterminate
Twinning tendency	0=None, 3=Slight, 5=Intermediate, 7=Pronounced
Plant hairiness	3=Glabrescent, 5=Short appressed hairs, 7=Pubescent
Leaf colour	3=Pale Green, 5=Variegated, 7=Dark green
Leaf marking	0=Absent, 1=Present
Flower colour	1=White, 2=Violet, 3=Mauvie-pink, 4=White with violet patches
Leaf size	1=Narrow (<10 cm), 3=Small (10 - 20 cm), 5=Medium (21 - 30

	cm), 7=Big (31-40 cm)
Terminal leaflet shape	1=Globose, 2=Sub–globose, 3=Sub–hastate, 4=Hastate
Plant pigmentation	0=None, 1=Very slight, 3=Moderate at the base and tips of petioles, 5=Intermediate, 7=Extensive, 9=Solid
Pod colour	1=Straw, 2=Dark tan, 3=Reddish straw, 4=Tan, 5=Greenish tan
Podtip colour	0=Absent, 1=Present
Pod attachment to peduncle	3=Pendant, 5=30o – 90o down from erect, 7=Erect
Pod curvature	0=Straight, 3=Slightly curved, 5=Curved, 7=Coiled
Pod wall thickness	3=Thin, 5=Intermediate, 7=Thick
Pod hairiness	3=Glabrescent, 5=Short appressed hairs, 7=Pubescent
seed coat colour	1=Reddish brown, 2=white, 3=Cream, 4=Cream with brown patches

3.5.2 Quantitative data

Three plants per accession were selected randomly and analysed for quantitative assessment. Measurements were taken and recorded in SI units.

3.5.2.1 Mean days to germination

Number of days from date of planting to germination was recorded for each accession and the mean was estimated and recorded.

3.5.2.2 Mean plant height

Plant height measurements were taken as the distance between the soil level or collar and apex of the plant. This measurement was done by using a 30-centimetre rule. Plant height was recorded for each plant and the mean was estimated and recorded.

3.5.2.3 Mean number of nodes

The number of nodes of each plants were counted and the mean was estimated and recorded.

3.5.2.4 Mean leaf length

The leaf length was taken by using a 30-centimetre rule. Measurement was done by taking the distance from the leaf base of the lamina to leaf apex for each plant. The mean was then estimated and recorded.

3.5.2.5 Mean leaf width

Leaf width measurement were taken using a 30-centimetre rule. The broadest part of the leaf of each plant was measured and the mean was estimated and recorded.

3.5.2.6 Mean number of leaves

The number of leaves of three plants per accession was obtained by counting both the matured and young leaves and the mean number of leaves of three plants per accession was estimated and recorded.

3.5.2.7 Mean number of branches

The number of branches of three plants per accession was counted and the mean of two plants per accession was estimated and recorded.

3.5.2.8 Mean petiole length

The length of two petiole per plant for three plants per accession was measured using a 30-centimetre rule from the node to the tip of the petiole. The average petiole length of three plants per accession was estimated and recorded.

3.5.2.9 Mean days to first flowering

The mean number of days of flowering per accession from days of germination to flowering were estimated and recorded.

3.5.2.10 Mean number of pods per peduncle

Number of pods per peduncle for three plants per accession was obtained by counting both the matured and the young pods per peduncle. The mean of three plants per accession was estimated and recorded.

3.5.2.11 Mean number of pods per plant

Two of pods per plant of three plants per accession was obtained through counting both matured and the young pods and the mean number of pods of three plant per accession were estimated and recorded.

3.5.2.12 Mean pod length

Two fully matured pods per plants of the three accession were measured using a string from the stylar end to the point of attachment of the pod to the stalk. The string was stretched on a 30-centimetre rule and the pod length was determined in centimeters. The mean pod length and its standard errors of three accesions were estimated and recorded.

3.5.2.13 Mean pod width

The pod width was taken by measuring the width of the same three pods which was used to measure the pod length. The measurement was done using a 30-centimetre rule. The mean pod width of three pods was calculated and recorded.

3.5.2.14 Mean number of locules per pod

Three pods were studied for this traits. Pod locules were recorded by counts. Three pods were broken along the dorsal sutures by the hand and ovules were counted starting from the stylar end to the basal end. Counts were taken for the total number of locules per pod. The measurement was done using the three matured pods for each accession and the mean locules per three pods were calculated and recorded.

3.5.2.15 Mean days to first mature pod

The mean number of days from germination to the first matured pod per accession was estimated and recorded.

3.5.2.16 Mean number of seeds per pod

Two pods per plant of the three accessions were threshed and the number of seeds in each pod was counted and mean number of seeds of two pods was estimated and recorded.

3.5.2.17 Mean number of seeds per plant

Two plants per three accessions were selected and the number of seeds in each pod per accession was counted. The mean number of seeds of two plants per accession was calculated and recorded.

3.5.2.18 Mean number of aborted seeds

Three pods were studied for the mean percentage seed set for each pod, the total number of seeds and the total number of locules were calculated and recorded. The mean number of aborted seeds of three pods were calculated and recorded

3.5.1.19 Mean percent seed set (*PA*)

Mean number of seeds per pod was expressed as a percentage over the mean total number of locule per pod. This was recorded as the mean percentage seed set per accession.

3.5.2.20 Mean seed length

A micrometre screw gauge was used to measure length of each of 10 randomly chosen seeds from each accession. The mean seed length was calculated and recorded.

3.5.2.21 Mean seed width

A micrometre screw gauge was used to measure the width of each of 10 randomly selected seeds from each accession. The mean seed width was calculated and recorded.

3.5.2.22 Mean seed thickness

A micrometre screw gauge was used to measure the thickness of each of 10 randomly selected seeds from each accession. The mean seed thickness was calculated and recorded.

3.5.1.23 Mean seed weight

The seeds of two plants per three the accessions were weighed separately using an electronic balance and mean seed weight for each accession was calculated and recorded.

3.6 TOTAL PHENOLIC COMPOUND ANALYSIS

3.6.1 Preparation of cowpea flour

100g of the cowpea seeds from each accessions were collected and pulverized by using an electronic blender into cowpea flour.

3.6.2. Preparation of sodium carbonate solution

A 50ml volumetric flask was filled with 20ml distilled water. A mass of 6.25g of sodium carbonate was weighed and dissolved in the distilled water. The solution was boiled, allowed to cool and then few crystals of sodium carbonate were added. The solution was made to stand for 24 h and then filtered. Distilled water was added up to the 25ml mark.

3.6.3 Extraction of samples for phytochemical studies

A mass of 0.5g of the cowpea flour was weighed using the electronic balance and poured into McCartney bottles. Twenty millilitres of 100% methanol was added and shaken. The bottles were covered and allowed to stand for 24 hours. After the 24 hour period, the sample in solution was filtered and the filtrate stored in tightly covered McCartney bottles at a temperature of 4 °C in the fridge.

3.6.4 Determination of phenolic acid content

Extract of the cowpea flour for each accession were analysed for phenolic compounds using the Folin-Ciocalteu method (Singleton and Rossi, 1965). After the 24 hour period, 1 ml of each extract was measured with a measuring cylinder and then diluted to 10 ml with distilled water in test tubes. Twenty microliters (20µl) of diluted samples were pipetted into cuvettes. A volume of 1.58 ml of distilled water and 100 µl Folin-Ciocalteu reagent was measured with a measuring cylinder and a 100 µl micropipette respectively and was added to the solution. The solution was shaken to mix. A volume of 300µl of sodium carbonate was pipetted and added to the solution after 5 min and shaken. The solution was placed in the oven for 30 min at a temperature of 40 °C. The cuvettes were taken out after the 30 min and allowed to stand for 90 min. The absorbance at 765 nm was determined against the blank methanol using the visible spectrophotometer. The concentration for the phenolic compounds for each accession was determined from the standard curves of linear equations (Table 2).

3.6.5 Determination of flavonoid content

A modified aluminium chloride colorimetric procedure was used for the determination of flavonoid content in the cowpea sample. A volume of 100µl of samples extract was pipetted and added to 500µl of distilled water and 30 µl of 5% sodium nitrite in cuvettes. The solutions were made to stand for 5 min after which 30 µl of aluminium chloride was added. The solutions were allowed to stand again for 6 min after which 200 µl of sodium hydroxide and 110µl of distilled water were added to the solutions and vortexed. The absorbance was taken at a wavelength of 425 nm for rutin and 415 nm for quercetin using the spectrophotometer. The concentration for individual flavonoid compounds were calculated according to their respective standard curves and the results expressed as mg/l of extract.

3.6.6 Standard curves

The standard curves used for the polyphenolic compounds are presented in Table 3.

Table 3: Polyphenolic compounds and their regression equation

Polyphenolic compound	**Regression equation**
Gallic acid	$y = 0.2263x + 0.1606$
Vanillic acid	$y = 0.1246x + 0.0794$
p-coumaric acid	$y = 0.0726x + 0.0874$
Rutin	$y = 0.0229x + 0.0301$
Quercetin	$y = 0.1548x + 0.0301$

3.6.7 Amino Acids Analysis

The following eighteen amino acids were analysed: L-Aspartic acid, Glutamine, L-Histidine, Isoleucine, L-Lysine, L-Cysteine, L-Methionine, DL-Beta-Phenyl-Alanine, D-Proline, LSerine, L-Threonine, L-Tyrosine, L-Valine, DL-Alpha-Alanine, B-Threonine, Trans-4- ydroxyl-Proline, L-Asparagine and L-Tryptophan.

3.6.7.1. Sample preparation

A standard solution was prepared by weighing 2.5 mg of the standard compound in 25 ml of ethanol and diluting to a concentration of 100 ppm. A mixed standard solution of 10 ppm was prepared from the stock solution, which was diluted to 1 ppm as a working solution. A weight of 0.5 g of cow pea flour was extracted into 20 ml of 100% methanol. The extracts were filtered through filter paper and a funnel into McCarntey tubes. The extracts were latter taken to Ghana Standard Authority for amino acid analysis.

3.6.7.2. Chromatography

The column used was Agilent Poroshell 120 Bonus RP 2.7 µm, 2.1 x 100 mm; the flow rate was 0.15 ml / min. Mobile phases were: 100% water, 0.1% formic acid (A) and 100% methanol, 0.1% formic acid (B). The gradient was 0 to 5% (B) over 5 minutes and 5 to 50% (B) over 15 minutes. The injection volume was 621. Mass spectrometry: MS-Aligent Triple Quadrupole 6420 was used to identify and quantify the compounds.

3.7 STATISTICAL ANALYSIS

STATA version 15 software was used for the following analyses: the percent frequency distribution of qualitative traits, summary statistics, Pearson correlation analysis, principal component analyses and cluster analyses.

Quantitative traits data taken were expose to analysis of variances (ANOVA) using 'R' software. This analysis was done to identify the uniqueness among the accessions and estimate the effects of environment and genes on morphological and phytochemical traits. Genotypic variance, phenotypic variance and environmental variance (Burton & De vane, 1953) with their corresponding coefficients of variation (Singh & Chaudhary, 1985) were used to estimate variability among the cowpea genotypes. The following formulae were adapted from (Belay & Fischa, 2020).

1. **Genotypic Variance**

   GV= (MSg −MSe)r,

   Where MSg = Mean Square of genotypes,

   MSe = Mean Square of error (environmental variance or δ^2e),

   r = number of replications;

2. **Phenotypic Variance**

   PV= *GV* +*MSe*,

   Where *GV* = Genotypic Variance

   MSe = Mean Square of error;

3. **Genotypic Coefficient of Variation**

   $$GCV = \frac{\sqrt{Genotypic\ variance}}{Grand\ mean}\ x\ 100$$

4. **Phenotypic Coefficient of Variation**

   $$PCV = \frac{\sqrt{Phenotypic\ variance}}{Grand\ mean}\ x\ 100$$

5. **Broad sense heritability**

   $H^2 = [(\sigma^2 g) / (\sigma^2 p)] \times 100$,

   Where, $\sigma^2 g$ and $\sigma^2 p$ are genotypic and phenotypic variances respectively.

6. **Genetic Advance**

   $GA = K\sigma p H^2$,

   Where, GA = expected genetic advance,

   K = the standardized selection differential at 5% selection intensity (K=2.063),

   σp = is phenotypic standard deviation on mean basis

   H^2 = heritability in broad sense.

7. **Genetic advance as percentage of population means**

   $GAM = KH^2$ (PCV)

   Where *GCV = Phenotypic Coefficient of Variation*

   K = the standardized selection differential at 5% selection intensity (K=2.063)

   H^2 = heritability in broad sense.

CHAPTER FOUR

4.0 RESULTS

4.1 MORPHOLOGICAL QUALITATIVE TRAITS

4.1.1 Frequency Distribution of Qualitative Traits

The frequency distributions of different classes of qualitative traits are shown in Table 4.

4.1.1.1 Growth pattern

All accessions showed indeterminate growth pattern.

4.1.1.2 Growth habit

There were three different phenotypic classes for growth pattern as follows: *erect, intermediate and semi – erect*. For the controls 67.86% exhibited *intermediate* growth habit, 32.14% showed *erect*. In the case of the test materials 91.04 % exhibited *erect* growth habit, 4.25% showed *intermediate* habit and 4.72% showed semi – erect growth habit.

4.1.1.3 Plant pigmentation

Plant pigmentation exhibited three different phenotypic classes. They were *intermediate, moderate and very slight*. For the control 10.72% showed *intermediate* pigmentation, while 54.76% showed *very slight*. 34.52% showed moderate pigmentation. In the test materials 0.31% were *intermediate* and 59.91% showed *very slight* while 39.78% were *moderate*.

4.1.1.4 Leaf shape

Terminal leaflet shape had three different phenotypic classes, namely; *globose, hastate and sub-globose*. For the control 66.67% showed *globose*, 33.33% showed *hastate*. In the test material 76.10% exhibited *globose* and 23.90% showed a *sub-globose*.

4.1.1.5 Leaf colour

Leaf colour was classified into two character states as *dark green* and *intermediate* colourations. Out of the 84 control plants, 64 of them were *dark green* representing 76.19% and 20 of them also had *intermediate* leaf color with a percentage of 23.81%. In the case test material, the least population frequency of 35.53% was recorded for *dark green* and the highest frequency of 64.47% was recorded for *intermediate*.

4.1.1.6 Twinning tendency

Twinning tendency had three different phenotypic classes, these were; *slight, intermediate* and *none*. For the control 19.05% showed *intermediate,* 55.95% showed *slight* and 25% showed *none*. The frequency scored for twinning tendency recorded for the test material were 0.31% for *intermediate*, 10.69% for *slight* and 88.99% for *none*.

4.1.1.7 Flower colour

Flower colour showed three character states: *white, violet* and *white with patches of violet*. For the control 66.67% was *white* and it was the dominant colour and 33.33% showed *violet*. In the test material, the flower colour, *white with patches of violet* showed 86.79%, 10.38% showed *white*, and 2.83% showed *violet*.

4.1.1.8 Pod tip colour

Two phenotypic classes of the pod tip colour were observed and recorded. For the control 33.33% of population showed *no colour* at the tip of the pod, whilst 66.67% had a *colouration* at the tip of their pod. In the case of the test material 37.89% showed *no colour* at the tip of the pod whereas 62.11% exhibited *colouration* at tip of the pod.

4.1.1.9 Leaf markings

All accessions showed leaf markings.

4.1.1.10 Leaf size

There were four different phenotypic class of leaf size recorded (*big*, *medium*, *small and narrow*). For the controls 23.81% showed *narrow* leaf size, 32.14% showed *big* and 44.05% showed *medium*. In the test materials 11.79% showed *big*, 16.19% showed *small* and 72.01% showed *medium.*

4.1.1.11 Pod attachment

Pod attachment to peduncle was classified into three character states namely; *pendant, erect and 30 - 90° down from erect. 30 - 90° down from erect* was predominant in the control (34.52%). However, *pendant* was dominant in both the test material (41.51%) and combined material (40.56%).

4.1.1.12 Pod thickness

There were three different phenotypic classes of pod thickness. They were *intermediate*, *thick and thin*. In the case of the control 67.86% showed *intermediate* and 32.14% showed *thick*. For the test materials, 51.26% showed *thin*, 41.51% showed *intermediate* and 7.23% showed *thick*.

4.1.1.13 Pod colour

Two phenotypic classes for pod colours were observed, these were: *dark tan and pale tan*. For the control 34.52% showed *dark tan* and 65.48% exhibited *pale tan*. In the case of test materials 37.42% showed *dark tan* and 62.58% showed *pale tan*.

4.1.1.14 Pod curvature

There were three phenotypic class observed for pod curvature, they were *curved, slightly curved and straight*. For the control 65.48% showed straight, 34.52% showed *slightly curved*. In the test material 44.03% showed *slightly curved* and 55.97% showed *curved*.

4.1.1.15 Pod hairiness

Two phenotypic classes of pod hairiness were observed these were *glabrescent* and *short appressed hair*. All the control exhibited *glabrescent*. In the case of the test material 82.70% exhibited *glabrescent* whereas 17.30% exhibited *short appressed hair*.

4.1.1.16 Seed coat colour

Three different phenotypic classes of the seed coat colour were recorded, they were: *reddish brown, white and cream*. For the control, 33.33% showed *reddish brown* 66.67% showed *white*. In the test material scored 33.96% showed *cream* colouration, 66.04 showed *white*.

Table 4: Frequency distribution of morphological traits for the 27 cowpea accessions

Traits	**Phenotypic Class**	**Control (%)**	**Test (%)**	**Combined (%)**
Growth pattern	Indeterminate	100.00	100.00	100.00
Growth habit	Erect	32.14	91.04	84.17
	Intermediate	67.86	4.25	11.67
	Semi-erect	0.00	4.72	4.17
Plant pigmentation	Intermediate	10.71	0.31	1.53
	Moderate	34.52	39.78	39.17
	Very slight	54.76	59.91	59.31
Leaf shape	Globose	66.67	76.10	75.00
	Hastate	33.33	0.00	3.89
	Sub-globose	0.00	23.90	21.11
Leaf colour	Dark green	76.19	35.53	40.28
	Intermediate green	23.81	64.47	59.72
Twinning tendency	Intermediate	19.05	0.31	2.50
	None	25.00	88.99	81.53
	Slight	55.95	10.69	15.97
Flower colour	Violet	33.33	2.83	6.39
	White	66.67	10.38	16.94
	White with patches of violet	0.00	86.79	76.67
Pod tip colour	Absent	33.33	37.89	37.36
	Present	66.67	62.11	62.64
Leaf markings	Present	100.00	100.00	100.00
Leaf size	Big	32.14	11.79	14.17
	Medium	44.05	72.01	68.75
	Narrow	23.81	0.00	2.78
	Small	0.00	16.19	14.31
Pod attachment	30 - 90° down from erect	34.52	28.77	29.44
	Erect	32.14	29.72	30.00
	Pendant	33.33	41.51	40.56
Pod thickness	Intermediate	67.86	41.51	44.58
	Thick	32.14	7.23	10.14
	Thin	0.00	51.26	45.28
Pod colour	Dark tan	34.52	37.42	37.08
	Pale tan	65.48	62.58	62.92
Pod curvature	Curved	34.52	55.97	49.44
	Slightly curved	0.00	44.03	42.92
	Straight	65.48	0.00	7.64
Pod hairiness	Glabrescent	100.00	82.70	84.72
	Short appressed hair	0.00	17.30	15.28
Seed coat colour	Reddish brown	33.33	0.00	3.89
	White	66.67	66.04	66.11
	Cream	0.00	33.96	30.00

4.2 CHI – SQUARE TEST OF ASSOCIATION AMONG QUALITATIVE TRAITS

4.2.1 Chi-square test of association in control material

Chi-square test of associations among the control is presented in Table 5. Seventy-eight (78) significant associations were observed among the qualitative traits.

Growth habit had a significant associated with plant pigmentation (χ^2 = 33.77, P = 0.000), terminal leaflet shape (χ^2 = 19.89, P = 0.00), leaf colour (χ^2 = 12.43, P = 0.000), twinning tendency (χ^2 = 13.76, P = 0.001), flower colour (χ^2 = 19.89, P = 0.000), pod tip colour (χ^2 = 19.89, P = 0.000), leaf size (χ^2 = 84.00, P = 0.000), pod attachment (χ^2 = 84.00, P = 0.000), pod thickness (χ^2 = 84.00, P = 0.000), pod colour (χ^2 = 20.98, P = 0.000), pod curvature (χ^2 = 20.98, P = 0.000), and seed coat colour (χ^2 = 19.84, P = 0.000).

Significant associations were observed between plant pigmentation and the following traits: terminal leaflet shape (χ^2 = 34.70, P = 0.00), leaf colour (χ^2 = 21.68, P = 0.000), twinning tendency (χ^2 = 19.54, P = 0.001), flower colour (χ^2 = 34.70, P = 0.000), pod tip colour (χ^2 = 34.70, P = 0.000), leaf size (χ^2 = 71.43, P = 0.000), pod attachment (χ^2 = 101.0435, P = 0.000), pod thickness (χ^2 = 33.77, P = 0.000), pod colour (χ^2 = 84.00, P = 0.000), pod curvature (χ^2 = 84.00, P = 0.000), and seed coat colour (χ^2 = 34.70, P = 0.000).

Significant associations were observed between terminal leaflet shape and the following traits: leaf colour (χ^2 = 52.50, P = 0.000), twinning tendency (χ^2 = 49.84, P = 0.000), flower colour (χ^2 = 84.00, P = 0.000), pod tip colour (χ^2 = 84.00, P = 0.000), leaf size (χ^2 = 55.78, P = 0.000), pod attachment (χ^2 = 84.00, P = 0.000), pod thickness

(χ^2 = 19.89, P = 0.000), pod colour (χ^2 = 22.15, P = 0.000), pod curvature (χ^2 = 22.15, P = 0.000), and seed coat colour (χ^2 = 84.00, P = 0.000).

High significant association was observed between leaf colour and; twinning tendency (χ^2 = 35.74, P = 0.000), flower colour (χ^2 = 52.50, P = 0.000), pod tip colour (χ^2 = 52.50, P = 0.000), leaf size (χ^2 = 84.00, P = 0.000), pod attachment (χ^2 = 52.50, P = 0.000), pod thickness (χ^2 = 12.43, P = 0.000), pod colour (χ^2 = 13.84, P = 0.000), pod curvature (χ^2 = 13.84 P = 0.000), and seed coat colour (χ^2 = 52.50, P = 0.000).

Twinning tendency was significantly associated with flower colour (χ^2 = 49.84, P = 0.000), pod tip colour (χ^2 = 49.84, P = 0.000), leaf size (χ^2 = 38.10, P = 0.000), pod attachment (χ^2 = 49.94, P = 0.000), pod thickness (χ^2 = 13.76, P = 0.001), pod colour (χ^2 = 11.26, P = 0.000), pod curvature (χ^2 = 11.26, P = 0.000), and seed coat colour (χ^2 = 49.84, P = 0.000).

Significant associations were observed between flower colour and the following seven qualitative traits: pod tip colour (χ^2 = 84.00, P = 0.000), leaf size (χ^2 = 55.78, P = 0.000), pod attachment (χ^2 = 84.00, P = 0.000), pod thickness (χ^2 = 19.89, P = 0.001), pod colour (χ^2 = 22.15, P = 0.004), pod curvature (χ^2 = 22.15, P = 0.004), and seed coat colour (χ^2 = 84.00, P = 0.000).

There was significant association observed between pod tip colour and the following qualitative traits: leaf size (χ^2 = 55.78, P = 0.000), pod attachment (χ^2 = 84.00, P = 0.000), pod thickness (χ^2 = 19.89, P = 0.001), pod colour (χ^2 = 22.15, P = 0.004), pod curvature (χ^2 = 22.15, P = 0.004), and seed coat colour (χ^2 = 84.00, P = 0.000).

Leaf size was significantly associated with pod attachment (χ^2 = 131.03, P = 0.000), pod thickness (χ^2 = 84.00, P = 0.001), pod colour (χ^2 = 56.26, P = 0.004), pod curvature (χ^2 = 56.26, P = 0.004), and seed coat colour (χ^2 = 55.78, P = 0.000). The following four qualitative traits pod thickness (χ^2 = 84.00, P = 0.001), pod colour (χ^2 = 84.00, P = 0.004), pod curvature (χ^2 = 84.00, P = 0.004), and seed coat colour (χ^2 = 84.00, P = 0.000), were significantly associated with pod attachment.

Pod thickness was significantly associated with pod colour (χ^2 = 20.98, P = 0.004), pod curvature (χ^2 = 20.98, P = 0.004), and seed coat colour (χ^2 = 19.89, P = 0.000). Pod colour scored a significant association with these two qualitative traits: pod curvature (χ^2 = 84.00, P = 0.004), and seed coat colour (χ^2 = 22.15, P = 0.000).

There was a significant association between pod curvature and seed coat colour (χ^2 = 22.15, P = 0.000).

Table 5: Chi-square test of association among 27 cowpea qualitative traits of control materials.

Traits	**Association**	**Control (χ^2)**
Growth Habit	Plant pigmentation	33.77***
	Terminal leaf shape	19.89***
	Leaf colour	12.43***
	Twining tendency	13.76***
	Flower colour	19.89***
	Pod tip colour	19.89***
	Leaf size	84.00***
	Pod attachment	84.00***
	Pod thickness	84.00***
	Pod colour	20.98***
	Pod curvature	20.98***
	Seed coat colour	19.89***
Plant pigmentation	Terminal leaf shape	34.70***
	Leaf colour	21.68***
	Twining tendency	19.54***
	Flower colour	34.70***
	Pod tip colour	34.70***
	Leaf size	71.43***
	Pod attachment	101.04***
	Pod thickness	33.77***
	Pod colour	84.00***
	Pod curvature	84.00***
	Seed coat colour	34.70***
Terminal leaf shape	Leaf colour	52.50***
	Twining tendency	49.84***
	Flower colour	84.00***
	Pod tip colour	84.00***
	Leaf size	55.78***
	Pod attachment	84.00***
	Pod thickness	19.89***
	Pod colour	22.15***
	Pod curvature	22.15***
	Seed coat colour	84.00***
Leaf colour	Twining tendency	35.74***
	Flower colour	52.50***
	Pod tip colour	52.50***
	Leaf size	84.00***
	Pod attachment	52.50***
	Pod thickness	12.43***
	Pod colour	13.84***
	Pod curvature	13.84***
	Seed coat colour	52.50***

Table 5 (Cont'd)

Traits	Association	Control (χ^2)
Twining tendency	Flower colour	49.84***
	Pod tip colour	49.84***
	Leaf size	38.10***
	Pod attachment	49.94***
	Pod thickness	13.76***
	Pod colour	11.26***
	Pod curvature	11.26***
	Seed coat colour	49.84***
Flower colour	Pod tip colour	84.00***
	Leaf size	55.78***
	Pod attachment	84.00***
	Pod thickness	19.89***
	Pod colour	22.15***
	Pod curvature	22.15***
	Seed coat colour	84.00***
Pod tip colour	Leaf size	55.78***
	Pod attachment	84.00***
	Pod thickness	19.89***
	Pod colour	22.15***
	Pod curvature	22.15***
	Seed coat colour	84.00***
Leaf size	Pod attachment	131.03***
	Pod thickness	84.00***
	Pod colour	56.26***
	Pod curvature	56.26***
	Seed coat colour	55.78***
Pod attachment	Pod thickness	84.00***
	Pod colour	84.00***
	Pod curvature	84.00***
	Seed coat colour	84.00***
Pod thickness	Pod colour	20.98***
	Pod curvature	20.98***
	Seed coat colour	19.89***
Pod colour	Pod curvature	84.00***
	Seed coat colour	22.15***
Pod curvature	Seed coat colour	22.15***

Significant level (*) = P<0.05, (**) = P<0.005 and (***) = P<0.0005

4.2.2 Chi-square test of association among qualitative traits in the test materials

Chi-square test of associations is shown in Table 6. Eighty-six (86) significant associations were observed among the qualitative traits.

Growth habit was significantly associated with the following qualitative traits: plant pigmentation ($\chi^2 = 84.32$, P = 0.000), terminal leaflet shape ($\chi^2 = 19.66$, P = 0.00), leaf colour ($\chi^2 = 101.83$, P = 0.000), twinning tendency ($\chi^2 = 59.93$, P = 0.000), flower colour ($\chi^2 = 9.53$, P = 0.049), pod tip colour ($\chi^2 = 102.62$, P = 0.000), leaf size ($\chi^2 = 220.84$, P = 0.000), pod attachment ($\chi^2 = 69.77$, P = 0.000), pod thickness ($\chi^2 = 45.78$, P = 0.000), pod colour ($\chi^2 = 32.67$, P = 0.000), pod curvature ($\chi^2 = 38.68$, P = 0.000), pod hairiness ($\chi^2 = 138.93$, P = 0.000) and seed coat colour ($\chi^2 = 17.87$, P = 0.000).

Significant association was observed between plant pigmentation and the following traits: terminal leaflet shape ($\chi^2 = 69.55$, P = 0.00), leaf colour ($\chi^2 = 37.93$, P = 0.000), twinning tendency ($\chi^2 = 20.93$, P = 0.001), flower colour ($\chi^2 = 17.31$, P = 0.002), pod tip colour ($\chi^2 = 45.56$, P = 0.000), leaf size ($\chi^2 = 140.16$, P = 0.000), pod attachment ($\chi^2 = 16.74$, P = 0.000), pod colour ($\chi^2 = 18.44$, P = 0.000), pod curvature ($\chi^2 = 10.48$, P = 0.005), pod hairiness ($\chi^2 = 6.09$, P = 0.048) and seed coat colour ($\chi^2 = 7.20$, P = 0.027).

Terminal leaflet shape was significantly associated with leaf colour ($\chi^2 = 110.01$, P = 0.000), twinning tendency ($\chi^2 = 85.98$, P = 0.000), flower colour ($\chi^2 = 18.73$, P = 0.000), pod tip colour ($\chi^2 = 34.39$, P = 0.000), leaf size ($\chi^2 = 137.11$, P = 0.000), pod attachment ($\chi^2 = 12.46$, P = 0.002), pod thickness ($\chi^2 = 75.92$, P = 0.000), pod colour ($\chi^2 = 59.42$, P = 0.000), pod curvature ($\chi^2 = 87.42$, P = 0.000), and pod hairiness ($\chi^2 = 49.82$, P = 0.000).

High significant associations were observed between leaf colour and the following traits: twinning tendency (χ^2 = 14.04, P = 0.001), flower colour (χ^2 = 47.68, P = 0.000), pod tip colour (χ^2 = 18.76, P = 0.000), leaf size (χ^2 = 69.31, P = 0.000), pod attachment (χ^2 = 45.81, P = 0.000), pod thickness (χ^2 = 9.36, P = 0.009), pod colour (χ^2 = 12.40, P = 0.000), Pod hairiness (χ^2 = 7.01, P = 0.008) and seed coat colour (χ^2 = 14.48, P = 0.000).

Twinning tendency had a significant association with pod tip colour (χ^2 = 20.40, P = 0.000), leaf size (χ^2 = 18.11, P = 0.001), pod attachment (χ^2 = 17.55, P = 0.002), pod thickness (χ^2 = 15.54, P = 0.004), pod curvature (χ^2 = 26.22, P = 0.000), and pod hairiness (χ^2 = 12.97, P = 0.002).

Significant associations were observed between flower colour and the following eight qualitative traits: pod tip colour (χ^2 = 46.98, P = 0.000), leaf size (χ^2 = 31.88, P = 0.000), pod attachment (χ^2 = 95.17, P = 0.000), pod thickness (χ^2 = 36.98, P = 0.000), pod colour (χ^2 = 11.56, P = 0.003), pod curvature (χ^2 = 76.12, P = 0.000), Pod hairiness (χ^2 = 11.95, P = 0.003), and seed coat colour (χ^2 = 41.04, P = 0.000).

There was significant association observed between pod tip colour and the following qualitative traits: leaf size (χ^2 = 99.01, P = 0.000), pod attachment (χ^2 = 98.66, P = 0.000), pod thickness (χ^2 = 47.26, P = 0.000), pod colour (χ^2 = 33.34, P = 0.000), pod curvature (χ^2 = 16.81, P = 0.004), pod hairiness (χ^2 = 45.81, P = 0.000), and seed coat colour (χ^2 = 20.37, P = 0.000).

Leaf size was significantly associated with pod attachment (χ^2 = 50.55, P = 0.000), pod thickness (χ^2 = 172.956, P = 0.001), pod colour (χ^2 = 103.84, P = 0.004), pod curvature (χ^2 = 48.40, P = 0.004), pod hairiness (χ^2 = 30.42, P = 0.000), and seed coat colour (χ^2 = 15.55, P = 0.000).

The following five qualitative traits pod thickness (χ^2 = 305.86, P = 0.000), pod colour (χ^2 = 186.40, P = 0.000), pod curvature (χ^2 = 215.75, P = 0.000), pod hairiness (χ^2 = 28.16, P = 0.000), and seed coat colour (χ^2 = 80.48, P = 0.000), were significantly associated with pod attachment.

There was a significant association between pod thickness and the following qualitative traits: pod colour (χ^2 = 355.45, P = 0.000), pod curvature (χ^2 = 413.84, P = 0.000), pod hairiness (χ^2 = 11.97, P = 0.003) and seed coat colour (χ^2 = 76.01, P = 0.000).

There was a significant association between pod colour and these three qualitative traits: pod curvature (χ^2 = 299.13, P = 0.000), pod hairiness (χ^2 = 8.99, P = 0.003) and seed coat colour (χ^2 = 20.50, P = 0.000).

Pod curvature was significantly associated with seed coat colour (χ^2 = 43.48, P = 0.000).

Pod hairiness also had a significant association with seed coat colour (χ^2 = 34.79, P = 0.000).

Table 6: Chi-square test of association among 27 cowpea qualitative traits of test materials.

Traits	Association	Test material (χ^2)
Growth Habit	Plant pigmentation	84.32***
	Terminal leaf shape	19.66***
	Leaf colour	101.83***
	Twining tendency	59.93***
	Flower colour	9.53*
	Pod tip colour	102.62***
	Leaf size	220.84***
	Pod attachment	69.77***
	Pod thickness	45.78***
	Pod colour	32.67***
	Pod curvature	38.68***
	Pod hairiness	138.93***
	Seed coat colour	17.87***
Plant pigmentation	Terminal leaf shape	69.55***
	Leaf colour	37.93***
	Twining tendency	20.93***
	Flower colour	17.31***
	Pod tip colour	45.56***
	Leaf size	140.16***
	Pod attachment	16.74***
	Pod thickness	4.01
	Pod colour	18.44***
	Pod curvature	10.48**
	Pod hairiness	6.09*
	Seed coat colour	7.20*
Terminal leaf shape	Leaf colour	110.10***
	Twining tendency	85.98***
	Flower colour	18.73***
	Pod tip colour	34.39***
	Leaf size	137.11***
	Pod attachment	12.46***
	Pod thickness	75.92***
	Pod colour	59.42***
	Pod curvature	87.42***
	Pod hairiness	49.82***
	Seed coat colour	0.22
Leaf colour	Twining tendency	14.04***
	Flower colour	47.68***
	Pod tip colour	18.76***
	Leaf size	69.31***
	Pod attachment	45.81***
	Pod thickness	9.36*
	Pod colour	12.40***
	Pod curvature	2.01
	Pod hairiness	7.01*
	Seed coat colour	14.48***

Table 5 (Cont'd)

Traits	Association	Test material (χ^2)
Twining tendency	Flower colour	3.47
	Pod tip colour	20.40***
	Leaf size	18.11***
	Pod attachment	17.55***
	Pod thickness	15.55***
	Pod colour	1.35
	Pod curvature	26.22***
	Pod hairiness	12.97***
	Seed coat colour	2.31
Flower colour	Pod tip colour	46.98***
	Leaf size	31.88***
	Pod attachment	95.17***
	Pod thickness	36.98***
	Pod colour	11.56***
	Pod curvature	76.12***
	Pod hairiness	11.95***
	Seed coat colour	41.04***
Pod tip colour	Leaf size	99.01***
	Pod attachment	98.66***
	Pod thickness	47.26***
	Pod colour	33.34***
	Pod curvature	16.81***
	Pod hairiness	45.81***
	Seed coat colour	20.37***
Leaf size	Pod attachment	50.55***
	Pod thickness	172.96***
	Pod colour	103.84***
	Pod curvature	48.40***
	Pod hairiness	30.42***
	Seed coat colour	15.55***
Pod attachment	Pod thickness	305.86***
	Pod colour	186.40***
	Pod curvature	215.75***
	Pod hairiness	28.16***
	Seed coat colour	80.48***
Pod thickness	Pod colour	355.45***
	Pod curvature	413.84***
	Pod hairiness	11.97***
	Seed coat colour	76.01***
Pod colour	Pod curvature	299.13***
	Pod hairiness	8.99***
	Seed coat colour	20.50***
Pod curvature	Pod hairiness	1.93
	Seed coat colour	43.48***
Pod hairness	Seed coat colour	34.79

Significant level (*) = P<0.05, (**) = P<0.005 and (***) = P<0.0005

4.2.3 Chi-square test of association among qualitative traits in the combined material

Chi-square test of associations is shown in Table 7. There were a total of 86 significant associations among the qualitative traits.

Significant associations were observed between growth habit and the following qualitative traits: plant pigmentation ($\chi^2 = 74.79$, P = 0.000), terminal leaflet shape ($\chi^2 = 243.87$, P = 0.00), leaf colour ($\chi^2 = 94.71$, P = 0.000), twinning tendency ($\chi^2 = 96.00$, P = 0.000), flower colour ($\chi^2 = 155.61$, P = 0.000), pod tip colour ($\chi^2 = 91.35$, P = 0.000), leaf size ($\chi^2 = 207.61$, P = 0.000), pod attachment ($\chi^2 = 69.91$, P = 0.000), pod thickness ($\chi^2 = 126.47$, P = 0.000), pod colour ($\chi^2 = 17.67$, P = 0.000), pod curvature ($\chi^2 = 145.63$, P = 0.000), pod hairiness ($\chi^2 = 25.04$, P = 0.000) and seed coat colour ($\chi^2 = 243.51$, P = 0.000).

Plant pigmentation had a significant association with terminal leaflet shape ($\chi^2 = 98.57$, P = 0.00), leaf colour ($\chi^2 = 53.77$, P = 0.000), twinning tendency ($\chi^2 = 53.28$, P = 0.000), flower colour ($\chi^2 = 66.40$, P = 0.000), pod tip colour ($\chi^2 = 27.83$, P = 0.000), leaf size ($\chi^2 = 137.75$, P = 0.000), pod attachment ($\chi^2 = 38.03$, P = 0.000), pod curvature ($\chi^2 = 134.92$, P = 0.005), pod hairiness ($\chi^2 = 6.09$, P = 0.021) and seed coat colour ($\chi^2 = 22.48$, P = 0.027).

Terminal leaflet shape was significantly associated with leaf colour ($\chi^2 = 136.13$, P = 0.000), twinning tendency ($\chi^2 = 42.35$, P = 0.000), flower colour ($\chi^2 = 492.08$, P = 0.000), pod tip colour ($\chi^2 = 73.08$, P = 0.000), leaf size ($\chi^2 = 673.09$, P = 0.000), pod attachment ($\chi^2 = 58.03$, P = 0.000), pod thickness ($\chi^2 = 133.70$, P = 0.000), pod colour ($\chi^2 = 70.32$, P = 0.000), pod curvature ($\chi^2 = 461.98$, P = 0.000), pod hairiness ($\chi^2 = 67.20$, P = 0.000) and seed coat colour ($\chi^2 = 721.76$, P = 0.000).

Significant association was observed between leaf colour and the following twinning tendency (χ^2 = 31.23, P = 0.001), flower colour (χ^2 = 86.72, P = 0.000), leaf size (χ^2 = 101.02, P = 0.000), pod attachment (χ^2 = 74.67, P = 0.000), pod thickness (χ^2 =39.27, P = 0.009), pod colour (χ^2 = 5.23, P = 0.022), pod hairiness (χ^2 = 13.36, P = 0.000) and seed coat colour (χ^2 = 32.17, P = 0.000).

Twinning tendency was significantly associated with pod tip colour (χ^2 = 121.46, P = 0.000), pod tip colour (χ^2 = 34.88, P = 0.000), leaf size (χ^2 = 41.15, P = 0.005), pod thickness (χ^2 = 59.05, P = 0.004), pod curvature (χ^2 = 101.13, P = 0.000), and seed coat colour (χ^2 = 24.53, P = 0.002).

Significant associations were observed between flower colour and the following eight qualitative traits: pod tip colour (χ^2 = 82.47, P = 0.000), leaf size (χ^2 = 341.22, P = 0.000), pod attachment (χ^2 = 109.58, P = 0.000), pod thickness (χ^2 = 29.20, P = 0.000), pod colour (χ^2 = 32.19, P = 0.000), pod curvature (χ^2 = 285.87, P = 0.000), pod hairiness (χ^2 = 8.86, P = 0.012), and seed coat colour (χ^2 = 469.41, P = 0.000).

Significant association observed between pod tip colour and the following qualitative traits: leaf size (χ^2 = 105.31, P = 0.000), pod attachment (χ^2 = 150.36, P = 0.000), pod thickness (χ^2 = 67.06, P = 0.000), pod colour (χ^2 = 48.70, P = 0.000), pod curvature (χ^2 = 14.01, P = 0.001), pod hairiness (χ^2 = 46.67, P = 0.000), and seed coat colour (χ^2 = 79.74, P = 0.000).

Leaf size was significantly associated with pod attachment (χ^2 = 47.64, P = 0.000), pod thickness (χ^2 = 339.40, P = 0.000), pod colour (χ^2 = 131.86, P = 0.004), pod curvature (χ^2 = 379.26, P = 0.004), pod hairiness (χ^2 = 26.79, P = 0.000), and seed coat colour (χ^2 = 531.50, P = 0.000).

The following five qualitative traits pod thickness (χ^2 = 261.26, P = 0.000), pod colour (χ^2 = 181.53, P = 0.000), pod curvature (χ^2 = 248.57, P = 0.000), pod hairiness (χ^2 =

27.57, P = 0.000), and seed coat colour (χ^2 = 118.41, P = 0.000), were significantly associated with pod attachment.

Significant association between pod thickness and the following qualitative traits: pod colour (χ^2 = 326.12, P = 0.000), pod curvature (χ^2 = 557.86, P = 0.000), pod hairiness (χ^2 = 14.66, P = 0.001) and seed coat colour (χ^2 = 140.08, P = 0.000).

Significant associations were observed between pod colour and these three qualitative traits: pod curvature (χ^2 = 269.26, P = 0.000), pod hairiness (χ^2 = 9.28, P = 0.002) and seed coat colour (χ^2 = 33.32, P = 0.000).

Pod curvature scored a significant association with pod hairiness (χ^2 = 11.44, P = 0.003) and seed coat colour (χ^2 = 416.68, P = 0.000).

Pod hairiness also had a significant association with seed coat colour (χ^2 = 51.01, P = 0.000).

Table 7: Chi-square test of association among 27 cowpea qualitative traits of the combined material

Traits	**Association**	**Combined (χ^2)**
Growth Habit	Plant pigmentation	74.79***
	Terminal leaf shape	243.87***
	Leaf colour	94.71***
	Twining tendency	96.00***
	Flower colour	155.61***
	Pod tip colour	91.35***
	Leaf size	207.61***
	Pod attachment	69.92***
	Pod thickness	126.47***
	Pod colour	17.67***
	Pod curvature	145.63***
	Pod hairiness	25.04***
	Seed coat colour	243.51***
Plant pigmentation	Terminal leaf shape	98.57***
	Leaf colour	53.77***
	Twining tendency	53.28***
	Flower colour	66.40***
	Pod tip colour	27.83***
	Leaf size	137.75***
	Pod attachment	38.03***
	Pod thickness	66.11***
	Pod colour	2.45
	Pod curvature	134.92***
	Pod hairiness	7.77
	Seed coat colour	22.48***
Terminal leaf shape	Leaf colour	136.13***
	Twining tendency	42.35***
	Flower colour	429.08***
	Pod tip colour	73.08***
	Leaf size	673.09***
	Pod attachment	58.03***
	Pod thickness	133.70***
	Pod colour	70.32***
	Pod curvature	461.98***
	Pod hairiness	67.20***
	Seed coat colour	721.76***
Leaf colour	Twining tendency	31.23***
	Flower colour	86.72***
	Pod tip colour	2.80
	Leaf size	101.02***
	Pod attachment	74.67***
	Pod thickness	39.26***
	Pod colour	5.23*
	Pod curvature	22.12***
	Pod hairiness	13.36***
	Seed coat colour	32.17***

Table 7 (Cont'd)

Traits	Association	Combined (χ^2)
Twining tendency	Flower colour	121.46***
	Pod tip colour	34.88***
	Leaf size	41.15***
	Pod attachment	7.62
	Pod thickness	59.05***
	Pod colour	1.36
	Pod curvature	101.14***
	Pod hairiness	0.29
	Seed coat colour	24.53***
Flower colour	Pod tip colour	82.47***
	Leaf size	341.22***
	Pod attachment	109.58***
	Pod thickness	29.20***
	Pod colour	32.19***
	Pod curvature	285.87***
	Pod hairiness	8.86*
	Seed coat colour	469.41***
Pod tip colour	Leaf size	105.31***
	Pod attachment	150.36***
	Pod thickness	67.06***
	Pod colour	48.70***
	Pod curvature	14.01***
	Pod hairiness	46.67***
	Seed coat colour	79.74***
Leaf size	Pod attachment	47.64***
	Pod thickness	339.40***
	Pod colour	131.86***
	Pod curvature	379.26***
	Pod hairiness	26.79***
	Seed coat colour	531.50***
Pod attachment	Pod thickness	261.26***
	Pod colour	181.53***
	Pod curvature	248.57***
	Pod hairiness	27.57***
	Seed coat colour	118.41***
Pod thickness	Pod colour	326.12***
	Pod curvature	557.86***
	Pod hairiness	14.66***
	Seed coat colour	140.08***
Pod colour	Pod curvature	269.26***
	Pod hairiness	9.28***
	Seed coat colour	33.32***
Pod curvature	Pod hairiness	11.44***
	Seed coat colour	416.68***
Pod hairiness	Seed coat colour	51.01***

Significant level (*) = P<0.05, (**) = P<0.005 and (***) = P<0.0005

4.3 VARIABILITY IN QUANTITATIVE MORPHOLOGICAL TRAITS

Means and their standard errors for morphological quantitative traits are presented in Table 8.

4.3.1 Days to germination

The test materials scored the highest mean number of days to germination of 3.60±0.03 days while the control scored the lowest mean number of days to germination of 3.40±0.07 days. The grand mean for days to germination was 3.57±0.03 days.

4.3.2 Petiole length

Mean petiole length of the control materials scored the highest mean value of 10.65±0.16 cm. The test material scored the lowest mean value of 9.79±0.06 cm. The grand mean for petiole length was 9.89±0.06cm.

4.3.3 Mean number of branches

The highest mean number of branches was scored by the test materials with value of 4.59±0.03. The control scored the least mean value of 4.38±0.05. The grand mean for number of branches was 4.57±0.02.

4.3.4 Mean number of leaves

Mean number of leaves for the test materials recorded the highest mean value of 42.40±0.31. The control recorded the least mean value of 39.19±0.70. The grand mean was 42.02±0.29.

4.3.5 Mean number of nodes

Mean number of nodes of the test material scored the highest mean value of 9.30±0.05. The number of nodes of the control scored the least mean value of 8.63±0.10. The grand mean of the number of leaves was 9.22±0.05.

4.3.6 Mean number of pod per peduncle

Mean number of pod per peduncle for the test material recorded the highest mean value of 2.97±0.02. The control scored the least mean value of 2.74±0.05. The grand mean for this traits was 2.94±0.02.

4.3.7 Mean Plant height

The mean plant height of the control recorded the highest mean value of 12.49±0.16. The test material scored the least mean value of 11.57±0.06. The grand mean of plant height was 11.67±0.06.

4.3.8 Mean leaflet length

Mean leaflet length of the control recorded the highest mean value of 10.40±0.17 cm. the test material scored the least mean value of 8.56±0.05. The grand mean for the leaflet length was 8.77±0.05 cm.

4.3.9 Mean leaflet width

Mean leaflet width of the test material recorded the highest mean value of 4.47±0.03 cm. The control scored the least mean value of 4.09±0.14. The grand mean for the leaflet length was 4.43±0.03 cm.

4.3.10 Days to first flowering

Mean days to first flowering of the control scored the highest mean value of 37.20±0.21 days. The test material scored the least mean value of 34.52±0.05 days. The grand mean was 34.84±0.06 days.

4.3.11 Days to first mature pod

The mean days to first mature pod of the control scored the highest mean value of 43.24±0.24 days. The mean value of 41.52±0.05 days, for the test material was the least. The grand mean was 41.72±0.05.

4.3.12 Mean pod length

The mean pod length of the control scored the highest mean value of 17.35±0.19 cm. the test material scored the least mean value of 16.90±0.09 cm. the grand mean was 16.95±0.08 cm.

4.3.13 Mean pod width

Mean pod width of the control scored the highest mean value of 0.96±0.02 cm. the test material scored the least mean value of 0.85±0.01 cm. the grand mean was 0.86±0. 01cm.

4.3.14 Number of locules per pod

Mean number of locules per pod of the test material recorded the highest mean value of 15.74±0.05. The control scored the least mean value of 15.36±0.22. The grand mean was 15.70±0.05.

4.3.15 Number of pods per plant

Mean number of pods per plant of the control had the highest mean value of 45.92±0.99 pods. The test had the least the mean value of 38.98±0.42. The grand mean was 39.79±0.40.

4.3.16 Mean number of seeds per pod

Mean number of seeds per pod of the test recorded the highest mean value of 15.15±0.06 seeds. The control recorded the least mean value of 14.87±0.21. The grand mean was 15.11±0.06 seeds.

4.3.17 Number of seeds per plant

Mean number of seeds per plant of the control recorded the highest mean value of 686.18±18.86 seeds. The test recorded the least mean value of 593.80±7.39 seeds. The grand mean of the number of seeds per plant was 604.58±6.98. This trait scored a Z-value of 4.30 and a p-value of 0.00

4.3.18 Mean number of seeds aborted

The mean number of seeds aborted of the test material scored the highest mean value of 0.60±0.03. The control scored the least mean value of 0.49±0.06. The grand mean for the number of seeds aborted was 0.59±0.03.

4.3.19 Percentage seed aborted

The mean percentage seed aborted of the test material scored the highest mean value of 3.79±0.21%. The control scored the least mean value of3.10±0.41%. The grand mean for the number of seeds aborted was 3.71±0.19%.

4.3.20 Mean seed length

The mean seed length of the control scored the highest mean value of 8.35±0.16 mm. the test material scored the least mean value of 7.02±0.03 mm. The grand mean for seed length was 7.17±0.04 mm.

4.3.21 Mean seed width

The mean seed width of the control score the highest mean value of 6.04±0.05 mm. The mean value of 5.47±0.04 mm for the test material was the least scored. The grand mean of seed width was 5.54±0.04 mm.

4.3.22 Mean seed thickness

The mean value of the control recorded the highest mean value of 4.97±0.05 mm. the mean value of 4.45±0.01 mm for the test material was the least scored. The grand mean for the seed thickness was 4.51±0.01 mm.

4.3.23 Mean seed weight

The mean seed weight of the control scored the highest mean value of 18.10±0.52 g. The test material scored the least mean value of 14.16±0.07 g. The grand mean for the seed weight was 14.62±0.10 g.

Table 8: Means and their standard errors for morphological quantitative traits in cowpea accessions

Traits	**Control**	**Test**	**Grand mean**	**Z-value**	**P-value**
DTG	3.40±0.07	3.60±0.03	3.57±0.03	-1.99	0.05
PTL	10.65±0.16	9.79±0.06	9.89±0.06	4.62	0.00
NB	4.38±0.05	4.59±0.03	4.57±0.02	-2.88	0.00
NL	39.19±0.70	42.40±0.31	42.02±0.29	-3.61	0.00
NN	8.63±0.10	9.30±0.05	9.22±0.05	-4.35	0.00
NPPPD	2.74±0.05	2.97±0.02	2.94±0.02	-4.13	0.00
PH	12.49±0.16	11.57±0.06	11.67±0.06	4.96	0.00
LL	10.40±0.17	8.56±0.05	8.77±0.05	12.30	0.00
LW	4.09±0.14	4.47±0.03	4.43±0.03	-3.74	0.00
DFF	37.20±0.21	34.52±0.05	34.84±0.06	17.08	0.00
APDLN	17.35±0.19	16.90±0.09	16.95±0.08	1.80	0.07
APDWD	0.96±0.02	0.85±0.01	0.86±0.01	6.01	0.00
ANLPP	15.36±0.22	15.74±0.05	15.70±0.05	-2.26	0.02
NPPPL	45.92±0.99	38.98±0.42	39.79±0.40	5.75	0.00
ANSPP	14.87±0.21	15.15±0.06	15.11±0.06	-1.50	0.13
DFMP	43.24±0.24	41.52±0.05	41.72±0.05	11.08	0.00
NSPPL	686.18±18.86	593.80±7.39	604.58±6.98	4.30	0.00
NSAB	0.49±0.06	0.60±0.03	0.59±0.03	-1.18	0.24
PA	3.10±0.41	3.79±0.21	3.71±0.19	-1.17	0.24
ASDLT	8.35±0.16	7.02±0.03	7.17±0.04	13.45	0.00
ASDWT	6.04±0.05	5.47±0.04	5.54±0.04	4.86	0.00
ASDTH	4.97±0.05	4.45±0.01	4.51±0.01	15.82	0.00
SDWG	18.10±0.52	14.16±0.07	14.62±0.10	14.67	0.00

DTG=Mean days to germination, PTL=Mean petiole length, NB=Mean number of branches, NL=Mean number of leaves, NPPPD=Mean number of pods per peduncle, PH= plant height, LL=Mean leaf length, LW=Mean leaf width, DFF=Mean days to first flowering, APDLN=Average pod length, PDWD=Average pod width, ANLPP=Average number of locus per plant, NPPPL=Number of pods per plant, NSAB=Average number of seed aborted, PA=Average percent seed abortion, ASDLT=Average seed length, ASDWT=Average seed width, ASDTH=Average seed thickness, SDWG=Seed weight

4.4 VARIABLITITY OF PHYTOCHEMICAL TRAITS

Results for summary statistics for phytochemical traits are presented in Tables 9 and 10.

4.4.1 Polyphenolic compounds

Means and their standard errors for individual polyphenolic compounds (phenols and flavonoids) are shown in Table 9.

4.4.1.1 Mean vanillic acid concentration (mg/l)

Mean vanillic acid concentration of the control recorded the highest mean value of 1.46±0.02 mg/ml. the test material recorded the lowest mean value of 1.14±0.02 mg/ml. The grand mean for vanillic acid concentration was 1.18±0.02.

4.4.1.2 Mean gallic acid concentration

Mean gallic acid concentration of the control recorded the highest mean value of 0.44±0.01mg/ml. the test material scored the least mean value of 0.27±0.01mg/ml. the grand mean of gallic acid was 0.29±0.01 mg/ml.

4.4.1.3 Mean P-coumaric acid concentration

Mean p-coumaric acid concentration of the control recorded the highest mean value of 2.39±0.04 mg/ml. the test material scored the least mean value of 1.85±0.03 mg/ml. the grand mean of p-coumaric acid concentration was 1.91±0.03 mg/ml

4.4.1.4 Mean rutin concentration (mg/l)

Mean rutin concentration of the control recorded the highest mean value of 11.19±0.55 mg/ml. The test material scored the least mean value of 9.80±0.14 mg/ml. The grand mean of rutin concentration was 9.96±0.14 mg/ml.

4.4.1.5 Mean quercetin concentration (mg/l)

Mean quercetin concentration of the control recorded the highest mean value of 3.08±0.07 mg/ml. The test material scored the least mean value of 2.71±0.03 mg/ml. The grand mean quercetin concentration was 2.74±0.03 mg/ml.

Table 9: Means (mg/ml) and standard error values for polyphenolic compounds in the cowpea.

Traits	Control	Test	Grand mean	Z-value	P-value
Van	1.46±0.02	1.14±0.02	1.18±0.02	6.36	0.00
Gal	0.44±0.01	0.27±0.01	0.29±0.01	6.37	0.00
Pca	2.39±0.04	1.85±0.03	1.91±0.03	6.36	0.00
Rutin	11.19±0.55	9.80±0.14	9.96±0.14	3.25	0.00
Que	3.08±0.07	2.71±0.03	2.74±0.03	3.51	0.00

Van=Vanillic acid, Gal=Gallic acid, Pca=P- coumaric acid, Rutin=Rutin, Que=Quercetin

4.4.2 Amino acids

Means and their standard error for individual amino acids are shown in Table 10.

4.4.2.1 Mean L-histidine concentration

Mean L-histidine concentration of the test material scored the highest mean value of 495.86±13.11ppb. The control scored the least mean value of 328.90±22.66 ppb. The grand mean of L-histidine concentration was 476.39±12.04 ppb.

4.4.2.2 Mean glycine concentration

Mean glycine of the test material scored the highest mean value of 453.34±94.90 ppb. The mean value of 46.08±2.22 ppb of the control, was the least mean value scored. The grand mean of glycine was 402.81±83.28 ppb.

4.4.2.3 Mean L-serine concentration

Mean L-serine concentration of the test material scored the highest mean value of 43.30±4.27 ppb. The mean value of 7.97±0.42 ppb of the control was the least. The grand mean of L-serine concentration was 37.66±3.64 ppb.

4.4.2.4 Mean L-aspartic acid concentration

Mean L-aspartic acid concentration of the test material scored the highest mean value of 51.04±1.86 ppb. The control scored the least mean value of 33.75±3.78 ppb. The grand mean of L-aspartic acid concentration was 48.81±1.72 ppb.

4.4.2.5 Mean L-lysine concentration

Mean L-lysine concentration of the test material scored the highest mean value of 12.81±0.88 ppb. The control scored the least mean value of 8.35±0.42 ppb. The grand mean of L-lysine acid concentration was 12.29±0.78 ppb.

4.4.2.6 Mean D-L-threonine concentration

Mean D-L-threonine concentration of the test material scored the highest mean value of 25.14±2.23 ppb. The mean concentration of the control was not detected. The grand mean of D-L-threonine concentration was 25.14±2.23 ppb.

4.4.2.7 Mean L-threonine concentration

Mean L-threonine concentration of the test material were the highest with a value of 44.70±2.91 ppb. The mean value of 12.68±1.13 ppb in the control was the least. The grand mean of L-threonine concentration was 38.60±3.07 ppb.

4.4.2.8 Mean Trans-4-hydroxyl-L-proline concentration

Mean Trans-4-hydroxyl-L-proline concentration of the control scored the highest mean value of 40.12±0.00 ppb. The mean value of 1.21±0.00 ppb of the test material was the least. The grand mean of Trans-4-hydroxyl-L-proline concentration was 22.83±4.69 ppb.

4.4.2.9 Mean D-proline concentration

Mean D-proline concentration of the test material scored the highest mean value of 93.97±5.86 ppb. The mean value of 49.38±2.59 ppb of the control was the least. The grand mean of D-proline concentration was 88.63±5.20 ppb.

4.4.2.10 Mean L-valine concentration

Mean L-valine concentration of the test material scored the highest mean value of 217.38±7.61 ppb. The mean value of 175.65±6.05 ppb of the control was the least. The grand mean of L-valine concentration was 212.51±6.78 ppb.

4.4.2.11 Mean L-methionine concentration

Mean L-methionine concentration of the test material scored the highest mean value of 38.24±1.33 ppb. The mean concentration of the control was not detected. The grand mean of L-methionine concentration was 38.24±1.33 ppb.

4.4.2.12 Mean L-asparagine concentration

The mean L-asparagine concentration of the test material scored the highest mean value of 114.93±13.43 ppb. The mean concentration of the control was not detected. The grand mean of L-asparagine concentration was 114.93±13.43 ppb.

4.4.2.13 Mean Iso-leucine concentration

Mean Iso-leucine concentration of the test material scored the highest mean value of 116.09±3.11 ppb. The control scored the least mean value of 95.76±5.19 ppb. The grand mean of Iso-leucine concentration was 113.63±2.81 ppb.

4.4.2.14 Mean L-leucine concentration

Mean L-leucine concentration of the control scored the highest mean value of 313.18±65.97 ppb. The test material scored the least mean value of 117.95±2.94 ppb. The grand mean of L-leucine concentration was 141.02±8.51 ppb.

4.4.2.15 Mean L-tyrosine concentration

Mean L-tyrosine concentration of the test material scored the highest mean value of 73.60±3.57 ppb. The control scored the least mean value of 45.93±2.22 ppb. The grand mean of L-tyrosine concentration was 70.37±3.18 ppb.

4.4.2.16 Mean D-L-B-phylalanine concentration

Mean D-L-B-phylalanine concentration of the test material scored the highest mean value of 196.45±3.69 ppb. The mean value of 180.85±15.01 ppb of the control was the least. The grand mean of D-L-B-phylalanine concentration was 194.63±3.70 ppb.

4.4.2.17 Mean L-tryptophan concentration

Mean L-tryptophan concentration of the test material scored the highest mean value of 1403.29±25.19 ppb. The mean value of 1334.57±76.19 ppb of the control was the least. The grand mean of L-tryptophan concentration was 1395.27±23.96 ppb.

Table 10: Means (ppb) and their standard error values for the amino acid concentrations in the cowpea

Traits	**Control**	**Test**	**Grand mean**	**Z-value**	**P-value**
Lhis	328.90±22.66	495.86±13.11	476.39±12.04	-4.51	0.00
Gly	46.08±2.22	453.34±94.90	402.81±83.28	-1.61	0.10
Lser	7.97±0.42	43.30±4.27	37.66±3.64	-3.60	0.00
Lasp	33.75±3.78	51.04±1.86	48.81±1.72	-3.42	0.00
Llys	8.35±0.42	12.81±0.88	12.29±0.78	-1.84	0.07
Dlthr	.	25.14±2.23	25.14±2.23		
Lthr	12.68±1.13	44.70±2.91	38.60±3.07	-5.27	0.00
Thlpro	40.12±0.00	1.21±0.00	22.83±4.69	0.00	0.00
Dpro	49.38±2.59	93.97±5.86	88.63±5.20	-2.80	0.00
Lval	175.65±6.05	217.38±7.61	212.51±6.78	-1.98	0.05
Lmet	.	38.24±1.33	38.24±1.33		
Lasn	.	114.93±13.43	114.93±13.43		
Isoleu	95.76±5.19	116.09±3.11	113.63±2.81	-2.36	0.02
Lleu	313.18±65.97	117.95±2.94	141.02±8.51	7.70	0.00
Ltyr	45.93±2.22	73.60±3.57	70.37±3.18	-2.80	0.01
Dlb	180.85±15.01	196.45±3.69	194.63±3.70	-1.35	0.18
Ltrp	1334.57±76.19	1403.29±25.19	1395.27±23.96	-0.92	0.36

Lhis =L-histidine**,** Gly=glycine, Lser=L-serine, Lasp= L-aspartic acid, Llys=L-lysine, Dlthr=D-L-threonine, Lthr=L-threonine, Thlpro= Trans-4-hydroxyl-L-proline, Dpro=D-proline, Lval=L-valine, Lmet=L-methionine, Lasn=L-asparagine, Isoleu=Iso-leucine, Lleu=L-leucine, Ltyr=L-tyrosine, Dlb= D-L-B-phylalanine, Ltrp= L-tryptophan.

4.5 ASSOCIATION AMONG QUANTITATIVE TRAITS OF 27 COWPEA ACCESSIONS

4.5.1 Morphological traits

4.5.1.1 Morphological traits of controls

Table 11 shows the pairwise correlation among the twenty-three (23) quantitative traits among the controls. There were one hundred and forty-five (145) significant associations ($P \leq 0.05$).

Days to germination had a positive correlation with average seed length (r = 0.23), mean seed thickness (r = 0.27) and seed weight (r = 0.23). Petiole length had a positive correlation with the following traits: number of branches (r = 0.47), number of nodes (r = 0.38), days to first flowering (r = 0.61), mean pod length (r = 0.52), mean number of seed per plant (r = 0.40), number of seed aborted (0.38), and percentage seed abortion (r = 0.27).

The number of branches was positively correlated with number of nodes (r = 0.91), days to first flowering (r = 0.46), mean pod length (r = 0.28), number of locule per pod (r = 0.44) and number of seed peer pod (r = 0.42).

The number of leaves had a positive correlation with number of pod (r = 0.59), leaflet width (r = 0.46) and mean seed width. Number of nodes recorded strong correlation with days to first flowering (r = 0.31), mean number of locule per pod (r = 0.33) and mean number of seed per pod (r = 0.31).

Number of pod per peduncle has a strong positive correlation with leaflet width (r = 0.73), mean seed length (r = 0.44), mean seed width (r = 0.68), mean seed thickness (r = 0.54) and seed weight (r = 0.45).

Leaflet width had a positive correlation with mean seed length (r = 0.53), mean seed width (r = 0.71), mean seed thickness (0.65) and seed weight (0.52).

Days to first flowering also recorded strong positive correlation with average pod length (0.52), mean number locule per pod (r = 0.68), mean number of seed per pod (r = 0.60) and number of seeds per plant (r = 0.52).

Mean pod length recorded a positive correlation with number of pod per plant (r = 0.50) and number of seed per plant (r = 0.52).

Mean pod width scored high correlation with mean seed length (r = 0.77), mean seed thickness (r = 0.64) and seed weight (r = 0.79).

Mean number of locule per pod had a strong positive correlation with mean number of seed per pod (r = 0.96) and number of seed per plant (r = 0.63).

Number of pod per plant had a positive correlation with number of seeds per plant (r = 0.86).

Mean number of seed per pod recorded a positive correlation with number of seeds per plant (r = 0.64).

Number of aborted seeds had a high positive correlation with percentage seed aborted (r = 0.97), mean seed length scored a highly positive correlation with mean seed width (r = 0.68), mean seed thickness (r = 0.91) and seed weight (r = 0.97).

Mean seed width had a positive correlation with mean seed thickness (r = 0.78) and seed weight (r = 0.65).

Mean seed thickness recorded a positive correlation with seed weight (r = 0.90).

Table 2: Pearson correlation coefficient among morphological quantitative traits of the controls

	DTG	PTL	NB	NL	NN	NPPPD	LW	DFF	APDLN	APDWD
DTG	1									
PTL		1								
NB		0.4712*	1							
NL		-0.4032*		1						
NN		0.3795*	0.9108*		1					
NPPPD		-0.5574*	-0.4248*	0.5974*		1				
PH				-0.2334*		-0.3890*				
LL				-0.2769*						
LW		-0.6301*	-0.4461*	0.4572*	-0.2964*	0.7254*	1			
DFF		0.6087*	0.4605*	-0.5620*	0.3113*	-0.7178*	-0.7612*	1		
APDLN		0.5185*	0.2796*	-0.4390*		-0.5304*	-0.4829*	0.5241*	1	
APDWD			-0.2376*			0.2600*	0.3718*	-0.2797*	0.3740*	1
ANLPP		0.4997*	0.4395*	-0.4508*	0.3265*	-0.6175*	-0.6564*	0.6820*	0.3081*	-0.5686*
NPPPL				-0.2150*		-0.2524*		0.2556*	0.5003*	
ANSPP		0.4049*	0.4233*	-0.3671*	0.3106*	-0.4917*	-0.5591*	0.5991*	0.2269*	-0.5492*
DFMP		0.2643*				-0.2579*		0.3931*		
NSPPL		0.2906*	0.2545*	-0.3774*		-0.4654*	-0.4204*	0.5194*	0.5186*	
NSAB		0.3818*		-0.3324*		-0.5004*	-0.4218*	0.3754*	0.3056*	
PA		0.2734*		-0.2553*		-0.4031*	-0.3269*	0.2905*	0.2360*	
ASDLT	0.2332*	-0.3119*	-0.3464*	0.2940*	-0.2668*	0.4435*	0.5332*	-0.4904*		0.7722*
ASDWT		-0.4980*	-0.4887*	0.4891*	-0.3536*	0.6835*	0.7062*	-0.7183*	-0.3515*	0.3840*
ASDTH	0.2678*	-0.4858*	-0.4614*	0.3696*	-0.3442*	0.5433*	0.6526*	-0.6407*		0.6390*
SDWG	0.2331*	-0.3187*	-0.3663*	0.2923*	-0.2824*	0.4454*	0.5247*	-0.5052*	0.2206*	0.7901*

DTG=Mean days to germination, PTL=Mean petiole length, NB=Mean number of branches, NL=Mean number of leaves, NPPPD=Mean number of pods per peduncle, PH= plant height, LL=Mean leaf length, LW=Mean leaf width, DFF=Mean days to first flowering, APDLN=Average pod length, PDWD=Average pod width, ANLPP=Average number of locus per plant, NPPPL=Number of pods per plant, NSAB=Average number of seed aborted, PA=Average percent seed abortion, ASDLT=Average seed length, ASDWT=Average seed width, ASDTH=Average seed thickness, SDWG=Seed weight

Table 11 (Cont'd)

	ANLPP	NPPPL	ANSPP	DFMP	NSPPL	NSAB	PA	ASDLT	ASDWT	ASDTH
ANLPP	1									
NPPPL		1								
ANSPP	0.9559*		1							
DFMP				1						
NSPPL	0.6312*	0.8623*	0.6408*	0.2170*	1					
NSAB	0.3041*					1				
PA						0.9726*	1			
ASDLT	-0.7427*	0.2532*	-0.6930*			-0.2787*		1		
ASDWT	-0.6846*		-0.5869*	-0.2784*	-0.3309*	-0.4189*	-0.3141*	0.6806*	1	
ASDTH	-0.7655*		-0.6913*		-0.2393*	-0.3615*	-0.2641*	0.9009*	0.7847*	1
SDWG	-0.7465*	0.2380*	-0.6987*			-0.2718*		0.9723*	0.6476*	0.8994*

APDLN=Average pod length, PDWD=Average pod width, ANLPP=Average number of locus per plant, NPPPL=Number of pods per plant, NSAB=Average number of seed aborted, PA=Average percent seed abortion, ASDLT=Average seed length, ASDWT=Average seed width, ASDTH=Average seed thickness, SDWG=Seed weight

4.5.1.2 Morphological traits of test material

The pairwise correlation among the twenty-three (23) quantitative traits among the test materials is presented in Table 12. One hundred and fourteen (114) significant associations ($P \leq 0.05$) were observed between morphological traits only.

The number of branches was positively highly correlated with number of leaves (r = 0.41), number of nodes (r = 0.93).

The number of leaves had a positive correlation with number of nodes (r = 0.46). Plant height had a strong positive correlation with leaflet length (r = 0.56), leaflet width (r = 0.32), mean pod length (r = 0.28) and seed weight (r = 0.26).

Leaflet length has a positive correlation with leaflet width (r = 0.69), mean pod length (r = 0.42), mean seed length (r = 0.31) and seed weight (r = 0.39).

Leaflet width had a positive correlation with mean pod length (r = 0.34), mean seed length (r = 0.37) and seed weight (r = 0.44).

Days to first flowering also recorded strong positive correlation with days to first matured pod (r = 0.92).

Mean pod length scored highly positive correlation with average pod width (r = 0.50), mean number of locule per pod (r = 0.32) mean seed thickness (r = 0.29) and seed weight (r = 0.74). Mean pod width scored high correlation with mean seed length (r = 0.35) and seed weight (r = 0.0.40).

Mean number of locules per pod had a strong positive correlation with number of pod plant (r = 0.31), mean number of seed per pod (r = 0.84) and number of seed per plant (r = 0.53).

Number of pod per plant had a positive correlation with number of seeds per plant (r = 0.94). Mean number of seed per pod recorded a positive correlation with number of seeds per plant (r = 0.56), number of seed aborted r = (0.46) and percentage aborted (r = 0.52).

Number of aborted seeds had a high positive correlation with percentage seed aborted (r = 0.99), mean seed length scored a highly positive correlation with mean seed width (r = 0.26), mean seed thickness (r = 0.52) and seed weight (r = 0.80).

Mean seed width had a positive correlation with mean seed thickness (r = 0.22) and seed weight (r = 0.19).

Mean seed thickness recorded a positive correlation with seed weight (r = 0.51).

Table 3: Pearson correlation coefficient among morphological quantitative traits of the test material

	DTG	PTL	NB	NL	NN	NPPPD	PH	LL	LW	DFF
DTG	1									
PTL		1								
NB			1							
NL			0.4124*	1						
NN			0.9270*	0.4560*	1					
NPPPD			0.1069*			1				
PH	0.1032*	0.0989*		-0.1725*		0.0856*	1			
LL	0.0990*	0.1919*		-0.1380*		0.1727*	0.5594*	1		
LW		0.1954*	-0.1059*	-0.0898*	-0.1038*		0.3271*	0.6868*	1	
DFF								0.2044*		1
APDLN	0.0833*	0.1550*	-0.2077*	-0.2366*	-0.1972*		0.2842*	0.4187*	0.3436*	
APDWD		0.0997*	-0.0797*	-0.1074*			0.1784*	0.2027*	0.1578*	
ANLPP		0.1061*						0.1067*		
NPPPL						0.1658*				
ANSPP										
DFMP	0.0951*		-0.1047*		-0.0944*			0.2003*	-0.0826*	0.9242*
NSPPL						0.1391*				
NSAB						0.0828*		0.0867*	0.0834*	
PA						0.0799*		0.0806*		
ASDLT		0.0917*	-0.1797*	-0.1866*	-0.1887*	-0.1382*	0.1056*	0.3110*	0.3661*	
ASDWT									0.1204*	
ASDTH		0.1517*	-0.1015*	-0.1396*	-0.1250*	-0.0786*		0.2174*	0.2434*	-0.1160*
SDWG		0.2460*	-0.2331*	-0.2181*	-0.2154*		0.2599*	0.3904*	0.4401*	

DTG=Mean days to germination, PTL=Mean petiole length, NB=Mean number of branches, NL=Mean number of leaves, NPPPD=Mean number of pods per peduncle, PH= plant height, LL=Mean leaf length, LW=Mean leaf width, DFF=Mean days to first flowering, APDLN=Average pod length, PDWD=Average pod width, ANLPP=Average number of locus per plant, NPPPL=Number of pods per plant, NSAB=Average number of seed aborted, PA=Average percent seed abortion, ASDLT=Average seed length, ASDWT=Average seed width, ASDTH=Average seed thickness, SDWG=Seed weight

Table 12 (Cont'd)

	APDLN	APDWD	ANLPP	NPPPL	ANSPP	DFMP	NSPPL	NSAB	ASDLT	ASDWT	ASDTH
APDLN	1										
APDWD	0.4985*	1									
ANLPP	0.3233*		1								
NPPPL			0.3064*	1							
ANSPP	0.3302*	0.0819*	0.8430*	0.2835*	1						
DFMP	-0.0940*					1					
NSPPL	0.1536*		0.5255*	0.9366*	0.5562*		1				
NSAB	-0.0783*		0.0884*		0.4614*		-0.1631*	1			
PA	-0.0955*				0.5245*		-0.2008*	0.9925*			
ASDLT	0.6457*	0.3519*	0.0932*			-0.0905*			1		
ASDWT	0.1420*		0.0795*						0.2624*	1	
ASDTH	0.2913*	0.1324*	0.1449*		0.1081*	-0.1280*			0.5186*	0.2219*	1
SDWG	0.7356*	0.4039*	0.0892*						0.7968*	0.1880*	0.5137*

APDLN=Average pod length, PDWD=Average pod width, ANLPP=Average number of locus per plant, NPPPL=Number of pods per plant, NSAB=Average number of seed aborted, PA=Average percent seed abortion, ASDLT=Average seed length, ASDWT=Average seed width, ASDTH=Average seed thickness, SDWG=Seed weight

4.5.1.3 Morphological traits of combine material

The pairwise correlation among the twenty-three (23) quantitative traits among the controls are presented in Table 13. There were one hundred and twenty-three (123) significant associations (P≤0.05).

The number of branches was positively correlated with number of leaves (r = 0.38) and number of nodes (r = 0.93).

The number of leaves had a positive correlation with nodes (r = 0.44). Plant height had a strong positive correlation with leaflet length (r = 0.51), leaflet width (r = 0.23), mean pod length (r = 0.28), mean pod width (r = 0.20) and seed weight (r = 0.23).

Leaflet length has a positive correlation with leaflet width (r = 0.45), mean pod length (r = 0.38), mean pod width (r = 0.25), mean seed thickness (r = 0.31) and seed weight (r = 0.38).

Leaflet width had a positive correlation with mean pod length (r = 0.21), mean seed thickness (r = 0.23) and seed weight (r = 0.33). Days to first flowering also recorded strong positive correlation with days to first matured pod (r = 0.81).

Mean pod length scored highly positive correlation with average pod width (r = 0.49), mean number of locules per pod (r = 0.31) mean seed thickness (r = 0.23) and seed weight (r = 0.51).

Mean pod width scored high correlation with average seed thickness (r = 0.29) and seed weight (r = 0.49).

Mean number of locules per pod had a strong positive correlation with number of pod per plant (r = 0.26), average number of seed per pod (r = 0.86) and number of seed per plant (r = 0.51).

Number of pods per plant had a positive correlation with mean number of seed pre pod (r = 0.25) and number of seeds per plant (r = 0.93).

Mean number of seed per pod recorded a positive correlation with number of seeds per plant (r = 0.55).

Number of aborted seeds had a high positive correlation with percentage seed aborted (r = 0.99).

Mean seed width had a positive correlation with average seed thickness (r = 0.30) and seed weight (r = 0.26).

Mean seed thickness recorded a positive correlation with seed weight (0.73).

Table 4: Pearson correlation coefficient among morphological quantitative traits of the combined materials.

	DTG	PTL	NB	NL	NN	NPPPD	PH	LL	LW	DFF
DTG	1									
PTL		1								
NB			1							
NL		-0.0818*	0.3809*	1						
NN			0.9256*	0.4369*	1					
NPPPD			0.0795*	0.0995*	0.0766*	1				
PH	-0.1204*	0.1287*		-0.1975*			1			
LL	-0.1314*	0.2373*		-0.1936*	-0.0766*		0.5080*	1		
LW			-0.1298*		-0.0974*	0.1767*	0.2327*	0.4499*	1	
DFF		0.1365*		-0.1671*	-0.1014*	-0.1531*	0.0855*	0.1184*	-0.2797*	1
APDLN	-0.0768*	0.1942*	-0.1789*	-0.2583*	-0.1804*		0.2814*	0.3785*	0.2073*	
APDWD		0.1033*	-0.1134*	-0.1100*	-0.1037*		0.2026*	0.2464*	0.1528*	0.1278*
ANLPP		0.1450*		-0.0751*					-0.0953*	0.0808*
NPPPL						0.0915*		0.1252*		0.1118*
ANSPP		0.0882*		-0.0740*					-0.1001*	
DFMP			-0.1098*	-0.1104*	-0.1347*	-0.0930*			-0.1566*	0.8095*
NSPPL							0.0824*	0.1260*	-0.0984*	0.1132*
NSAB		0.0887*								
PA		0.0737*								
ASDWT			-0.1015*		-0.1074*			0.1252*	0.1250*	
ASDTH		0.1212*	-0.1798*	-0.1172*	-0.2054*		0.1327*	0.3107*	0.2306*	0.0897*
SDWG		0.1660*	-0.2500*	-0.1443*	-0.2470*		0.2335*	0.3819*	0.3307*	0.1141*

DTG=Mean days to germination, PTL=Mean petiole length, NB=Mean number of branches, NL=Mean number of leaves, NPPPD=Mean number of pods per peduncle, PH= plant height, LL=Mean leaf length, LW=Mean leaf width, DFF=Mean days to first flowering, APDLN=Average pod length, PDWD=Average pod width, ANLPP=Average number of locus per plant, NPPPL=Number of pods per plant, NSAB=Average number of seed aborted, PA=Average percent seed abortion, ASDLT=Average seed length, ASDWT=Average seed width, ASDTH=Average seed thickness, SDWG=Seed weight

Table 13 (Cont'd)

	APDLN	APDWD	ANLPP	NPPPL	ANSPP	DFMP	NSPPL	NSAB	ASDWT	ASDTH
APDLN	1									
APDWD	0.4887*	1								
ANLPP	0.3070*		1							
NPPPL	0.1079*		0.2598*	1						
ANSPP	0.3103*		0.8631*	0.2499*	1					
DFMP		0.1164*		0.0781*		1				
NSPPL	0.1929*		0.5125*	0.9305*	0.5476*		1			
NSAB			0.1139*		-0.4033*		-0.1493*	1		
PA	-0.0754*				-0.4740*		-0.1912*	0.9913*		
ASDWT	0.1313*	0.1224*							1	
ASDTH	0.2318*	0.2923*	-0.1110*	0.1425*	-0.0854*	0.0790*	0.0819*		0.2985*	1
SDWG	0.5132*	0.4916*	-0.2017*	0.1201*	-0.1623*	0.1142*			0.2562*	0.7311*

APDLN=Average pod length, PDWD=Average pod width, ANLPP=Average number of locus per plant, NPPPL=Number of pods per plant, NSAB=Average number of seed aborted, PA=Average percent seed abortion, ASDLT=Average seed length, ASDWT=Average seed width, ASDTH=Average seed thickness, SDWG=Seed weight

4.5.2 Phytochemical traits

4.5.2.1 Phytochemical traits of controls

The Pearson correlation among the phytochemical traits of the controls is shown in Table 14. Seventy-six (76) significant associations ($P \leq 0.05$) were observed between the phytochemical traits.

Vanillic acid was highly correlated with gallic acid (r = 1.00), quercetin (r = 0.61), and L-tyrosine (r = 0.62). Gallic acid strongly positively correlated with p- coumaric acid (r = 1.00), quercetin (r = 0.61) and L-tyrosine (r = 0.61).

p-coumaric acid was positively correlated quercetin (r = 0.61), and L-tyrosine (r = 0.62). Rutin was highly correlated with quercetin (r = 0.82). L-histidine was positively correlated with L-serine (r = 0.45), L-aspartic acid (r = 0.84) and L-lysine (r = 0.54).

Glycine was highly correlated with D-proline (r = 0.52), Iso-leucine (r = 0.81), L-leucine (r = 0.79), L-tyrosine (r = 0.64), D-L-B-phylalanine (r = 0.73) and L-tryptophan (r = 0.75).

L-aspartic acid was positively correlated with L-lysine (r = 0.43).

L-lysine was positively correlated with L-valine (r = 0.68). D-proline was highly correlated Iso-leucine (r = 0.50), L-leucine (r =.64) and D-L-B-phylalanine (r = 0.65).

Iso-leucine was highly positively correlated with L-leucine (r = 0.75), D-L-B-phylalanine (r = 0.83) and L-tryptophan (r = 0.83).

L-leucine was strongly correlated with D-L-B-phylalanine (0.73) and L-tryptophan (r = 0.58).

L-tyrosine was strongly correlated with D-L-B-phylalanine (0.51) and L-tryptophan (r = 0.67). D-L-B-phylalanine had a positive coreelation with L-tryptophan (r = 0.84

Table 5: Correlation coefficient among phytochemical traits of the controls

	Van	Gal	Pca	Rutin	Que	Lhis	Gly	Lser	Lasp	Llys	Dpro	Lval	Isoleu	Lleu	Ltyr	Dlb
Van	1															
Gal	1.0000*	1														
Pca	1.0000*	1.0000*	1													
Rutin	0.3082*	0.3082*	0.3086*	1												
Que	0.6100*	0.6104*	0.6105*	0.8167*	1											
Lhis				-0.5635*	-0.2275*	1										
Gly	0.3907*	0.3917*	0.3911*		0.3142*		1									
Lser	0.2905*	0.2899*	0.2900*	-0.4067*		0.4537*		1								
Lasp						0.8425*	-0.6663*		1							
Llys	0.3709*	0.3709*	0.3706*		0.2474*	0.5418*			0.4314*	1						
Dpro				-0.4495*			0.5226*				1					
Lval	0.2784*	0.2783*	0.2784*		0.3461*	0.4298*			0.2690*	0.6810*		1				
Isoleu							0.8112*		-0.7711*	-0.3268*	0.4973*	-0.5211*	1			
Lleu					0.2890*	-0.2702*	0.7945*		-0.3332*		0.6425*	-0.4338*	0.7458*	1		
Ltyr	0.6181*	0.6181*	0.6183*				0.6425*		-0.8071*				0.3685*		1	
Dlb						-0.4239*	0.7377*		-0.8295*	-0.4903*	0.6485*	-0.5828*	0.8343*	0.7316*	0.5137*	1
Ltrp						-0.4051*	0.7519*	0.2593*	-0.9129*	-0.4684*	0.2184*	-0.4881*	0.8319*	0.5830*	0.6722*	0.8420*

Van=Vanillic acid, Gal=Gallic acid, Pca=P- coumaric acid, Rutin=Rutin, Que=Quercetin, Lhis =L-histidine, Gly=glycine, Lser=L-serine, Lasp= L-aspartic acid, Llys=L-lysine, Dlthr=D-L-threonine, Lthr=L-threonine, Thlpro= Trans-4-hydroxyl-L-proline, Dpro=D-proline, Lval=L-valine, Lmet=L-methionine, Lasn=L-asparagine, Isoleu=Iso-leucine, Lleu=L-leucine, Ltyr=L-tyrosine, Dlb= D-L-B-phylalanine, Ltrp= L-tryptophan.

4.5.2.2 Phytochemical traits of test material

The Pearson correlation among the phytochemical traits of the test materials are indicated in Table 15. One hundred and twenty-one (121) significant associations ($P \leq 0.05$) were observed between the phytochemical traits.

Vanillic acid was highly correlated with gallic acid (r = 1.00) and P-coumaric acid (r = 1.00). Gallic acid strongly positively correlated with P- coumaric acid (r = 1.00) and L-methionine (r = 1.00).

p-coumaric acid was positively correlated with L-methionine (r = 1.00).

Rutin was highly correlated with quercetin (r = 0.71) and D-L-threonine (r = 0.81). L-histidine was positively correlated with L-aspartic acid (r = 0.84) and L-methionine (r = 1.00).

Glycine was highly correlated with L-methionine (r = 1.00). L-serine is positively correlated with L-lysine (r = 0.93), D-L-threonine (r = 0.98), L-threonine (r = 1.00), D-proline (r = 0.87), L-valine (r = 0.56), L-asparagine (r = 1.00), Iso-leucine (r = 0.79), and L-leucine (r = 0.93).

L-aspartic acid is highly correlated with D-L-threonine (r = 1.00).

L-lysine had a positive correlation with L-asparagine (r = 0.84), Iso-leucine (r = 0.77), L-leucine (r = 0.75) and L-tyrosine (r = 0.93).

L-threonine was positively correlated with D-proline (r = 0.92) and Iso-leucine (r = 0.99). D-proline was highly correlated L-methionine (r = 1.00), L-asparagine (r = 0.55) and Iso-leucine (r = 0.78).

L-valine had a strong correlation with L-methionine (r = 1.00), L-asparagine (r = 0.93), L-leucine (r = 0.43) and L-tyrosine (r = 0.68).

L-methionine recorded a positive correlation with L-tyrosine and D-L-B-phylalanine was (r = 1.00).

L-asparagine was positively correlated with L-tyrosine (r = 0.88) and L-tryptophan (r = 0.65).

L-leucine (r = 0.95) and L-tyrosine (r = 0.82) were positively correlated with Iso-leucine.

L-leucine was positively correlated with L-tyrosine (r = 0.80).

D-L-B-phylalanine was correlated with L-tryptophan (r = 0.45).

Table 6: Pearson correlation coefficient among phytochemical traits of the test

	Van	Gal	Pca	Rutin	Que	Lhis	Gly	Lser	Lasp	Llys
Van	1									
Gal	1.0000*	1								
Pca	1.0000*	1.0000*	1							
Rutin				1						
Que				0.7138*	1					
Lhis				-0.2183*	-0.1946*	1				
Gly	-0.1840*	-0.1837*	-0.1838*	0.1294*		-0.2252*	1			
Lser	0.1446*	0.1447*	0.1446*					1		
Lasp				-0.1665*	-0.1360*	0.8181*	-0.2251*		1	
Llys	0.1784*	0.1785*	0.1784*					0.9269*		1
Dlthr				0.8108*	-0.6509*	-0.4623*	-0.7432*	0.9750*	1.0000*	
Lthr	-0.3629*	-0.3621*	-0.3628*	-0.8689*	-0.8651*	0.6229*	-0.5637*	1.0000*		
Dpro					-0.1118*		-0.0853*	0.8657*		0.3592*
Lval	0.1345*	0.1345*	0.1344*					0.5610*		0.6052*
Lmet	1.0000*	1.0000*	1.0000*		-1.0000*	1.0000*	1.0000*			
Lasn	-0.9401*	-0.7533*	-0.9333*	-0.9557*	-0.9557*			1.0000*		0.8362*
Isoleu	0.1976*	0.1976*	0.1977*		-0.0903*			0.7863*		0.7677*
Lleu	0.1925*	0.1925*	0.1925*					0.7825*		0.7512*
Ltyr	0.1517*	0.1518*	0.1518*					0.9265*		0.9371*
Dlb	0.1457*	0.1456*	0.1457*	0.1613*	0.1241*			0.2501*		0.1899*
Ltrp						-0.2386*	0.1447*	0.2328*		0.2299*

Van=Vanillic acid, Gal=Gallic acid, Pca=P- coumaric acid, Rutin=Rutin, Que=Quercetin, Lhis =L-histidine, Gly=glycine, Lser=L-serine, Lasp= L-aspartic acid, Llys=L-lysine, Dlthr=D-L-threonine, Lthr=L-threonine, Thlpro= Trans-4-hydroxyl-L-proline, Dpro=D-proline, Lval=L-valine, Lmet=L-methionine, Lasn=L-asparagine, Isoleu=Iso-leucine, Lleu=L-leucine, Ltyr=L-tyrosine, Dlb= D-L-B-phylalanine, Ltrp= L-tryptophan.

Table 15 (Cont'd)

	Dlthr	Lthr	Dpro	Lval	Lmet	Lasn	Isoleu	Lleu	Ltyr	Dlb
Dlthr	1									
Lthr	1.0000*	1								
Dpro	0.3301*	0.9218*	1							
Lval			0.2600*	1						
Lmet			1.0000*	1.0000*	1					
Lasn			0.5544*	0.9335*		1				
Isoleu	0.3603*	0.9872*	0.7833*	0.3894*		-0.9163*	1			
Lleu	0.3674*		0.2259*	0.4289*		-0.8447*	0.9540*	1		
Ltyr			0.3894*	0.6772*	1.0000*	0.8824*	0.8213*	0.8008*	1	
Dlb			0.1526*	0.2496*	1.0000*		0.3348*	0.3115*	0.2809*	1
Ltrp			0.1964*			0.6509*	0.2804*	0.2126*	0.2579*	0.4540*

Dlthr=D-L-threonine, Lthr=L-threonine, Thlpro= Trans-4-hydroxyl-L-proline, Dpro=D-proline, Lval=L-valine, Lmet=L-methionine, Lasn=L-asparagine, Isoleu=Iso-leucine, Lleu=L-leucine, Ltyr=L-tyrosine, Dlb= D-L-B-phylalanine, Ltrp= L-tryptophan.

4.5.2.3 Phytochemical traits of combine material

The Pearson correlation among the phytochemical traits of the combine material is presented in Table 16. One hundred and forty-four (144) significant associations ($P \leq 0.05$) were observed between the phytochemical traits.

Vanillic acid was highly correlated with gallic acid (r = 1.00) and p- coumaric acid (r = 100).

Gallic acid strongly positively correlated with P- coumaric acid (r = 1.00) and L-methionine (r = 1.00).

p-coumaric acid was positively correlated with L-methionine (r = 1.00).

Rutin was highly correlated with quercetin (r = 0.72), D-L-threonine (r = 0.81) and thlpro (r = 1.00).

L-histidine was positively correlated with L-aspartic acid (r = 0.81), L-threonine (r = 0.54) and L-methionine (r = 1.00).

Glycine was highly correlated with L-methionine (r = 1.00). L-serine had a positive correlated with L-lysine (r = 0.92), D-L-threonine (r = 0.98), L-threonine (r = 0.99), D-proline (r = 0.86), L-valine (r = 0.56), L-asparagine (r = 1.00), Iso-leucine (r = 0.77), and L-tyrosine (r = 0.92).

L-aspartic acid is highly correlated with D-L-threonine (r = 1.00). L-lysine was positively correlated with L-valine (r = 0.61), L-asparagine (r = 0.84), Iso-leucine (r = 0.74) and L-tyrosine (r = 0.93).

D-L-threonine recorded highly positive correlation with L-threonine (1.00).

L-threonine was positively correlated with D-proline (r = 0.92), Iso-leucine (0.99) and D-L-B-phylalanine (r = 0.44).

Trans-4-hydroxyl-L-proline was positively correlated with L-tryptophan (r = 1.00). D-proline was highly correlated L-methionine (r = 1.00), L-asparagine (0.55) and Iso-leucine (r = 0.77).).

L-valine had a strong correlation with L-methionine (1.00), L-asparagine (r = 0.93), and L-tyrosine (r = 0.67).

L-methionine recorded a positive correlation with L-tyrosine (r = 1.00) and D-L-B-phylalanine was (r = 1.00).

L-asparagine was positively correlated with L-tyrosine (r = 0.88) and L-tryptophan (r = 0.65).

Iso-leucine scored a high positive correlation with L-leucine (r = 0.40) and L-tyrosine (r = 0.80).

D-L-B-phylalanine was correlated with L-tryptophan (r = 0.52).

Table 7: Pearson correlation coefficients among phytochemical traits of the combined material

	Van	Gal	Pca	Rutin	Que	Lhis	Gly	Lser	Lasp	Llys
Van	1									
Gal	1.0000*	1								
Pca	1.0000*	1.0000*	1							
Rutin	0.0767*	0.0765*	0.0766*	1						
Que				0.7193*	1					
Lhis	-0.0952*	-0.0952*	-0.0953*	-0.2614*	-0.2134*	1				
Gly	-0.1906*	-0.1903*	-0.1904*	0.1054*		-0.2036*	1			
Lser	0.0937*	0.0937*	0.0937*					1		
Lasp				-0.1519*	-0.1311*	0.8112*	-0.2023*		1	
Llys	0.1584*	0.1585*						0.9240*		1
Dlthr				0.8108*	-0.6509*	-0.4623*	-0.7432*	0.9750*	1.0000*	
Lthr	-0.5691*	-0.5688*	-0.5690*	-0.8582*	-0.8657*	0.5381*		0.9941*	-0.9910*	
Thlpro	-1.0000*			1.0000*	1.0000*	-1.0000*				
Dpro				-0.0810*	-0.1218*		-0.0776*	0.8641*		0.3618*
Lval	0.1155*	0.1155*	0.1155*					0.5635*		0.6071*
Lmet	1.0000*	1.0000*	1.0000*		-1.0000*	1.0000*	1.0000*			
Lasn	-0.9401*	-0.7533*	-0.9333*	-0.9557*	-0.9557*			1.0000*		0.8362*
Isoleu	0.1617*	0.1617*	0.1618*		-0.1033*			0.7660*		0.7438*
Lleu	0.1411*	0.1412*	0.1411*	0.1328*	0.1029*	-0.1237*		0.1741*	-0.1497*	0.2013*
Ltyr	0.1281*	0.1282*	0.1282*		-0.0794*			0.9243*		0.9320*
Dlb	0.1112*	0.1112*	0.1113*	0.0847*	0.0784*	-0.0916*		0.2152*	-0.1806*	0.1555*
Ltrp						-0.2400*	0.1369*	0.2243*	-0.1727*	0.2041*

Van=Vanillic acid, Gal=Gallic acid, Pca=P- coumaric acid, Rutin=Rutin, Que=Quercetin, Lhis =L-histidine, Gly=glycine, Lser=L-serine, Lasp= L-aspartic acid, Llys=L-lysine, Dlthr=D-L-threonine, Lthr=L-threonine, Thlpro= Trans-4-hydroxyl-L-proline, Dpro=D-proline, Lval=L-valine, Lmet=L-methionine, Lasn=L-asparagine, Isoleu=Iso-leucine, Lleu=L-leucine, Ltyr=L-tyrosine, Dlb= D-L-B-phylalanine, Ltrp= L-tryptophan.

Table 16 (cont'd)

	Dlthr	Lthr	Thlpro	Dpro	Lval	Lmet	Lasn	Isoleu	Lleu	Ltyr	Dlb
Dlthr	1										
Lthr	1.0000*	1									
Thlpro			1								
Dpro	0.3301*	0.9191*	-1	1							
Lval			-1.0000*	0.2628*	1						
Lmet				1.0000*	1.0000*	1					
Lasn				0.5544*	0.9335*		1				
Isoleu	0.3603*	0.9865*	-1.0000*	0.7733*	0.3699*		-0.9163*	1			
Lleu	0.3674*						-0.8447*	0.4065*	1		
Ltyr		0.3440*	-1.0000*	0.3946*	0.6742*	1.0000*	0.8824*	0.8064*	0.2256*	1	
Dlb		0.4427*		0.1576*	0.1933*	1.0000*		0.3789*	0.3873*	0.2701*	1
Ltrp		0.3357*	1.0000*	0.1902*			0.6509*	0.3254*	0.2484*	0.2611*	0.5194*

Dlthr=D-L-threonine, Lthr=L-threonine, Thlpro= Trans-4-hydroxyl-L-proline, Dpro=D-proline, Lval=L-valine, Lmet=L-methionine, Lasn=L-asparagine, Isoleu=Iso-leucine, Lleu=L-leucine, Ltyr=L-tyrosine, Dlb= D-L-B-phylalanine, Ltrp= L-tryptophan.

4.6 RELATIVE CONTRIBUTION OF TRAITS TO OBSERVED VARIABILITY

4.6.1 Quantitative agro-morphological traits

4.6.1.1 Quantitative agro-morphological traits in the controls

The results of the principal component analysis for the control is shown in Table 17. The eigenvalue for the first principal component analysis was 8.01 and this represented 36.00 % of the total variation. The eigenvalue for the second principal component analysis was 3.28 which represented 15.00 % of the total variation. The third principal component analysis recorded an eigenvalue of 2.16, representing 10.00 % of the total variation. The eigenvalue for the fourth principal component was 1.70, representing 8.00 % of the total variation. The eigenvalues for fifth and six principal components were 1.32 and 1.11 with each representing 6.00 % and 5.00% of the total variation respectively. The seventh principal component had an eigenvalue of 0.90, representing 4.00% of the total variation. The first six principal component explained 80% of the observed variability. The traits contributing to PC1 were PTL, NB, DFF, ANLPP and ANSPP. The traits contributing significantly to PC2 were APDLN, APDWD, NPPPL, ASDLT and ASDTH. PC3 was highly positively correlated with NPPL and NSPPL. The traits contributing to PC 4 were PTL, NB and NN. PH, LL, LW and DFF contributed significantly to PC5. The traits contributing significantly to PC6 were LL, NPPL and NSPPL.

Table 8: Principal component analysis for quantitative morphological traits of the controls

Variable	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7
DTG	-0.06	0.13	0.08	-0.09	-0.58	-0.02	0.15
PTL	0.24	0.12	-0.07	0.21	-0.06	-0.04	0.28
NB	0.21	-0.02	0.14	0.55	0.04	0.08	0.01
NL	-0.20	-0.17	0.08	0.20	-0.08	0.12	-0.05
NN	0.15	-0.05	0.11	0.62	0.04	0.13	-0.03
NPPPD	-0.28	-0.16	0.09	0.02	0.01	0.19	0.14
PH	0.07	0.13	0.00	0.08	0.40	-0.64	-0.40
LL	0.07	0.10	-0.12	-0.08	0.56	0.47	0.30
LW	-0.29	-0.06	0.03	-0.04	0.35	0.08	0.01
DFF	0.30	0.13	0.01	-0.01	-0.11	-0.11	0.18
APDLN	0.14	0.44	0.03	0.14	-0.06	0.05	0.05
APDWD	-0.20	0.35	-0.02	0.16	0.07	-0.08	0.08
ANLPP	0.32	-0.05	0.15	-0.12	0.01	0.07	-0.07
NPPPL	0.06	0.40	0.25	-0.19	0.03	0.24	-0.24
ANSPP	0.28	-0.09	0.32	-0.12	0.03	0.02	-0.02
DFMP	0.10	0.14	-0.07	-0.14	0.15	-0.35	0.63
NSPPL	0.20	0.27	0.35	-0.21	0.05	0.20	-0.17
NSAB	0.17	0.12	-0.53	-0.02	-0.07	0.16	-0.20
PA	0.12	0.12	-0.57	0.00	-0.07	0.15	-0.21
ASDLT	-0.27	0.33	0.03	0.11	-0.01	0.01	0.06
ASDTH	-0.30	0.22	0.06	0.03	-0.03	-0.03	-0.09
SDWG	-0.27	0.33	0.02	0.11	-0.02	0.01	0.01
Eigenvalue	8.01	3.28	2.16	1.70	1.32	1.11	0.90
Difference	4.73	1.12	0.47	0.38	0.21	0.20	0.04
Proportion (%)	36.00	15.00	10.00	8.00	6.00	5.00	4.00
Cumulative (%)	36.00	51.00	61.00	69.00	75.00	80.00	84.00

DTG=Mean days to germination, PTL=Mean petiole length, NB=Mean number of branches, NL=Mean number of leaves, NPPPD=Mean number of pods per peduncle, PH= plant height, LL=Mean leaf length, LW=Mean leaf width, DFF=Mean days to first flowering, APDLN=Average pod length, PDWD=Average pod width, ANLPP=Average number of locus per plant, NPPPL=Number of pods per plant, NSAB=Average number of seed aborted, PA=Average percent seed abortion, ASDLT=Average seed length, ASDWT=Average seed width, ASDTH=Average seed thickness, SDWG=Seed weight

4.6.1.2 Quantitative agro-morphological traits in the the test materials

The results of the principal component analysis for quantitative traits are shown in Table 18. The first nine components explained 81.00% of the total variations. The eigenvalue for the first principal component analysis was 4.20 which represented 19.00 % of the total variation. The eigenvalue for the second principal component analysis was 3.00 which represented 14.00 % of the total variation. The third and fourth principal component analysis recorded an eigenvalue of 2.38 and 1.99, representing 11.00 and 9.00% of the total variation respectively. The eigenvalue for the fifth principal component was 1.69, representing 8.00 % of the total variation. The eigenvalues for sixth and seventh principal components were 1.45 and 1.13 with each representing 7.00% and 5.00% of the total variation respectively. The eight principal component had an eigenvalue of 1.03, representing 5.00% of the total variation. The ninth component scored an eigenvalue of 0.91 contributing to a total variation of 4.00%. The first nine component explained 81% of the observed variability. The traits contributing significantly to PC1 were LL, APDLN, ASDLT and SDWG. The traits contributing significantly to PC2 were ANLPP, NPPPL, ANSPP and NSPPL. PC3 was highly positively correlated with nb, NN, LL, NSAB and PA. The traits contributing to PC 4 were DFF, ANLPP, NPPPL, NSAB and PA. The following traits NB, NN, DFF and DFMP contributed significantly to PC5. The traits contributing significantly to PC6 were ASDTH and SDWG. The traits contributing to PC 8 were DTG and PTL. The traits that contributed significantly to PC9 were PTL, NPPPD and APDWD.

Table 9: Principal component analysis for quantitative morphological traits of the tests material

Variable	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8	PC 9
DTG	-0.02	0.00	-0.10	0.08	-0.03	0.21	0.56	0.44	0.15
PTL	0.14	-0.05	0.09	0.04	0.04	0.02	-0.16	0.68	0.42
NB	-0.17	0.11	0.43	-0.05	0.38	0.15	0.04	0.00	-0.03
NL	-0.18	0.08	0.27	-0.03	0.21	0.20	-0.04	0.02	-0.03
NN	-0.17	0.11	0.43	-0.06	0.40	0.16	0.04	0.00	-0.04
NPPPD	0.00	0.06	0.16	0.20	0.03	-0.33	0.12	-0.06	0.53
PH	0.21	-0.03	0.16	0.02	0.14	-0.46	0.03	-0.01	-0.16
LL	0.31	-0.07	0.27	0.01	0.06	-0.38	0.07	0.10	-0.16
LW	0.29	-0.12	0.16	0.02	0.08	-0.26	0.09	0.19	-0.29
DFF	-0.08	-0.05	-0.34	0.37	0.45	-0.04	0.02	0.03	-0.12
APDLN	0.40	0.03	-0.02	0.00	0.12	0.08	-0.08	-0.21	0.17
APDWD	0.23	-0.04	-0.04	0.01	0.26	0.07	-0.01	-0.36	0.49
ANLPP	0.17	0.34	0.04	0.28	-0.06	0.12	-0.46	0.13	-0.05
NPPPL	0.05	0.37	0.10	0.31	-0.18	0.01	0.40	-0.14	-0.03
ANSPP	0.17	0.47	-0.09	0.00	0.05	0.03	-0.33	0.14	-0.04
DFMP	-0.08	-0.04	-0.36	0.37	0.43	-0.06	0.02	0.06	-0.13
NSPPL	0.09	0.47	0.07	0.26	-0.15	0.01	0.24	-0.09	-0.05
NSAB	-0.03	-0.31	0.24	0.47	-0.19	0.14	-0.15	-0.05	-0.01
PA	-0.04	-0.34	0.24	0.45	-0.18	0.13	-0.12	-0.07	0.00
ASDLT	0.36	-0.12	-0.03	-0.06	0.09	0.33	0.10	-0.13	-0.09
ASDTH	0.26	-0.05	0.03	-0.03	-0.04	0.34	0.09	0.15	-0.25
SDWG	0.41	-0.13	-0.02	-0.03	0.12	0.22	0.13	-0.02	0.03
Eigenvalue	4.20	3.00	2.38	1.99	1.69	1.45	1.13	1.03	0.91
Difference	1.20	0.62	0.40	0.29	0.24	0.32	0.11	0.11	0.06
Proportion (%)	19.00	14.00	11.00	9.00	8.00	7.00	5.00	5.00	4.00
Cumulative (%)	19.00	33.00	44.00	53.00	60.00	67.00	72.00	77.00	81.00

DTG=Mean days to germination, PTL=Mean petiole length, NB=Mean number of branches, NL=Mean number of leaves, NPPPD=Mean number of pods per peduncle, PH= plant height, LL=Mean leaf length, LW=Mean leaf width, DFF=Mean days to first flowering, APDLN=Average pod length, PDWD=Average pod width, ANLPP=Average number of locus per plant, NPPPL=Number of pods per plant, NSAB=Average number of seed aborted, PA=Average percent seed abortion, ASDLT=Average seed length, ASDWT=Average seed width, ASDTH=Average seed thickness, SDWG=Seed weight

4.6.1.3 Quantitative agro-morphological traits in the combined materials

The results of the principal component analysis for quantitative traits of the combined materials are shown in Table 19. The first nine components explained 81.00% of the total variations. The eigenvalue for the first principal component analysis was 4.18 which represented 19.00 % of the total variation. The eigenvalue for the second principal component analysis was 3.04 which represented 14.00 % of the total variation. The third and fourth principal component analysis recorded an eigenvalue of 2.34 and 2.12, representing 10.00% and 10.00% of the total variation respectively. The eigenvalue for the fifth principal component was 1.74, representing 8.00 % of the total variation. The eigenvalues for sixth and seventh principal components were 1.49 and 1.20 with each representing7.00% and 5.00% of the total variation respectively. The eight principal components had an eigenvalue of 0.97, representing 4.00% of the total variation. The ninth component scored an eigenvalue of 0.92 contributing to a total variation of 4.00%. The first nine component explained 81% of the observed variability. The traits contributing significantly to PC1 were LL, ASDLT, ASDTH and SDWG. The traits contributing significantly to PC2 were ANLPP, NPPPL, ANSPP and NSPPL. PC3 was highly positively correlated with NB, NN and LW. The traits contributing to PC 4 were NB NN, NSAB and PA. The following traits NB, NN, DFF and DFMP contributed significantly to PC5. The traits contributing significantly to PC6 were DTG, ANSPP and NSPPL. The traits contributing to PC 8 were DTG and PTL. The traits that contributed significantly to PC9 were PTL, PH and APDWD.

Table 10: Principal component analysis for quantitative morphological traits of the combined material

Variable	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8	PC 9
DTG	-0.02	-0.01	-0.09	-0.06	0.07	0.29	0.15	0.77	0.28
PTL	0.12	0.04	-0.04	0.18	-0.02	-0.25	0.21	0.48	0.04
NB	-0.21	0.08	0.31	0.29	0.39	-0.14	0.09	0.06	-0.04
NL	-0.19	-0.03	0.26	0.10	0.27	0.12	0.08	-0.16	0.13
NN	-0.22	0.06	0.33	0.28	0.39	-0.14	0.09	0.05	-0.02
NPPPD	-0.04	-0.01	0.19	0.10	-0.09	0.16	-0.43	-0.06	0.70
PH	0.20	0.03	0.10	0.17	-0.06	-0.33	-0.38	0.14	-0.24
LL	0.29	0.00	0.14	0.23	-0.07	-0.22	-0.31	0.15	-0.15
LW	0.19	-0.14	0.32	0.04	-0.20	-0.03	-0.25	0.12	0.11
DFF	0.12	0.09	-0.47	0.11	0.37	-0.17	-0.14	-0.04	0.10
APDLN	0.33	0.13	0.10	0.06	-0.13	-0.17	0.27	-0.12	0.19
APDWD	0.29	-0.03	0.07	0.01	0.13	-0.09	0.16	-0.22	0.34
ANLPP	0.01	0.42	-0.06	0.23	-0.26	-0.11	0.26	-0.06	0.13
NPPPL	0.10	0.34	-0.01	0.20	0.07	0.49	-0.21	-0.01	-0.18
ANSPP	0.03	0.51	0.04	-0.06	-0.13	-0.16	0.17	-0.02	0.12
DFMP	0.11	0.04	-0.46	0.07	0.36	-0.13	-0.22	-0.05	0.20
NSPPL	0.10	0.46	0.01	0.15	0.01	0.36	-0.13	-0.02	-0.13
NSAB	-0.04	-0.24	-0.18	0.54	-0.21	0.12	0.14	-0.07	0.01
PA	-0.04	-0.28	-0.18	0.52	-0.19	0.13	0.12	-0.08	0.00
ASDLT	0.40	-0.12	0.10	-0.03	0.17	0.14	0.20	-0.08	-0.02
ASDTH	0.34	-0.09	0.08	-0.02	0.17	0.22	0.11	0.01	-0.17
SDWG	0.42	-0.13	0.11	-0.02	0.17	0.14	0.12	-0.02	0.01
Eigenvalue	4.18	3.04	2.14	2.12	1.74	1.49	1.20	0.97	0.92
Difference	1.14	0.90	0.02	0.38	0.25	0.30	0.22	0.05	0.05
Proportion (%)	19.00	14.00	10.00	10.00	8.00	7.00	5.00	4.00	4.00
Cumulative (%)	19.00 %	33.00 %	43.00 %	52.00 %	60.00 %	67.00 %	72.00 %	77.00 %	81.00 %

DTG=Mean days to germination, PTL=Mean petiole length, NB=Mean number of branches, NL=Mean number of leaves, NPPPD=Mean number of pods per peduncle, PH= plant height, LL=Mean leaf length, LW=Mean leaf width, DFF=Mean days to first flowering, APDLN=Average pod length, PDWD=Average pod width, ANLPP=Average number of locus per plant, NPPPL=Number of pods per plant, NSAB=Average number of seed aborted, PA=Average percent seed abortion, ASDLT=Average seed length, ASDWT=Average seed width, ASDTH=Average seed thickness, SDWG=Seed weight

4.6.2 Phytochemical traits.

4.6.2.1 Phytochemical traits in the control

The results of the principal component analysis for the phytochemical traits of the control are presented in Table 20. The eigenvalue for the first principal component analysis was 7.30 which represented 46.00% of the total variation. The eigenvalue for the second principal component analysis was 3.56 which represented 22.00% of the total variation. The third principal component analysis recorded an eigenvalue of 2.35, representing 15.00% of the total variation. The eigenvalues for the fourth and fifth principal components were 1.65 and 1.14 with each representing 10.00% and 7.00 % of the total variation respectively. The five principal component, explained 100.00 % of the total variation. The second component was highly correlated with rutin and quercetin. The third component was highly correlated with L-lysine. The fourth component was highly correlated with D-proline. The fifth component was highly positive correlated with L-valine.

Table 20: Principal component analysis for phytochemical traits of the control

Variable	PC 1	PC 2	PC 3	PC 4	PC 5
Gal	0.22	0.35	-0.13	0.15	-0.34
Pca	0.22	0.34	-0.13	0.15	-0.34
Rutin	0.17	0.45	0.13	-0.03	0.15
Que	0.17	0.43	0.06	0.16	0.27
Lhis	-0.32	0.19	0.20	-0.06	0.11
Gly	0.34	0.07	0.19	-0.11	0.12
Lser	0.07	0.14	-0.46	0.38	0.37
Lasp	-0.29	0.21	0.14	0.34	-0.05
Llys	-0.08	0.25	0.51	-0.18	-0.24
Dpro	0.15	-0.26	0.24	0.51	0.17
Lval	-0.17	0.27	-0.13	-0.37	0.50
Isoleu	0.30	-0.11	0.25	-0.24	0.23
Lleu	0.27	-0.01	0.39	0.21	0.12
Ltyr	0.30	0.04	-0.26	-0.27	-0.26
Dlb	0.33	-0.24	0.02	0.06	0.01
Ltrp	0.34	-0.04	-0.11	-0.22	0.15
Eigenvalue	7.30	3.56	2.35	1.65	1.14
Difference	3.75	1.20	0.70	0.52	1.14
Proportion (%)	46.00	22.00	15.00	10.00	7.00
Cumulative (%)	46.00	68.00	82.00	93.00	100.00

Van=Vanillic acid, Gal=Gallic acid, Pca=P- coumaric acid, Rutin=Rutin, Que=Quercetin, Lhis =L-histidine, Gly=glycine, Lser=L-serine, Lasp= L-aspartic acid, Llys=L-lysine, Dlthr=D-L-threonine, Lthr=L-threonine, Thlpro= Trans-4-hydroxyl-L-proline, Dpro=D-proline, Lval=L-valine, Lmet=L-methionine, Lasn=L-asparagine, Isoleu=Iso-leucine, Lleu=L-leucine, Ltyr=L-tyrosine, Dlb= D-L-B-phylalanine, Ltrp= L-tryptophan.

4.6.2.2 Phytochemical traits in the test materials

The results of the principal component analysis for the phytochemical traits of the test materials are shown in Table 21. The eigenvalue for the first principal component analysis was 6.49 which represented 41.00% of the total variation. The eigenvalue for the second principal component analysis was 2.51 which represented 16.00% of the total variation. The third principal component analysis recorded an eigenvalue of 1.98, representing 12.00% of the total variation. The eigenvalues for the fourth and fifth principal components were 1.55 and 1.24 with each representing 10.00% and 8.00 % of the total variation respectively. The sixth principal component analysis recorded an eigenvalue of 0.83, representing 5.00% of the total variation. The first six principal component, explained 100.00 % of the total variation. The second component was highly correlated with rutin and quercetin. The third component was highly correlated with L-lysine. The fourth component was highly correlated with D-proline. The fifth component was highly positive correlated with L-valine. The sixth component is highly correlated with glycine.

Table 11: Principal component analysis for phytochemical traits of the test material

Variable	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6
Gal	0.11	0.37	0.37	0.41	-0.17	0.09
Pca	0.11	0.37	0.37	0.41	-0.17	0.09
Rutin	-0.05	-0.25	0.54	-0.20	0.22	0.13
Que	-0.06	-0.29	0.56	-0.22	0.13	0.07
Lhis	-0.04	0.48	-0.03	-0.35	0.23	0.25
Gly	-0.05	-0.26	-0.10	0.03	-0.37	0.85
Lser	0.36	-0.03	-0.02	-0.16	-0.04	-0.06
Lasp	0.01	0.46	-0.04	-0.28	0.39	0.30
Llys	0.38	0.00	-0.02	-0.09	-0.10	0.01
Dpro	0.37	-0.07	-0.09	0.00	0.08	0.01
Lval	0.38	-0.01	-0.01	-0.08	-0.10	-0.07
Isoleu	0.35	-0.04	0.01	0.03	0.11	0.10
Lleu	0.35	-0.08	0.05	-0.08	0.01	0.11
Ltyr	0.39	-0.01	-0.04	-0.08	-0.04	0.01
Dlb	0.13	-0.14	0.11	0.35	0.54	0.00
Ltrp	0.00	-0.17	-0.30	0.45	0.45	0.25
Eigenvalue	6.49	2.51	1.98	1.55	1.24	0.83
Difference	3.98	0.52	0.43	0.32	0.40	0.29
Proportion (%)	41.00	16.00	12.00	10.00	8.00	5.00
Cumulative (%)	41.00	56.00	69.00	78.00	86.00	91.00

Van=Vanillic acid, Gal=Gallic acid, Pca=P- coumaric acid, Rutin=Rutin, Que=Quercetin, Lhis =L-histidine, Gly=glycine, Lser=L-serine, Lasp= L-aspartic acid, Llys=L-lysine, Dlthr=D-L-threonine, Lthr=L-threonine, Thlpro= Trans-4-hydroxyl-L-proline, Dpro=D-proline, Lval=L-valine, Lmet=L-methionine, Lasn=L-asparagine, Isoleu=Iso-leucine, Lleu=L-leucine, Ltyr=L-tyrosine, Dlb= D-L-B-phylalanine, Ltrp= L-tryptophan.

4.6.2.3 Phytochemical traits in the combined material

The results of the principal component analysis for the phytochemical traits of the combined materials are shown in Table 22. The eigenvalue for the first principal component analysis was 5.60 which represented 35.00% of the total variation. The eigenvalue for the second principal component analysis was 2.55 which represented 16.00% of the total variation. The third principal component analysis recorded an eigenvalue of 2.15, representing 13.00% of the total variation. The eigenvalues for the fourth and fifth principal components were 1.71 and 1.27 with each representing 11.00% and 8.00% of the total variation respectively. The sixth principal component had an eigenvalue 0.85, which contributed 5.00% of the total variation. The seventh principal component had an eigenvalue of 0.68, representing 4.00% of the total variation.

Table 12: Principal component analysis for phytochemical traits of the combined material

Variable	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7
Gal	0.10	-0.02	0.61	-0.17	-0.25	0.11	0.11
Pca	0.10	-0.02	0.61	-0.17	-0.25	0.11	0.11
Rutin	-0.04	0.32	0.20	0.54	0.16	0.05	0.18
Que	-0.06	0.35	0.18	0.57	0.07	0.00	0.09
Lhis	-0.03	-0.46	0.14	0.11	0.42	0.26	-0.02
Gly	-0.05	0.14	-0.26	0.05	-0.30	0.88	0.03
Lser	0.38	-0.06	-0.09	0.15	-0.03	-0.04	0.03
Lasp	0.01	-0.45	0.15	0.12	0.44	0.24	0.08
Llys	0.41	-0.07	-0.04	0.09	-0.10	0.03	-0.04
Dpro	0.40	0.01	-0.12	0.01	0.07	0.00	0.06
Lval	0.40	-0.07	-0.05	0.11	-0.12	-0.04	0.03
Isoleu	0.36	0.10	0.01	-0.04	0.15	0.07	-0.07
Lleu	0.10	0.32	0.19	-0.12	0.27	0.15	-0.83
Ltyr	0.41	-0.04	-0.06	0.06	-0.03	0.03	0.04
Dlb	0.15	0.34	0.08	-0.23	0.36	-0.05	0.26
Ltrp	0.03	0.31	-0.11	-0.42	0.35	0.18	0.39
Eigenvalue	5.60	2.55	2.15	1.71	1.27	0.85	0.68
Difference	3.06	0.39	0.44	0.44	0.43	0.17	0.22
Proportion (%)	35.00	16.00	13.00	11.00	8.00	5.00	4.00
Cumulative (%)	35.00	51.00	64.00	75.00	83.00	88.00	93.00

Van=Vanillic acid, Gal=Gallic acid, Pca=P- coumaric acid, Rutin=Rutin, Que=Quercetin, Lhis =L-histidine, Gly=glycine, Lser=L-serine, Lasp= L-aspartic acid, Llys=L-lysine, Dlthr=D-L-threonine, Lthr=L-threonine, Thlpro= Trans-4-hydroxyl-L-proline, Dpro=D-proline, Lval=L-valine, Lmet=L-methionine, Lasn=L-asparagine, Isoleu=Iso-leucine, Lleu=L-leucine, Ltyr=L-tyrosine, Dlb= D-L-B-phylalanine, Ltrp= L-tryptophan.

4.7 INTER-RELATIONSHIPS AMONG ACCESSIONS

4.7.1 Morphological traits

Morphological data were used to determine the Euclidean distances among the 27 cowpea accessions and a dendrogram was designed (Figure 1). The cluster groups formed and the number of observations in each cluster from the dendrogram are shown in Table 23. Distances between the clusters formed are recorded in Table 24. The dendrogram generated five (5) main clusters among the 23 morphological traits at a distance of 200. Cluster 1 represented 4 accessions (Asontem, T3, T5, T22) and were characterized by least days to germination (3.58), highest mean number of branches (4.93), least mean number of leaves (41.26), highest mean number of nodes (9.83), least mean leaflet width (3.69), the highest mean days to first flowering, least mean number of pods per peduncle (2.81), least average pod width (0.80), highest mean number of pods per plant (49.50), the highest average number of seed per pod (15.97), highest mean days to first matured pod (42.01), highest mean number of seeds per plants (795.75), least average seed length (6.68) and least mean seed weight (12.98). Cluster 2 was made up of 5 accessions (Kirkhouse, T7, T16, T19, T23) and were characterized by highest mean days to germination (3.61), highest mean petiole length (10.58), highest mean plant height (12.40), highest mean leaflet length (9.69), highest leaflet width (4.80) and highest mean number of pod per peduncle (3.14). A total of 6 accessions (Wang Kae, T1, T2, T4, T14, and T15) were recorded in cluster 3. These accessions were characterized with least mean number of branches (4.21), least mean number of nodes (8.51), least mean days to first flowering (34.60), highest average pod length (17.96), highest pod width (0.91), highest average seed length (7.75), highest average seed width (5.75), highest average seed thickness (4.63) and highest mean seed weight (16.55). Cluster 4 was made up of 8 accessions (T6, T13, T18, T9, T21, T11, T12, and T20) and they were characterized by highest mean number of number of leaves (42.82) and least mean days to first matured pod (41.60). Cluster 5 was made up of 4 accessions (T8, T10, T24, and T17) and they were noted for the following characters; least average pod length (15.59), least mean number of locules per pod (15.12), least mean number of seeds per plant (474.31) and highest mean number of seed aborted (0.67). The greatest distance of 321.89 was observed between clusters 1 and 5 whereas the lowest distance of 48.45 was observed between clusters 2 and 3 (Table 24). There was no significant association between the cluster groups ($X^2900=930$, $P>0.05$).

Table 13: Major cluster group formed from the dendrogram for 23 morphological traits in cowpea accessions

Cluster groups	**Number of observations**	**List of accessions**
Cluster1	4	Asontem, T3, T5, T22
Cluster2	5	Kirkhouse, T7, T16, T19, T23
Cluster3	6	Wang kae, T1, T2, T4, T14, T15
Cluster4	8	T6,T13, T18, T9, T21, T11, T12, T20
Cluster5	4	T8, T10, T24, T17

Table 14: Distance between cluster centroids for 23 morphological traits in cowpea accessions

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	0.00	198.76	150.41	250.45	321.89
Cluster 2	198.76	0.00	48.45	51.77	123.22
Cluster 3	150.41	48.45	0.00	100.17	171.61
Cluster 4	250.45	51.77	100.17	0.00	71.47
Cluster 5	321.89	123.22	171.61	71.47	0.00

$X^2900=930$ at 5% probability level P= 0.237

Table 15: Mean value of morphological traits for 5 groups revealed by cluster analysis

Traits	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Grand centroid
DTG	3.58	3.61	3.52	3.59	3.60	3.58
NB	4.93	4.58	4.21	4.73	4.46	4.58
NL	41.26	41.56	41.65	42.82	42.56	42.06
NN	9.83	9.27	8.51	9.60	8.99	9.24
PTL	9.53	10.58	10.05	9.81	9.32	9.89
PH	11.93	12.40	11.74	11.43	10.91	11.68
LL	8.92	9.69	8.95	8.43	7.84	8.76
LW	3.69	4.80	4.61	4.53	4.26	4.43
DFF	35.59	34.67	34.60	34.67	34.88	34.82
NPPPD	2.81	3.14	2.97	2.91	2.88	2.95
APDLN	16.42	17.33	17.96	16.96	15.59	16.97
APDWD	0.80	0.90	0.91	0.85	0.84	0.86
ANLPP	16.54	15.64	15.58	15.66	15.12	15.69
NPPPL	49.50	39.51	42.82	36.26	32.83	39.77
ANSPP	15.97	15.11	15.07	15.02	14.44	15.10
DFMP	42.01	41.65	41.64	41.60	41.84	41.71
NSPPL	795.75	597.27	645.56	545.66	474.31	603.90
NSAB	0.57	0.53	0.50	0.64	0.67	0.58
PA	3.41	3.39	3.23	4.04	4.37	3.70
ASDLT	6.68	7.36	7.74	7.07	6.78	7.17
ASDWT	5.38	5.68	5.75	5.44	5.36	5.53
ASDTH	4.48	4.58	4.63	4.45	4.41	4.51
SDWG	12.98	15.19	16.55	14.40	13.12	14.62

DTG=Mean days to germination, PTL=Mean petiole length, NB=Mean number of branches, NL=Mean number of leaves, NPPPD=Mean number of pods per peduncle, PH= plant height, LL=Mean leaf length, LW=Mean leaf width, DFF=Mean days to first flowering, APDLN=Average pod length, PDWD=Average pod width, ANLPP=Average number of locus per plant, NPPPL=Number of pods per plant, NSAB=Average number of seed aborted, PA=Average percent seed abortion, ASDLT=Average seed length, ASDWT=Average seed width, ASDTH=Average seed thickness, SDWG=Seed weight

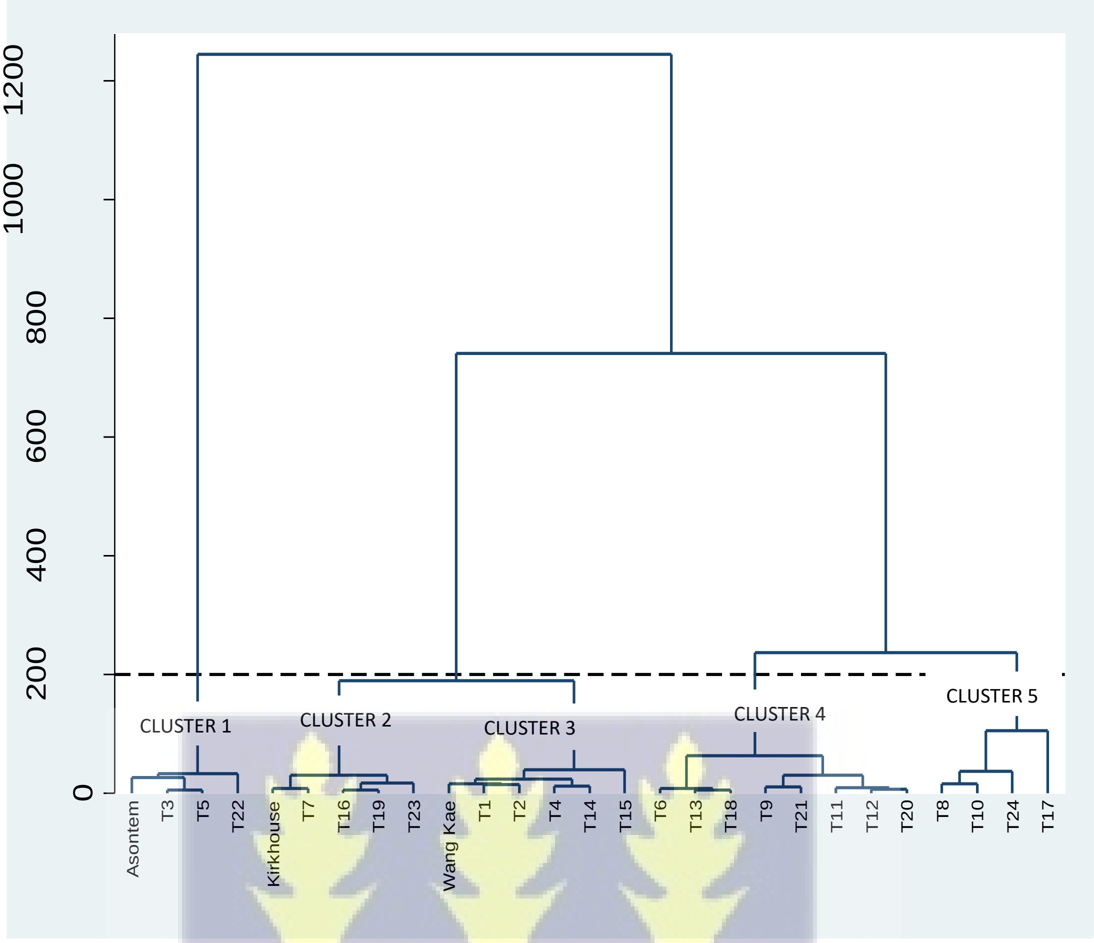

Figure 1: Dendrogram showing the relationship among 27 cowpea accessions based on morphological traits.

4.7.2 Phytochemical Traits

Phytochemical data were used to calculate the Euclidean distances among the 27 cowpea accessions and a dendrogram was designed (Figure 2). The cluster groups formed and the numbers of observations in each cluster and accessions in each cluster are shown in Table 26. Distances between the clusters formed were also recorded in Table 27. The dendrogram generated four major clusters among the 18 phytochemical traits at a distance of 1500.

12 accessions (Asontem, T23, Wang kae, T7, T1, T21, T2, T11, T20, T15, T5, and T2) formed the cluster 1. These were characterized by having the highest in all mean concentrations of the following amino acids: L-serine (73.57ppb), L-lysine (15.98ppb), D-L-threonine (6.75ppb), L-threonine (10.53 ppb), Trans-4-hydroxyl-L-proline (3.44), L-valine (243.83), L-methionine (6.43 ppb), Iso-leucine (127.80 ppb), =L-leucine (184.23 ppb) and L-tyrosine (89.12 ppb). Cluster 2 comprised 13 accessions (kirkhouse, T13,T9,T6,T8,T18,T3,T4,T16,T24,T10,T22) and were characterized with high mean concentrations for the following amino acids: Vanillic acid (1.24 ppb), Gallic acid (0.33 ppb), P- coumaric acid (2.03 ppb), L-histidine (568.21 ppb), D-proline (93.62 ppb) and L-asparagine (21.09 ppb). T14 was the only accession to represent the cluster 3 and had high mean concentration of glycine (6012.02 ppb), D-L-B-phenylalanine, (229.49) and L-tryptophan (2065.61 ppb). Cluster 4 was represent by a single accession (T17) and recorded high mean concentration for rutin (13.74 ppb), quercetin (3.44 ppb) and L-aspartic acid (63.24 ppb).

The greatest inter cluster distance of 6056.61 was observed between clusters 2 and 3 and the lowest distance of 627.54 was observed between clusters 1 and 2 (Table 27).

There was no significant association between the cluster groups ($X^2$900 = 930, P>0.05).

Table 16: Major cluster group formed from the dendrogram for 18 phytochemical traits in cowpea accessions

Cluster groups	Number of observations	List of accessions
Cluster1	12	Asontem, T23, Wang kae, T7, T1, T21, T2, T11, T20, T15, T5, T2
Cluster2	13	kirkhouse, T13,T9,T6,T8,T18,T3,T4,T16,T24,T10,T22
Cluster3	1	T14
Cluster4	1	T17

Table 17: Distance between cluster centroids for 18 phytochemical traits in cowpea accessions

	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	0	627.54	5983.81	3166.98
Cluster 2	627.54	0	6056.61	3163.58
Cluster 3	5983.81	6056.61	0	2913.29
Cluster 4	3166.98	3163.58	2913.29	0

Table 18: Mean value of phytochemical traits for 4 groups revealed by cluster analysis

Traits	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Grand centroid
Van	1.2	1.24	0.67	0.66	1.18
Gal	0.3	0.33	0.01	0	0.29
Pca	1.95	2.03	1.04	1.02	1.92
Rutin	10.72	8.97	10.85	13.74	9.99
Que	2.91	2.62	1.85	3.44	2.75
Lhis	389.86	568.21	276.21	525.13	476.54
Gly	43.43	43.22	6012.02	3190.95	380.96
Lser	73.57	16.63	17.42	23.28	42.21
Lasp	45.44	49.95	33.41	63.24	47.83
Llys	15.98	9.32	10.56	6.39	12.22
Dlthr	6.75	0.71	0	0	3.34
Lthr	10.53	5.2	0	0	7.18
Thlpro	3.44	0	0	0	1.53
Dpro	88.01	93.62	53.82	60.39	88.42
Lval	243.83	190.71	171.92	168.5	212.8
Lmet	6.43	0	0	0	2.86
Lasn	0	21.09	0	0	10.16
Isoleu	127.8	100.68	116.42	95.95	113.14
Lleu	184.23	102.37	128.1	93	139.36
Ltyr	89.12	53.37	74.52	52.18	70
Dlb	213.1	179.51	229.49	139.55	194.81
Ltrp	1671.47	1083.74	2065.61	1390.62	1392.69

Van=Vanillic acid, Gal=Gallic acid, Pca=P- coumaric acid, Rutin=Rutin, Que=Quercetin, Lhis =L-histidine, Gly=glycine, Lser=L-serine, Lasp= L-aspartic acid, Llys=L-lysine, Dlthr=D-L-threonine, Lthr=L-threonine, Thlpro= Trans-4-hydroxyl-L-proline, Dpro=D-proline, Lval=L-valine, Lmet=L-methionine, Lasn=L-asparagine, Isoleu=Iso-leucine, Lleu=L-leucine, Ltyr=L-tyrosine, Dlb= D-L-B-phylalanine, Ltrp= L-tryptophan.

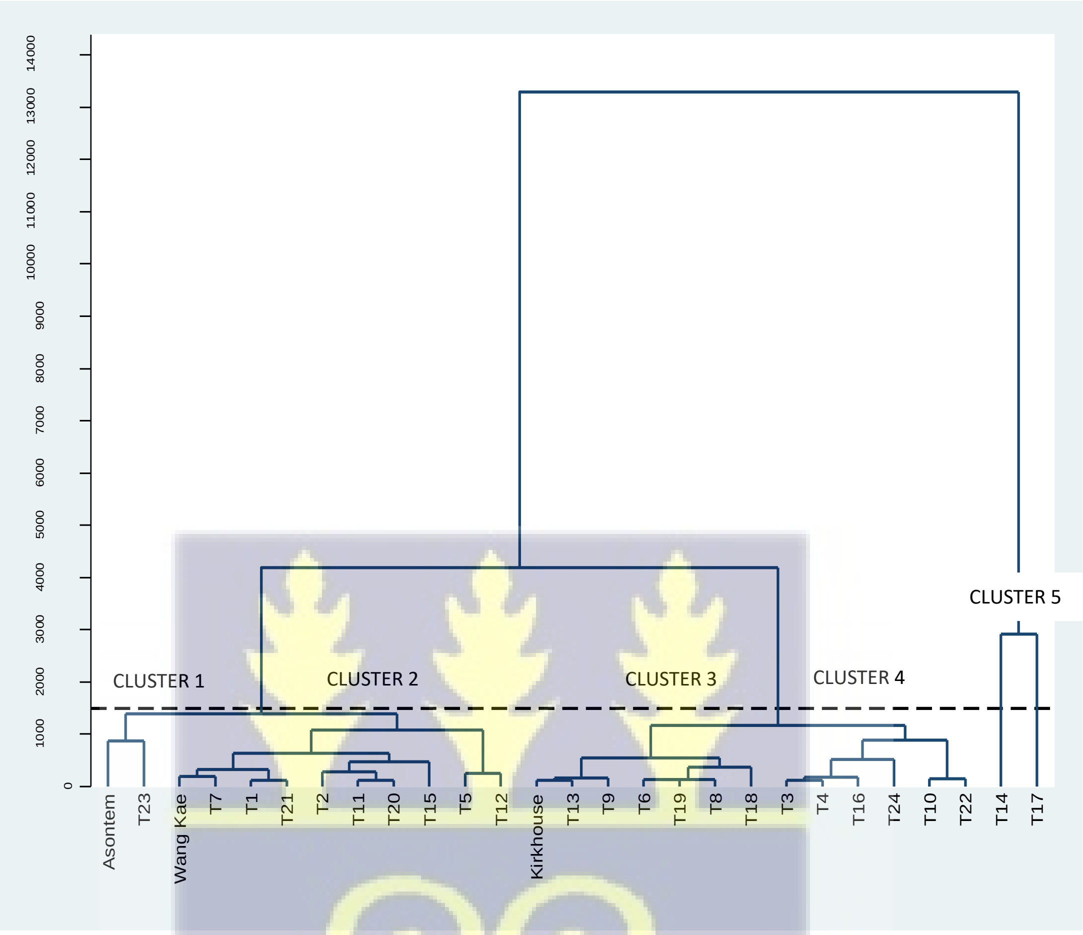

Figure 2: Dendrogram showing the relationship among 27 cowpea accessions based on phytochemical traits.

4.8 GENETIC VARIABILITY, HERITABILITY AND EXPECTED GENETIC ADVANCE

4.8.1 Morphological traits

Analysis of variance showing F-value, estimates of phenotypic and genotypic variances and coefficient of variations, broad-sense heritability, critical difference, genetic advance and genetic advance as percent of mean among morphological quantitative traits were presented in Table 29. The number of seeds per plant gave the highest genotypic variance (80841.20) and phenotypic variance (107162.90) while the lowest genotypic variance (0.09) and phenotypic variance (0.10) were recorded by mean days to germination and mean seed thickness respectively. The number of node showed low (≤20%), PCV (7.89%) and GCV (6.84%). This trend could also be seen in mean days to first flowering with PCV (10.39%) and GCV (9.87%). Mean number of locules per pod recorded PCV (16.79%) and GCV (14.81%). Mean number of seed per plant scored PCV (17.53%) and GCV (14.89%). Similarly, mean days to first matured pod recorded low PCV and GCV values of 5.89% and 5.89% respectively. Mean seed thickness exhibited similar trend, it recorded PCV (18.45%) and GCV (17.96%).

Low (≤20%) broad sense heritability values were recorded for all the morphological traits and ranged from 0.33% for days to germination to 0.99% for seed weight. However all traits scored above 0.60% with exception of days to germination (0.33%) and average seed width (0.55%).

The number of aborted seeds scored the highest genetic advance (as percentage mean) value of 269.76% whereas, days to first matured pod scored the lowest value of 8.94%. The following morphological traits recorded genetic advance above 60%; petiole length (69.34%), leaflet length (74.62), leaflet width (82.29%), average pod length (67.69%), average pod width (63.46%), number of pod per plant (73.83), number of seeds per plant (84.14), percentage abortion (255.25%) and average seed length (76.29%)

Table 19: ANOVA, Estimates of environmental, phenotypic and genotypic variances and coefficient of variations, broad-sense heritability, genetic advance and genetic advance as percent of mean among morphological traits in cowpea

Traits	F	σ^2 e	σ^2 g	σ^2 p	ECV	GCV	PCV	H^2%	GA	GAM
DTG	2.50***	0.65	0.33	0.98	22.57	15.98	27.65	0.33	0.68	19.02
NB	22.90***	0.23	1.66	1.89	10.44	28.22	30.09	0.88	2.49	54.52
NL	7.43***	48.10	103.04	151.14	16.50	24.16	29.25	0.68	17.27	41.09
NN	20.57***	1.05	6.84	7.89	11.10	6.84	7.89	0.87	5.02	54.39
PTL	29.58***	1.29	12.26	13.54	11.46	35.38	37.20	0.91	6.86	69.34
PH	30.13***	1.29	12.57	13.87	9.75	30.37	31.90	0.91	6.95	59.58
LL	39.99***	0.84	10.87	11.71	10.43	37.59	39.01	0.93	6.55	74.62
LW	26.11***	0.42	0.42	3.92	14.61	42.26	44.72	0.89	3.64	82.29
DFF	28.70***	1.28	11.83	13.11	3.25	9.87	10.39	0.90	6.73	19.32
NPPPD	10.60***	0.18	0.58	0.76	14.46	25.88	29.65	0.76	1.37	46.54
APDLN	74.52***	1.32	32.28	33.60	6.77	33.52	34.20	0.96	11.47	67.69
APDWD	15.41***	0.02	0.09	0.10	15.45	33.86	37.23	0.83	0.55	63.46
ANLPP	11.55***	1.54	5.41	6.95	7.90	14.81	16.79	0.78	4.23	26.93
NPPPL	10.55***	83.99	267.25	351.24	23.03	41.09	47.10	0.76	29.38	73.83
ANSPP	8.77***	1.96	5.07	7.02	9.25	14.89	17.53	0.72	3.94	26.06
DFMP	9.43***	1.58	4.45	6.03	3.02	5.06	5.89	0.74	3.73	8.94
NSPPL	10.21***	26321.70	80841.20	107162.90	26.84	47.03	54.15	0.75	508.72	84.14
NSAB	6.13***	0.54	0.93	1.48	126.07	164.86	207.54	0.63	1.58	269.76
PA	5.72***	22.00	34.63	56.63	126.31	158.46	202.64	0.61	9.48	255.25
ASDLT	175.73***	0.12	7.18	7.30	4.89	37.35	37.67	0.98	5.47	76.29
ASDWT	4.67***	0.94	1.15	2.09	17.53	19.38	26.13	0.55	1.64	29.62
ASDTH	55.36***	0.04	0.66	0.69	4.22	17.96	18.45	0.95	1.63	36.01
SDWG	453.30***	0.40	60.36	60.76	4.33	53.14	53.32	0.99	15.95	109.11

DTG=Mean days to germination, PTL=Mean petiole length, NB=Mean number of branches, NL=Mean number of leaves, NPPPD=Mean number of pods per peduncle, PH= plant height, LL=Mean leaf length, LW=Mean leaf width, DFF=Mean days to first flowering, APDLN=Average pod length, PDWD=Average pod width, ANLPP=Average number of locus per plant, NPPPL=Number of pods per plant, NSAB=Average number of seed aborted, PA=Average percent seed abortion, ASDLT=Average seed length, ASDWT=Average seed width, ASDTH=Average seed thickness, SDWG=Seed weight, MS= Mean squares, CD5%=Critical Difference (CD) 5%, CD1%=Critical Difference (CD) 1%, σ2 e =Environmental Variance, σ2 g =Genotypic Variance, σ2 p =Phenotypic Variance, ECV= Environmental Coefficient of Variance, GCV= Genotypic Coefficient of Variance, PCV=Phenotypic Coefficient of Variance, H2%= Heritability (Broad Sense), GA= Genetic Advance, GAM= Genetic Advance as percentage of mean

4.8.2 Phytochemical traits

Analysis of variance showing F-value, estimates of phenotypic and genotypic variances and coefficient of variations, broad-sense heritability, critical difference, genetic advance and genetic advance as percent of mean among phytochemical traits are presented in Table 30. The phenotypic variance (σ^2_p) was higher than the genotypic variance (σ^2_g) for all phytochemical traits evaluated with the exception of D-L-threonine and L-asparagine. The phytochemical trait glycine scored the highest genotypic (13593070.00) and phenotypic (16636080.00) variance while the lowest genotypic (0.51) and phenotypic (0.52) value was recorded by gallic acid. High (≥20%) phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed in the phytochemical traits except for glycine and L-serine, L-aspartic acid, D-L-threonine, L-threonine, D-proline, L-asparagine, Iso-leucine and L-leucine which did not show genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV). Low (≤20%) broad sense heritability values were observed in all phytochemical traits and ranging from 0.73% for D-L-B-phenylalanine to 1.00% for D-L-threonine, L-threonine L-asparagine. The phytochemical traits gallic acid recorded the highest genetic advance (as percentage mean) value of 508.07% whereas the trait, D-L-B-phenylalanine scored the lowest value of 126.8% for genetic gain.

Table 30: ANOVA, Estimates of phenotypic and genotypic variances, coefficient of variations, broad-sense heritability, genetic advance and genetic advance as percent of mean among phytochemical traits in 27 accessions of cowpeas.

Traits	F	σ2 e	σ^2 g	σ^2 p	ECV	GCV	PCV	H^2%	GA	GAM
Van	411.42***	0.01	1.70	1.71	9.45	110.59	110.99	0.99	2.67	226.98
Gal	412.21***	0.00	0.51	0.52	21.14	247.55	248.46	0.99	1.47	508.07
Pca	411.73***	0.04	5.00	5.03	10.00	116.96	117.38	0.99	4.59	240.06
Rutin	95.75***	3.07	96.91	99.98	17.58	98.80	100.35	0.97	19.97	200.38
Que	79.52***	0.15	4.00	4.15	14.25	72.88	74.26	0.96	4.04	147.34
Lhis	11.48***	71862.33	251000.31	322862.64	56.27	105.17	119.28	0.78	909.98	191.02
Gly	14.40***	3043014.00	13593070.00	16636080.00				0.82	6865.30	
Lser	32.99***	2158.18	23012.90	25171.07				0.91	298.80	
Lasp	21.28***	502.84	3399.70	3902.54				0.87	112.11	
Llys	11.22***	303.81	1035.42	1339.23	141.82	261.82	297.77	0.77	58.28	474.25
Dlthr	4.9E+30***	0.00	1111.87	1111.87				1.00	68.69	
Lthr	810.91***	5.85	1578.87	1584.72				1.00	81.70	
Dpro	11.11***	13490.04	45455.37	58945.40				0.77	385.68	
Lval	16.21***	19873.10	100750.95	120624.05	66.34	149.36	163.43	0.84	597.58	281.20
Lasn	5.1E+32***	0.00	21125.60	21125.60				1.00	299.41	
Isoleu	13.55***	3413.73	14278.49	17692.22				0.81	221.14	
Lleu	13.67***	32805.02	138505.78	171310.81				0.81	689.35	
Ltyr	12.28***	4969.78	18687.00	23656.78	100.18	194.26	218.57	0.79	250.28	355.66
Dlb	9.03***	7374.48	19738.65	27113.13	44.12	72.19	84.60	0.73	246.94	126.88
Ltrp	13.76***	279015.26	1186853.04	1465868.30	37.86	78.08	86.77	0.81	2019.37	144.73

Van=Vanillic acid, Gal=Gallic acid, Pca=P- coumaric acid, Rutin=Rutin, Que=Quercetin, Lhis =L-histidine**,** Gly=glycine, Lser=L-serine, Lasp= L-aspartic acid, Llys=L-lysine, Dlthr=D-L-threonine, Lthr=L-threonine, Thlpro= Trans-4-hydroxyl-L-proline, Dpro=D-proline, Lval=L-valine, Lmet=L-methionine, Lasn=L-asparagine, Isoleu=Iso-leucine, Lleu=L-leucine, Ltyr=L-tyrosine, Dlb= D-L-B-phenylalanine, Ltrp= L-tryptophan, MS= Mean squares, CD5%=Critical Difference (CD) 5%, CD1%=Critical Difference (CD) 1%, σ2 e =Environmental Variance, σ2 g =Genotypic Variance, σ2 p =Phenotypic Variance, ECV= Environmental Coefficient of Variance, GCV= Genotypic Coefficient of Variance, PCV=Phenotypic Coefficient of Variance, H2%= Heritability (Broad Sense), GA= Genetic Advance, GAM= Genetic Advance as percentage of mean

CHAPTER FIVE

5.0 DISCUSSION

5.1 PHENOTYPIC VARIABILITY OF AGRO-MORPHOLOGICAL AND PHYTOCHEMICAL TRAITS OF COWPEA

5.1.1 Morphological qualitative characterization

Genetic diversity is very essential in improving crops genetically. However, the effective use of the genetic diversity in modern day germplasm collections requires a good knowledge about their characteristics. Characterization of cowpea accessions is traditionally based on their morphological and agro-morphological traits.

In this study growth habit showed three (3) different forms namely: erect, intermediate and semi-erect. Erect growth habit was the most dominant (84.17%) in the entire population. This observation is not in accordance with a study by Lazaridiet al. (2017) who used qualitative and quantitative traits to characterize phenotypic diversity in local cowpea populations collected from Greece. He reported seven different forms of growth habit with a frequency of 37% for an erect growth habit. In this study, there were three different phenotypic classes observed for plant pigmentation: intermediate, moderate and very slight. Very slight was the most predominant in the entire population with a frequency of 59.31%. The current findings do not corroborate with what Lesly (2005) observed the least frequency of 3.6% for very slight class in cowpea. The difference may be due to environmental conditions and differences in cowpea genotypes used. Furthermore, in this present study terminal leaflet shape had three different phenotypic classes: globose, sub-globose and hastate, with globose (75%) being predominant in the entire population. The present work is in contrast with the work of Pottorff *et al.*; (2012), they reported six different categories of terminal leaflet shape: globose, hastate, sub-globose, sub-hastate, strip and ovate lanceolate. Again this observation in the current work is in contrast to Doumbia *et al*. (2013), who also observed similar forms of terminal leaflet shape and reported sub-globose forms to be predominant in genotypes from Mali while sub-hastate was the predominant form in genotypes from Ghana. The variance in the reports may be due to the differences in cowpea accessions used in the various works and environmental conditions.

In this current study, two different phenotypic classes were observed for leaf colour, they were: dark green and intermediate green. The current work agrees with Kumar (2016) who observed two classes of leaf colour: green and dark green. However, this current findings does not agree with the observation made by Ahamed *et al.* (2014). They reported three leaf colour types pale green, intermediate green and dark green leaf type. In this study twinning tendency recorded three different phenotypic classes: none, slight and intermediate. None twinning was predominant in the entire population with a frequency of 81.53%. The current study agrees with the work of Lazaridi *et al.* (2017). They observed that the absence of twinning (73.7%) as the most frequent with intermediate twinning (7.4%) as the lowest frequency for twinning tendency. This current work however, agrees with Hutchinson *et al.* (2017) who reported a high frequency for none twinning in 28 cowpea accessions. In the current study three phenotypic classes was observed for flower colour, they were: white, violet and white with violet patches. The findings in this current work contradict the findings of Bozokalfa *et al.* (2017), they observed 2 phenotypic classes for flower colour, white and violet with frequencies of 62.5 and 37.5% respectively. All plants in the entire population had leaf markings. The finding in this present work is in contrast with the work of Zoryeku (2019) who reported no marking in cowpea accessions. The difference in the reports could be attributed to differences in cowpea genotypes used.

Ahamed *et al.* (2014) in their study reported that all the accessions studied had 30-90° down to erect pod attachment to peduncle. This is in contrast with results from this study. The present study revealed three different classes for pod attachment to peduncle, these were: 30-90° down from erect, erect and pendant. The differences in the reports may be attributed to differences in genotype and sample size. In this current work, pod colour recorded were mainly pale tan (62.92%) and dark tan (37.08%), this does not agree with the work of Nortey (2017) who reported straw coloured pods (62.33%) for cowpea accessions. In this current study, curved pod curvature was predominant in the entire population, this is contradiction to the findings of Bozokalfa *et al.* (2017). They observed that pods were mainly straight (68.8%), and few genotypes (25%) showed slightly curved pods. In this current study, three different phenotypic class were observed for seed coat colour. They were: reddish brown, white and cream, with white (66.11%) being the dominant trait in the entire population. However Onwubiko (2020) observed three seed coat colours namely; milky, white and red, which does not agree with this current work.

5.1.2 Morphological quantitative characterization

In this current work, mean petiole length recorded in the entire population was 9.89±0.06cm. This is in contrast to the findings by Singh (1997) who reported a figure of 13.02 cm. The results from this current study showed the mean number of branches as 4.57±0.02 for the entire population, this figure is much higher than the 3.88 reported by Lesly (2005). The number of nodes reported in this current work was 9.22±0.05 for the whole population. The figure in this study is relatively higher than that of Kouam *et al.* (2018), who studied cowpea and reported the mean number of nodes as 4.78. The dissimilarity may be due to the differences in cowpea genotypes and the location. In this current study, the mean value for number of pods per peduncle was 2.94±0.02. This was in an agreement with the value of 2.94±0.14 reported by Walle *et al.* (2019), In this study, the mean terminal leaflet length and width were 8.77±0.05 cm and 4.43±0.03 cm respectively which was in disagreement with Walle *et al.* (2019) who reported mean terminal leaf length and leaf with as 11.57±0.57 and 9.34±0.91 cm respectively. The number of leaves reported in this present study was 42.02±0.29, this is much higher than 13.10 reported by Musvosvi (2009). In this study, the cowpea accessions took an average of 34.84±0.06 days to flower. The result observed in this study is lower than that of Lesly (2005), who reported the mean days to flowering of cowpea genotypes as 54.80 days. The differences may be due to environmental factors and the cowpea genotypes used in these studies. The shortest flowering time is an advantage, as high temperatures and low humidity can be avoided. In this present work the mean number of pods per plant was 39.79±0.40, this much higher than one reported by Walle *et al.* (2019), they reported a mean number of pods per plant to be 27.83±1.62, however the mean value reported in the current work is much lower than the 76.77±4.17 recorded by Kouam *et al.* (2018). The mean value of pod length was reported as 16.95±0.08 cm in this current study and this much lower than the mean value of 38.00 cm reported by Singh (1997). In this present work, the number of locules per pod recorded is higher the mean value 13.10 for this same trait reported by Musvosvi (2009). This diference may be due to the differences in cowpea genotypes used and sample size.

In the entire population the mean number of seeds per pod was 15.11±0.06, this higher than and contradicts the mean number of seeds per pod of 12.74±1.14 reported by Walle *et al.*, (2019). In this current study, the value 7.17±0.04 mm in the entire population was recorded for the mean seed length is smaller than the result of

Milosevic (2013) who reported a mean seed length of 10.57 mm on the study of cowpea. The difference may be due to the cowpea genotype used. In the present work mean seed width was 5.54±0.04 mm this contradicts the findings of Milosevic (2013) who reported a value of 5.84 mm. In this study, the mean seed thickness was 4.51±0.01 mm. There were differences between this result and the one obtained in a similar study by Hamid *et al.*, (2016) who had 4.97 mm for seed thickness. The difference in the mean value obtained in this study and that of Hamid *et al.*, (2016) could be due to differences in genotypes and locations. The mean 100-seed weight recorded in this current work was 14.62±0.10 g. this is similar to the observation made by Bozokalfa *et al.* (2017), they reported a value of 14.29 g.

5.1.3 Phytochemical traits

Elhardallou *et al.* (2015) reported that valine, methionine and tryptophan were absent in the cowpea accessions they studied. These findings do not agree with the results of this current work, where valine, methionine and tryptophan were all present in the cowpea genotypes used. Frota *et al.* (2017) reported the presence cysteine in their work, this is in contrast with the present study, where cysteine weren't detected. In this current work, the mean value of L-Histidine was 476.39±12.04 ppb which much higher than mean value of 0.77 ppb reported by Elharadallou *et al.* (2015) on the study of cowpea. The dissimilarity may be due to the different type of cowpea accessions used. In this current study, the mean estimated value for iso-leucine was 113.63±2.81 ppb. A study by Frota *et al.* (2017) reported a mean concentration of4.5±0.03 ppb. The observations from the present work contradicts that of the previous study. In the present study the following amino acids: aspartic acid, asparagine and tryptophan appeared in amounts higher than those reported by Rangel *et al.* (2004) and Elhardallou *et al.* (2015) whom work on the same trait in cowpea accessions. The differences in the results obtained in the present study and the results of other researchers maybe attributed to dissimilarities in sample size and accessions used. In this current study, D-L-B-phenylalanine concentration recorded a mean value of 194.63±3.70 ppb which is significantly higher than the mean concentration of 2.00 ppb scored for the same trait by Elharadallou *et al*. (2015), who also worked on cowpea. In this current study 70.37±3.18 ppb was the mean value of L-Tyrosine recorded, this disagrees with figures reported by Elharadallou *et al*. (2015), who reported a mean value of 3.33 ppb for the same traits.

5.2 ASSOCIATION AMONG AGRO-MORPHOLOGICAL AND PHYTOCHEMICAL TRAITS OF COWPEA

Correlation analysis is very important in breeding programmes and also in traits identification, classification and selection. A total of one hundred and forty-five (145) and one hundred and thirteen (113) significant associations ($P \leq 0.05$) were observed between morphological traits in the control and test material respectively. However in the phytochemical traits, the significant association observed among the control and test material were seventy-six (76) and.one hundred and twenty-one (121) respectively. Furthermore, the study showed that number of seed per plant had a positive significant correlation with plant height, leaflet length, days first flowering, pod length, number of locule per pods, number of pod per plant and number of seeds per plant. This current result is in accordance with Sabale *et al*. (2019). The current study reveal results that suggest that significant correlations were observed among the polyphenolic compounds in entire population. The associations between and within groups of phenols and flavonoids for the entire population were significant. These results are in line with the study by Alidu *et al.* (2020) who observed strong correlations among phenolic acids and flavonoids. In the current work, low correlation values were also observed in the association between some traits this is agreement with the explanations by Lopes *et al.* (2017) in their study.

5.3 GENETIC VARIABILITY, HERITABILITY ANS RESPONSE TO SELECTION FOR AGRO-MORPHOLOGICAL AND PHYTOCHEMICAL TRAITS COWPEA

The genetic component evaluation of quantitative character is an essential tool in crop genetic improvement programmes in almost all crops species. Hence, understanding the extent of genetic variability, estimating heritability and character associations in crop species is pivotal, and gives the basis for selection and genetic improvement programmes (Idahosa et al. 2010). Significant differences were observed among genotypes for all quantitative traits. The analysis of variance indicated that the F value for the morphological quantitative traits were all highly significant ($P<0.001$). This current study is in accordance with the study done by Gerrano et al. (2015), Srinivas et al. (2016), Suganthi and Murugan (2008), Withanage (2005) and Malarvizhi et al. (2005). They reported the existence of important genetic variation among *V. unguiculata* genotypes. The same observation was reported for *V. mungo* (Veeramani et al. 2005), another crop from the same genus. The coefficient of variation shows the relationship between the relative amounts of variability among agro-morphological traits (Sharma 1988). The genetic component analysis in this study revealed that the phenotypic variance (σ^2 p) was higher than or equal to genotypic variance (σ^2 g) regarding all the traits evaluated. This report is consistent with a study by Murugan (2008) who reported higher value for phenotypic variance than genotypic variance. Moreover, Owusu et. al., (2021) observed similar results which indicated that the genotypic variance values were higher than environmental variance values. In this t study, environmental and phenotypic coefficients of variance were moderate while genotypic coefficient of variance was low in almost all cases except mean days to germination, number of pod per plant, number of seeds aborted and percentage abortion. In the current work, the phenotypic coefficient of variance value was higher than genotypic coefficient variance value. This study is consistent with a study by Withanage (2005). He reported same trends between the environmental and genotypic coefficients of variance.

Heritability aids in knowing the level of environmental influence on the expression of a phenotypic trait. According to Robinson et al. (1949), heritability values is an important observation that helps the breeder to know the extent to which the improvement of a trait is can be done through selection. Broad sense heritability is categorized as low (<40%), medium (40–59%), moderately high (60-79%) and very high (≥80%) (Singh, 2001). All other traits fall within the range of low heritability. This finding is in contrast with a study by Belay & Fischa (2020) on cowpea, who reported high estimate of heritability for all its studied traits. The differences may be attributed to the cowpea genotypes used for the study. Genetic Advance as percent of the mean, according to Johnson et al. (1955), is grouped as high when exceeding 20%, moderate when between 10 and 20% and is considered as low when below 10%. In this current study, genetic advance was high for number of pod per plant (29.38) and number of seed per plant (508.72), these finfings are in accordance to the observation made by Gerrano *et, al.*, (2015) who reported higher genetic advance for the same traits. Phytochemical components (individual phenols, flavonoids and amino acids) of cowpea and other crops form part of the important nutrients in diets. In this current study, the analysis showed highly significant (P<0.001) for almost all the traits.

Highly significant mean square values explains adequate variability among the cowpea genotypes (Belay & Fischa, 2020). In this current study, the critical difference at 5 % and at 1 % were found highest in glycine. In the current study, the results showed the highest environmental, genotypic and phenotypic coefficients of variations values as 3043014.00, 13593070.00 and 16636080.00respectively for glycine. This association of all the highest values of the parameters (ECV, GCV and PCV) to one particular trait may be due high content of this trait in the germplasm of the studied trait. Noubissié *et al*. (2012) reported highest environmental, genotypic and phenotypic coefficients of variations values of 450.71, 407.35 and 288.63 respectively for total phenols among three different cowpea genotypes. The highest heritability value observed in the phytochemical traits was 1.00, this is higher than the value reported by Noubissié *et al*. (2012) on cowpea total phenols as component of phytochemical traits, and he reported highest heritability value of 0.9343 for total phenols among three cowpea accessions. John et al. (1955) classified genetic advance into three categories: less than (<) 10% as low, 10-20% as moderate as and more than (>) 20% as high genetic advance. In this current, based on the classification, all the amino acids were high. With the phenols, rutin scored a moderate value of 19.97 and this in agreement to the work done by Noubissié *et al*. (2012) reported genetic advance figure of 23.77, 15.78 and 18.17 for total phenols.

5.4 INTERRELATIONSHIPS AMONG COWPEA ACCESSIONS BASED ON AGRO-MORPHOLOGICAL AND PHYTOCHEMICAL TRAITS

Principal component analysis was used to identify variables describing the phenotypic diversity of the genotypes. It is believed that the first principal component accounts for maximum variability in the data with respect to succeeding components (Syafii *et al*.; 2015).

For morphological quantitative traits, 33% of total variability between the traits can be explained by the PC1 and PC2. Mean pod length (0.33), mean seed length (0.40), seed thickness (0.34) and 100-seed weight (0.42) contributed importantly to the construction of the PC1. The highest PC2 contribution is provided by average number locules per pod (0.42), average number seed per pod (0.51) and number of seed per plant (0.46). This observation does not agree with Udensi & Edu (2015), who carried out principal component analysis on 13 traits in 30 cowpea accessions from Nigeria. They reported a three principle component contributing to 82.23% of the total variability. The difference may due the number of genotypes used and the number of traits analysed. However, in the phytochemical traits, 55% of total variability between the traits can be explained by the PC1 and PC2. The traits the contributed more in PC1 are L-lysine (0.41), D-proline (0.40), L-valine (0.40), and L-tyrosine (0.41). The highest PC2 contribution is provided by rutin (0.32), quercetin (0.35), L-leucine (0.32) and = L-tryptophan (0.31). This results does not agree with the total variation value of 86% reported by M. Avanza *et. al*., (2013) for the first two principal component when they work on four local cowpea varieties grown in the Northeast of Argentina. The principal component analysis (PCA) allowed the characterization of the cowpea accession used in the current study.

In this present study, the dendrogram constructed based on the data from morphological quantitative traits showed five major clusters (1, 2, 3, 4 and 5) for the 27 accessions studied. However, the results in this current work does not agree with the observation made by Ajayi & Adesoye (2013), who reported two major clusters formed from the dendrogram, when they worked on 10 cowpea accessions. The centroid distances between all clusters showed high divergence (P>0.05), indicating wide diversity among genotypes in the five different clusters. The range of intra- and inter-cluster distance was 48.45 to 250.45 units to 48.45 to 321.89 units respectively. This result was in disagreement the figures reported by Walle *et al* (2019). They reported an interval of 6.08 to 22.72 units and 17.37 to 41.62 units between six clusters. In the present work, perfect correlation existed among the phenolic acids and very strong associations among the flavonoids in the entire population. The results for the dendrogram generated four major clusters among the phytochemical traits at a distance of 1500. Cluster 1 was highly associated with high amino acid concentration, however cluster two was highly associated with polyphenolic compound concentration. The range of intra- and inter-cluster distance was 627.54 to 5983.81 units to 627.54 to 3166.98 units respectively. The cluster distances observed in the study indicates that the intra and inter cluster distances were more genetically divergent from each other.

CHAPTER SIX

6.0 CONCLUSION & RECOMMENDATIONS

6.1 CONCLUSION

This current study showed differences between the 27 cowpea genotypes used on the basis of qualitative, quantitative and phytochemical traits. The knowledge gained in the current work provides useful information about the diversity and breeding value of the cowpea accessions used. It also provides a useful database for selecting the top performing accessions to be used in future breeding programs.

The phenotypic assessment of plant genetic resources is an essential tool for identifying potential parents and interesting traits that can be used in crop improvement programmes. This study of the 23 quantitative traits showed that, there is high genetic variability among the 27 cowpea genotypes in terms of number of days to germination, mean number of leaves, number of pods per plant, number of nodes, days to first flowering, number of pods per plant, number of seed per pod, number of seeds per plants and seed weight. This important genetic variability was confirmed by cluster and principal component analysis. These suggest high potential for selection and further screening of the acessions and possibility of release for food and nutritional security in Ghana and beyond. The accessions T3, T5, T22 showed more promising for earliness and yield related traits, hence could be selected for further screening and multi-location evaluation.

Different classes of qualitative traits were observed for the test materials, control and combined materials in the frequency distribution. The Chi-square test of association indicated a high number of significant associations between the qualitative traits of the cowpea genotypes which shows the dependence of one trait on the other. This should facilitate selection for traits with significant positive association. The study revealed strong significant correlations between the quantitative traits of the cowpea accessions, which also shows the dependency relationships among the traits, which will enhance selection.

This study confirms that cowpea seeds are a very good source of proteins and mineral elements and polyphenolic compounds. The maximum amount of phenolic acid content was found to be in the controls. Moreover, quercetin and rutin were most abundant in the control compared to test material. This suggest that the germplasm has to be augmented to obtain additional sources for improvement of quercetin and rutin. The cowpea test materials recorded the highest concentrations for all the amino acids compared to the controls, and this can be confimed from cluster 1 (Table 25). Hence, there is a need to consider these varieties in the selection for cowpea breeding programmes in nutrition enhencement. The different groups of phytochemical traits contributed to the genetic variation. In addition, some phytochemical traits were strongly related, which will facilitate their selection.

The germplasm clustered into five and four major groups under the quantitative morphological and phytochemical traits respectively indicating the relationship between the cowpea genotypes based on the character. Members of a cluster tended to showed common and useful characteristics. This will help plant breeders to select parent from complementary clusters for their breeding programmes. This points out that the clustered traits may be expressed by a particular or similar genes.

It was revealed from this current study that performance and selection could be projected dependably if the choice of individuals is based on traits with high broad sense–heritability estimates in addition to high genetic advance. Heritability was high in phytochemical compared to the morphological traits. This indicate that the collections will be useful for cowpea breeding programmes in morphological traits which showed high diversity and heritability.

6.2 RECOMMENDATION

1. High yielding germplasm such as T3, T5 and T22 from cluster 1 can be selected and incorporated into breeding programs to ensure food security in Ghana and elsewhere.
2. Further work must be done to improve the study on variation by using molecular markers.
3. Poor yielding accessions should be maintained and replanted to further evaluate their yield performance.

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APPENDICES

Appendix 1: Marginal analysis showing accessions that significantly (P<0.05) performed below and above the grandmean for morphological traits

	DTG					PTL					NB					NL				
Accessions	means	sem	con	F	P	means	sem	con	F	P	means	sem	con	F	P	means	sem	con	F	P
Asontem	3.58	0.16	0.00	0.00	1.00	9.67	0.22	-0.22	1.01	0.31	4.08	0.09	-0.50	29.18	0.00	38.38	1.37	-3.67	7.52	0.01
Kirkhouse	4.07	0.16	0.50	10.59	0.00	8.78	0.22	-1.11	27.12	0.00	5.04	0.09	0.46	25.65	0.00	46.52	1.34	4.46	11.51	0.00
Wang kae	3.63	0.16	0.05	0.12	0.73	10.10	0.22	0.20	0.91	0.34	4.15	0.09	-0.43	22.25	0.00	41.67	1.34	-0.39	0.09	0.77
T1	3.32	0.15	-0.26	2.92	0.09	12.09	0.21	2.20	109.08	0.00	4.75	0.09	0.17	3.76	0.05	33.93	1.32	-8.13	39.57	0.00
T2	3.28	0.15	-0.30	4.19	0.04	9.78	0.21	-0.12	0.32	0.57	4.24	0.09	-0.34	14.59	0.00	41.97	1.29	-0.09	0.01	0.94
T3	3.19	0.16	-0.39	6.15	0.01	7.48	0.22	-2.42	122.82	0.00	4.88	0.09	0.31	11.06	0.00	49.81	1.37	7.75	33.51	0.00
T4	3.92	0.16	0.35	4.95	0.03	9.07	0.22	-0.82	14.27	0.00	4.50	0.09	-0.08	0.69	0.41	45.46	1.37	3.40	6.46	0.01
T5	3.33	0.16	-0.24	2.56	0.11	9.97	0.22	0.08	0.13	0.72	4.22	0.09	-0.35	15.22	0.00	36.85	1.34	-5.21	15.67	0.00
T6	3.40	0.16	-0.18	1.26	0.26	7.46	0.23	-2.43	119.93	0.00	4.80	0.10	0.22	5.60	0.02	44.00	1.39	1.94	2.03	0.15
T7	3.41	0.16	-0.17	1.24	0.26	9.85	0.22	-0.04	0.04	0.85	3.59	0.09	-0.98	117.29	0.00	39.67	1.34	-2.39	3.30	0.07
T8	3.30	0.16	-0.28	3.40	0.07	9.94	0.22	0.05	0.06	0.81	5.00	0.09	0.42	21.68	0.00	44.67	1.34	2.61	3.94	0.05
T9	3.32	0.16	-0.26	2.65	0.10	9.46	0.23	-0.43	3.79	0.05	5.80	0.10	1.22	168.23	0.00	40.52	1.39	-1.54	1.27	0.26
T10	3.70	0.16	0.13	0.68	0.41	10.39	0.22	0.50	5.38	0.02	4.67	0.09	0.09	0.98	0.32	40.56	1.34	-1.50	1.30	0.25
T11	3.68	0.15	0.10	0.45	0.50	9.10	0.21	-0.79	14.20	0.00	4.61	0.09	0.03	0.12	0.73	40.25	1.32	-1.81	1.96	0.16
T12	3.46	0.15	-0.11	0.57	0.45	10.47	0.21	0.58	7.58	0.01	4.89	0.09	0.32	12.52	0.00	46.25	1.32	4.19	10.53	0.00
T13	3.93	0.15	0.35	5.75	0.02	11.02	0.21	1.12	29.57	0.00	4.28	0.09	-0.30	11.74	0.00	41.79	1.29	-0.26	0.04	0.84
T14	3.64	0.16	0.06	0.16	0.69	10.30	0.23	0.41	3.37	0.07	4.80	0.10	0.22	5.60	0.02	45.52	1.39	3.46	6.44	0.01
T15	3.39	0.15	-0.18	1.52	0.22	7.31	0.21	-2.59	151.08	0.00	4.04	0.09	-0.54	36.71	0.00	39.96	1.32	-2.09	2.62	0.11
T16	3.63	0.15	0.06	0.15	0.70	10.82	0.21	0.92	20.62	0.00	4.43	0.09	-0.14	2.76	0.10	40.90	1.27	-1.16	0.86	0.36
T17	3.41	0.16	-0.17	1.24	0.26	10.80	0.22	0.90	17.83	0.00	4.78	0.09	0.20	4.89	0.03	47.37	1.34	5.31	16.33	0.00
T18	3.39	0.15	-0.18	1.52	0.22	10.50	0.21	0.61	8.34	0.00	4.04	0.09	-0.54	36.71	0.00	38.86	1.32	-3.20	6.13	0.01
T19	4.04	0.16	0.46	8.26	0.00	11.50	0.23	1.61	50.35	0.00	4.54	0.10	-0.04	0.13	0.71	40.50	1.42	-1.56	1.25	0.26
T20	3.54	0.15	-0.04	0.08	0.78	9.81	0.21	-0.09	0.16	0.69	5.14	0.09	0.57	40.17	0.00	40.61	1.32	-1.45	1.26	0.26
T21	3.86	0.17	0.29	2.89	0.09	11.39	0.24	1.49	39.98	0.00	4.55	0.10	-0.03	0.10	0.75	38.23	1.48	-3.83	6.96	0.01
T22	3.73	0.16	0.15	0.97	0.32	11.31	0.22	1.42	42.16	0.00	4.46	0.09	-0.12	1.55	0.21	40.12	1.37	-1.94	2.10	0.15
T23	3.85	0.16	0.27	2.99	0.08	9.46	0.22	-0.43	3.91	0.05	4.35	0.09	-0.23	6.21	0.01	43.69	1.37	1.64	1.49	0.22
T24	3.58	0.16	0.01	0.00	0.97	9.29	0.23	-0.60	7.03	0.01	4.96	0.10	0.38	15.73	0.00	47.50	1.42	5.44	15.30	0.00
Grand mean	**3.57**	**0.83**		**2.49**	**0.00**	9.89	1.62		**29.67**	**0.00**	**4.57**	**0.64**		**22.63**	**0.00**	**42.02**	**7.72**		**7.39**	**0.00**

Appendix 1 (cont'd)

	NN					NPPPD					PH					LL				
Accessions	means	sem	con	F	P	means	sem	con	F	P	means	sem	con	F	P	means	sem	con	F	P
Asontem	8.35	0.20	-0.89	20.35	0.00	3.00	0.08	0.05	0.42	0.51	11.81	0.23	0.13	0.36	0.55	9.08	0.18	0.31	3.12	0.08
Kirkhouse	10.26	0.20	1.02	27.50	0.00	2.81	0.08	-0.13	2.65	0.10	11.22	0.22	-0.45	4.31	0.04	7.33	0.18	-1.43	67.82	0.00
Wang kae	8.30	0.20	-0.94	23.52	0.00	3.00	0.08	0.05	0.44	0.51	12.41	0.22	0.73	11.30	0.00	10.26	0.18	1.49	74.01	0.00
T1	9.11	0.19	-0.13	0.48	0.49	2.21	0.08	-0.73	84.97	0.00	12.88	0.22	1.20	31.40	0.00	10.86	0.17	2.09	150.21	0.00
T2	8.48	0.19	-0.76	16.22	0.00	3.00	0.08	0.05	0.47	0.49	12.21	0.21	0.53	6.38	0.01	10.10	0.17	1.34	63.60	0.00
T3	10.32	0.19	1.08	32.06	0.00	3.25	0.08	0.30	14.61	0.00	13.04	0.22	1.36	40.38	0.00	9.50	0.17	0.74	18.56	0.00
T4	9.08	0.20	-0.16	0.67	0.41	3.08	0.08	0.13	2.52	0.11	9.85	0.23	-1.83	67.87	0.00	6.85	0.18	-1.92	117.52	0.00
T5	8.81	0.20	-0.42	4.77	0.03	3.04	0.08	0.09	1.26	0.26	14.83	0.22	3.16	210.01	0.00	9.56	0.18	0.79	20.73	0.00
T6	9.64	0.21	0.40	3.94	0.05	2.96	0.09	0.01	0.03	0.87	10.60	0.23	-1.07	22.58	0.00	8.00	0.18	-0.76	17.97	0.00
T7	7.19	0.20	-2.05	111.59	0.00	2.93	0.08	-0.02	0.06	0.80	12.81	0.22	1.14	27.36	0.00	8.89	0.18	0.12	0.51	0.47
T8	10.04	0.20	0.80	16.82	0.00	3.63	0.08	0.68	71.47	0.00	12.74	0.22	1.07	23.92	0.00	9.94	0.18	1.18	46.12	0.00
T9	11.68	0.21	2.44	146.26	0.00	2.96	0.09	0.01	0.03	0.87	12.52	0.23	0.85	13.97	0.00	8.96	0.18	0.20	1.18	0.28
T10	9.56	0.20	0.32	2.64	0.10	3.19	0.08	0.24	8.73	0.00	12.22	0.22	0.55	6.31	0.01	9.98	0.18	1.22	49.06	0.00
T11	9.36	0.19	0.12	0.38	0.54	2.89	0.08	-0.05	0.45	0.50	10.64	0.22	-1.03	23.21	0.00	7.60	0.17	-1.17	46.78	0.00
T12	9.96	0.19	0.72	14.39	0.00	2.61	0.08	-0.34	18.24	0.00	10.71	0.22	-0.96	20.11	0.00	6.75	0.17	-2.01	139.16	0.00
T13	8.52	0.19	-0.72	14.77	0.00	2.83	0.08	-0.12	2.31	0.13	10.31	0.21	-1.36	41.97	0.00	7.17	0.17	-1.59	89.89	0.00
T14	9.72	0.21	0.48	5.67	0.02	2.88	0.09	-0.07	0.63	0.43	11.20	0.23	-0.47	4.41	0.04	9.42	0.18	0.66	13.22	0.00
T15	8.21	0.19	-1.03	28.78	0.00	2.68	0.08	-0.27	11.37	0.00	12.11	0.22	0.43	4.08	0.04	8.75	0.17	-0.01	0.01	0.93
T16	8.90	0.19	-0.34	3.37	0.07	3.03	0.08	0.09	1.28	0.26	11.55	0.21	-0.12	0.36	0.55	9.27	0.17	0.50	9.24	0.00
T17	9.59	0.20	0.35	3.30	0.07	3.00	0.08	0.05	0.44	0.51	10.22	0.22	-1.45	44.41	0.00	9.04	0.18	0.27	2.46	0.12
T18	8.07	0.19	-1.17	37.36	0.00	2.79	0.08	-0.16	4.09	0.04	10.29	0.22	-1.39	42.06	0.00	9.11	0.17	0.34	4.03	0.05
T19	9.17	0.21	-0.07	0.13	0.72	2.83	0.09	-0.11	1.75	0.19	12.08	0.24	0.41	3.14	0.08	9.50	0.19	0.74	16.00	0.00
T20	9.73	0.20	0.49	6.16	0.01	2.81	0.08	-0.14	2.84	0.09	10.87	0.23	-0.81	13.30	0.00	7.52	0.18	-1.25	49.52	0.00
T21	9.14	0.22	-0.10	0.23	0.63	2.86	0.09	-0.08	0.86	0.35	12.86	0.25	1.19	24.42	0.00	8.82	0.20	0.05	0.08	0.78
T22	9.12	0.20	-0.12	0.39	0.53	3.04	0.08	0.09	1.25	0.26	12.73	0.23	1.06	22.64	0.00	8.92	0.18	0.16	0.80	0.37
T23	8.88	0.20	-0.35	3.21	0.07	3.50	0.08	0.55	45.25	0.00	10.38	0.23	-1.29	33.79	0.00	7.85	0.18	-0.92	26.93	0.00
T24	10.29	0.21	1.05	26.14	0.00	2.75	0.09	-0.20	5.27	0.02	10.13	0.24	-1.55	45.13	0.00	7.63	0.19	-1.14	38.38	0.00
Grand mean	**9.22**	**1.34**		**20.40**	**0.00**	**2.95**	**0.50**		**10.52**	**0.00**	**11.67**	**1.64**		**29.23**	**0.00**	**8.77**	**1.42**		**39.55**	**0.00**

Appendix 1 (cont'd)

	LW					DFF					APDLN					APDWD				
Accessions	means	sem	con	F	P	means	sem	con	F	P	means	sem	con	F	P	means	sem	con	F	P
Asontem	4.90	0.13	0.47	14.28	0.00	35.08	0.22	0.25	1.37	0.24	16.77	0.23	-0.20	0.81	0.37	0.84	0.03	-0.03	1.15	0.28
Kirkhouse	3.50	0.12	-0.93	58.24	0.00	34.89	0.22	0.07	0.10	0.76	15.00	0.22	-1.97	82.15	0.00	0.75	0.03	-0.12	21.90	0.00
Wang kae	5.01	0.12	0.58	22.62	0.00	35.89	0.22	1.07	24.88	0.00	18.09	0.22	1.12	26.83	0.00	1.14	0.03	0.28	121.19	0.00
T1	2.48	0.12	-1.95	264.59	0.00	39.61	0.21	4.78	518.61	0.00	18.91	0.22	1.94	82.90	0.00	0.89	0.03	0.03	1.37	0.24
T2	4.78	0.12	0.34	8.41	0.00	36.10	0.21	1.28	38.45	0.00	15.16	0.21	-1.80	73.95	0.00	0.86	0.02	0.00	0.02	0.88
T3	3.36	0.13	-1.08	74.60	0.00	34.96	0.22	0.14	0.41	0.52	14.62	0.23	-2.35	112.66	0.00	0.90	0.03	0.03	1.78	0.18
T4	4.12	0.13	-0.32	6.51	0.01	34.50	0.22	-0.32	2.19	0.14	15.79	0.23	-1.18	28.46	0.00	0.81	0.03	-0.05	4.51	0.03
T5	4.15	0.12	-0.28	5.29	0.02	34.70	0.22	-0.12	0.31	0.58	19.50	0.22	2.53	135.99	0.00	0.97	0.03	0.10	16.69	0.00
T6	4.24	0.13	-0.19	2.32	0.13	34.12	0.23	-0.70	10.02	0.00	16.90	0.23	-0.07	0.09	0.76	0.82	0.03	-0.04	2.84	0.09
T7	5.00	0.12	0.57	21.48	0.00	34.48	0.22	-0.34	2.54	0.11	20.13	0.22	3.16	212.03	0.00	0.94	0.03	0.08	9.78	0.00
T8	4.43	0.12	-0.01	0.00	0.95	34.44	0.22	-0.38	3.13	0.08	15.65	0.22	-1.32	36.95	0.00	0.80	0.03	-0.06	5.74	0.02
T9	4.96	0.13	0.52	16.97	0.00	35.04	0.23	0.22	0.96	0.33	17.90	0.23	0.93	17.11	0.00	0.92	0.03	0.06	4.61	0.03
T10	4.88	0.12	0.45	13.44	0.00	35.00	0.22	0.18	0.69	0.41	19.80	0.22	2.83	169.68	0.00	0.95	0.03	0.08	11.21	0.00
T11	4.52	0.12	0.08	0.50	0.48	34.25	0.21	-0.57	7.42	0.01	17.41	0.22	0.44	4.31	0.04	0.86	0.03	0.00	0.02	0.90
T12	3.87	0.12	-0.57	22.14	0.00	35.75	0.21	0.93	19.49	0.00	15.06	0.22	-1.91	79.75	0.00	0.78	0.03	-0.09	12.45	0.00
T13	4.26	0.12	-0.17	2.18	0.14	35.24	0.21	0.42	4.11	0.04	13.55	0.21	-3.42	265.12	0.00	0.74	0.02	-0.12	24.75	0.00
T14	5.08	0.13	0.65	25.98	0.00	34.32	0.23	-0.50	5.13	0.02	19.72	0.23	2.75	149.18	0.00	0.92	0.03	0.06	4.61	0.03
T15	4.82	0.12	0.39	10.44	0.00	34.39	0.21	-0.43	4.18	0.04	16.80	0.22	-0.16	0.59	0.44	0.83	0.03	-0.03	1.66	0.20
T16	4.70	0.12	0.27	5.27	0.02	33.90	0.21	-0.92	20.59	0.00	18.33	0.21	1.37	43.75	0.00	0.89	0.02	0.02	0.77	0.38
T17	4.70	0.12	0.27	4.76	0.03	33.89	0.22	-0.93	19.06	0.00	15.64	0.22	-1.33	37.47	0.00	0.74	0.03	-0.12	24.02	0.00
T18	4.66	0.12	0.23	3.58	0.06	34.11	0.21	-0.72	11.59	0.00	18.62	0.22	1.65	59.66	0.00	0.89	0.03	0.02	0.78	0.38
T19	4.88	0.13	0.44	11.65	0.00	33.58	0.23	-1.24	29.99	0.00	19.72	0.23	2.75	143.29	0.00	1.05	0.03	0.18	46.72	0.00
T20	4.55	0.12	0.12	1.00	0.32	33.75	0.21	-1.07	26.05	0.00	14.88	0.22	-2.09	96.22	0.00	0.74	0.03	-0.12	24.74	0.00
T21	5.23	0.14	0.79	34.61	0.00	35.27	0.24	0.45	3.64	0.06	17.59	0.25	0.62	6.76	0.01	1.00	0.03	0.14	24.84	0.00
T22	5.04	0.13	0.61	23.63	0.00	34.23	0.22	-0.59	7.38	0.01	16.30	0.23	-0.67	9.18	0.00	0.83	0.03	-0.04	2.32	0.13
T23	3.87	0.13	-0.57	20.79	0.00	34.58	0.22	-0.25	1.27	0.26	15.15	0.23	-1.82	67.61	0.00	0.78	0.03	-0.09	11.05	0.00
T24	3.73	0.13	-0.70	29.59	0.00	34.13	0.23	-0.70	9.50	0.00	15.15	0.23	-1.82	62.87	0.00	0.70	0.03	-0.16	36.06	0.00
Grand mean	**4.43**	**0.89**		**26.11**	**0.00**	**34.84**	**1.60**		**28.68**	**0.00**	**16.95**	**2.20**		**74.31**	**0.00**	**0.86**	**0.16**		**15.46**	**0.00**

Appendix 1 (cont'd)

	NPPPL					ANSPP					DFMP					NSPPL				
Accessions	means	sem	con	F	P	means	sem	con	F	P	means	sem	con	F	P	means	sem	con	F	P
Asontem	28.38	1.80	-11.39	41.80	0.00	14.44	0.27	-0.66	6.00	0.01	42.08	0.25	0.36	2.23	0.14	416.04	31.78	-187.86	36.31	0.00
Kirkhouse	50.56	1.76	10.78	38.85	0.00	15.70	0.27	0.60	5.16	0.02	41.78	0.24	0.06	0.07	0.79	796.67	31.19	192.77	39.65	0.00
Wang kae	48.93	1.76	9.15	27.99	0.00	12.98	0.27	-2.12	64.24	0.00	42.89	0.24	1.18	24.16	0.00	642.76	31.19	38.86	1.61	0.20
T1	48.96	1.73	9.19	29.23	0.00	16.52	0.26	1.42	29.62	0.00	44.00	0.24	2.29	94.71	0.00	811.95	30.62	208.05	47.83	0.00
T2	40.17	1.70	0.40	0.06	0.81	15.03	0.26	-0.07	0.07	0.79	42.83	0.23	1.11	23.25	0.00	605.19	30.09	1.29	0.00	0.97
T3	33.50	1.80	-6.27	12.68	0.00	14.10	0.27	-1.01	13.95	0.00	41.96	0.25	0.25	1.04	0.31	474.44	31.78	-129.46	17.24	0.00
T4	45.81	1.80	6.03	11.73	0.00	14.19	0.27	-0.91	11.41	0.00	41.62	0.25	-0.10	0.16	0.69	650.38	31.78	46.48	2.22	0.14
T5	41.11	1.76	1.34	0.60	0.44	15.56	0.27	0.45	2.93	0.09	41.70	0.24	-0.01	0.00	0.97	644.31	31.19	40.41	1.74	0.19
T6	49.04	1.83	9.27	26.65	0.00	16.16	0.28	1.06	14.83	0.00	41.44	0.25	-0.27	1.22	0.27	797.88	32.41	193.98	37.28	0.00
T7	38.96	1.76	-0.81	0.22	0.64	16.04	0.27	0.93	12.47	0.00	41.48	0.24	-0.23	0.94	0.33	632.35	31.19	28.45	0.86	0.35
T8	38.63	1.76	-1.14	0.44	0.51	14.94	0.27	-0.16	0.36	0.55	41.44	0.24	-0.27	1.27	0.26	582.72	31.19	-21.18	0.48	0.49
T9	38.36	1.83	-1.41	0.62	0.43	14.66	0.28	-0.44	2.60	0.11	41.44	0.25	-0.27	1.22	0.27	562.90	32.41	-41.00	1.67	0.20
T10	40.33	1.76	0.56	0.10	0.75	15.09	0.27	-0.01	0.00	0.97	42.00	0.24	0.29	1.43	0.23	609.61	31.19	5.71	0.03	0.85
T11	32.89	1.73	-6.88	16.38	0.00	15.32	0.26	0.22	0.71	0.40	41.07	0.24	-0.64	7.48	0.01	498.38	30.62	-105.52	12.30	0.00
T12	32.64	1.73	-7.13	17.59	0.00	15.98	0.26	0.88	11.44	0.00	42.71	0.24	1.00	18.14	0.00	523.18	30.62	-80.72	7.20	0.01
T13	36.55	1.70	-3.22	3.71	0.05	13.91	0.26	-1.19	21.61	0.00	42.24	0.23	0.53	5.22	0.02	508.40	30.09	-95.50	10.42	0.00
T14	36.56	1.83	-3.21	3.20	0.07	14.68	0.28	-0.42	2.37	0.12	41.28	0.25	-0.43	3.06	0.08	542.32	32.41	-61.58	3.76	0.05
T15	35.75	1.73	-4.02	5.60	0.02	14.84	0.26	-0.26	1.03	0.31	41.32	0.24	-0.39	2.79	0.10	543.48	30.62	-60.42	4.03	0.05
T16	35.80	1.67	-3.97	5.84	0.02	15.43	0.26	0.33	1.73	0.19	41.00	0.23	-0.71	9.86	0.00	557.00	29.59	-46.90	2.60	0.11
T17	41.30	1.76	1.52	0.77	0.38	15.28	0.27	0.18	0.44	0.51	41.00	0.24	-0.71	8.91	0.00	634.63	31.19	30.73	1.01	0.32
T18	40.79	1.73	1.01	0.35	0.55	16.39	0.26	1.29	24.62	0.00	41.14	0.24	-0.57	5.91	0.02	668.95	30.62	65.05	4.68	0.03
T19	40.08	1.87	0.31	0.03	0.87	14.98	0.29	-0.12	0.19	0.66	40.75	0.26	-0.96	14.51	0.00	594.19	33.08	-9.71	0.09	0.76
T20	49.43	1.73	9.66	32.26	0.00	15.50	0.26	0.40	2.34	0.13	40.82	0.24	-0.89	14.43	0.00	776.50	30.62	172.60	32.92	0.00
T21	37.77	1.95	-2.00	1.10	0.30	14.77	0.30	-0.33	1.28	0.26	42.09	0.27	0.38	2.04	0.15	560.05	34.55	-43.85	1.68	0.19
T22	38.35	1.80	-1.43	0.66	0.42	15.50	0.27	0.40	2.17	0.14	41.23	0.25	-0.48	3.94	0.05	594.65	31.78	-9.25	0.09	0.77
T23	36.81	1.80	-2.97	2.83	0.09	15.13	0.27	0.03	0.01	0.91	41.62	0.25	-0.10	0.16	0.69	544.00	31.78	-59.90	3.69	0.06
T24	36.42	1.87	-3.36	3.36	0.07	14.63	0.29	-0.48	2.91	0.09	41.33	0.26	-0.38	2.26	0.13	532.38	33.08	-71.52	4.87	0.03
Grand mean	**39.79**	**10.62**		10.55	0.00	**15.11**	**1.59**		8.76	0.00	**41.72**	**1.44**		9.29	0.00	**604.58**	**187.17**		10.24	0.00

Appendix 1 (cont'd)

	SDLT					SDWD					SDTH					SDWG				
Acessions	means	sem	con	F	P	means	sem	con	F	P	means	sem	con	F	P	means	sem	con	F	P
Asontem	6.78	0.07	-0.39	32.98	0.00	5.68	0.19	0.14	0.60	0.44	4.43	0.04	-0.09	5.45	0.02	13.96	0.12	-0.66	29.44	0.00
Kirkhouse	6.42	0.07	-0.75	129.24	0.00	5.21	0.19	-0.32	3.07	0.08	4.41	0.04	-0.10	7.83	0.01	12.55	0.12	-2.07	300.22	0.00
Wang kae	10.34	0.07	3.17	2286.91	0.00	6.41	0.19	0.87	22.65	0.00	5.52	0.04	1.01	775.59	0.00	24.85	0.12	10.22	7300.20	0.00
T1	7.26	0.07	0.09	1.78	0.18	5.57	0.18	0.04	0.05	0.83	4.54	0.04	0.03	0.54	0.46	14.52	0.12	-0.10	0.78	0.38
T2	7.54	0.07	0.37	32.80	0.00	6.16	0.18	0.62	12.38	0.00	4.89	0.04	0.38	116.47	0.00	15.28	0.12	0.65	31.68	0.00
T3	6.36	0.07	-0.81	145.50	0.00	5.14	0.19	-0.40	4.53	0.03	4.16	0.04	-0.35	91.08	0.00	11.46	0.12	-3.17	676.02	0.00
T4	7.04	0.07	-0.13	3.70	0.05	5.59	0.19	0.06	0.10	0.76	4.25	0.04	-0.26	48.82	0.00	14.36	0.12	-0.26	4.70	0.03
T5	6.73	0.07	-0.44	43.74	0.00	5.09	0.19	-0.45	6.00	0.01	4.25	0.04	-0.26	53.01	0.00	15.08	0.12	0.45	14.29	0.00
T6	6.83	0.07	-0.34	25.11	0.00	5.53	0.19	0.00	0.00	0.98	4.58	0.04	0.07	3.52	0.06	12.73	0.13	-1.89	232.57	0.00
T7	8.04	0.07	0.87	171.14	0.00	5.54	0.19	0.01	0.00	0.98	4.61	0.04	0.10	7.47	0.01	16.76	0.12	2.14	318.60	0.00
T8	6.65	0.07	-0.52	61.03	0.00	5.50	0.19	-0.04	0.04	0.84	4.57	0.04	0.06	2.95	0.09	12.84	0.12	-1.78	221.75	0.00
T9	7.24	0.07	0.07	0.91	0.34	5.48	0.19	-0.05	0.07	0.79	4.46	0.04	-0.06	2.25	0.13	14.72	0.13	0.10	0.63	0.43
T10	8.30	0.07	1.12	287.25	0.00	5.69	0.19	0.16	0.73	0.39	4.44	0.04	-0.07	3.63	0.06	17.19	0.12	2.57	460.84	0.00
T11	7.72	0.07	0.54	69.60	0.00	5.66	0.18	0.13	0.50	0.48	4.67	0.04	0.16	20.09	0.00	14.97	0.12	0.35	8.75	0.00
T12	6.56	0.07	-0.61	87.84	0.00	5.47	0.18	-0.06	0.13	0.72	4.33	0.04	-0.19	27.26	0.00	13.13	0.12	-1.50	161.92	0.00
T13	6.25	0.07	-0.93	209.19	0.00	4.98	0.18	-0.55	9.76	0.00	4.38	0.04	-0.13	14.40	0.00	12.10	0.12	-2.53	478.07	0.00
T14	7.90	0.07	0.73	112.35	0.00	5.63	0.19	0.09	0.24	0.62	4.49	0.04	-0.02	0.22	0.64	16.58	0.13	1.96	248.92	0.00
T15	7.58	0.07	0.41	38.97	0.00	5.59	0.18	0.05	0.08	0.78	4.51	0.04	0.00	0.00	0.98	15.15	0.12	0.53	20.28	0.00
T16	7.59	0.06	0.42	44.04	0.00	5.68	0.18	0.14	0.69	0.41	4.78	0.03	0.27	61.01	0.00	15.29	0.12	0.67	34.47	0.00
T17	6.65	0.07	-0.52	61.16	0.00	5.34	0.19	-0.19	1.10	0.30	4.51	0.04	0.00	0.01	0.90	13.61	0.12	-1.01	71.42	0.00
T18	7.65	0.07	0.48	54.31	0.00	6.56	0.18	1.02	32.12	0.00	4.63	0.04	0.11	10.46	0.00	14.65	0.12	0.03	0.05	0.82
T19	7.62	0.07	0.45	40.46	0.00	5.72	0.20	0.19	0.91	0.34	4.58	0.04	0.07	3.27	0.07	16.41	0.13	1.79	199.34	0.00
T20	6.23	0.07	-0.94	208.94	0.00	5.19	0.18	-0.34	3.60	0.06	4.38	0.04	-0.13	13.74	0.00	12.11	0.12	-2.51	456.32	0.00
T21	7.46	0.07	0.29	15.61	0.00	5.78	0.21	0.24	1.43	0.23	4.70	0.04	0.19	23.56	0.00	16.06	0.14	1.43	117.68	0.00
T22	6.67	0.07	-0.50	55.80	0.00	5.35	0.19	-0.18	0.93	0.33	4.42	0.04	-0.09	5.65	0.02	14.21	0.12	-0.41	11.36	0.00
T23	5.78	0.07	-1.40	428.03	0.00	4.67	0.19	-0.86	21.38	0.00	4.10	0.04	-0.41	126.87	0.00	12.20	0.12	-2.42	395.75	0.00
T24	6.46	0.07	-0.71	102.18	0.00	5.22	0.20	-0.31	2.58	0.11	4.22	0.04	-0.29	57.37	0.00	12.07	0.13	-2.55	406.58	0.00
Grand mean	**7.17**	**0.95**		176.04	0.00	**5.54**	**1.03**		4.66	0.00	**4.51**	**0.33**		54.93	0.00	**14.62**	**2.64**		452.10	0.00