ASSESSMENT OF VIARIABILITY IN FRUIT QUALITY CHARACTERISTICS AND LEVELS OF SOME BIOACTIVE COMPOUNDS IN AFRICAN EGGPLANT (*Solanum aethiopicum* L.) GERMPLASM IN GHANA

BY

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DECLARATION

I, Percy Nimako Yamoah, declare that except for the reference to other people's work, which have been duly cited and acknowledged, this thesis is the result of my original findings and this thesis has neither in whole, or part, been presented for a degree in Ghana or elsewhere.

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ABSTRACT

In order to determine genetic variability in some accessions of Africa eggplant, open field experiments were conducted in two separate locations, one at University of Ghana farm, Legon and the other at the Forest and Horticultural Crops Research Centre (FOHCREC), Okumaning-Kade simultaneously. The experimental design used was the Randomized Complete Block Design (RCBD) with three (3) replications. The combined analysis of variance was carried out for the data gathered. The effect of genotype, location and their interaction was significant for most of the characters studied. From the combined analysis of variance, location variance (σ^2_L) was higher than genotypic variance (σ^2_G) counterparts for most vegetative traits studied except for leaf area. However, the effects of location on the expression of yield and yield component traits was not very much pronounced as evidenced in the high estimated values of σ^2_G than the corresponding σ^2_L for almost all yield and yield component traits. Most of these traits also recorded high values of heritability (h^2). Leaf area recorded the highest value of genetic gain (44243.51 %) whiles stem girth scored the lowest estimated value of 0.26 %. Generally, the estimated PCV was higher than the corresponding GCV for all the characters. However, the difference between PCV and GCV were observed to be narrow for most traits studied indicating the role of genetic factors in the expression of the traits. The bioactive compounds studied in the present experiment correlated with number of traits with weak correlated coefficients. And also character association analysis reviewed that accessions with less fruits per plant and those with larger fruit sizes got ripened earlier, which gives an indication for optimum harvesting time to reduce lose and enhances fruit life span. Garden egg genotypes 14 – 030, A12, A10, 14 – 026 and A4 produced better yield across locations and are potentially valuable source of genetic materials that could be used for further crop improvement programmes.

DEDICATIONS

I dedicate this work to the loving memory of my dearest mother, Mrs. Margaret Tawiah-Yamoah for her endearing love, encouragement and support both financially and the edging spirit , as well as the entire Yamoah family.

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LIST OF ABBREVIATIONS

AA	Ascorbic acid
ANOVA	Analysis of Variance
Av. P	Available Phosphorus
Ave. FWT	Average fruit weight
CC	Chlorophyll Content
CLCA	Complete Linkage
CSMA	Canopy span at maturity
DFL	Days to50% flowering
DFR	Days to fruiting
DMT	Days to maturity
DNA	Deoxyribonucleic Acid
DRP	Days to ripening
ECV	Error Coefficient of Variation.
EGA	Expected genetic advance
EGGNET	Eggplant Genetic Resource Network
FAO	Food and Agricultural Organization
FDM	Fruit diameter
FLT	Fruit length
FS	Fruit size
FWT/PLT	Fruit weight per plot
G	Genotype

GAM	Genetic advance of the mean.
GCV	Genotypic coefficient of variation
GCV	Genotypic coefficient of variation
GM	Grand mean
GMO	Genetically Modified Organism
H^2b	Broad sense heritability
HCl	Hydrochloric Acid
$HClO_4$	Perchloric acid
HNO_3	Nitric Acid
K	Potassium
LA	Leaf area
LSD	Least significant difference
m	Mean
MDC	Multidimensional Scaling
ml	Millilitre
MLCA	Median Linkage
mm	Millimetre
Mn	Magnesium
N.P.K	Nitrogen Phosphorous Potassium
NFR	Number of fruits
NL	Number of leaves

PCA	Principal Component Analysis
PCOA	Principal Coordinate Analysis
PCV	Phenotypic coefficient of variation
PHT	Plant height
Q^2E	Error variance
Q^2G	Genotypic variance
Q^2_L	Location variance
Q^2LxG	Genotype by location interaction
Q^2P	Phenotypic variance
Q^2P	Phenotypic variance
R	Correlation Coefficient
RCBD	Randomized Complete Block Design
RL	Root length
SG	Stem girth
SLCA	Single Linkages
t/ha	Ton/hectare
ISSS	International Society of Soil Science
WAT	Weeks after transplanting
WK	Week
X	Population mean
Y/T	Yield per ton

Zn	Zinc
GEI	Genotype by Environment Interaction
USDA	United States Department of Agriculture
IPGRI	International Plant Genetic Resources Institute
ISRIC	International Soil Reference and Information Centre
UPGMC	Unweighted paired group method using centroids
FOHCREC	Forest and Horticultural Crops Research Centre
UNESCO	United Nations Educational, Scientific and Cultural Organization
UPOV	International Union for the Protection of New Varieties of Plants
UPGMA	Unweighted paired group method with arithmetic mean
PPMED	Policy, Planning, Monitoring and Evaluation Division (Ghana)

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CHAPTER ONE

1.0 INTRODUCTION

Vegetables are widely grown in most parts of sub-Saharan Africa and they constitute the most affordable and sustainable source of micronutrients in human diets. The choice of a vegetable is dependent on its diversity of usage and economic value. African eggplant or garden egg (*Solanum aethiopicum* L.) is an important vegetable utilized in various households in West Africa (Gyiele, 1999).

The cultivated African eggplant constitutes a major agricultural industry especially in the tropical and sub-tropical regions. Akinlosotu (1979) acknowledged that the crop production levels could reach 8 ton/ha to 22 ton/ha depending on the variety. However, the country's national average output is about 8 ton/ha under rain-fed conditions but with increasing potential to about 18 tones/ha under irrigation (PPMED, 2005).

Garden egg can be eaten raw or cooked. There are varieties of garden eggs which have been processed and canned into puree, whole peeled, diced as well as in various forms of sauces have gained consumers' acceptability.

The fruits of garden egg come in a wide array of sizes, shapes and colours (Chen *et al.*, 2001). The benefits include nutritional as well as medicinal values (Horna *et al.*, 2007; Okon *et al.*, 2010).

Scarlet eggplant, as the crop is popularly known in West Africa, is produced for domestic consumption. It is the third most consumed vegetable in Ghana and also as a commercial crop for export (Daunay *et al.*, 2001).

Increasing knowledge regarding the enormous contribution of diet on health has changed the perception to as the role of vegetables, resulting in new dietary strategies that are unveiling the use for various forms of vegetables.

Diet does not only provide adequate nutrients for our metabolic up keep, but also contribute to the improvement of human health. There are several important bioactive compounds in plants that are believed to benefit human health. The sources need to be identified and production boosted up for the food market to complement a balanced diet.

Phytochemical investigation in garden eggplant composition and relatives of this genus has revealed the presence of high levels of essential bioactive compounds most being vitamins and minerals (Chinedu *et al*., 2011; Aliero, 2007 and Cipollini & levey, 1997).

Characterization of African eggplant germplasm in Ghana has been mostly with respect to morphological traits (Nkansah, 2001; Ofori *et al*., 2008). To some limited extent, molecular characterization has also been done to link phenotypic with genotypic variability.

Desired cultivars of vegetables with improved fruit quality traits, especially appreciable levels of essential bioactive compounds are indeed a pressing need for a nutritional and better market value. The development through crop improvement programmes of such vegetables has received relatively little attention notably in African eggplant.

The depth of information on the variability of various bioactive compounds in African eggplant accessions in Ghana is very limited. Furthermore, association between fruit physical quality traits and the levels of bioactive compounds has not been studied.

Research on eggplant (*Solanum melongena*) has indicated appreciable amount of potassium, zinc and vitamin C content in some varieties (Ramaswamy and Rege 1977a, b; Bajaj *et al.*, 1990 and Bender, 2009).

The specific objectives of the study were to:

a. Assess the variability in Vitamin C, Potassium, Magnesium and Zinc among accessions of African eggplants available to University of Ghana.
b. To assess the association between levels of bioactive compounds and the fruits physical quality traits.
c. To assess the association between fruit quality traits and fruit yield
d. Estimate heritability and expected genetic advance based on selection among these accessions
e. Estimate the strength of genotype-environment interaction for K, Mg, Zn and vitamin C content in the accessions studied.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 The Origin, Botany and Distribution

African eggplant (*Solanum aethiopicum* L.) is believed to have evolved from *Solanum anguivi* and *Solanum distichum* as a result of domestication in tropical Africa. Its production is much more concentrated intensively in West and East Africa (Norman, 1992; Grubben and Denton, 2004). It has being categorised under four groups, namely: Gilo, Shum, Kumba and Acculeatum (Lester and Niakan, 1986).

Solanum aethiopicum L. is a shrub that may either be an annual or perennial herb depending on the cultivar or the agronomic practices or both. Its height can extend up to about 200 cm tall, densely and heavily-branched with a root system extending both vertically and laterally. The upper shoot including the leaves may at times have prickles and stallete hairs. The floral are hermaphrodite with regular (4-10) merous, 2-15 mm long pedicel, most at times white but seldom pale purple in colour (PROTA, 2004).

The flowers are single or arranged in cluster of two flowers or more with the stigma bulging out either above termed long styled flower, on the same level which is referred as medium styled flower or below it known as diminutive or short styled flower anther tips. The long and medium styled flowers at most times have a well-developed nodule, superior pollen absorption capacity with permissible tissue rich in polysaccharide, protein and other nutrients.

As observed, cross pollination is effectively promoted in flower arrangement where the anther tips of the stigma is referred to as long styled flowers whereas the short styled flowers are evident by a tiny, diminished gynoecium which is often sterile, a relatively small stigma with immature papillae as well as a spatial separation of anther pores and a low sugar content

precludes pollen germination hence results in pollen drop (Passam and Bolmatis, 1997; Chen, 2001; Sekara and Bieniasz, 2008). Diminutive styled flowers are however less exposed to the prevailing weather conditions and may remain receptive for long hours. The fruit shapes are in the category of globose to depressed globose, ellipsoid, ovoid or fusiform berry and can be either smooth or grooved with fruit size ranging from 1 to 6 cm long. They also exhibit these shades of colours (red, white, cream, yellow and pinkish to orange) depending on the stage of maturity (Handique and Sarma, 1995; Chen, 2001; Diggle and Miller, 2004; Lester and Seck, 2004; PROTA, 2004).

2.2 Geographical Distribution of Garden Eggs

The Solanaceae family members are well adapted to different agro-ecological environments, which are widely spread across the globe (Knapp *et al.,* 2004). African eggplant (*Solanum aethiopicum* L.) is increasingly gaining popularity in the world (Pessarakli and Dris, 2003).

Garden egg originated from tropical Africa, but it can also be found in South America and Asia with occasional productions in southern part of France and Italy (Norman, 1992). The crop is widely cultivated across most of the African continent, and more intensively in West and East Africa (Danquah-Jones, 2000).

In Ghana, the production of garden eggs is throughout the country, but commercial production is concentrated mostly in the forest zone

2.2 Utilization and Importance of Garden Eggs

The leaves and immature fruits of African eggplant are used as a vegetable which is taken in stews, sauces and soups. The fruits can also be consumed raw. African eggplant fruit is rich in iron making it extremely valued locally (Macha, 2005; Gruère *et al.,* 2007). It also has

appreciable levels of other bioactive compounds, which help in maintaining the normal function of the heart and regulate blood pressure as well as protect the heart against cholesterol effects. Lawande and Chavan (1998) acknowledged that African eggplant is a fairly good source of iron, calcium, phosphorus, potassium and vitamin B group.

The vegetable has also been identified to play an important role in some socio-cultural settings as it is offered as a gift to visitors, in marriage ceremonies, outdooring and other social events basically as a sign of blessings, fruitfulness and good-will in some notable cultures in sub-Saharan African (Chinedu *et al.*, 2011). The medicinal properties of garden egg are also impeccable, as it has been acknowledged for its role on nutritional security for most people in Africa. It has been deemed significant in ensuring food security and sustainability. The production of this crop can also help to foster rural development and to a large extent land-care cover (Horna *et al.*, 2007; Okon *et al.*, 2010).

Chinedu *et al*., (2011) also reported that African eggplant is very imperative in terms of its native medicinal folklore which is used to treat certain infirmities because of its reserves of micronutrients, vitamins and proteins which can be used to address potential deficiencies. In addition, some parts such as the roots have been acknowledged and used as medicine for treating uterine complaints, eye pressure disorder (Glaucoma) and tetanus (Igwe *et al.*, 2003; Grubben &Denton, 2004; Lester & Seck, 2004; Horna *et al.*, 2007; Okon *et al.*, 2010).

The Igbo community in Nigeria can hardly do without the consumption of African eggplant because of its immense contribution to good vision. A study reviewed that the consumption of garden egg fruits may be of great benefit to glaucoma patients (White, 2010).

2.3 Yield and Production pattern in Ghana

African eggplant is one of the most important vegetable crops cultivated in Ghana and represents one of the main sources of income for many rural farmers and their households in the forest zone of the country (Danquah-Jones, 2000; Owusu Ansah *et al.*, 2001; Grubben & Denton, 2004).

Asenso-Okyere *et al.*, (2000) estimated that about 4,305 families are actively involved in the production of vegetable crops including eggplants in our country. It is believed that approximately 97% of total production of garden egg in Ghana occupies less than a hectare of farm land and almost a little bit above half of the total production levels get to consumers.

Norman (1992) reported that most of the local accessions of African eggplant can give an average yield of about 35-40 fruits per plant or an average weighing of about 0.9 to a 1 kg per plant. However, fruit size has been noted to decrease with increasing number of fruits.

A productivity study by Olympio and Schippers (1995), PROTA (2004) and Lester and Seck (2004) reported that African eggplant has a potential yield of approximate 225 ton/ha. An African eggplant is likely to produce about 500 g to 800 g weight of fruit per plant, based on the variety cultivated and to a larger extent conditions prevailing during that particular production season. The market preferred fruit weight for African eggplant basically, ranges from about 30 to 40 g per fruit. However, the local eggplant cultivated without irrigation may yield figures ranging from 5 to 8 ton/ha whiles those cultivated under irrigation may yield approximately 12 to 20 ton/ha. Improved cultivars grown under favourable conditions are most likely to reach yield levels of 50-80 ton/ha.

Daunay *et al.*, (2001) reported that African eggplant production stands as a commercial crop for the local market as well as for export. Approximately 750 metric tons of African eggplant fruits

were exported from Ghana in 1997 and this constituted about 5% of the total production at that time (Danquah-Jones, 2000). However, Horna *et al.,* (2007) acknowledged that relatively a smaller percentage of the total national production around 30,000 metric tons is exported internationally. According to Gruère *et al.,* (2007) the production levels of African eggplant in places such as Greater Accra, Volta and Brong-Ahafo Regions, have their yields and prices comparatively higher than in the other regions of Ghana. This provides producers an optimum recovery of their investments.

2.4 Genetic Divergence among the African eggplant in Ghana

Genetic diversity arises predominately as a modification(s) in the linear sequence of nucleotides in DNA. This comes as a result of mutations occurring in the coding region of genes, or the spacer regions within and between genes bringing about variability in the number of copies of genes, the linkage relation between several genes or indeed in an entire chromosome. A small portion of these changes translates into protein variation, characters, physiological, marker polymorphisms and morphological diversities in agronomic characters, resultant produce and ultimately into variability in accessions given different names most at times by breeders, farmers and marketers (Brown, 2008).

According to Mostafa *et al*., (2011) genetic variability studies provide the intellects of genetic relationships among populations and hence guide assigning lines to specific heterogeneous groups that help in identification of parents and hence choice selection for hybridization. Precise information on evaluation of genetic diversity helps to specify the source of a particular trait within notable genes in a germplasm. Multivariate analysis acts as a useful apparatus to quantify the extent of divergence between the biological populations at genotypic level and to assess the

relative contribution of different components to the total divergence both inter and intra cluster levels (Murty and Arunachalam, 1966).

Rao (2004) acknowledged that the fundamental part of global food security on food and agriculture depends largely on the existing plant genetic resources and also on the ability to improve the self-sufficiency in vegetable crop production and advancement in its breeding programs.

African eggplant varies in several agronomic and quality traits. These traits include branching habit, plant height, time of flowering, time to fruit maturity, fruit size, fruit shape, immature fruit colour, fruit yield and taste are the most perceptible characters that vary among the available genotypes currently (Osei *et al*., 2010; Frary *et al*., 2007 and Ofori *et al*., 2008). Also, wide diversities exist in African eggplants, their related species and landraces as it were observed in the plant's morphological, physiological and biochemical properties as observed by (Daunay *et al*., 1991; Collonier *et al*., 2001 and Ofori *et al*., 2008).

The ability to characterize the divergences that exist in African eggplant is indispensable for effective management and sustainable use of genetic resources in breeding programmes. Primary characterization involves measuring plant characters that can be recorded easily through visual surveillance at different plant growth stages. Such traits include plant height, canopy spread, leaf area, number of leaves, fruit shape, size and colour, plant prickliness and hairiness. Secondary characterization deals with more complicated morphological traits of agronomic importance such as pest and disease resistance, fruit set, yield potential and biochemical properties (Ayad *et al*., 1995).

Morphological crop descriptors allow a quick and easy discrimination between phenotypes. They are generally highly heritable traits that can easily be recorded through visual observations and expressed in basically all environments. Morphological descriptors for *Solanum aethiopicum* L. and its close relative have been developed by International Plant Genetic Resources Institute/ Food and Agricultural Organization (IPGRI/FAO), Eggplant Genetic Resource Network (EGGNET) and International Union for the Protection of New Varieties of Plants (UPOV) that provide internationally accepted definitions for these descriptors which include a complete description of important quantitative and qualitative traits exemplified by figures and measured either in metric or arbitrary scale.

To carry out an effective breeding program, information concerning the extent and nature of genetic diversity within a crop species is of prime importance. It is very useful for characterizing individual accessions and cultivars and as a general guide in the selection of the parents for hybridization (Furini and Wunder, 2004). Better knowledge on genetic diversity or genetic similarity could also help to sustain long term selection gain (Chowdhury *et al*., 2002).

Sharma and Jana (2002) reported that, assessment of genetic diversity in a species is a necessity for the initiation of an efficient breeding program, as it provides a basis for tailoring desirable genotypes. Furthermore, a previous knowledge of the structure of the genetic variation within a large collection of germplasm may be of great help on decisions on management procedures, as well as on breeding approaches to use in on going and future breeding programs (Kumar *et al*., 2007).

Improvement in yield and quality at most times are attained by picking out genotypes of outstanding character combinations existing in nature or by hybridization. Selection of parents' base on divergence analysis would be more auspicious for a hybridization programs (Singh and

Gopalakrishman, 1999). Genetically, parents that are highly variable are likely to segregate or have high heterotic crosses or both. The more diverse the parents are the greater the chances of obtaining high heterotic first filial generations and broad spectrum of diversities in segregating generations. Understanding genetic relationship within and among cultivars could increase hybrid vigour and reduce re-selection within existing germsplasm (Arunachalam, 1981).

Genetic divergence study also enables one to select the genetically diverse parents to obtain the enviable recombinant in the segregating generations of eggplants.

Studying genetic diversity is critical to success in plant breeding. It provides substantial information about genetic divergence and provides the opportunity for specific breeding objectives. It identifies parental combinations exploitable to create segregating progenies with maximum genetic potential for further selection, as demonstrated by Aremu *et al.*, 2007. It exposes the genetic variability in diverse populations and provides justification for introgression and ideotype breeding programmes to enhance crop performance.

Choice of parents has been identified to be the first basic step in meaningful breeding programme (Rahim *et al*., 2010). Furthermore, the choice of parent selection in diversity studies is valuable because it is a means of creating useful variations in subsequent progenies. Diversity studies on garden eggs at their respective primitive levels will lead to the development of widely distributed cultivars and varieties with proven characteristics based on stability and adaptability of performance with consistent tolerance to adverse weather conditions and resistance to diseases.

Mohammadi *et al*., (2010), acknowledged that appropriate parent selection for hybridization in flax using a definite diversity study technique, increased flax yield tremendously.

2.4.1 Diversities in African Eggplant Agronomic Traits

African eggplant is a hermaphrodite crop but extremely heterogeneous due to cross-pollination (Horna *et al*., 2007). The species varies considerable in several agronomic traits, as a wide variation has been witnessed in plant height, fruit shape, immature fruit colour, fruit size, diameter of corolla, petiole length, leaf area etc. (Blay, 1978; Chinedu *et al*., 2011; Osei *et al*., 2010; Gisbert *et al.*, 2006). African eggplant varieties also vary in traits such as branching habit, time of flowering, time of fruit maturity and fruit yield (Blay, 1978).

Desmukh *et al*., (1986), categorized PCV and GCV values in classes which were cited by Abrefa and Ofori (2012). The following classes are; high (>20%), medium (10-20%) and low (<10%). Degwione *et al*., (2011) also acknowledged that PCV values ranged from 6.8% in fruit diameter to 27.8% in number of seeds per fruit and GCV ranged from 4.0% in fruit diameter to 22.7% in fruit length. The development of effective breeding programme depends extensively on genetic diversity.

Rana and Kalloo (1989) stated that the number of fruits per plant has a close bearing on total fruit yield in tomato. Therefore, the varieties showing high number of fruits per plant might be high yielding. In spite of the number and size, fruit weight also contributes directly to total yield.

Saeed *et al*., (2007) revealed that diversities among the accessions, on the basis of coefficient of variability were higher in characters like number of fruits per plant and number of flowers per plant. This emphasizes that the genetic material was rich in diversities for those characters mentioned (Singh, 2004).

Kaushik *et al*., (2011), revealed that the magnitudes of GCV and PCV were almost proportional to the number of leaves, days to 50% flowering, fruit diameter, fruit length and fruit yield except

for plant height and fruit shelf life indicating that the impact of the environment on the expression of these traits. On the other hand, with respect to plant height and fruit shelf life, the magnitude of PCV was greater than their respective GCV denoting a strong influence of environmental factors in their expression. The magnitude of genotypic and phenotypic coefficient of variation was higher for number of leaves at 30 days after transplanting, fruit length and fruit yield. The number of leaves at 30 days after transplanting, fruit length and fruit yield depict greater genotypic and phenotypic variability among the genotypes and also the sensitiveness of these attributes for mating further modifications by selection. Similar observations were also made in tomato by Singh and Narayan (2004), Mehta and Asati (2008) and Sharma *et al*., (2009).

Yildirim *et al*., (1997) reported that both tuber number and tuber weight as yield components were associated with tuber yield, but they indicated that tuber numbers were of more prime significance than average tuber weight. Also the number of tubers in a plant and the percent of dry matter percent had a positive and significant correlation with tuber yield. However, according to Hosseinzadeh (2002), correlation between the number of tubers in each plant and tuber yield were not significant as also similar findings were acknowledged by Siyadat *et al.*, (2000). Also, negatively significant correlation was observed between tuber weight and number of tubers according to the correlation analysis in sweet-potato as reviewed by (Islam *et al.,* 2002; Tsegaye *et al.,* 2006)

2.4.2 Diversities in Fruit Quality Traits in African Eggplant

Wide variations exist within the vegetative and fruit characters both within and between the African eggplant species including variations in fruit shape, immature fruit colour, fruit firmness, fruit size, fruit weight, (Ofori *et al.*, 2008 and Osei *et al*., 2010)

The fruit colour ranges from whitish to dark green, yellowish to creamy, reddish to pinkish depending on the stage of maturity with taste varying from sweet to bitter depending on the saponin content of the cultivar. The fruit shape may be round or oval with smooth, grooved or ribbed surfaces (Cebula *et al.*, 2007). At full maturity, the fruits turn red or reddish-orange due to increasing carotene content.

There are many different sizes and shapes of garden egg. The shape of the fruit varies from elongated to round and fruits may have ridges or present a smooth appearance (Gisbert *et al.*, 2006; Osei *et al.*, 2010; Chinedu *et al.*, 2011).

The fruit is a globose to depressed globose, ellipsoid, ovoid or fusiform berry, 1-6 cm long, smooth to grooved, red or orange in colour (Handique and Sarma, 1995; Chen, 2001; Diggle and Miller, 2004; Lester and Seck, 2004; PROTA, 2004).

The fruit shape, fruit size, fruit colour and taste are the most obvious characters that vary among cultivars (Frary *et al.*, 2007). Choice of garden egg variety depends on usage as immature fruits basically in stew and sauce preparation but fully matured fruits or those at ripening stage are preferred for soups (Gyiele, 1999). In Nigeria, the varieties with green immature fruit colour are preferred as fruits whiles in Ghana varieties with cream or white immature fruit colour are preferred for use as vegetable (Horna *et al.*, 2007).

Fruit quality is a combination of physical and chemical characteristics accompanied by sensory properties such as appearance, texture, taste and aroma, nutritional values, chemical compounds, mechanical properties, and functional properties (Kramer and Twigg, 1966; Velišek and Cejpek, 2007

2.4.3 Diversities of Bioactive Compounds in Fruits of African eggplant

In African eggplant, numerous landrace species have been upheld to be untapped sources of valuable genetic variability, including nutritional and industrial quality traits. Actually, crop improvement strategies are focused not only on the traditional areas of yield enhancement and disease resistance but, also driven by recent plant molecular farming, or "Bio-Pharming" researches for specific protein production to compliment both animal and human health (Kant *et al*., 2011; Twyman *et al*., 2012).

In particular, during these past few decades, most research has focused on the enhancement of bioactive compounds, given that biochemicals present in fruits and vegetables may help prevent chronic diseases such as cancer, arthritis, glaucoma and heart disease (Fernie *et al.*, 2006; Harrigan *et al.*, 2007a).

Genetic contributing factors to nutritional quality have long been studied. Nonetheless, it is only recently that researchers have started investigations into bioactive compounds and metabolites such as minerals, vitamins, antioxidants and phenols of various vegetables such as iron in garden eggs (Horna *et al*., 2007; Okon *et al*., 2010) and carotenoid content in tomato (Liu *et al.*, 2003a).

Recently, conscious advocates on health awareness have progressively informed consumers to look for food sources that supply adequate amount of vitamins and minerals and these are

important constituents essential for humans for a healthy life, which has given the platform for fruits and vegetables to contribute to these demands.

Numerous studies have shown that fruits and vegetables are rich sources of nutrients as well as non-nutrient molecules (bioactive compounds) with antioxidant or other physiological effects, and it seems likely that given adequate bioavailability, these compounds may be key constituents of a healthy diet. The health promoting properties of plant-based foods have largely been attributed to their wide range of phytochemicals, many present at relatively high levels.

These pharmacological properties have been attributed to the presence of certain chemical substances in the plants, such as fiber, ascorbic acid, phenols, anthocyanin, glycoalkaloids and a chaconine. (Sanchez-Mata *et al.*, (2010); Alozie *et al.*, (1978))

2.5 Relationship between Fruits Physical characters and Bioactive Compounds

Association studies reveal reliable information for genetic breeding, since they help to facilitate, pinpoint and ascertain the proportion of the phenotypic that has the relation to causes associated with genetics, as well as aid in verifying whether the selection for a known trait influences the expression of another. Again, it helps to measure indirect gains due to selection on correlated characters, and to evaluate the complexity of the character (Cruz *et al.*, 1988; Tiwari and Upadhyay, 2011). According to Dighe (1995) it was observed that the visual characteristic of the fruits physical traits was found to influence the presence of various bioactive compounds present. If two traits reveal high genetic association, it is very likely to obtain a gain in one of them through indirect selection of the other character. This is advantageous when a trait of high commercial value has low heritability, when put side by side with the associated character.

This implies that selection may be based on either the trait having high heritability or the one that is more easily evaluated, with the objective of co-inheriting the associated character. Haydar *et al.*, (2007) acknowledged an association between fruit yield and the number of fruits per plant. However, Singh *et al.*, (1977) observed that the number of locules per fruit associates negatively with the number of fruits per raceme.

Tasisa *et al.*, (2012) analysis revealed a positive and significant genotypic and phenotypic association of average fruit yield per plant with fruit clusters and fruits per plant. Also, Ghosh *et al.*, (2010) and Anjum *et al.*, (2009) acknowledged positive and significant phenotypic and genotypic association between tomato yield traits with emphasis on fruit yield and fruit number per plant.

Stevens *et al.*, (2008) further reported that vitamin A acts as a molecule which contributes significantly to tomatoes' resistance to most stress response as well as to its storageability in post-harvest fruit quality.

Bajaj (1979) found that fruits with shapes longer than broad have on the average large amount of dry matter, amino proteins, total water-soluble sugars, phenols and free reducing sugars.

Sidhu *et al.*, (1982) and Bajaj *et al.*, (1979) reported that white cultivars of eggplants, independent of the shape of fruit whether broader than long, longer than broad or as long as broad, lack the compound anthocyanin.

Flick *et al.*, (1978) and Bajaj *et al.*, (1990) observed that potassium is more abundant in violet cultivars of eggplant than the other varieties.

Ramaswamy and Rege (1977a,b) reported that zinc is found in appreciable levels in white cultivars of eggplant than the rest and it has a positive correlation with alcohol dehydrogenase.

Zinc (Zn) is an essential trace element for plants, which helps in regulating the carbohydrate metabolism, protein synthesis, cellular differentiation and replication (Swietlik, 1999, Pathak and Kapil, 2004).

2.6 Estimation of Genetic Diversity

The apposite statistical tool or the measuring indicators of diversity to use has long been a matter of dialogue (Magurran, 2003). Numerous researches have engaged variant data sources and types from different crops to study genetic variability. Such data sources include morphological and agronomic, pedigree, biochemical and molecular data (Aremu and Ibrinde, 2011).

Aremu *et al*., (2008), acknowledged that selection of statistical methods to be used is reliant on the achievable objectives spelled out in the studies.

According to Franco *et al*., (2001), one needs to be careful, considerate on the approaches when measuring genetic variability within and between crop populations in research. Such considerations include:

1. The use of multivariate data collected from morphological characters. Such data may effectively display discrete, continuous, binomial or ordinal variables.

2. The use of multiple sets arising from morphological, biochemical and DNA-based data. Use of such multiple data sets in variability studies help to disclose the tolerability in terms of strength and constraints in the choice of each of the data sets. A research in phylogenetic relationships among Triticeae species using individual and combined analysis of data sets consisting of

morphological and GMO-based characters revealed divergent results in the analyzed individual and combined data.

3. Expected objective to be achieved. This dictates choice of statistical tool in measuring genetic distance and the level of clustering of the intragenic factors in use. Diversity recorded in the measurement of genetic variability in genotype relationships are based on genetic distances and class rankings.

Genetic associations among and within genotypes can be acknowledged and categorised using multivariate grouping methods. The use of established multivariate statistical algorithm is important in classifying genotypes from germplasm, accessions, lines, and other races into distinct and variable ranks depending on genotype performance. The frequently used techniques regardless of the data source (morphological, biochemical and molecular marker data) are cluster analysis, Principal Component Analysis (PCA), Principal Coordinate Analysis (PCOA), Canonical Correlation and Multidimensional Scaling (MDS).

According to Amenu (2011), Cluster analysis presents patterns of relationships between genotypes and hierarchical mutually exclusive grouping such that similar descriptions are mathematically gathered into same cluster.

Principal components, canonical and multidimensional analyses are also used to derive a 2- or 3-dimensional scatter plot of individuals such that the geometrical distances among individual genotypes reflect the genetic distances among them.

Cluster and principal component analyses can be jointly used to explain the variations in breeding materials in genetic diversity studies.

2.6.1 Estimation of G × E Interaction

The relative performance of genotypes for quantitative characters such as yield, fruit quality and other traits, vary from one environment to another. Thus, to develop a genotype with high yield; fruit quality ability and consistency, absolute attention should be given to the importance of stable performance for the genotypes under different environments and their interactions which had significant bearing on breeding for superior varieties buffering (Allard and Bradshaw, 1964).

According to Kang (1998), the expression of a gene is subject to a varying environment; on that regard, genotypic expression of a phenotype is environmentally dependant. Constancy in performance of a genotype over a wide range of environments is a needed attribute and relies largely upon magnitude of genotype-environment interaction (Ahmad *et al.,* 1996). For stabilizing crop yield and quality, it is necessary to ascertain stable genotypes suitable for a wide range of environments. To characterize such individuals, genotype by environment interactions are of major concern for a breeder, because such interactions conflict the selection of the superior cultivars by altering their relative productiveness in varied environments (Eagles and Frey, 1977). Consistency analysis is a must-do technique for measuring the adaptability of diverse crop varieties to varying environments (Morales *et al.,* 1991).

Environmental factors such as the prevailing soil, moisture, temperature, light intensity and quality, humidity, rainfall, photoperiod, and cultural practices, most at times, influence performance of a given genotype from location to location. These factors most often have significant effect on gene regulation, which in turn can affect the gene expression controlling the character of interest and ultimately result in different phenotypic expressions among locations.

According to Khalil *et al*., (2011) the yield and fruit qualities of crops in nature, most often, exhibit Genotype-Environment Interaction. And this necessitates evaluation of accessions at

several locations (Kang, 2004; Fan *et al.*, 2007). It has also been shown by Comstock and Moll (1963) that correlation between phenotypic and genotypic values was significantly reduced by Genotype-Environment Interaction affecting progress of selection. This is because, relative categorization of major characters often fluctuates across several locations hence possibility of pinpointing single superior genotype poses trickiness or difficulty (Khalil *et al.*, 2011; Abdulai *et al.*, 2007).

Consistency analysis defines the true performance of an accession when it is significantly reproducible in distinct locations (Brown and Caligari, 2008). As acknowledged by Khalil *et al.*, (2011), several stability statistic studies have been proposed to categorise Genotype by Environment Interaction (GEI) (Becker and Leon, 1988; Piepho, 1998; Truberg and Huhn, 2000). This method is divided into two major groups; thus Univariate and Multivariate stability statistics (Lin *et al*., 1986). Joint regression is the most popular among the univariate methods because of its ease in computing and application (Becker and Leon, 1988), which also serves as a conceptual model for genotypic stability (Romagosa and Fox, 1993). Genotype-environment interaction and phenotypic stability of solanum spp. have been studied by several plant breeders and researchers including Panthee *et al*., (2012), Hosamani (2010), Shalini (2009), Mandal *et al.*, (2000), Ortiz and Izquierdo (1994).

2.6.2 Estimation of Correlation between Agronomic Traits and Fruit Quality Traits

Phenotypic correlations are estimated using values measured directly from the experimental field(s) as a result of the diversities that exist environmentally on gene expression and only the genetic portion of phenotypic correlations is used to chaperon breeding programs, because it represents the components that would be passed on onto the next generation.

Correlation studies provides plant breeders the tool for selection procedure in their breeding programs, since they enable to pinpoint and estimates the proportion of the phenotypic correlation that is associated with genetic cause and also to verify whether the selection for a known trait influences simultaneous selection of another. Again, helps to quantify indirect gains due to selection on correlated traits, and to evaluate the complexity of the traits (Cruz *et al*., 1988; Tiwari and Upadhyay, 2011).

If two characters exhibit high genetic correlation, it is possible to obtain a gain in one of them through indirect selection of the other trait. This is advantageous when a character of high economic value has low heritability, when compared to the associated trait. This implies that selection may be based on either the character having high heritability or the one that is more easily evaluated, with the objective of co-inheriting the associated trait. In general, breeders consider 0.5 a high correlation coefficient (Miranda *et al*., 1988).

Haydar *et al*., (2007) observed a correlation between tomato fruit yield and the number of fruits per plant. On the other hand, Singh *et al.,* (1977) observed that the number of locules per fruit of tomato correlates negatively with the number of fruits per raceme.

According to Tasisa *et al*., (2012), a research observation on tomato reviewed a positive and high genotypic and phenotypic correlation for average fruit yield per plant with fruit clusters and fruits per plant. In addition, Ghosh *et al.,* (2010) and Anjum *et al*., (2009) acknowledged that there was a positive and significant phenotypic and genotypic correlation between tomato yield traits stressing on fruit yield and fruit number per plant.

Abrefa and Ofori (2012) reported that plant height at flowering disclosed significant and a high positive association with fruit length at both phenotypic and genotypic levels in *garden egg*

(Solanum gilo Raddi*).* Swamy *et al*., (2003) also acknowledged a positive association between plant height at flowering and fruit length in groundnut. Nonetheless, Denton and Nwangburuka's (2011) analysis revealed a significant negative association at phenotypic level and a positive correlation at genotypic level between plant height and fruit length in *Solanum anguivi*.

Haydar *et al*., (2007), revealed that positive associations of traits in tomato may lead to increasing fruit quality and yield traits. Fruit quality and yield are complex characters associated with a number of fruits per plants and the fruits physical attributes. It is one of the main aims of the plant breeder to figure out which selection programs that targets to improve this parameter. Most changes that occur in plant yield are evidenced in one or more characters associations (Graffius, 1964).

Fruit quality and yield are complex traits with polygenic inheritance, and correlation studies seems to serves as a blue print to selection of characters that aim to have a positive correlation with such characters. Correlation studies in solanum spp. breeding programs are useful when highly heritable traits are associated with important characters like fruit quality and yield.

2.6.3 Estimation of Heritability among Traits

Broad-sense heritability estimates the total genetic effects influencing a trait and includes additive, dominance, and epistatic effects (Nyquist, 1991). In cross-pollinated species, narrow sense heritability is typically more useful to plant breeders because it measures the additive gene effects, which are passed on to the progeny more predictably than dominant or epistatic gene effects. However, when working with apomictic or asexually propagated crops, in which hybrid

vigor and both additive and non-additive gene actions are fixed, estimates of broad-sense heritability are more appropriate (Poehlman and Sleper, 1995).

Assessment of genetic diversity is the most suitable statistical tool to find out the degree of heritability, genetic coefficient of variation and response to selection using the realistic selection intensity for character of interest.

Heritability helps the plant breeder to formulate effective breeding tactics. Reports on high heritability and genetic advance for number of fruit/plant and average fruit weight in tomato had been earlier acknowledged (Mittal *et al.,* 1996). Some other research fellows realized moderate to high genotypic coefficient of variation and phenotypic variability, heritability and genetic advance for number of flowers, number of fruits per plant and fruit yield; and arrived at the fact that yield was positively associated with number of fruits per plants (Srivastava *et al.,* 1998). According to Mohanty (2003), there was high genetic variability, coefficient of variation and heritability for number of branches per plant, number of fruits per plant, fruit weight, plant height and number of days to harvest in tomato and in addition revealed that number of fruits per plant and average fruit weight had positive and directly link to tomato yield.

Makeen *et al.,* (2007) acknowledged that there were great significant differences for all traits with high magnitude of heritability for plant height and testa weight when they evaluated twenty mung bean genotypes to estimate genetic variability, heritability and genetic advance for quantitative traits. Characters with high heritability had less influenced by the environment but on the other hand traits with low heritability were mostly influenced by environmental factors.

According to Abrefa and Ofori (2012), fruit diameter recorded the least heritability value of 34.5% followed by number of fruiting branches scoring 54.7%. Fruit length had the highest

heritability estimate of 94.7% and days to flowering followed with 83.5%. The heritabilities for fruit weight, height at flowering and number of seeds per fruit were 76.0%, 74.1% and 66.3% respectively.

Nwangburuka and Denton (2011) also obtained marks close to scorings recorded for *Solanum anguivi* L. used in similar trial. In a related study, Islam and Uddin (2009), high heritability estimates of 91.5% for fruit length and 62.7% for days to first flowering in *Solanum melongena* were recorded. They emphasized that the high heritability values obtained for fruit length, days to 50% flowering, fruit weight and height at flowering revealed that selection could be practiced for these agronomic traits.

Saeed *et al.*, (2007) stated that the value of heritability for number of fruits per plant was 0.96 which showed that about 96% of estimate of diversity was under genetic regulation and the coefficient of variability which was 13.92%, indicated that 96% of 13.92% variation could be transferred to the progeny. Singh and Mandhar (2004) also acknowledged that, the relatively low value of coefficient of variability of 7.69% and heritability of 0.36 suggested that the trait was partially under the influence of genes. The value of high broad sense heritability (0.9715) was estimated for yield per plant, thus 97% of the variation obtained was genetically determined. The results also confirms with the findings of Mittal *et al.*, (1996) and Mohanty (2003).

The highest value of broad sense heritability (0.97) for yield per plant showed that about 97% of the variation observed for this trait was genetically determined and would be passed onto the next generation (Singh, 2004). Similar results were also obtained by Srivastava *et al.*, (1998), and Mohanty (2003).

Kaushik *et al*., (2011) also indicated that the heritability in broad sense ranges from 58.2 fruit to 99.9 for fruit weight. The high heritability was obtained for all number of leaves, days to 50% flowering, fruit length, fruit diameter and fruit yield and for plant height and fruit shelf life (58%). Pradeepkumar *et al*., (2001), Haydar *et al*., (2007) and Hidayatullah *et al*., (2008) also had similar values as reported above.

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Assessment of fruit physical Quality and Bioactive Compounds Diversity in 14 Accessions of African Eggplant.

Two field experiments were carried out at Legon and Kade representing different agro-ecological zones.

3.1.1 Experiment 1: Evaluation at the University of Ghana, Legon

The experiment was conducted at the University of Ghana Farm, Legon located between latitude of 50˚ 38′45′ N and longitude 00˚ 11′13′ E (Cobbina, 1987), between December, 2014 and April 2015. The soil type on the farm is classified as the Adenta series, a savannah Acrisol (FAO/UNESCO, 1999). According to USDA classification the soil is approximately 150 cm deep, moderately well-drained and occurring on the middle slope of Legon hill where it is gentle to medium (2%-3%). The soil profile consists of about 23 cm dark brown to reddish brown sandy clay loam topsoil slightly sticky with a weak, fine granular structure with few to common fine, medium root distribution and below this is about 17 cm thick yellowish red sandy clay containing few fine roots and few fine quartz and ironstone concretions (Brammer, 1967).

The conditions that represented the coastal savannah zone

During the experimental period, minimum and maximum temperatures ranged from 20.3-24.2˚C and 31.4-35.2˚C, rainfall distribution ranged between 12.3 and 20.8 mm while relative humidity ranged between 61 and 88%.

Table 3.1: Mean Monthly Temperature (˚C), Rainfall (mm) and Relative Humidity (%).

Month	Temperature (˚C)		Rainfall (mm)	Relative Humidity (%)	
	Minimum	Maximum		Minimum	Maximum
December	22.6	32.4	13.5	63	88
January	23.9	33.5	12.3	67	86
February	22.9	34.1	12.4	67	88
March	24.2	35.2	14.9	61	86
April	21.3	31.4	20.8	68	88

Source: Ghana Meteorological Agency, Mempasem, Legon, 2015

3.1.2 Experiment II: Evaluation at the Forest and Horticultural Crops Research Centre, Kade

The experiment was carried out between January, 2015 and May, 2015 at the Forest and Horticultural Crops Research Centre (FOHCREC) Okumaning, Kade, located at latitude 60˚ 09′ and 60˚ 06′ N and longitude 00˚ 55′ and 00˚ 49′ W and 135.9 m above sea level. The centre is located in the semi-deciduous forest agro-ecological zone of Ghana in the Kwaebibrem district of the Eastern Region, 175km NE of Accra.

The soils of the research area developed from procambian phyllitic rocks of Nzima-Bekwai-Kokofu series (ISSS/ISRIC/FAO, 1998; Adu, 1992; FAO, 1988) made up of argillaceous sediments metamorphosed into phylite. It's well drained and Ochrosol of forest type, one of the best Soil Groups classified in Ghana soil system (Brammer, 1962; Owusu-Benoah *et al.*, 2000) and are generally accommodated as Acrisols in the FAO/NESCO Revised Legend (FAO, 1998) and as Utisols in Soil Taxonomy (Soil Survey Staff, 1998). The soil has an isohyperthermic moisture and temperature regimes respectively (Van Wambeke, 1982; Owusu-Benoah *et al.*, 2000).

The climate of the area is humid tropical, with an average annual temperature of about 28˚C. The rainfall has the bi-modal pattern with a 30-year average approximation of 1,433mm. The peak season ranges from June to November, with a brief dry spell in August. The dry season is from December to March. The maximum and minimum relative humidity ranged from 47.7% to 96.4% and 39.5% to 47.7% respectively during the period of the study.

During the experimental period, minimum and maximum temperatures ranged from 20.5-23.5˚C and 32.6-34.1˚C, rainfall distribution ranged between 12.2 and 67.5 mm while relative humidity ranged between 42.3 and 96.95%.

Table 3.2: Mean Monthly Temperature (˚C), Rainfall (mm) and Relative Humidity (%).

Month	Temperature (˚C)		Rainfall (mm)	Relative Humidity (%)	
	Minimum	Maximum		Minimum	Maximum
January	22.9	32.6	44.4	39.5	94.5
February	20.5	33.3	12.2	45.1	99.1
March	23.5	32.8	53.8	46.1	98.6
April	22.3	34.1	67.5	47.7	99.4
May	21.4	33.3	19.6	39.6	96.4

Source: FOHCREC Meteorological Centre, Okumaning, Kade, 2014/2015.

3.1.3 Germplasm used for the study

The genetic material comprised fourteen (14) garden egg accessions. Seeds were obtained from the existing collections at The Department of Crop Science, University of Ghana, Legon and Forest and Horticultural Crops Research Centre (FOHCREC), Okumaning, Kade. These

accessions were A1, A2, A3, A4, A7, A11, A9, 14-026, 14-030, 14-027, A12, Green, A10, and Legon 1.

Accessions A1, A2, A3, A4, A7, A9, A10, A11, A12 and Legon 1 are existing collections at the Department of Crop Science, University of Ghana. However, apart from Legon 1 which has had improvement programs carried on, the rest are basically wild type collections undergoing selection on various quantitative properties and consumer preference characteristics. On the other hand accessions 14-026, 14-030, 14-027 and Green are locally grown varieties in various farming communities in the Eastern Region.

3.1.4 Nursery, Field Preparation and Planting

Seeds of each of the accessions were nursed in carbonized rice husks popularly known as "Bio char" contained in plastic nursing cell trays on the 29th of November, 2014 at the Sinna's gardens, Department of Crop Science, University of Ghana, Legon, Accra and that of Forest and Horticultural Crops Research Centre (FOHCREC), Okumaning, Kade was also initiated on 29th December same year at their nursery session.

Three seeds were sown per cell in the nursing tray and later pricked out to one per tray two weeks after planting. Ridomil was applied at the rate of 3 g/L of water to the seedlings a day after pricking out to prevent damping off disease. N.P.K. 19-19-19 at a rate of 70-90 g/L was applied in solution to the seedlings about three weeks after nursing.

This was repeated at weekly interval to provide nutrients to the seedlings. Cydim Super at the rate of 2 ml/L was sprayed onto the leaves of the seedlings to prevent leaf miners and white flies. Daily watering was carried out in the absence of rain.

The experimental area was ploughed and then harrowed. Lining and pegging was done a day before transplanting. Five weeks-old seedlings were then transferred to the University of Ghana Farm and FOHCREC experimental field respectively.

3.1.5 Experimental Design and Field Layout

A Randomized Complete Block Design (RCBD) with three replications was used on the field. The seedlings were planted at 80 cm x 80 cm between rows and 80 cm x 80 cm within rows. Each accession was planted in two rows with five plants per row providing a total of 10 plants per accession. Data were collected from six tagged plants (three from each of the middle rows) throughout the experiment with the exception of fruit length and diameter for which plant two, three, four and five were used.

3.1.6 Agronomic/Cultural Practices

N.P.K. (15-15-15) was applied to the seedlings a day after transplanting as a starter solution. Cydim Super was applied at the rate of 35ml/15L of water every two weeks to control leaf miners, white flies and grass hoppers. N.P.K. (19-19-19) at the rate of 250 kg/ha was applied to each plant in a form of foliar one week after transplanting and Multi-K at the rate of 125 kg/ha was also applied in split doses at flowering and fruiting.

Weeding was done as and when necessary and watering was done daily since production was done during the Harmattan season hence the soil was basically dry throughout the growing season. The physiologically matured fruits were harvested using a knife.

3.1.7 Data Collection and analysis

Data collection was categorised into vegetative, reproductive and yield characteristics. Six record plants per each accession were used in both locations

3.1.7.1 Vegetative Characteristics

Number of leaves per plant: The number of leaves of the six record plants was counted when the plants were two, four and six weeks old after transplanting.

Plant height (cm): A meter rule was used to measure the height of the six record plants from the soil level to the tip when the plants were two, four and six weeks old after transplanting.

Chlorophyll content (nm): A chlorophyll content meter was used to measure the leaf chlorophyll content at record plants when the plants were at 2, 4, and 6 weeks after transplanting.

Stem girth (mm): Electronic vernier caliper was used to measure the girth of the stem at 4cm from the soil surface of the six record plants at two, four and six weeks old after transplanting.

Destructive sampling (g): A whole plant was up-rooted carefully with the root bulk intact. The soil and organic particles attached to the roots were washed off gently and dabbed with cellulose tissue. The fresh weight of the roots, stem and the leaves were taken with electronic balance. After which it was dried in the oven at 65^{o}C for five days and reweighed for their dry weights. This was done for the six record plants and at 2,4 and 6 weeks after transplanting.

3.1.7.2 Reproductive Characteristics

Leaf area at flowering (m^2): The length and breadth of the leaves were taken by plucking eight (8) leaves from each accession and with the aid of a cork borer a defined disc with precise diameter were created from the leaves and by ratio leaf area was calculated.

Canopy span at flowering (cm): A steel tape was used to measure the two broad diagonals of the canopy of the six record plants when flowering.

Days to first flowering: The number of days from transplanting to the appearance of the first flower was recorded.

Destructive sampling at flowering (g): A whole plant was up rooted with the root bulk intact. After which the soil attached to the roots were washed off gently to have the roots remain intact. It was then dabbed with cellulose tissue. The fresh weight of the roots, stem and the leaves were taken with electronic balance. After which they were dried in the oven at 65^{o}C for five (5) days and reweighed for their dry weights.

Days to 50% flowering: The number of days from transplanting to the days three of the six record plants had their flowers appearing.

Number of fruits per plot: The total number of fruits for each of the six plants was counted.

3.1.7.3 Yield and yield characteristics

Days to fruit formation: Number of days to fruit formation covered the period from seedling emergence to time of first fruit formation.

Days to first harvest: Number of days from seedling emergence to time of first fruit harvest.

Number of days to maturity: Days from seedling emergence to time of the first physiologically mature fruit.

Number of fruits per plant: The total number of mature fruits per plant was counted at each harvest and the mean computed.

Fruit weight (g): The total number of fruits per plot per harvest was weighed and the mean computed.

Fruit length (cm): The lengths of five mature fruits per record plant were measured from the base of the fruit stalk to the apex of the fruit using a vernier caliper and the mean calculated.

Fruit diameter (cm): The diameters of five mature fruits per record plant were measured at the middle portion of the fruits using a vernier caliper and the mean calculated.

Fruit yield per plant (g): The sum of mature fruits per plant at harvest beginning from first harvest to the last harvest was computed to obtain the total yield per plant.

Fruit yield (ton/ha): $$\textbf{Yield (ton/ha)} = = \frac{Area\ of\ hectare\ X\ Yield\ per\ plot}{Area\ of\ plot\ X\ 100}$$

3.1.7.4 Data Analysis

Genstat statistical software, model: 12th edition was used for data analysis. Means, ranges and standard errors were determined for all quantitative traits. Quantitative morphological data were subjected to Analysis of Variance (ANOVA) to assess significance of the differences among accessions. The least significant difference (LSD) was used to separate the mean performance of genotypes that were significantly different.

The estimation of genotypic and phenotypic variances was calculated in accordance with the explanation by Obilana and Fakorede, (1981) and that of genetic (r_G) and phenotypic correlations (r_P) were estimated according to Akhtar *et al.*, (2011). Heritability and genetic advance were estimated according to the methods suggested by (Hanson *et al.*, 1956) and (Robinson, 1955) respectively.

Table 3.4 Format for the analysis of variance

Source of variation	DF	Mean square	Expected means square
Replication (R)	r-1	MS_b (M1)	
Location	l-1	MSl (M2)	$\sigma^2_e + r\sigma^2_{gl} + rg\,\sigma^2_l$
Genotype (G)	g-1	MS_g (M3)	$\sigma^2_e + r\sigma^2_{gl} + rl\sigma^2_g$
Genotype x Location (GxL)	(g-1) (l-1)	MS_{ge} (M4)	$\sigma^2_e + r\,\sigma^2_{gl}$
Residual	(gl-1) (r-1)	MSe (M5)	σ^2_e
Total	(glr-1		

Where MS_l = Mean square due to location; MSg = Mean square due to genotype; MS_{gl}= Mean square due to genotype x location; MSe = Error mean square; MSe = Error mean square, σ^2_l = Location variance, $\sigma^2 gl$ = Genotype by location variance, σ^2_e = Error variance, r = Number of replications, l = Number of locations, g = Number of genotypes and e = experimental error.

Table 3.5: Computing Estimates of Variance Components

Variance component	Determination method
Replication (R)	(M1 – M5)/GL
Location (L)	(M2- M4)/GL
Genotype (G)	(M3 – M4)/RG
G × L	(M4-M5)/M5
Pooled error (E)	(M5)

$$VP = 1 + \frac{VE}{rl} + \frac{VE}{l} + VG$$

Where,

VG = Genotypic variance, VP= Phenotypic variance, VGL= Variance due to genotype X location

VGLR = Variance due to genotype, location and replication, r = Replication, l = Location, VE= Variance due to error

3.3.1 Correlation Coefficient of Variation

Estimates of correlation coefficients were determined to show the degree of association between yield and its components, and among yield components. The genetic (r_G) and phenotypic correlations (r_P) between two characters, X and Y, were estimated according to Akhtar *et al.*, (2011).

$$r_G = \frac{COV_{G(XY)}}{\sqrt{V_{G(X)} \cdot V_{G(Y)}}}$$

Where,

$COV_{G\,(XY)}$ = Genetic covariance among trait X and Y.

$V_{G(X)}$ and $V_{G(Y)}$ = Genetic variance for trait X and Y, respectively.

$$r_P = \frac{COV_{P(XY)}}{\sqrt{V_{P(X)} \cdot V_{P(Y)}}}$$

Where,

$COV_{P\,(XY)}$ = Phenotypic covariance among traits X and Y

$V_{P(X)}$ and $V_{P(Y)}$ = Phenotypic variance for traits X and Y, respectively.

Broad Sense heritability (H) was estimated as:

$$H = \frac{\delta_g^2}{\delta_g^2 + \delta_{e/r}^2}$$

According to Johnson et al. (1955), response to selection or expected genetic advance (as a percentage of the mean) after one generation of selection was calculated at 10% selection intensity using the following formula:

$$GA = \frac{i\sigma p h^2}{m} X\ 100$$

$$GA(X\ \%) = \frac{i\sigma_g \sqrt{h^2}}{m} X\ 100$$

$$GA\ (X\ \%) = iGCVh$$

Where GA = genetic advance; σ_p is the phenotypic standard deviation, h^2 is the broad sense heritability and *m* is the mean of the unselected population and *i* is the selection differential.

The genetic correlation between yield (A) and other traits (B) ($r_{G(AB)}$)were calculated from the genetic variance and covariance components from the ANOVA as follows:

$$r_{G(AB)} = \sigma_{G(AB)} / \sqrt{(\sigma^2_{G(A)} . \sigma^2_{G(B)})}$$

Where $\sigma_{G(AB)}$ is the genetic covariance between traits A and B. This was estimated by summing up the two traits and estimating the variance of the resulting data using the mean squares from the ANOVA. The $\sigma^2_{G(A)}$ and $\sigma^2_{G(B)}$ are the genetic variances of traits A and B respectively.

Principal Component Analysis was carried out using 18 vegetative, reproductive and quality traits subjected to Principal Component Analysis and Cluster analysis was done to determine the relationship between the garden egg accessions.

3.2 Variation in Bioactivities (Vitamin C, Zinc, Potassium and Magnesium) Among fourteen (14) African Garden Egg Accessions

This analysis was carried out at the Department of Food and Nutrition Science in collaboration with the Ecological Laboratory Project, University of Ghana. Samples of the accessions were transported to these locations in clean containers.

At the laboratories, samples were thoroughly washed with ordinary water and then with doubly distilled water. The stalks were removed and the edible portion of the fruits was analyzed. From each of the garden egg accessions sub-samples were selected and sliced into pieces using a carbon steel knife on a plastic slicing board. The sliced sub-samples were homogenized by thorough mixing. Each sub-sample was further homogenized in a home-styled blender with stainless steel blades. From the homogenized samples, twenty grams (20 g) were taken for the analysis of each mineral.

3.2.1 Analysis of Vitamin C

For the analysis of vitamin C, determination was done on the same day of harvest to counteract the instability of the ascorbic acid. Vitamin C was determined by using the procedure as outlined by AOAC International Methods of Analysis Vol. 16 Method 967.2; The Indophenol Method (Zvaigzne *et al.,* 2009; Nielsen *et al.,*1998).

Aliquots in oxalic acid solution are titrated with standardized sodium 2,6-dichlorophenolindophenol dye to a faint pink colour that persists for 5 to 10 seconds. This method is limited to juices of light colour because red pigments obscure the end point.

Preparation of Indophenol Dye, Oxalic Acid and Dye

1. **Indophenol dye- 0.04%was obtained as follows**

To obtain 0.04% of Indophenol dye, 0.2g of Sodium 2,6-dichorophenolindophenol was weighed and dissolved in 200ml of water contained in a beaker, after which it was filtered through No.4 Whatman paper into 500ml volumetric flask and made up to volume at 20^{o}C and stored in a refrigerator.

2. **Oxalic acid – 0.4% was obtained as below**

To obtain 0.4% of Oxalic acid, 4gm of oxalic acid was dissolved in water and diluted to 1,000ml.

Standardization of Dye

2 to 3g potassium iodine was dissolved in about 5ml. water in 50ml. Erlenmeyer flask (triplicate). 15ml dye was added with a pipette and then 10ml, 1N HCL. They were mixed and allowed to stand for 2minutes. A freshly prepared 0.01N sodium thiosulfate was used to titrate from a micro burette. (20ml 0.1N in 200ml volumetric flask at 20^{o}C) using 1 to 2ml starch, until there was no change in colour when one drop or less is added. The titration was completed in 1minute.

Determination Procedure

Since harvesting was done at the physiological maturity stage, the fruits were virtually juiceless to have employed the juice extractor. Therefore 20g of each of the samples was accurately weighed, chopped into pieces by the use of a carbon steel knife and macerated in a high speed home styled blender,

20ml of the extract was pipetted into 100ml volumetric flask. It was then made up to the volume with 0.4% oxalic acid and was filtered through No.4 Whatman filter paper. A 10ml aliquot was

pipetted for titration; 15ml oxalic acid (0.4%) was added and titrated in a 50ml. Erlenmeyer flask with 0.04% dye to a faint pink end point which lasted for about 5 to 10 seconds. Titration was completed in one minute and the total amount of dye used did not exceed 1.5ml. A micro-burette was used to pipette the dye. The amounts of Ascorbic acid present in the samples were calculated as follows:-

Calculations

If 15ml dye required 5.25ml sodium thiosulfate

$$\text{Dye Equivalent} = \frac{1}{1000} \times \frac{ml\ Na_2S_2O_3 \times Normality\ of\ Na_2S_2O_3 \times 88 \times 1000}{ml\ of\ dye}$$

15 ml Dye required 5.25 ml of $Na_2S_2O_3$

Normality of $Na_2S_2O_3$ = 0.01N

Molar Mass of Ascorbic Acid (A.A) = 88

A.A per 100g Sample = Dye equivalent × Titre value × Dilution Factor

Dilution Factor (ml) = 10

3.2.2 Analysis of the Minerals

Sampled garden eggs from the various accessions were chopped into pieces with the aid of carbon steel knife, sun dried for few days to optimum required value of dryness and milled into';/. powder after which a wet digestion was carried out to eliminate the organic matter component from the samples before the various samples from both experimental fields were analyzed for these minerals. About 5g of the samples was measured into a 250 ml beaker. 25mls of concentrated HNO_3 was added turning the medium yellowish and the beaker was covered with a watch glass. The sample was digested with care on a hot plate in a fume chamber until all the

organic matter had been oxidized. This took about 20 to 30 minutes top. The pale yellow solution obtained indicated completion of the oxidation process was then cooled and 1ml 70% perchloric acid ($HClO_4$) was added with care. Digestion was continued until the solution was almost colourless (thus, when all the HNO_3 added was removed) the solution was cooled slightly after the digestion process, and about 30 ml of distilled water was added and allowed to boil for about 10 minutes then filtered when hot through No. 4 Whatman filter paper into a 100mls volumetric flask. The beaker was washed well with distilled water and filtered. The flask was then cooled and made up to the 100mls mark. This solution was used for these minerals analysis Potassium (K), Magnesium (Mn) and Zinc (Zn). And they were determined using the Perkin Elmer Atomic Absorption Spectrophotometer (AAS; Model Analyst 400) and the results were recorded in milligram (mg). The amount of mineral content present was calculated as follows:-

Calculations

$$\text{Mineral Content (mg)} = \frac{AAS\ Reading}{1000} \times \frac{100}{1000} \times \frac{100}{Wt.\ of\ Sample}$$

CHAPTER FOUR

4.0 RESULTS

Table 4.1: Soil Fertility Profile Results of the Locations

SAMPLE	H_2O(1:1)	KCL(1:1)	%N	OC%N	Av. P (mg/kg)	K (ppm)	Ca (ppm)	Mg (C Mol/Kg)
KADE	5.51	4.2	1.93	0.25	2.64	0.21	2.1	1.4
LEGON	5.18	3.82	0.99	0.11	7.36	0.13	2.0	1.2

Source: Dept. of Soil Science Laboratory

4.2 Variability of growth and yield of garden egg genotypes

Growth and development traits were scored at 2, 4 and 6 weeks after planting. Flowering of plants occurred around six weeks after transplanting and therefore data from sixth week after planting were used.

4.2.1 Plant height at week six

For plant height at six weeks after planting, the genotype x environment interaction was significant ($p < 0.001$). The mean values ranged from 57.25 – 86.25 cm at Kade. At Legon the mean values among the genotypes ranged from 31.22 – 48.83 cm (Table 4.2). Across the two locations mean values ranged from 46.24 – 79.50. The highest and lowest mean values were recorded by genotypes A11 and A1 respectively at Kade while genotypes 14-026 and A12 scored the highest and lowest values respectively at Legon.

Table 4.2 Mean plant height at week six

GENOTYPE	Plant height at week 6 (cm)		
	KADE	LEGON	COMBINED LOCATIONS
A1	57.3	35.2	46.2
A2	85.3	43.0	64.2
A3	60.7	36.4	48.5
A4	79.8	32.9	56.4
A7	81.6	40.2	60.9
A9	84.4	40.9	62.7
A10	64.6	32.9	48.8
A11	86.3	44.7	65.5
A12	69.0	31.2	50.1
14-026	75.3	48.8	62.1
14-027	76.3	39.9	58.1
14-030	74.8	42.3	58.6
GREEN	79.5	34.2	79.5
LEGON 1	78.9	38.7	78.9
MEAN	75.3	38.7	56.9
GCV	92.79	68.23	8.42
PCV	105.52	81.99	10.96

4.2.2 Number of leaves at week six

The combined data showed that effects of genotype, location and Genotype x Location interaction were significant (P <0.05). The mean values for the trait ranged from 82.0 - 186.0 at Kade while at Legon the mean values ranged from 47.0 – 73.0 (Table 4.3). Across the two locations mean values ranged from 69.0 – 129.0. The highest and lowest mean values for the trait

were recorded by genotypes A12 and A3 respectively at Kade while genotypes A12 and A2 scored the highest and lowest mean values respectively at Legon.

Table 4.3 Mean number of leaves at week six after transplanting

GENOTYPE	Number of leaves at week 6 (cm)		
	KADE	LEGON	COMBINED LOCATIONS
A1	86	52	69
A2	152	47	99
A3	82	71	76
A4	162	44	103
A7	137	50	94
A9	167	50	108
A10	143	59	101
A11	160	50	105
A12	186	73	129
14-026	177	60	199
14-027	132	63	97
14-030	175	64	199
GREEN	170	61	116
LEGON 1	143	53	98
MEAN	148.0	57.0	102.4
GCV	256.4	99.53	00.0
PCV	258.3	117.4	15.9

4.1.9 Chlorophyll content for week six

Based on the combined analysis of variance effects of genotype and location were significantly ($P < 0.01$) different. The effect of Genotype x Location interaction were not significantly ($P < 0.05$) different. The mean values for chlorophyll content at week six ranged from 24.33 – 37.08

nm at Kade. At Legon the mean values ranged from 38.29 – 73.23 nm (Table 4.4). Across the two locations mean values ranged from 33.32 nm – 55.16 nm. The highest and lowest mean values were scored by genotypes 14-026 and A3 respectively at Kade while genotypes 14-026 and A1 scored the highest and lowest values respectively at Legon.

Table 4.4 Mean chlorophyll content at week six

GENOTYPE	Chlorophyll content at week 6 (cm)		
	KADE	LEGON	COMBINED LOCATIONS
A1	31.5	38.3	34.9
A2	29.7	43.6	33.9
A3	24.8	39.8	33.3
A4	26.8	39.8	37.1
A7	24.4	49.7	37.1
A9	30.5	50.4	40.5
A10	34.4	55.1	44.7
A11	27.9	43.9	35.9
A12	26.1	40.7	33.4
14-026	37.1	73.2	55.2
14-027	34.9	61.7	48.3
14-030	28.7	45.2	36.9
GREEN	35.9	46.4	41.2
LEGON 1	25.9	44.8	35.4
MEAN	29.9	48.7	33.9
GCV	256.4	118.5	13.2
PCV	258.3	134.6	16.1

4.1.11 Stem girth at week six

The combined analysis of variance for stem girth at week six showed that genotype, location and Genotype x Location interaction effects were significantly (< 0.01) different. The mean values for stem girth at week six ranged from 10.10 – 18.06 mm at Kade. But at Legon, the mean values among the genotypes ranged from 10.45 – 12.85 mm (Table 4.5). Across the two locations mean values for stem girth at week six ranged from 10.97 – 14.56 mm. The highest and lowest mean

values were recorded by genotypes A2 and LEGON 1 respectively at Kade while genotypes LEGON 1 and A1 recorded the highest and the lowest mean values at Legon.

Table 4.5 Mean stem girth at week six

GENOTYPE	Stem girth at week 6 (cm)		
	KADE	LEGON	COMBINED LOCATIONS
A1	11.9	10.5	11.2
A2	18.1	12.8	15.4
A3	11.7	12.2	11.9
A4	13.9	11.9	12.9
A7	10.9	11.6	11.3
A9	16.2	10.5	13.4
A10	10.8	11.2	10.9
A11	17.8	11.4	14.6
A12	12.9	12.3	12.6
14-026	14.4	12.7	13.6
14-027	12.7	11.5	12.1
14-030	14.0	11.4	12.7
GREEN	14.9	12.2	13.5
LEGON 1	10.1	12.9	11.5
MEAN	13.6	11.8	12.7
GCV	67.6	1.6	0.01
PCV	68.0	22.5	0.01

4.1.12 Leaf area

Combined analysis for leaf area showed that the effects of location and Genotype x Location interaction were significantly (< 0.01) different while genotype effect was found to be non-significant (P < 0.05). The mean values for leaf area ranged from 1902.0 – 4894.0 at Kade. However, at Legon mean values for leaf area ranged from 1818.0 - 5146.0 (Table 4.6). Across the two locations mean values for leaf area among the genotypes ranged from 2064.0 – 5020.0.

The highest and lowest mean values for leaf area were scored by genotypes A10 and GREEN respectively at Kade while genotypes A10 and A4 scored the highest and lowest values respectively at Legon.

Table 4.6 Mean leaf area

GENOTYPE	Leaf area (cm^2)		
	KADE	LEGON	COMBINED LOCATIONS
A1	2563	2499	2531
A2	2115	2542	2531
A3	3272	3406	3339
A4	2318	1818	2068
A7	3408	3202	3305
A9	2767	2840	2803
A10	4894	5146	5020
A11	3129	2978	3054
A12	3341	3454	3398
14-026	3883	4139	4011
14-027	3716	3466	3591
14-030	2122	2265	2193
GREEN	1902	2226	2064
LEGON 1	3717	3398	3558
MEAN	3082	3098	3090
GCV	1510.7	1016.0	0.27
PCV	1510.8	1538.2	0.27

4.1.13 Canopy span

Combined analysis for canopy span showed that the effects of genotypes, location and Genotype x Location interaction were significantly (< 0.01) different. The mean values for canopy span ranged from 84.43 – 99.17 at Kade. However, at Legon mean values for leaf area ranged from 83.53 – 98.43 (Table 4.7). Across the two locations mean values for leaf area among the genotypes ranged from 84.20 – 98.43. The highest and lowest mean values for leaf area were

scored by genotypes A10 and A1 respectively at Kade while genotypes A2 and A3 scored the highest and lowest values respectively at Legon.

Table 4.7 Mean canopy span at maturity

GENOTYPE	Canopy span at maturity (cm)		
	KADE	LEGON	COMBINED LOCATIONS
A1	17.4	15.0	16.2
A2	21.3	21.2	21.3
A3	22.3	22.5	22.4
A4	18.1	17.3	17.7
A7	18.3	17.8	18.1
A9	19.2	19.7	19.4
A10	21.6	19.5	20.6
A11	20.9	22.3	21.6
A12	20.6	21.0	20.8
14-026	21.9	20.3	21.2
14-027	19.8	19.2	19.5
14-030	22.2	21.7	21.9
GREEN	18.9	21.2	20.0
LEGON 1	18.8	18.1	18.4
MEAN	20.1	19.8	19.9
GCV	50.8	46.8	4.9
PCV	51.4	46.9	5.0

4.1.14 Root length

The combined analysis of variance for root length showed that genotype effect was significantly (< 0.01) different while effects of location and Genotype x Location interaction were not significant. The mean values for root length ranged from 11.60 – 30.00 cm at Kade while at Legon, the mean values among the genotypes ranged from 12.50 – 22.07 cm (Table 4.8). Across the two locations mean values for root length ranged from 12.05 – 25.58 cm. The highest and

lowest mean values were recorded by genotypes GREEN and 14-026 respectively at Kade while genotypes 14-027 and 14026 recorded the highest and the lowest mean values respectively at Legon.

Table 4.8 Mean root length

GENOTYPE	Root length (cm)		
	KADE	LEGON	COMBINED LOCATIONS
A1	17.4	15.0	16.2
A2	21.3	21.2	21.3
A3	22.3	22.5	22.4
A4	18.1	17.3	17.7
A7	18.3	17.8	18.1
A9	19.2	19.7	19.4
A10	21.6	19.5	20.6
A11	20.9	22.3	21.6
A12	20.6	21.0	20.8
14-026	21.9	20.3	21.2
14-027	19.8	19.2	19.5
14-030	22.2	21.7	21.9
GREEN	18.9	21.2	20.0
LEGON 1	18.8	18.1	18.4
MEAN	20.1	19.8	19.9
GCV	00.0	00.0	21.9
PCV	36.9	48.5	33.3

4.2 GENOTYPES PERFORMANCE FOR YIELD TRAITS ACROSS THE TWO LOCATIONS

4.2.1 Days to 50 % flowering

Based on the combined analysis of variance, effects of genotype, location and genotype-by-location interaction were significantly ($P < 0.01$) different for days to 50 % flowering. Mean performance of the genotypes for days to 50 % flowering ranged from 15.0 – 28.0 and 15.0 – 29.0 at Kade and Legon respectively (Table 4.9). Across the two locations values for days to 50

% flowering among the genotypes ranged from 15.0 – 29.0. The highest and lowest mean values were scored by genotypes A7 and A3 at each of the two locations.

Table 4.9 Mean Days to 50% flowering

GENOTYPE	Days to 50% Flowering		
	KADE	LEGON	COMBINED LOCATIONS
A1	28.0	28.0	28.0
A2	23.0	22.0	23.0
A3	15.0	15.0	15.0
A4	18.0	19.0	19.0
A7	28.0	29.0	29.0
A9	21.0	22.0	22.0
A10	18.0	20.0	19.0
A11	28.0	28.0	28.0
A12	23.0	24.0	24.0
14-026	22.0	23.0	23.0
14-027	23.0	25.0	24.0
14-030	18.0	18.0	18.0
GREEN	26.0	28.0	27.0
LEGON 1	22.0	23.0	23.0
MEAN	22.0	23.0	22.8
GCV	86.7	85.2	17.8
PCV	86.9	85.5	17.9

4.1.2 Days to fruiting

The combined analysis of variance showed that effects of genotype, location and genotype-by-location interaction were significantly ($P < 0.01$) different for days to fruiting. The mean values for days to fruiting ranged from 22.0 – 38.0 at Kade. At Legon the mean values for days to fruiting among the genotypes ranged from 24.0 – 40.0 (Table 4.10). Across the two locations mean values for days to fruiting among the genotypes ranged from 23.0 – 39.0. The highest and

lowest mean values were scored by genotypes A11 and A3 respectively at Kade while genotypes A7 and A3 scored the highest and lowest values respectively at Legon.

Table 4.10 Mean days to fruiting

GENOTYPE	Days to Fruiting		
	KADE	LEGON	COMBINED LOCATIONS
A1	37.0	35.0	36.0
A2	35.0	35.0	35.0
A3	22.0	24.0	23.0
A4	27.0	28.0	27.0
A7	39.0	40.0	39.0
A9	33.0	36.0	34.0
A10	27.0	30.0	29.0
A11	38.0	37.0	37.0
A12	33.0	37.0	35.0
31.014-026	31.0	33.0	32.0
14-033.027	33.0	39.0	36.0
14-030 27.0	27.0	27.0	27.0
GREEN	33.0	37.0	35.0
LEGON 1	32.0	32.0	32.0
MEAN	32.0	34.0	32.0
GCV	84.1	80.4	13.8
PCV	85.5	81.6	14.2

4.1.3 Days to fruit maturity

Combined analysis showed that effect of genotype was significantly (< 0.01) different while location and genotype-by-location effects were non-significant (P < 0.05). The mean values for days to fruit maturity ranged from 31.0 – 55.0 at Kade. But at Legon, the mean values for days to fruit maturity among the genotypes ranged from 30.0 – 48.0 (Table 4.11). Across the two locations mean values for days to fruit maturity among the genotypes ranged from 31.0 – 50.0. The highest and lowest mean values were scored by genotypes 14-027 and A3 respectively at Kade while genotypes A7 and A3 scored the highest and lowest values respectively at Legon.

Table 4.11 Mean days to fruit maturity

GENOTYPE	Days to Fruit Maturity		
	KADE	LEGON	COMBINED LOCATIONS
A1	44.0	46.0	45.0
A2	41.0	44.0	43.0
A3	31.0	30.0	31.0
A4	33.0	35.0	34.0
A7	45.0	48.0	47.0
A9	41.0	45.0	43.0
A10	34.0	36.0	35.0
A11	44.0	44.0	44.0
A12	42.0	41.0	41.0
14-026	37.0	39.0	38.0
14-027	55.0	45.0	50.0
14-030	34.0	37.0	35.0
GREEN	42.0	44.0	43.0
LEGON 1	38.0	42.0	40.0
MEAN	40.0	41.0	40.6
GCV	91.4	78.5	12.8
PCV	101.2	79.7	13.7

4.1.4 Days to fruit ripening

Based on the combined analysis of variance effects of genotype and genotype-by-location interaction were significantly ($P < 0.01$) different for days to fruit ripening. However, a location effect was not significant for the trait. The mean values for days to fruit ripening ranged from 41.0 – 53.0 at Kade. At Legon the mean values ranged from 38.0 – 53.0 (Table 4.12). Across the two locations mean values ranged from 40.0 – 53.0. The highest and lowest mean values were scored by genotypes 14-027 and A10 respectively at Kade while genotypes 14-027 and A3 scored the highest and lowest values respectively at Legon.

Table 4.12 Mean days to fruit ripening

GENOTYPE	Days to Fruit Ripening		
	KADE	LEGON	COMBINED LOCATIONS
A1	52.0	53.0	52.0
A2	48.0	49.0	49.0
A3	42.0	38.0	40.0
A4	41.0	41.0	41.0
A7	52.0	53.0	52.0
A9	48.0	52.0	50.0
A10	41.0	42.0	41.0
A11	52.0	50.0	51.0
A12	48.0	48.0	48.0
14-026	44.0	44.0	44.0
14-027	53.0	53.0	53.0
14-030	42.0	42.0	42.0
GREEN	48.0	51.0	49.0
LEGON 1	44.0	46.0	45.0
MEAN	47.0	47.0	46.9
GCV	60.4	73.9	9.5
PCV	61.3	74.7	9.7

4.1.5 Number of fruits per plant

Combined analysis for number of fruits per plant showed that effects of genotype, location and Genotype x Location interaction were significantly (< 0.01) different. The mean values for number of fruits per plant ranged from 4.0 – 15.0 at Kade. However, Legon recorded the value ranging from 4.0 – 24.0 as their means values (Table 4.13). Across the two locations mean values for number of fruits per plant among the accessions ranged from 4.0 – 16.0. The highest and lowest mean values were scored by genotypes A12 and Legon 1 respectively at Kade while genotypes A10 and Legon 1 scored the highest and lowest values respectively at Legon.

Table 4.13 Mean Number of Fruits per Plant

GENOTYPE	Number of Fruit Per Plant		
	KADE	LEGON	COMBINED LOCATIONS
A1	6.0	8.0	7.0
A2	9.0	8.0	8.0
A3	8.0	13.0	10.0
A4	11.0	7.0	9.0
A7	10.0	10.0	10.0
A9	7.0	6.0	7.0
A10	9.0	24.0	16.0
A11	7.0	16.0	11.0
A12	15.0	15.0	15.0
14-026	6.0	16.0	11.0
14-027	6.0	5.0	6.0
14-030	16.0	17.0	16.0
GREEN	10.0	13.0	11.0
LEGON 1	4.0	4.0	4.0
MEAN	9.0	12.0	10.2
GCV	99.5	151.2	26.4
PCV	111.7	164.7	36.9

4.1.6 Fruit length

The combined analysis of variance showed that effects of genotype, location and genotype-by-location interaction were significantly ($P < 0.01$) different for fruit length. The mean values for fruit length ranged from 4.50 – 7.13 cm at Kade. At Legon the mean values for fruit length among the genotypes ranged from 4.16 – 6.40 cm (Table 4.14). Across the two locations mean values for fruit length among the genotypes ranged from 4.33 – 6.36 cm. The highest and lowest mean values were scored by genotypes GREEN and A1 respectively at Kade while genotypes A12 and A1 scored the highest and lowest values respectively at Legon.

Table 4.14 Mean Fruit length

GENOTYPE	Fruit length (cm)		
	KADE	LEGON	COMBINED LOCATIONS
A1	4.50	4.16	4.33
A2	5.50	5.10	5.30
A3	5.23	4.50	4.86
A4	4.53	5.13	4.83
A7	5.60	5.10	5.35
A9	5.16	6.10	5.63
A10	6.06	5.03	5.55
A11	6.20	5.53	5.86
A12	6.33	6.40	6.36
14-026	5.63	5.10	5.36
14-027	6.16	5.10	5.63
14-030	5.33	5.10	5.21
GREEN	7.13	5.53	6.33
LEGON 1	6.56	6.13	6.35
MEAN	5.71	5.28	5.50
GCV	30.31	26.37	10.49
PCV	30.66	26.63	12.29

4.1.7 Fruit diameter

The combined analysis of variance showed that effects of genotype, location and genotype-by-location interaction were significantly ($P < 0.01$) different for fruit length. The mean values for fruit diameter ranged from 3.66 – 6.06 cm at Kade. At Legon the mean values ranged from 4.06 – 5.53 cm (Table 4.15). Across the two locations mean values for fruit diameter among the genotypes ranged from 3.90 – 5.73 cm. The highest and lowest mean values were scored by genotypes 14-026 and A12 respectively at Kade while genotypes LEGON 1 and A1 scored the highest and lowest values respectively at Legon.

Table 4.15 Mean fruit diameter

GENOTYPE	Fruit Diameter (cm)		
	KADE	LEGON	COMBINED LOCATIONS
A1	4.23	4.06	4.15
A2	5.16	4.10	4.63
A3	5.33	4.93	5.13
A4	5.06	4.16	4.61
A7	5.16	4.33	4.75
A9	4.46	4.20	4.33
A10	4.10	4.53	4.31
A11	5.78	5.20	5.48
A12	3.66	4.13	3.90
14-026	6.06	5.06	5.56
14-027	5.16	4.13	4.65
14-030	4.16	4.63	4.40
GREEN	3.83	4.33	4.08
LEGON 1	5.93	5.53	5.73
MEAN	4.86	4.52	4.69
GCV	35.23	21.61	9.20
PCV	35.69	22.38	10.94

4.1.9 Average fruit weight

The combined analysis of variance showed that effects of genotype and genotype-by-location interaction were significantly ($P < 0.01$) different for average fruit weight. The effect of location was not significantly different for the trait. The mean values for average fruit weight ranged from 33.3 – 75.8 g at Kade. At Legon the mean values for average fruit weight among the genotypes ranged from 23.6 – 57.2 g (Table 4.16). Across the two locations mean values for average fruit weight among the genotypes ranged from 33.1 – 61.6 g. The highest and lowest mean values were scored by genotypes A4 and A1 respectively at Kade while genotypes 14-026 and 14-027 scored the highest and lowest values respectively at Legon.

Table 4.16 Mean Average Fruit Weight

GENOTYPE	Average Fruit Weight (g)		
	KADE	LEGON	COMBINED LOCATIONS
A1	33.3	50.1	41.7
A2	45.8	37.0	41.4
A3	63.9	35.9	49.9
A4	75.8	47.3	61.6
A7	50.6	38.1	44.3
A9	51.4	44.7	48.1
A10	56.6	38.5	47.6
A11	68.0	35.3	51.6
A12	55.7	42.2	49.0
14-026	56.0	57.2	56.6
14-027	48.4	23.6	36.0
14-030	46.7	48.6	47.6
GREEN	59.6	46.4	53.0
LEGON 1	38.7	27.5	33.1
MEAN	53.6	40.9	47.2
GCV	133.2	120.1	7.4
PCV	153.7	141.5	16.2

4.1.10 Fruit weight per plot

Combined analysis for number of fruits per plant showed that effect of genotype, location and Genotype x Location interaction were significantly (< 0.01) different. The mean values for fruits weight per plot at Kade ranged from 168.0 – 835.0 g while at Legon the mean values ranged from 99.0 g – 918.0 g (Table 4.17). Across the two locations mean values among the genotypes ranged from 134.0 – 785.0 g. The highest and lowest mean values were recorded by genotypes A4 and LEGON 1 respectively at Kade while genotypes A10 and LEGON 1 scored the highest and lowest values respectively at Legon.

Table 4.17 Mean of Fruit Weight per Plot

GENOTYPE	Weight of Fruit Per Plot (g)		
	KADE	LEGON	COMBINED LOCATIONS
A1	204.0	405.0	304.0
A2	407.0	299.0	353.0
A3	468.0	459.0	464.0
A4	835.0	344.0	589.0
A7	517.0	378.0	447.0
A9	342.0	282.0	312.0
A10	495.0	918.0	707.0
A11	476.0	557.0	516.0
A12	795.0	622.0	708.0
14-026	330.0	881.0	605.0
14-027	327.0	119.0	223.0
14-030	748.0	822.0	785.0
GREEN	563.0	583.0	573.0
LEGON 1	168.0	99.0	134.0
MEAN	477.0	483.0	480.0
GCV	857.1	1072.4	30.3
PCV	941.2	1189.3	40.7

4.1.8 Fruit size

Based on the combined analysis of variance effects of genotype and genotype-by-location interaction were significantly ($P < 0.01$) different for fruit size. However, location effect was not significant for the trait. The mean values for fruit size at Kade ranged from 0.54 -1.12. At Legon the mean values ranged from 0.64 – 1.09 cm (Table 4.18). Across the two locations mean values ranged from 0.61 – 1.06 cm. The highest and lowest mean values were scored by genotypes A4 and GREEN respectively at Kade while genotypes A3 and A12 scored the highest and lowest values respectively at Legon.

Table 4.18 Mean Fruit size

GENOTYPE	Fruit Size (cm)		
	KADE	LEGON	COMBINED LOCATIONS
A1	0.94	0.98	0.96
A2	0.80	0.94	0.87
A3	1.02	1.09	1.06
A4	1.12	0.81	0.96
A7	0.92	0.85	0.89
A9	0.87	0.69	0.78
A10	0.68	0.90	0.79
A11	0.93	0.94	0.94
A12	0.58	0.64	0.61
14-026	1.08	0.99	1.04
14-027	0.84	0.81	0.85
14-030	0.78	0.91	0.85
GREEN	0.54	0.78	0.66
LEGON 1	0.91	0.90	0.90
MEAN	0.86	0.85	0.87
GCV	45.25	37.56	0.23
PCV	42.42	36.25	0.19

4.1.11 Fruit yield

Based on the combined analysis of variance effects of genotype and genotype-by-location interaction were significantly ($P < 0.01$) different for fruit yield. However, location effect was not significantly ($P < 0.05$) different for the trait. The mean values for fruit yield at Kade ranged from 2.63 – 13.05 ton/ha. At Legon the mean values ranged from 1.55 – 14.35 t/ha (Table 4.19).

Across the two locations mean values ranged from 2.09 – 12.27. The highest and lowest mean values were recorded by genotypes A4 and LEGON 1 respectively at Kade while genotypes A10 and LEGON 1 scored the highest and lowest values respectively at Legon.

Table 4.19 Mean Yield

GENOTYPE	Yield (ton/ha)		
	KADE	LEGON	COMBINED LOCATIONS
A1	3.18	6.33	4.75
A2	6.36	4.67	5.52
A3	7.32	7.18	7.25
A4	13.05	5.37	9.21
A7	8.07	5.91	6.99
A9	5.35	4.40	4.87
A10	7.74	14.35	11.04
A11	7.43	8.70	8.07
A12	12.42	9.71	11.07
14-026	5.16	13.77	9.46
14-027	5.12	1.87	3.49
14-030	11.69	12.84	12.27
GREEN	8.79	9.10	8.95
LEGON 1	2.63	1.55	2.09
MEAN	7.45	7.55	7.50
GCV	107.15	134.02	30.26
PCV	117.68	148.64	40.71

4.3 PERFORMANCE OF GENOTYPES FOR BIOACTIVE COMPOUNDS COMPONENTS

4.3.1 Ascorbic acid content

The combined analysis of variance for ascorbic acid content showed that effects of genotype were significantly ($P < 0.01$) different. However, effects of location and Genotype x Location interaction were not significant for the trait. The mean performance of the genotypes for ascorbic acid content at Kade ranged from 1.380 – 1.846 mg/g and at Legon mean values ranged from 1.210 – 1.892 mg/g respectively (Table 4.20). Across the two locations mean values ranged from 1.336 – 1.846 mg/g respectively. The highest and lowest mean values at Kade were recorded by

genotypes A10 and 14-027 respectively. At Legon, the highest and lowest mean values were recorded by genotypes A9 and A3respectively.

4.3.2 Magnesium content

The combined analysis of variance for magnesium content in the fruit showed that effects of genotype, location and Genotype x Location interaction were not significantly ($P < 0.01$) different. The mean performance of the genotypes for magnesium content at Kade ranged from 0.250 – 0.356 ppm respectively and at Legon mean values ranged from 0.247 – 0.288 ppm respectively (Table 4.21). Across the two locations mean values ranged from 0.259 – 0.779 ppm respectively. The highest and the lowest mean values at Kade were recorded by genotypes GREEN and A1. At Legon, the highest and lowest mean values were recorded by genotypes GREEN and 14-030 respectively.

Table 4.20 Mean ascorbic acid

Genotype	Ascorbic acid (AA) mg/g		
	Kade	Legon	Combined locations
A1	1.792	1.479	1.635
A10	1.846	1.843	1.845
A11	1.514	1.491	1.503
A12	1.673	1.738	1.706
14-026	1.600	1.549	1.575
14-027	1.380	1.292	1.336
14-030	1.504	1.525	1.515
A2	1.536	1.336	1.436
A3	1.569	1.210	1.389
A4	1.548	1.671	1.610
A7	1.713	1.700	1.707
A9	1.799	1.892	1.846
GREEN	1.513	1.407	1.407
LEGON 1	1.565	1.562	1.564
Mean	1.611	1.550	1.580
GCV	7.615	13.83	8.801
PCV	10.59	16.27	9.890

Table 4.21 Mean magnesium (Mn)

Genotype	Magnesium (Mn) ppm		
	Kade	Legon	Combined locations
A1	0.250	0.280	0.265
A10	0.287	0.261	0.275
A11	0.276	0.254	0.265
A12	0.268	0.260	0.264
14-026	0.267	0.250	0.259
14-027	0.291	0.255	0.273
14-030	0.290	0.247	0.268
A2	0.273	0.279	0.276
A3	0.276	0.257	0.267
A4	0.292	0.266	0.779
A7	0.299	0.265	0.282
A9	0.285	0.282	0.284
GREEN	0.356	0.288	0.322
LEGON 1	0.286	0.275	0.280
Mean	0.357	0.266	0.311
GCV	0.001	1.876	4.151
PCV	45.23	2.512	43.59

4.3.3 Potassium content

Based on the combined analysis of variance for potassium content in the fruit effect of genotype was significantly ($P < 0.01$) different while location and Genotype x Location effects were also not significant. The mean performance of the genotypes for potassium content at Kade ranged from 0.987 – 1.490 ppm and at Legon mean values ranged from 0.870 – 1.383 ppm respectively (Table 4.22). Across the two locations mean values ranged from 0.950 – 1.437 ppm. The highest and the lowest mean values for potassium content at Kade were recorded by genotypes A10 and 14.026 respectively. At Legon, the highest and lowest mean values were recorded by genotypes A10 and 14-027 respectively.

4.3.4 Zinc

The combined analysis of variance for zinc content in the fruit showed that genotype and Genotype x Location interaction were significantly ($P < 0.01$) different. However a location effect was not significantly different ($P < 0.05$). The mean performance of the genotypes for zinc content at Kade ranged from 0.0009 – 0.0073 ppm respectively and at Legon mean values ranged from 0.0002 – 0.0090 ppm respectively (Table 4.33). Across the two locations mean values ranged from 0.009 – 0.0058 ppm respectively. The highest and the lowest mean values at Kade were recorded by genotypes A9 and A1. At Legon, the highest and lowest mean values were recorded by genotypes A1 and GREEN respectively.

Table 4.22 Mean Potassium (K)

Genotype	Potassium (K)		
	Kade	Legon	Combined locations
A1	0.993	0.953	0.973
A10	1.490	1.383	1.437
A11	1.090	1.083	1.087
A12	1.043	1.007	1.025
14-026	0.987	0.977	0.982
14-027	1.030	0.870	0.950
14-030	1.010	0.967	1.988
A2	1.090	1.123	1.107
A3	1.007	1.017	1.012
A4	1.060	1.003	1.035
A7	1.153	1.090	1.122
A9	1.177	1.123	1.150
GREEN	1.210	1.260	1.235
LEGON 1	1.187	1.183	1.185
Mean	1.109	1.074	1.074
GCV	9.360	11.51	11.76
PCV	12.64	13.04	12.02

Table 4.23 Mean Zinc (Zn)

	Zinc (Zn)		
Genotype	**Kade**	**Legon**	**Combined locations**
A1	0.0009	0.0090	0.0049
A10	0.0019	0.0058	0.0039
A11	0.0014	0.0013	0.0014
A12	0.0009	0.0009	0.0009
14-026	0.0017	0.0012	0.0015
14-027	0.0049	0.0025	0.0038
14-030	0.0024	0.0087	0.0056
A2	0.0016	0.0025	0.0021
A3	0.0017	0.0009	0.0013
A4	0.0016	0.0009	0.0013
A7	0.0010	0.0007	0.0009
A9	0.0073	0.0042	0.0058
GREEN	0.0067	0.0002	0.0035
LEGON 1	0.0015	0.0017	0.0016
Mean	0.0026	0.0029	0.0016
GCV	4.1148	5.2369	0.0001
PCV	4.2210	5.4152	0.6511

4.4 DESTRUCTIVE SAMPLED TRAITS

4.4.2 Leaf dry weight

Based on the combined analysis of variance, effects of genotype, location and Genotype x Location interaction were not significantly ($P < 0.05$) different. The mean performance of the genotypes for leaf dry weight at Kade ranged from 2.56 – 7.04 g and at Legon mean values ranged from 2.83 – 7.65 g respectively (Table 4.24). Across the two locations mean values ranged from 2.70 – 6.94 g. The highest and the lowest mean values for leaf dry weight at Kade was recorded by genotypes A3 and A11 respectively. At Legon, the highest and lowest mean values were recorded by genotypes A12 and A11 respectively.

Table 4.24 Mean Leaf Dry Weight

GENOTYPE	Leaf Dry Weight (g)		
	KADE	LEGON	COMBINED LOCATIONS
A1	4.37	4.25	4.31
A2	4.45	3.42	3.93
A3	7.02	7.47	7.26
A4	5.57	5.65	5.26
A7	3.83	4.57	4.20
A9	5.53	5.73	5.63
A10	3.90	3.98	3.94
A11	2.56	2.83	2.70
A12	6.22	7.65	6.94
14-026	4.89	6.80	5.85
14-027	6.37	5.92	6.14
14-030	7.17	4.87	6.02
GREEN	3.90	3.72	3.81
LEGON 1	5.63	6.07	5.88
MEAN	5.11	5.21	5.16
GCV			
PCV			

4.4.4 Stem dry weight

The combined analysis of variance for stem dry weight showed that genotype, location and Genotype x Location interaction were not significantly ($P < 0.05$) different. The mean performance of the genotypes for stem dry weight at Kade ranged from 0.52 – 2.27 g and at Legon mean values ranged from o.55 – 1.75 g (Table 4.25). Across the two locations, mean values ranged from 0.53 – 1.93. The highest and the lowest mean values at Kade were recorded by genotypes 14-030 and A11 respectively. At Legon, the highest and the lowest mean values were recorded by genotypes LEGON 1 and A11respectively.

Table 4.25 Mean Stem Dry Weight

GENOTYPE	Stem Dry Weight (g)		
	KADE	LEGON	COMBINED LOCATIONS
A1	0.61	0.66	0.64
A2	0.94	0.68	0.81
A3	1.39	1.55	1.47
A4	1.00	1.20	1.10
A7	1.29	1.21	1.25
A9	1.40	1.31	1.36
A10	0.72	0.73	0.72
A11	0.52	0.55	0.53
A12	0.91	1.55	1.23
14-026	1.66	1.71	1.69
14-027	1.74	1.31	1.52
14-030	2.27	1.15	1.71
GREEN	1.78	1.28	1.53
LEGON 1	2.11	1.75	1.93
MEAN	1.31	1.19	1.25
GCV	0.00	0.00	0.20
PCV	65.8	54.5	0.20

4.4.6 Root dry weight

The combined analysis of variance for root dry weight showed that effects of genotype, location and Genotype x Location interaction were not significantly ($P < 0.05$) different. The mean performance of the genotypes for root dry weight at Kade ranged from 0.78 – 1.77 g and at Legon mean values ranged from 0.70 – 1.25 g (Table 4.25). Across the two locations mean values ranged from 0.75 – 1.35 g. The highest mean value at Kade was recorded by genotype A3 while genotypes A2 and A11recorded the lowest values. At Legon, the highest and the lowest mean values were recorded by genotypes 14-030 and A10 respectively.

Table 4.25 Mean Root Dry Weight

GENOTYPE	Root Dry Weight (g)		
	KADE	LEGON	COMBINED LOCATIONS
A1	0.87	0.71	0.79
A2	0.78	0.72	0.75
A3	1.77	1.56	1.67
A4	1.04	1.10	1.07
A7	1.08	0.81	0.95
A9	1.01	0.91	0.96
A10	1.11	0.70	0.90
A11	0.78	0.80	0.79
A12	1.49	1.16	1.33
14-026	1.16	1.08	1.12
14-027	1.18	1.05	1.11
14-030	1.45	1.25	1.35
GREEN	0.90	1.00	0.95
LEGON 1	0.86	0.83	0.84
MEAN	1.10	0.98	1.05
GCV	0.00	0.00	39.0
PCV	101.9	96.9	39.0

4.5 THE VARIANCE COMPONENTS OF THE STUDIED CHARACTERS

4.5.1 Variance component for vegetative traits

Variance components estimated across the two locations are shown in Table 4.15. Among the vegetative traits, variance due to location (σ^2_L) was higher than the corresponding genotypic variance for number of leaves, stem girth, plant height and chlorophyll content. However, genotypic variance was higher than the corresponding location variance for leaf area, root length and canopy span. The estimated phenotypic variance (σ^2_P) was higher than the genotypic variance for all the vegetative traits studied. Also, variance due to environment (σ^2_E) was higher than the corresponding genotypic variance for almost all traits except canopy span. With the exception of number of leaves and stem girth, Variance due to genotype (σ^2_G) was found to be higher than the Genotype x Location variance ($\sigma^2_{G\,x\,L}$) counterparts for all other vegetative traits. The difference between GCV and PCV was narrow for all traits except number of leaves and stem girth.

4.5.2 Heritability

Heritability estimated for vegetative characters across the two locations are shown in Tables 4.17. Among the vegetative traits studied, leaf area, root length, canopy span, plant height and chlorophyll content recorded high (> 60 %) estimates of heritability. However, heritability values estimated for number of leaves and stem girth was very low (< 10 %). Stem girth recorded the lowest estimated broad sense heritability (1%) while the highest estimated value of 97 % was recorded by leaf area among the various vegetative traits.

4.5.3 Estimated genetic gain for vegetative traits

The estimated values of genetic gain for the vegetative traits expressed as genetic advance as percentage of mean (GAM) over the locations is presented in Tables 4.26. Apart from number of leaves and stem girth all the remaining traits recorded higher values of genetic gain (> 20 %). Leaf area recorded the highest value (44243.51 %) whiles stem girth scored the lowest estimated value of genetic gain (0.26 %).

Table 4.26 Mean of vegetative characters

	Variance Components			Heritability and Genetic gain	
Vegetative Characters	Q^2_G	Q^2_P	Q^2_E	H^2_b	**EGA(% of mean)**
Leaf area	683562.17	701853.17	1134510.00	0.97	1367124.33
Root length	2.82	3.24	20.86	0.87	5.65
Canopy span	20.29	21.21	0.85	0.96	40.58
No. of leaves	0.00	265.16	62.43	00.0	0.00
Stem girth	0.02	1.73	1.10	1.00	0.03
Plant height	23.0	38.97	39.05	0.59	46.02
Chlorophyll Content	26.99	40.21	47.17	0.67	53.99

Q^2_G = genotypic variance; Q^2_E = error variance; Q^2_P= phenotypic variance; H^2_b = broad sense heritability; EGA=Expected genetic advance of the mean.

4.5.4 Variance components for yield and yield components

Variance components estimated over locations for yield and yield component traits are shown in Table 4.27. Among the yield and yield component traits, estimated genotypic variance was higher than the corresponding variance due to location (σ^2_L) for almost all traits except average fruit weight. The estimated phenotypic variance (σ^2_P) was higher than the genotypic variance for all the yield and yield component traits studied.

Traits including number of fruits, average fruit weight, fruit weight per plot and fruit yield recorded lower values of environmental variance (σ^2_E) than the corresponding genotypic variance (σ^2_G) while the rest of the traits recorded higher values for genotypic variance (σ^2_G) than the corresponding environmental variance. Among the yield and yield component traits, σ^2_G was found to be higher than the corresponding $\sigma^2_{G \times L}$ for most traits except number of fruits, average fruit weight fruit weight per plot and fruit yield. The difference between GCV and PCV was observed to be narrow for almost all the traits studied.

4.5.5 Estimates of heritability for yield and yield components

The estimated values of heritability for yield and yield component traits over the combined locations are presented in Tables 4.27. Among the yield and yield component traits studied, the estimates of heritability was higher (> 60 %) for most traits except number of fruits, average fruit weight, fruit weight per plot and fruit yield which recorded moderate estimates.

4.5.6 Estimates of genetic gain yield and yield components

Genetic gain expressed as genetic advance as percentage of mean (GAM) over the locations is presented in Tables 4.27. Almost all the yield and yield component traits recorded high (> 20 %)

values of genetic gain (GAM). However, fruit diameter and fruit length recorded moderate (10 – 20 %) and low (< 10 %) estimated values of heritability.

Table 4.27 Mean of yield components

	Variance Components			Heritability and Genetic gain	
Yield Components	**Q^2_G**	**Q^2_P**	**Q^2_E**	**H^2_b**	**EGA(% of mean)**
Days to 50% flowering	16.66	16.82	0.40	0.99	33.33
Days to fruiting	20.24	21.53	2.10	0.94	40.48
Days to maturity	26.99	30.28	12.20	0.89	53.99
Days to ripening	19.91	20.94	1.60	0.95	39.83
Fruit diameter	0.24	0.33	0.05	0.73	0.49
Fruit length	0.26	0.36	0.03	0.71	0.51
Number of fruits	7.23	14.18	12.71	0.51	14.46
Ave. fruit weight	12.15	58.18	86.83	0.21	24.30
Fruit weight/plot	21093.83	38191.83	30969.00	0.55	42187.67
Yield/ton	5.15	9.32	7.56	0.55	10.30

Q^2_L = Location variance; Q^2G = genotypic variance; Q^2E = error variance; Q^2P= phenotypic variance; EGA = expected genetic advance of percentage of the mean

4.5.7 Variance components for destructive sample traits

Variance components estimated for all the destructive sample traits are shown in Table 4.28. The estimated genotypic variance (σ^2_G) was higher than the corresponding variance due to location (σ^2_L) as well as variance due to Genotype x Location interaction (σ^2_{GxL}) for all traits. With the exception of root fresh weight, all the destructive sample traits recorded higher values of environmental variance (σ^2_E) than the corresponding genotypic variance (σ^2_G). The estimated phenotypic variance (σ^2_P) was higher than the genotypic variance (σ^2_G) counterparts for all the

destructive sample traits studied. The difference between GCV and PCV was observed to be narrow for almost all the traits studied.

4.5.8 Estimates of heritability for destructive sample traits

The estimated values of heritability for destructive sample traits over the combined locations are presented in Tables 4.28. Among the traits studied, the estimate of heritability was higher (> 0.60) for all traits. The highest and lowest heritability estimates were recorded by leaf fresh weight (0.96) and root fresh weight (0.65) respectively.

4.5.9 Estimates of genetic gain destructive sample traits

Genetic gain expressed as genetic advance as percentage of mean (GAM) computed over the combined locations for the destructive sample traits is presented in Tables 4.28. Most of the traits recorded high (> 20 %) values of genetic gain (GAM) except root dry matter and fresh weights which recorded moderate values (10 – 20 %). The highest estimate of GAM was recorded by leaf fresh weight (698.03 %) while the lowest values were recorded by root dry weight (11.80 %).

Table 4.28 Mean destructive sampled

Distractive Sampled	**Variance Components**			**Heritability and Genetic gain**	
Characters	**Q^2_G**	**Q^2_P**	**Q^2_E**	**H^2_b**	**EGA(% of mean)**
Leaf dry weight	1.53	1.78	8.66	0.86	3.06
Root dry weight	0.06	0.07	0.30	0.92	0.12
Stem dry weight	0.15	0.19	0.66	0.78	0.30

Q^2_L = Location variance; Q^2G = genotypic variance; Q^2E = error variance; Q^2P= phenotypic variance; H^2_b = broad sense heritability; EGA = expected genetic advance of the mean.

4.5.10 Variance components for fruit bioactive compounds

Variance components estimated for all the fruit bioactive compounds traits are shown in Table 4.29. The estimated values for genotypic (σ^2_G), location (σ^2_L), Genotype x Location interaction and environmental variance (σ^2_{GxL}) for all traits were very low (< 10). The estimated phenotypic variance (σ^2_P) was higher than the corresponding genotypic variance (σ^2_G) for zinc (Zn), manganese (Mn), and ascorbic acid (AA) while estimated values σ^2_G and σ^2_P were the same for potassium (K). The difference between GCV and PCV was observed to be narrow for almost all the bioactive compounds studied.

4.5.11 Estimates of heritability for fruit bioactive compound traits

The estimated values of heritability for bioactive compounds the combined locations are presented in Tables 4.29. Among the traits studied, the estimate of heritability was higher (>0.60) for potassium (K) and ascorbic acid composition. The highest and lowest heritability estimates were recorded by potassium (0.96) and Zinc (Zn) (0.00) respectively.

4.5.12 Estimates of genetic gain

Genetic gain expressed as genetic advance as percentage of mean (GAM) computed over the combined locations for the bioactive compounds is presented in Tables 4.29. Generally, a very low (< 10) estimate of genetic gain was recorded by all the bioactive compounds.

Table 4.29 Mean of Bioactive components

	Variance Components			Heritability and Genetic gain	
	Q^2_G	Q^2_P	Q^2_E	H^2_b	EGA(% of mean)
K	0.02	0.02	0.02	0.96	0.03
Zn	0.00	0.00	0.00	0.00	0.00
Mn	0.00	0.02	0.11	0.01	0.00
AA	0.02	0.02	0.03	0.79	0.04

Q^2_G = genotypic variance; Q^2_E = error variance; Q^2_P= phenotypic variance; H^2_b = broad sense heritability; EGA = expected genetic advance.

4.6 PEARSON'S CORRELATION MATRIX AMONG TRAITS

4.5.1 Pearson's correlation coefficient among yield, yield component characters and bioactive compounds

The associations among selected agronomic characters and fruit bioactive compounds of fourteen accessions of African eggplant analysed across the two locations has been shown (Table 4.30). Positive and significant association was observed for fruit weight per plot with number of fruits per plant (r = 0.864) and average fruit weight (r = 0.455). Fruit yield correlated positively and significantly with number of fruits per plant (r = 0.864), average fruit weight (r = 0.455) and fruit weight per plot. A significantly positive association was observed between trait pairs days to fruiting and days to flowering (r = 0.881), fruit size and fruit length (r = 0.654) as well as potassium and fruit length (0.0271). Days to fruit maturity associated positively and significantly with days to flowering (r = 0.701) and days to fruiting (r = 0.708). Number of days to fruit ripening showed a significantly positive association with number of days to flowering (r = 0.839), number of days to fruit ripening (r = 0.853) and number of days to fruit maturity (0.773).

Magnesium showed a weak positive and significant correlation with number of fruits per plot (r = 0.215) and fruit yield (r = 0.215).

On the other hand, a negative and significant correlation was observed for number of days to fruit ripening and number of fruits per plant (r = - 0.276), fruit weight per plot (r = - 0.217), and fruit yield p (r = - 0.881). There was a significantly negative association between number of days to fruit maturity and number of fruits per plant (r = - 0.216), fruit weight per plot (r = - 0.281) and fruit yield (r = 0.281). Also, a negative and significant association was observed between numbers of days to fruit ripening and number of fruits per plant (r = - 0275), fruit weight per plot (r = - 0.317), and fruit yield (r = - 317). Fruit diameter associated negatively and significantly with fruit size (r = - 0.677) and Zinc (0.221).

Table 4.30 The Pearson's correlation coefficient among yield, yield components and bioactive compounds

Traits	Ave.FWT	FWT/PLT	Y/T	DFL	DFR	DMT	DRP	FDM	FLT	FS	K	Zn	Mn	AA
NFR	-0.008	**0.864****	**0.864****	-0.149	-0.111	**-0.216***	**-0.275***	-0.202	-0.118	0.073	0.120	0.120	0.084	-0.004
Ave.FWT	-	**0.455***	**0.455***	-0.156	**-0.276***	-0.197	-0.171	0.159	0.078	-0.017	0.077	0.087	0.179	0.004
FWT/PLT		-	**1.000****	-0.198	**-0.217***	**-0.281***	**-0.317***	-0.131	-0.070	0.071	0.104	0.128	**0.215***	-0.021
Y/T			-	-0.198	**-0.217***	**-0.281***	**-0.317***	-0.131	-0.070	0.071	0.104	0.128	**0.215***	-0.021
DFL				-	**0.881****	**0.701****	**0.839****	-0.052	0.160	0.138	-0.029	-0.043	-0.096	0.011
DFR					-	**0.708****	**0.853****	-0.107	0.170	0.174	-0.028	-0.077	-0.131	0.054
DMT						-	**0.773****	-0.098	0.190	0.175	0.021	0.146	-0.138	0.017
DPR							-	-0.151	0.156	0.195	-0.091	0.050	-0.109	0.001
FDM								-	0.099	**-0.677****	-0.035	**-0.221***	0.041	-0.145
FLT									-	**0.654****	**0.271***	-0.067	-0.119	0.118
FS										-	0.208	0.102	-0.103	0.194
K											-	0.084	0.027	0.319
Zn												-	-0.006	0.086
Mn													-	0.033

FLT = Fruit length; FS = Fruit size; NFR = Number of fruits; Ave. FWT = Average fruit weight; FWT/PLT = Fruit weight per plot; Y/T = Yield per ton; DFL = Days to50% flowering; DFR = Days to fruiting: DMT = Days to maturity; DRP = Days to ripening; FDM = Fruit diameter; K = Potassium; Mn = Magnesium; Zn = Zinc; AA = Ascorbic acid;=significant (P<0.05), **=high significant (P<0.01).*

4.5.2 Pearson's correlation coefficient among vegetative, yield and yield component characters

The Pearson's correlation coefficient among vegetative, yield and yield component characters of fourteen accessions of African eggplant analysed across the two locations has been shown (Table 4.31). A positive and significant association was observed for fruit weight per plot with number of fruits per plant (r = 0.864) and average fruit weight (r = 0.455). Fruit yield correlated positively and significantly with number of fruits per plant (r = 0.864), average fruit weight (r = 0.455) and fruit weight per plot (r = 1.00). A significantly positive association was observed between trait pairs days to fruiting and days to flowering (r = 0.881), fruit size and fruit length (r = 0.654) as well as leaf area and fruit diameter.

Days to fruit maturity associated positively and significantly with days to flowering (r = 0.701) and days to fruiting (r = 0.708). Number of days to fruit ripening showed a significantly positive association with number of days to flowering (r = 0.839), number of days to fruit ripening (r = 0.853) and number of days to fruit maturity (0.773). Root length correlated positively and significantly with fruit length (r = 0.234), and fruit size (r = 0.286). The association of plant height with average fruit weight (r = 0.495), fruit diameter (r = 0.353) and fruit length (r = 0.330) were significantly positive. Number of leaves showed a positive and significant correlation with average fruit weight (r = 0.454) and fruit length (r = 0.389) and plant height (r = 0.879).Stem girth also correlated positively and significantly with average fruit weight (r = 0.311) and plant height (r = 0.555).

However, a negative and significant correlation was observed for number of days to fruit ripening and average fruit weight (r = - 0.276), fruit weight per plot (r = - 0.217), and fruit yield (r = - 0.217).

Table 4.31 The Pearson's correlation coefficients among vegetative, yield and yield component characters

Characters	Ave.FWT	FWT/PLT	Y/T	DFL	DFR	DMT	DRP	FDM	FLT	FS	LA	RL	PHT	NL	CC	SG
NFR	-0.008	**0.864****	**0.864****	-0.149	-0.111	**-0.216***	**-0.275***	-0.202	-0.118	0.073	0.195	0.048	-0.172	-0.093	0.177	-0.001
Ave.FWT	-	**0.455***	**0.455***	-0.156	**-0.276***	-0.197	-0.171	0.159	0.078	-0.017	-0.029	0.069	**0.495***	**0.454***	**-0.348***	**0.311***
FWT/PLT		-	**1.000****	-0.198	**-0.217***	**-0.281***	**-0.317***	-0.131	-0.070	0.071	0.124	0.103	0.071	0.126	0.035	0.135
Y/T			-	-0.198	**-0.217***	**-0.281***	**-0.317***	-0.131	-0.070	0.071	0.124	0.103	0.071	0.126	0.035	0.135
DFL				-	**0.881****	**0.701****	**0.839****	-0.052	0.160	0.138	-0.106	-0.039	0.002	-0.095	0.085	0.055
DFR					-	**0.708****	**0.853****	-0.107	0.170	0.174	-0.048	-0.059	-0.060	-0.149	0.200	0.061
DMT						-	**0.773****	-0.098	0.190	0.175	-0.006	-0.001	0.007	-0.100	0.092	0.001
DRP							-	-0.151	0.156	0.195	-0.140	0.039	0.049	-0.084	0.020	0.056
FDM								-	0.099	**-0.677****	**0.226***	-0.156	**0.353***	0.180	-0.173	0.191
FLT									-	**0.654****	0.134	**0.234***	**0.330***	**0.389***	-0.200	0.144
FS										-	-0.069	**0.286***	-0.001	0.191	-0.035	-0.017
LA											-	0.038	0.034	0.047	0.055	-0.039
RL												-	0.054	0.091	0.047	0.042
PHT													-	**0.879****	**-0.630****	**0.555****

FLT = Fruit length; FS = Fruit size; NFR = Number of fruits; Ave. FWT = Average fruit weight; FWT/PLT = Fruit weight per plot; Y/T = Yield per ton; DFL = Days to50% flowering; DFR = Days to fruiting: DMT = Days to maturity; DRP = Days to ripening; FDM = Fruit diameter; PHT = Plant height; SG = Stem girth; NL = Number of leaves; LA = Leaf area; RL = Root length; CSMT = Canopy span at maturity; CC= Chlorophyll content;=significant (P<0.05), **=high significant (P<0.01)*

4.5.3 Pearson's correlation coefficient among vegetative and fruit bioactive compounds characters

The Pearson's correlation coefficient among vegetative characters, yield and yield components of selected accessions of African eggplant analysed across the two locations has been shown (Table 4.32). A positive and significant association was between number of leaves and plant height(r = 0.879). Stem girth correlated positively and significantly with plant height (r = 0.555) and number of leaves (r = 0.537). A positive and significant association was observed for canopy span at maturity with plant height (r = 0.223), number of leaves (r = 0.290) and stem girth (r = 0.295). There was a positive and significant association between potassium and leaf area (r = 0.350) and canopy span at maturity (r = 0.344). Zinc correlated positively with root length (r = 0.273) and canopy span at maturity (r = 0.259). Ascorbic acid content correlated positively and significantly with leaf area (r = 0.331).

A negative significant association was observed for chlorophyll content and plant height (r = -0.630) and number of leaves (r = 0.628). Also, a significant and positive association between stem girth and chlorophyll content (r = -275).

Table 4.32 The Pearson's correlation coefficients among vegetative characters and bioactive compounds

Characters	RL	PHT	NL	CC	SG	CSMT	K	Zn	Mn	AA
LA	0.038	0.034	0.047	0.055	-0.039	-0.058	**0.350***	0.020	-0.101	**0.331***
RL	-	0.054	0.091	0.047	0.042	0.150	-0.099	**0.273***	-0.049	-0.207
PHT		-	**0.879****	**-0.630****	**0.555****	**0.223***	0.111	0.012	0.148	0.034
NL			-	**-0.628****	**0.537****	**0.290***	0.120	-0.004	0.128	0.060
CC				-	**-0.275***	0.070	-0.197	-0.046	-0.149	-0.115
SG					-	**0.295***	0.002	0.019	0.071	-0.073
CSMT						-	**0.344***	**0.259***	-0.063	-0.028
K							-	0.084	0.027	0.319
Zn								-	-0.006	0.086
Mn									-	0.033

PHT = Plant height; SG = Stem girth; NL = Number of leaves; CC= Chlorophyll content; LA = Leaf area; RL = Root length; CSMT = Canopy span at maturity; K = Potassium; Mn = Magnesium; Zn = Zinc; AA = Ascorbic acid;=significant (P<0.05), **=high significant (P<0.01).*

5.0 DISCUSSIONS

5.1 PERFORMANCE OF GARDEN EGG ACCESSIONS

Vegetative, yield and yield component traits are economically important quantitative characters that influence the overall productivity of crops including garden eggs. The performance of a genotype for these quantitative traits is influenced by both genetic and environmental factors which define the variations that occur in crops. The present study revealed a significant variation among the genotypes, locations and their interaction for most of the studied traits. This indicated the possibility of differential response of the genotypes to different locations. Thus, the performance of garden egg accessions evaluated varied across the two locations for most traits. Generally, the performance of the accessions for most vegetative traits was higher at Kade as compared to the corresponding accessions studied at Legon. The relatively higher fruit yield at Legon than Kade in the present study perhaps suggested that vegetative traits did not play significant role in the overall yield performance of the genotypes. Plant height recorded in this study across the two locations ranged from 46.24 – 79.50 cm which was higher than values recorded by Nahid (2012) who recorded plant height range of 31 – 52 cm.

Phenological development characters including number of days to flowering, number of days to fruiting and number of days to fruit maturity play a significant role in the productivity of a crop (Awal and Ikeda, 2003). They are valuable characters considered in selecting genotypes required to obtain increased fruit productivity. In the present investigation, garden egg genotypes produced at Kade were earlier in flowering, fruiting and attainment of fruit maturity. Across the two experimental locations, four accessions A3, 14 – 030, A10 and A4 comparatively displayed earlier phenological development in flowering, fruiting and maturity. These genotypes represent

valuable accessions for selection in crop improvement programmes aimed at increasing garden egg productivity.

In the present study, fruit yield recorded ranged from 2.09 t/ha – 12.27 t/ha across the two locations and lower than previous finding by Adamczewska-Sowinska and Krygier (2013) and Nahid (2012) who reported yield varies in a range of 11.77 – 29.67 ton/ha and 5.75 – 33.43 ton/ha respectively. Differences in findings could be attributed to differences in accessions evaluated, as well as variation in the experimental locations. Garden egg genotypes 14 – 030, A12, A10, 14 – 026 and A4 produced better yield across locations and are potentially valuable source of genetic materials that could be used for further crop improvement programmes. According to Osman *et al.,* (2013), a common observation in crop studies is the association between yields and yield components traits. Comparatively, these genotypes also recorded higher values of one or more of essential characters like number of fruits per plant, average fruit weight, fruit weight per plant, fruit size and fruit length. This implied that such traits are economically important determinants of yield in garden eggs. Based on the present study, fruit length ranged from 4.33 – 6.36 cm while average number of fruits per plant ranged from 4 – 16. Based on a similar study conducted by Nahid (2012), fruit length ranged from 10 – 26 cm while the maximum and minimum values of number of fruits per plant recorded were 11 and 42. Differences in values reported could be due to differences in the accessions evaluated as well as season and experimental location. Generally, vegetables including eggplant are rich source of many essential bioactive compounds. Ascorbic acid is a bioactive compound with antioxidant property (ability to neutralize free radicals) in the human body, and hence play important role in reducing heart and cancer related incidence. Eggplant also represents essential source of many important mineral elements. In the present study, fruits' bioactive compounds varied

considerably among the eggplant accessions. Ascorbic acid varied among the accessions and ranged from 1.336 – 1.846 mg/g. In a related study carried out by Singh (2014) in tomato, the reported ascorbic acid content ranged 12.65 – 15.63 mg/100g. Mineral elements studied in this experiment included manganese, potassium and zinc. The amount of mineral elements recorded in these elements ranged from 0.265 – 0.284 ppm (manganese), 0.973 – 1.437 ppm (potassium) and 0.0009 – 0.0056 ppm (zinc). In a related study by Salisu *et al*., (2012) that determined trace elements in some fruits and vegetables mean values recorded were 2.39±0.11 mg/dm3 (zinc) and 0.31±0.02 mg/dm3 (manganese).

5.2 VARIANCE COMPONENTS, HERITABILITY AND GENETIC ADVANCE

Knowledge about genetic variability in a crop is fundamental in crop improvement programmes as it aids in planning efficient breeding programmes (Kumar *et al*., 2007). In the present study, the estimate of variance components including GCV and PCV was recorded for almost all the traits studied which suggested an existence of variability among the genotypes and locations. Cebula and Ambroszczyk (1999) reported an existence of wide variability in garden eggs in several traits like reproductive, fruit physical and quality traits. Generally, a higher estimate PCV than the corresponding GCV for almost all traits revealed the relative significant role of environmental factors on the expression of the traits. From the combined analysis of variance, location variance (σ^2_L) was higher than genotypic variance (σ^2_G) counterparts for most vegetative traits studied except leaf area. This implied that differences in location significantly affected the expression of those traits.

However, the effects of location on the expression of yield and yield component traits was not very much pronounced as evidenced in the high estimated values of genotypic variances than the

corresponding location variances for almost all yield and yield component traits. Most of these traits also recorded high values of heritability. This implied that the expression of yield and yield component traits were under strong genetic control. An exception was fruit weight per plant where variance due to location was rather higher. Fruit weight per plot was therefore influenced by differences in environmental conditions prevalent in the two experimental locations, thus a lower heritability value was observed for the trait. Destructive sample characters were not affected by location because results of the variance components indicated higher estimated σ^2_G than the corresponding location variances (σ^2_L). Also, no estimate of $\sigma^2_{G \times L}$ was recorded for almost all destructive sample traits studied in this experiment, thus high estimated values for heritability were recorded.

The estimates of higher values of variance due to genotype-by-location interaction ($\sigma^2_{L \times G}$) than the corresponding genotypic variance for some traits in the present study suggest that the two locations differed in both altitude and climatic factors (Usman, 2013). This finding also indicated that the performance of the accessions differed across the two locations. The effects due to $\sigma^2_{L \times G}$ resulted in lower estimated values of heritability for such traits. The significance of Genotype x Location interaction and its effects on the expression of traits have been reported in previous studies by Panthee (2012) and Causse, *et al*., (2003) in tomato. According to Khan *et al*., (2013), the significant estimate of σ^2_{LxG} for a trait suggests that individual location analysis of such traits is recommended. The ratio, σ^2_G:$\sigma^2_{G \times L}$ was close to unity only for fruit length and fruit yield per plant, thus suggesting that large proportion of genotypic factors than environment resulted in the observed variability among the genotypes.

The relative amount of variability due to genetic factors in a crop's accession could be obtained through the estimate of heritability. Based on the present study, most of the vegetative, yield

components, destructive sample traits and the bioactive compounds recorded high broad sense heritability estimates which indicated that they were highly controlled by inherent genetic factors. This suggests that selection of accessions for most of the traits could be effective at early generation. In contrast, traits that recorded low values of broad sense heritability values are influenced by environmental factors. Selection for such traits would not be effective at early generation. According to Falconer and Mackay (1996), heritability estimated along with high advance provide useful information about the kind of gene action involved in the expression of trait as well as the scope for selection. Results of the present study showed high broad sense heritability estimate along with high genetic advance for most of the vegetative and destructive sample traits, as well as yield and yield components. This suggests that selection for those traits could be effective. Findings from previous study by Ofori *et al.*, (2012) and Islam and Uddin recorded high (> 60 %) estimated heritability values for fruit length and days to flowering which are in agreement with the present study where high estimates of heritability were recorded for the same trait. Contrary to the present findings where moderate value of heritability was recorded for fruit yield per plant, Singh (2004) and Kaushik *et al*., (2011) reported the highest broad sense heritability estimate for fruit yield. Among the bioactive compounds high estimate of broad sense heritability was recorded for potassium (K) and ascorbic acid (AA) whose genetic gains were very low. This implied that selection for such traits in crop improvement programmes would not be effective.

5.3 CHARACTER ASSOCIATION IN GARDEN EGGS

From the results of the present study, fruit yield showed a positive and significant association with number of fruits, average fruit weight and fruit weight per plot. These results suggest the possibility for selection of those traits to maximize fruit yield.

Nahid (2012) observed that, number of fruits per plant associated positively with fruit yield which is in line with similar findings in the present study. On the other hand, the observed negative correlation of fruit yield with days to fruiting, fruit maturity and fruit ripening implied that selection pressure for either of those traits could possibly result in a positive gain in yield (Kubi, 2013). It also indicated that genotypes that attain early fruiting, maturity and ripening stage of development are high yielding. The correlation coefficient between fruit size and the other characters showed a significant estimate for fruit diameter and fruit length, the former scored negative and the later positive. This observation indicated that accessions with smaller fruit diameter as well as longer fruit length produced bigger fruit size. This again suggest that indirect selection for accessions which produce smaller fruit diameter and longer fruit length could result in increased fruit size in African eggplant.

Leaf area correlated significantly and positively only with number of days to fruit maturity which suggests that late maturing accessions have large leaf area. A weak positive correlation between root length and fruit length was significant and indicated that that selection for either of the trait pairs could be possible to improve upon the other. Plant height significantly and positively associated with average fruit weight, fruit length and fruit diameter and implied that tall accessions produced high average fruits which have high fruit length and diameter. This finding was in agreement with that of Abrefa and Ofori (2012) and Swamy *et al*., (2003) who observed a significant and positive association between plant height at flowering and fruit length. Also, a significantly positive association was observed for number of leaves with average fruit weight, fruit length and plant height. Thus, accessions with high number of leaves also produced high fruit weight and fruit length and were comparatively taller. The present results agree with findings by Kauskik *et al.,* (2011) who recorded a positive significant correlation between

number of leaves and fruit length. In this experiment, chlorophyll content showed highly significant and positive association with plant height and number of leaves, implying that shorter accessions and those with fewer number of leaves contain high chlorophyll content.

The bioactive compounds studied in the present experiment correlated with a number of traits with weak correlated coefficients. Potassium showed a significant and positive association with number of fruits per plant and canopy span at maturity. This indicated that selection for accessions with high number of fruits per plant and canopy span could lead to increased potassium composition in African eggplant. Similarly, zinc showed a significant and positive association with leaf area and canopy span at maturity which suggests the possibility for selection of the traits to enhance zinc composition. The association of manganese with fruit weight per plant and fruit yield was weak and positive. Thus, selection for accessions with high fruit weight per plant and longer fruits could result in a relative increase in manganese content.

CHAPTER SIX

6.0 CONCLUSIONS AND RECOMMENDATION

6.1 CONCLUSIONS

1. Systematic breeding programmes aimed at improving eggplant fruit yield and fruit quality traits require information on the nature and magnitude of genetic variability, heritability and character association in agronomic and fruit quality traits in the crop. Results of the present study revealed an existence of useful genetic variability in the genotypes. The estimate of moderate to high GCV, high broad sense heritability as well as high genetic gain for almost all characters associated with vegetative and yield components suggest the potential for selection and utilization of suitable genotypes based on different parameters to obtain high yield and fruit quality characteristics

2. Following the present findings, promising African eggplant genotypes based on their fruit yield (t/ha) across locations were 14 – 030, A 10 and A 12

3. African eggplant genotypes A 10 followed by 14 – 026 showed superior yield performance in Legon whiles A 4 and A 12 ranked highest in Kade respectively.

4. Across the two locations, A 12 and 14 – 030 were found to be superior among the genotypes performing relatively well in the various vegetative and yield components characters considered in this present study.

5. On the average, highest amount of fruit bioactive compounds contents obtained across the two locations were recorded by African eggplant genotypes A10 and A 4 respectively.

6. The average amounts of potassium and ascorbic acid were at more appreciable levels in most genotypes considered in this current study than magnesium and zinc composition. The amount of zinc present in all genotypes is significantly below the toxic levels but enough to activate various metabolic processes.

7. Generally, the performance of the genotypes evaluated differed across locations due to the interaction between the genotypes and environment. The expressions of most traits were influenced by effects of genetic and environmental factors as well as their interaction.

8. Number of fruits per plant, fruit weight per plot and average fruit weight per plant showed a positive and strong association with fruit yield and are potentially useful traits as indirect selection indexes for future yield improvement programs.

9. And also character association analysis acknowledged a weak and positive linkage between number of days to fruit ripening to number of fruits per plant and average fruit weight per plant has helped in widening the insight to time of harvesting and fruits shelf life. Accessions with less number of fruits per plant and those with larger fruits got ripened earlier, which give an indication for optimum harvesting time to reduce fruits lose and improvements in post-harvest management in fruit life span.

6.2 RECOMMENDATIONS

1. The results of the current study showed that African eggplant genotypes have prospects for commercial production under both experimental locations by virtue of their performance in fruit yield even during the off season when this study was initiated.

2. The present study was carried out under a single growing season; hence further evaluation of the genotypes could be conducted over multiple seasons or locations. The evaluation of the genotypes across multiple seasons and years along with appropriate stability analysis procedure can further be carried out to identify stable African eggplant genotypes for fruit yield and other important chemical composition traits defining fruit quality characteristics. This will also provide an in depth information regarding G x E interaction and eggplant fruit yields.

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APPENDIX

APENDIX I: MEAN SQUARES OF YIELD AND YIELD COMPONENTS

Source of Variation	DF	Means Squares				
		DFL	DFR	DMT	DRP	FDM
Replication	2	1.3214	4.619	19.73	1.798	0.30250
Location	1	12.1905	66.964	22.01	2.012	2.43440
Genotype	13	100.9194	129.184	181.69	125.627	1.99876
Genotype x Location	13	0.9341	7.734	19.73	6.140	0.54235
Residual	54	0.3955	2.101	12.20	1.600	0.04620
Total	83	-	-	-	-	-
CV (%)	-	17.71	14.89	15.63	9.92	14.51
Grand mean	-	22.8	32.70	40.58	46.99	4.69
Lsd (0.05) L	1	0.2751	0.634	1.528	0.553	0.0940
Lsd (0.05) G	13	0.7280	1.678	4.042	1.464	0.2488
Lsd (0.05) G x L	13	1.0295	2.373	5.717	2.071	0.3519

**Significant P < 0.05; ns = Not significant at 0.05; CV = Coefficient of variability; DFL = Days to flowering; DFR = Days to fruiting: DMT = Days to maturity; DRP = Days to ripening; FDM = Fruit diameter; L= Location; G = Genotypes; G x L = Genotype location interaction.*

APPENDIX II: MEANS SQUARES OF YIELD AND YIELD COMPONENTS

Source of Variation	DF	**Means Squares**					
		FLT	**FS**	**NFR**	**Ave. Fwt**	**Fwt/Plt**	**Y/T**
Replication	2	0.12250	0.00476	20.32	0.10	29629	7.23
Location	1	3.77190	0.00004	148.19	3399.55	897	0.22
Genotype	13	2.17282	0.09876	85.08	349.09	229151	55.95
Genotype x Location	13	0.63652	0.03376	41.70	276.20	30969	25.05
Residual	54	0.03262	0.00224	12.71	86.83	102588	7.56
Total	83	-	-	-	-	-	-
CV (%)	-	12.98	20.15	54.18	29.59	56.21	56.21
Grand mean	-	5.50	0.87	10.18	47.2	480	7.50
Lsd (0.05) L	1	0.0790	0.02070	1.56	77.0	4.08	1.20
Lsd (0.05) G	13	0.2091	0.05475	4.13	203.7	10.79	3.18
Lsd (0.05) G x L	13	0.2957	0.07743	5.84	288.1	15.25	4.50

**Significant P < 0.05; ns = Not significant at 0.05; CV = Coefficient of variability; FLT = Fruit length; FS = Fruit size; NFR = Number of fruits; Ave. FWT = Average fruit weight; FWT/PLT = Fruit weight per plot; Y/T = Yield per ton; L= Location; G = Genotypes; G x L = Genotype location interaction.*

APPENDIX III: MEANS SQUARES OF FRUIT BIOACTIVE COMPOUNDS

Source of Variation	DF	Means Squares			
		K	Zn	Mn	AA
Replication	2	0.10615	1.022	0.1074	0.7025
Location	1	0.02538	2.750	0.1748	0.0790
Genotype	13	0.10344	1.896	0.1103	0.1468
Genotype x Location	13	0.00448	2.026	0.1093	0.0306
Residual	54	0.01743	1.128	0.1107	0.0331
Total	83	-	-	-	-
CV (%)	-	16.26	95.25	9.27	16.39
Grand mean	-	1.092	0.003	0.331	1.550
Lsd (0.05) L	1	0.0578	0.00047	0.1456	0.0796
Lsd (0.05) G	13	0.1528	0.00123	0.3851	0.2106
Lsd (0.05) G x L	13	0.2161	0.00174	0.5447	0.2978

**Significant P < 0.05; ns = Not significant at 0.05; CV = Coefficient of variability; DF = Degree of freedom; K = Potassium; Mn = Magnesium; Zn = Zinc; AA = Ascorbic acid; L= Location; G = Genotypes; G x L = Genotype location interaction.*

APPENDIX IV: MEANS SQUARES OF VEGETATIVE CHARACTERS

Source of Variation	DF	Means Squares			
		PHT (WK2)	SG (WK 2)	NL (WK 2)	CC (WK 2)
Replication	2	12.407	4.0143	2.585	6.86
Location	1	1095.719	0.0288	30.020	3053.93
Genotype	13	16.998	1.6803	4.565	112.10
Genotype x Location	13	12.605	0.0230	4.064	20.56
Residual	54	4.557	0.2759	2.372	55.58
Total	83	-	-	-	-
CV (%)	-	32.51	14.89	29.58	32.81
Grand mean	-	14.13	4.83	6.16	29.54
Lsd (0.05) L	1	0.934	0.2299	0.674	3.262
Lsd (0.05) G	13	2.471	0.6083	1.783	8.630
Lsd (0.05) G x L	13	3.495	0.8602	2.521	12.205

**Significant P < 0.05; ns = Not significant at 0.05; CV = Coefficient of variability; PHT = Plant height; SG = Stem girth; NL = Number of leaves; CC= Chlorophyll content; L= Location; G = Genotypes; G x L = Genotype location interaction.*

APPENDIX V: MEANS OF SQUARES OF VEGETATIVE CHARACTERS

Source of Variation	DF	Means Squares			
		PHT (WK4)	SG (WK 4)	NL (WK 4)	CC (WK 4)
Replication	2	31.76	15.443	115.73	60.85
Location	1	14674.95	169.865	16693.46	5568.29
Genotype	13	92.83	3.307	209.49	269.68
Genotype x Location	13	58.15	2.931	124.48	131.49
Residual	54	20.58	4.225	89.74	23.87
Total	83	-	-	-	-
CV (%)	-	52.00	53.64	25.32	31.97
Grand mean	-	28.17	7.75	33.1	47.86
Lsd (0.05) L	1	1.985	0.899	4.14	2.137
Lsd (0.05) G	13	5.252	2.379	10.97	5.655
Lsd (0.05) G x L	13	7.427	3.365	15.51	7.998

**Significant P < 0.05; ns = Not significant at 0.05; CV = Coefficient of variability; PHT = Plant height; SG = Stem girth; NL = Number of leaves; CC= Chlorophyll content; L= Location; G = Genotypes; G x L = Genotype location interaction.*

APPENDIX VI: MEANS SQUARES OF VEGETATIVE CHARACTERS

Source of Variation	DF	Means Squares						
		LDW(v)	LFW(v)	RDW(v)	RFW(v)	RL(v)	SDW(v)	SFW(v)
Replication	2	26.575	1952.7	0.8663	9.204	159.97	1.3307	125.46
Location	1	0.225	13.1	0.3464	0.044	0.20	0.3062	0.31
Genotype	13	10.699	925.0	0.4020	3.800	83.73	1.1366	50.10
Genotype x Location	13	1.518	39.2	0.0320	1.326	9.97	0.2500	8.09
Residual	54	8.656	499.1	0.2978	3.678	17.69	0.6571	27.53
Total	83	-	-	-	-	-	-	-
CV (%)	-	54.39	53.56	50.69	42.25	34.18	65.20	61.33
Grand mean	-	5.16	42.3	1.05	4.32	16.01	1.25	8.89
Lsd (0.05) L	1	1.288	9.78	0.2390	0.840	1.842	0.3550	2.297
Lsd (0.05) G	13	3.408	25.88	0.6322	2.222	4.873	0.9392	6.079
Lsd (0.05) G x L	13	4.820	36.60	0.8941	3.142	6.891	1.3282	8.596

**Significant P < 0.05; ns = Not significant at 0.05; CV = Coefficient of variability; LDW = Leaf dry weight; LFW = Leaf fresh weight; RDW = Root dry weight; RFW = Root fresh weight; RL = Root length; SDW = Stem dry weight; SFW = Stem fresh weight; L= Location; G = Genotypes; G x L = Genotype location interaction.*

APPENDIX VII: MEANS SQUARES OF REPRODUCTIVE CHARACTERS

Source of Variation	DF	Means Squares			
		PHT (WK6)	SG (WK 6)	NL (WK 6)	CC (WK 6)
Replication	2	287.22	1.72	49.70	308.53
Location	1	28110.63	69.15	174174.11	7413.53
Genotype	13	233.81	10.38	1590.96	241.28
Genotype x Location	13	95.76	10.28	1603.03	79.32
Residual	54	39.05	1.10	62.43	47.17
Total	83	-	-	-	-
CV (%)	-	36.08	17.33	50.20	33.93
Grand mean	-	56.97	12.68	102.36	39.29
Lsd (0.05) L	1	2.73	0.460	3.46	3.01
Lsd (0.05) G	13	7.23	1.216	9.15	7.95
Lsd (0.05) G x L	13	10.23	1.719	12.93	11.24

**Significant P < 0.05; ns = Not significant at 0.05; CV = Coefficient of variability; PHT = Plant height; SG = Stem girth; NL = Number of leaves; CC= Chlorophyll content; L= Location; G = Genotypes; G x L = Genotype location interaction.*

APPENDIX VIII: MEANS SQUARES OF REPRODUCTIVE CHARACTERS

Source of Variation	DF	Means Squares			
		LA (R)	LDW (R)	LFW (R)	RDW (R)
Replication	2	10058726	246.59	10075	35.09
Location	1	5759	0.82	5	3.21
Genotype	13	4211119	86.67	2337	34.67
Genotype x Location	13	109746	0.43	93	1.20
Residual	54	1134510	32.84	1280	24.67
Total	83	-	-	-	-
CV (%)	-	41.74	32.60	36.59	77.93
Grand mean	-	3090	19.54	104.5	6.09
Lsd (0.05) L	1	466.4	2.509	15.67	2.175
Lsd (0.05) G	13	1234.0	6.639	41.45	5.754
Lsd (0.05) G x L	13	1745.1	9.388	58.61	8.138

**Significant P < 0.05; ns = Not significant at 0.05; CV = Coefficient of variability; LA = Leaf area; LDW = Leaf dry weight; LFW = Leaf fresh weight; RDW =Root dry weight;L= Location; G = Genotypes; G x L = Genotype location interaction.*

APPENDIX IX: MEANS SQUARES OF REPRODUCTIVE CHARACTERS

Source of Variation	DF	Means Squares				
		RFW (R)	RL(R)	SDW (R)	SFW (R)	CSMT (R)
Replication	2	73.1	27.56	65.98	886	0.57
Location	1	6.6	2.27	1.43	30	32.81
Genotype	13	176.5	19.41	17.03	1414	127.28
Genotype x Location	13	12.3	2.47	1.03	46	5.54
Residual	54	114.2	20.86	19.43	1030	0.85
Total	83	-	-	-	-	-
CV (%)	-	62.04	21.05	49.47	50.39	5.13
Grand mean	-	16.4	19.93	8.35	60.1	91.47
Lsd (0.05) L	1	4.68	2.000	1.930	14.05	0.404
Lsd (0.05) G	13	12.38	5.291	5.106	37.18	1.069
Lsd (0.05) G x L	13	17.51	7.482	7.222	52.58	1.512

**Significant P < 0.05; ns = Not significant at 0.05; CV = Coefficient of variability; RFW = Root fresh weight; RL = Root length; SDW = Stem dry weight; SFW = Stem fresh weight; CSMT = Canopy span at maturity; L= Location; G = Genotypes; G x L = Genotype location interaction.*