GENETIC VARIABILITY AND ASSOCIATION IN YIELD AND YIELD RELATED TRAITS IN ANCHOTE [*Coccinia abyssinica* (LAM.) COGN.]

M.Sc. Thesis

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GENETIC VARIABILITY AND ASSOCIATION IN YIELD AND YIELD RELATED TRAITS IN ANCHOTE [*Coccinia abyssinica* (LAM.) COGN.]

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APPROVAL SHEET

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As thesis research advisor, I hereby certify that I have read and evaluated this thesis prepared, under my guidance, by **Tilahun Wondimu**, entitled: **Genetic Variability and Association in Yield and Yield related traits in Anchote [*Coccinia abyssinica* (Lam.) Cogn.] Accessions.** I recommend that it be accepted as fulfilling thesis requirement.

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DEDECATION

I dedicate this thesis manuscript to my wife **DESISTU NEFEBASA**, for her dedicated partnership in the success of my life.

STATEMENT OF AUTHOR

First, I declare that this thesis is my work and all sources of materials used for this thesis have been duly acknowledged. This thesis has been submitted in partial fulfillment of the requirements for M.Sc. degree at the Jimma University College of Agriculture and Veterinary Medicine and is deposited at the University Library to be made available to borrowers under rules of the library. I strictly declare that this thesis is not submitted to any other institution anywhere for the award of any academic degree, diploma, or certificate.

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BIOGRAPHICAL SKETCH

Tilahun Wondimu was born on 28 April 1974 in Jimma-Rare Woreda, Horro-Guduru Wollega Zone, Oromia, Ethiopia. He attended his school at Lelise Wayu Elementary and Junior Secondary School from 1979 to 1986. He pursued his Secondary School education at Gedo High School from 1986 to 1990 in West Shoa Zone. He joined Jimma College of Agriculture graduated with a diploma in Plant Science on August 8, 1992. After graduation, he was employed by the Ministry of Agriculture and served for nine years on different designations in West Shoa Zone. In 2003 he joined Jimma University and graduated with Bachelor of Science Degree in Horticultural Science on July 12, 2006. After that he was employed by Oromia Agricultural Research Institute as researcher and has been working until he rejoined Jimma University in 2010 for MSc in Plant Breeding.

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ABBREVIATIONS

ANOVA	Analysis of Variance
AVRDC	Asian Vegetable Research and Development Center
BARC	Bako Agricultural Research Center
CCC	Cubic Clustering Criteria
CIP	International Potato Center
CT	Column Total
CV	Coefficient of Variation
DZARC	Debre Zeit Agricultural Research Center
ECPGR	European Cooperative Program for Plant Genetic Resources
ENBSA	Ethiopian National Biodiversity Strategy and Action
FYM	Farm Yard Manure
GA	Genetic advance
GAM	Genetic Advance as Percent of Mean
GCV	Genotypic Coefficient of Variation
GC	Ground Cover
H'	Shannon Weaver Diversity Index
H^2	Heritability (Broad Sense)
IPGRI	International Plant Genetic Resources Institute
IBCRE	Institute of Biodiversity Conservation Research of Ethiopia
IBPGR	International Board of Plant Genetic Resource
JARC	Jimma Agricultural Research Center
JUCAVM	Jimma University College of Agricultural and Veterinary Medicine
LSD	Least Significant Difference
PCV	Phenotypic Coefficient of Variation
PCA	Principal Component Analysis
RCBD	Randomized Complete Block Design
SAS	Statistical Analysis Software
SNNP	Southern Nations, Nationalities and Peoples

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GENETIC VARIABILITY AND ASSOCIATION IN YIELD AND RELATED TRAITS IN ANCHOTE [*Coccinia abyssinica* (LAM.) COGN.]

ABSTRACT

Anchote (Coccinia abysinica) is an endemic perennial trailing plant found both as cultivated and wild in Ethiopia. It has been in cultivation for a long period of time and has important economic (food, feed and income), socio-cultural and medicinal values. The objective of the present study was to estimate the extent of genetic variability and character association among anchote yield and yield related traits. Accordingly, forty nine anchote accessions from major anchote growing regions of west and south parts of Ethiopia were collected and tested at Bako Agricultural Research Center, western Ethiopia in 2011 main cropping season. The treatments were arranged in 7x7 simple lattice design. Variance component methods were used to estimate phenotypic and genotypic variation, heritability and genetic advance. Association of traits also estimated both at genotypic and phenotypic level using standard method. The accessions differed highly significantly for most of the characters and relatively wide range of mean for most characters, indicating the existence of variation among the tested accessions. High genotypic coefficient of variation along with high heritability and genetic advance was obtained from hundred seed weight, number of seeds per fruit, number of fruits per plant, average root yield per plant, total root yield, marketable root yield and average fruit yield, showing the possibility of anchote yield improvement through selection. Average root yield was positively and significantly ($P<0.01$) associated at genotypic and phenotypic level with root diameter ($rg = 0.858$ and $rp = 0.593$) and it also showed positive and highly significant association with root length ($rg = 0.482$ and $rp = 0.345$) signifying that indirect improvement would be very effective. Genotypic path coefficient analysis revealed that root diameter (0. 478), exerted maximum positive direct effect on average root yield per plant suggesting its possible utilization to improve root yield per plant. D^2 analysis showed the 49 anchote accessions grouped into five clusters and this makes the accessions to become moderately divergent. Principal component analysis showed that the first three principal components explained about 93.50% of the total variation. Average fruit yield per plant and root diameter showed positive direct effect on average root yield, this character may be included as a component of indirect selection. Finally, genetic information for anchote especially at molecular level does not yet exist. Therefore, efficient utilization of anchote landraces for future breeding needs morphological diversity supported by molecular marker system.

1. INTRODUCTION

Anchote (*Coccinia abssynica*) is one of the most well-liked indigenous root crops of the family Cucurbitaceae which is found both as cultivated and wild in Ethiopia (FAO, 1996). It is adapted well to south and western parts of the country between 1300 to 2800m.a.s.l. It prefers soil pH of 4.5 to 7.5, mean minimum and mean maximum temperature of 12^{o}Cand 28^{o}C, and rain fall ranging from 800 to 1200 mm/year (BARC, 2004).

Anchote is imperative, because of its economic (food, feed and income), medicinal and socio-cultural values (Abera,1995; Abdisa, 2000). It is mainly grown for its storage root yield conversely, leaf and fruit also used as a vegetable among the growers. As a food, it is rich sources of carbohydrate, vitamins, minerals, protein and calcium as compared to other root crops (Amsalu *et al.,* 2008; Habtamu, 2011). Habitually, its storage root is served as a side dish with cereals as; *'kitifo', 'lankata'* (finely grounded tuber), '*wot'*, soup, and '*murmura*' (boiled tuber cut in pieces). Similarly, the leaf and fruit also primed as *'Wot'* and served as a side dish with bread or *'injera'* (Abera, 1995). Moreover, traditional practitioners use *anchote* to treat different type of diseases such as diabetes, gonorrhea, tuberculosis, asthma and cholesterol lowering (Amare, 1985).

In Ethiopia the production of root and tuber in general and anchote in particular is less. JARC (2005) estimated that the total arable land coverage by root and tuber crops including anchote and its return in Wollega was 5066 ha and 69,754 tons, respectively. Amare (2003) also witnessed that a farmer in western parts of Wollega usually allocate 400 to 600 square meters of land for anchote production mainly for home consumption. Its productivity show a discrepancy based on genotypes, soil fertility level, location and cultural practices used. Under farmers condition it can yield 20 to 30tha^{-1} (Abera, 1995; BARC, 2004). However, under research condition it has a potential to yield of up to 73tha^{-1} (Desta, 2011) and 76.45tha^{-1} (Daba *et al*., 2012).

The estimation of genetic parameters is needed to understand the genetic architecture of yield and yield contributing components. Besides, an information about the mode of inheritance, type of gene action and heritability of the yield contributing components helps immensely for plant breeder to decide about the proper breeding procedure to be adopted and the characters on which the selection has to be made so that selection is effective (Chandrasekhar, 2006). Most of the quantitative characters, which are of economic value, are highly influenced by environment. However, highly heritable characters which are less influenced by environment and associated with yield can be serving as an indicator of yield in breeding program.

In spite of the long history of cultivation and consumption, anchote have not been taken up for systematic research work in order to understand the genetic architecture and manipulation in an improvement programme. Yielding ability is a prime example of quantitative trait and is of obvious importance for improvement. On the other hand for want of information on genetic variability, the crop has not been exploited to the fullest extent possible. As a result, appreciable improvement has not been made in terms of yield and disease and insect pest resistance because of less attrition given plus lack of information on the genetic bases of the crop (Abdisa, 2000). Due to the less attention given to anchote, there is no variety so far developed and released.

The development of high yielding and stable varieties requires a continuous supply of new germplasm as sources of desirable genes and /or gene complex. The primary sources of such genes are landraces, introductions, weedy, and wild relatives of a crop plants. The utilization of such germplasm requires identification of the areas of diversity of various characters of agronomic importance, especially within the center of diversity (Harlan, 1992). Therefore, the study of genetic diversity of anchote at Bako is worthwhile, since the area lies within the center of diversity of the crop.

There are traditional selection practices being followed by farmers (especially by women) to have anchote with desirable quality (Abera, 1995). Among the quality attributes cooking

quality, shelf life and early tuber formation are some of them. With regards to genetic diversity there is no satisfactory research information in anchote. Recently Desta (2011) and Daba *et al. (*2012) tried to generate information for some traits of the crop and reported variation among the character studied. However, the study has three major limitations. First, the number of accession used was few (10-36 accessions) plus collected from limited location so that drowning conclusion from such genotypes does not give true picture of the crop traits. Second, Desta (2011) characterized the crop out off its center of diversity (in central high land of Ethiopia (Debre Zeit)) while the traits are best expresses itself in the center of diversity than elsewhere in the world because of environmental factors. Third, the generated information was more of nutritional quality of the crop than yield and yield related traits while, indirect selection for yield depends on yield related traits than its quality parameters. Because of these and other reasons, efficient utilization of anchote genetic resources still requires compressive, systematic and intensive characterization to enrich anchote germplasm data basis and to identify accessions for utilization in breeding program.

Therefore, the study was aimed to contribute towards such pressing needs and designed with the following objectives:-

- To assess the extent of genotypic and phenotypic variability among anchote accessions grown in Western Ethiopia
- To assess the association of yield and yield related trait of anchote accessions
- To investigate the level of genetic divergence among the anchote accessions

2. LITERATURE REVIEW

2.1Taxonomic Classification of Anchote

The scientific name of anchote is *Coccinia abyssinica*. This species belongs to the family *Cucurbitaceae* (Abera, 1995). The most recent taxonomic classification of the family *Cucurbitaceae* is given by Jeffery (1980) who classified the family into two subfamilies: *Zanonioideae* and *Cucurbitoideae*, with several tribes. The tribes of subfamily *cucurbitoideae* includes; *Melothrieae*, *Schizopeponeae*, *Joliffieae*, *Trichosantheae*, *Benincaseae* (subtribe *Benincasinae* (genus *coccinia*)), tribe *cucurbiteae*, tribe *Cyclanthereae* and tribe *Sicyoeae*.

According to this taxonomic classification, the genus *Coccina* belongs to the sub tribe *Beninccaseae* of the tribe *Benincasinae*. The genus *Coccinia* is made up of 30 species of which eight are reported to be occurring in Ethiopia. The species recorded in flora of Ethiopia since 1995 include: *Coccinia abysinica* (Lam.) Cogn. *C. adoensis* (Hochst. Ex. A. Rich.) Cogn.), *C.grandis* (L.) Voigh (Syn. *C. indica* Wight and Arn.), *C. megarrhiza*, C. Jeffrey and *C. schliebenni* Harms. The remaining three species have not so far been described and named according to the rules for giving scientific names for the plants. Of this species it is only *Coccinia abyssinica* that is grown for its edible tuberous root (Abera, 1995). *Coccinia grandis* has edible fruits and is native to Southeast Asia (Rehm and Espig, 1991)

Other cucurbits recorded as having edible storage roots are buffalo gourd (*Cucurbita foetidissima)* and Chayote (*Sechium eduulis*) (Esquinas-Alcazar and Guilck, 1983). These three cucurbits (Anchote, Buffalo and Chayote) with edible tuberous roots are divers in their centers of origin or diversity. That of Chayote is in the tropics of Latin America and *Baffalo* is in arid areas of southwest USA and north central Mexico (Esquinas-Alcazar and Gulick,

1983). Anchote is indigenous and endemic to Ethiopia (Amare 1973, Terefe 1982, FAO 1996; Schipper, 2000).

Other species of *Coccinia* which have been reported (Amare, 1985) to produce underground perennial tuberous organs in the arid tropics and various subtropical regions of the world includes: *C. indica, C. engleri, C. jatrophacolla, C. renmannii, and C. sessiofolia*. He also reported other cucurbits with tuberous roots such as *Citrullus naudinianua*, *Trichosanthes cucumberoides*, *T. japonica, and T. mulliloba*.

Anchote has both vegetative (root, vine and leaf) and reproductive (flower, fruit and seeds) parts. Besides, it has a modified underground storage structure called tuberous root which is the economic part of this plant. The cucurbit seeds consist of an embryo and two cotyledons covered with a seed coat. The processes of germination are typical of dicots with epigeal germination. Imbibition is followed by biochemical activity, and elongation and emergence of the radicle. The hypocotyl emerges from the seed coat and lengthens to push the hypocotyls hook above the soil surface. Exposed to light, the hook straightens, pulling the cotyledons out of the soil where they expand and begin photosynthesis. The length of time required for cucurbit germination in a moist environment depends on the temperature (Liz, 2007).

Anchote leaves are heart shaped to palmatelly lobed with slightly toothed margins and arise singly at each node (Abera, 1995). Those leaves on the main stem (vine) and lower branches gradually become shaded because of the creeping and intermingling nature of the shoot that prevent light from penetrating to the bottom parts of the plant. The newly born and immature leaves are concentrated on the top part of the plant. Though, anchote foliage green color intensity were not clearly characterized, cucurbits foliage color ranges from deep green, yellowish green, light green to dark purple (Diez *et al*., 2005). The stem (vine) and leaves stalk (petiole) of anchote are solid as contrary to the cucurbits. Tendrils arise from each node and help the shoots climb up a support. On the contrary, tendrils interleave the plants and make weeding, cultivation and harvesting difficult (Abera, 1995).

According to Abera (1995), anchote shoot (vine) start to appear after seed germinations or from the root tubers at the beginning of the rainy season and it can grow to 4 to 5 meters when provided with support. Further he pointed out each main shoot has 3 to 4 branches (vines) which arise from the lower nodes and this vines give rise to the tendrils, leaves and inflorescences. According to Loy (2004) the number and length of branches in cucurbits vary depending on species and cultivar. Similarly, he reported the existence of genetic variations that lead to reduced internodes length and shorter vines in all genera of cucurbits.

Anchote starts to develop flowers after 75 days of planting when the vines start to cover the ground. It appears at each node along with tendril and leaves. Anchote flower is cleistogameous (automatic self–pollination under closed-marriage) in nature (Desta, 2011). Its fruits fully mature after 60 days of fruit setting. In line with this, Liz (2007) reported Watermelons and muskmelons typically mature 42 to 46 days after pollination, while winter squash and pumpkins take 50 to 90 days to reach harvest maturity.

Indicators of harvest maturity vary depending on the crop. Cucumbers and summer squash are usually harvested based on size. Muskmelons form an abscission layer between the peduncle and fruit so they "slip" from the vine when fully ripe; commercial harvest occurs after the layer begins to form but before the melon falls off the vine. Watermelon harvest maturity is identified by yellowing of the ground spot and wilting of tendril near the place of fruit attachment (Wien, 1997). As far as anchote is concerned immature fruits show light green with whitish patches on the entire fruit structure and upon repining the fruit give red or yellow color with white patches indicating harvesting time (Amare, 1985).

The size, number and weight of the mature fruit are influenced by genetics, environment, and plant conditions during development of the flower and fruit. Conditions that reduce the amount of assimilate available tend to decrease the size of individual fruit. Increased plant density, greater numbers of fruit per plant, and reduced water supply tend to decrease fruit

size (Fabeiro *et al*., 2002). Like fruit size, soluble solids tend to be lower under conditions that reduce assimilate level and high night temperatures, reduced leaf area, increased numbers of fruit per plant and increased plant density can all reduce soluble solids (Wien, 1997). Similarly, Abera (1995) noted on average anchote fruit can weigh 50-100g. Other researchers also reported high variability in number of seeds per fruit and seed weights. For instance, Tesfaye and Abebe (1988) reported 94-156 seeds per fruit, Amare (1985) noted 153 seeds per fruit and Abera (1995) 78 to 160 seeds per fruit.

The tuberous root is an economic and modified underground parts of anchote plant. It can vary with age of the plant, soil physical properties, harvesting time and genotypes. Variability based on genotypes is by far very important for selection program. Typically anchote has large root diameter which can weigh 0.30 to 2.00kg and its shape also vary from spherical to cone (Abera, 1995). Properly washed *anchote* storage root has white or red surface color while its flesh is mostly whitish to brown/ yellow. It is also variable in flesh water and fiber content which aids in traditional selection of the genotypes (Aschalew *et al*., 2009).

2.2 Cultural Practices and Production of Anchote

The practices of anchote cultivation and utilization have been passing orally from generation to generation with very little recorded information. The role of women with this regards is valuable because they select anchote genotypes with desirable quality for the next generation; harvest anchote at right harvesting time for different purpose and prepare, process and taste for its quality and finally they market and distribute anchote products (Abera, 1995).

Anchote input requirement is low as compared to most vegetables (Desta, 2011). However, Anchote can respond well to 5-8tha^{-1} of farm yard manure (FYM), which is as equivalent as 46/20 kg ha^{-1} N/P (Girma and Hailu, 2009). Intermittently, farmers in the western Oromia

have been accustomed to burn some plant residue on farm land to upgrade the fertility of the soil for proper growth and development of anchote (Aschalew *et al.,* 2009).

Anchote is mainly propagated by seeds and sometimes by its storage root. The optimum inter and intera row spacing for its production is 40-60cm and 10-20cm, respectively (Girma and Hailu, 2009). It needs loose soil for easy root penetration. The crop is planted in June and harvested after 3-4 months (JARC, 2005). Storage roots for domestic consumption are dug out daily and surplus tubers are allowed to stay in the ground for several months. As it stays long in the ground after maturity, the tubers become larger, stringier, and more difficult to cook. The above-ground portion of the plant is allowed to grow un staked if the tuber is to be harvested in less than a year, but if a "gubbo" crop of one-year-old tubers is desired or if the plant is to be used for seed production, then a trellis is provided on which the vine is supported (Amare, 1985).

In Ethiopia the production of root and tuber in general and anchote in particular is infrequent. Cognizant of this vegetables and root crops together are cultivated on 281 thousand hectares, 2.6 percent of total area cultivated in Ethiopia; of which root crops accounted for 174, 826 hectares of land and 14,732, 919 quintals (Alemayeu *et al.,* 2011). JARC (2005) as well estimated the total arable land coverage by root and tuber crops and its production in Wollega was 5066 ha and 69,754 tons, respectively. Amare (2003) also witnessed that a farmer in western parts of Wollega usually allocate 400 to 600 square meters of land for anchote production mainly for home consumption.

The productivity of anchote varies based on genotypes, soil fertility level, location and cultural practices that we apply. Under farmer condition anchote can yield 20 to 30tha^{-1} (Abera, 1995; BARC, 2004). However, under research condition it has a potential to yield 73 tha^{-1} (Desta, 2011) and 76.45 tha^{-1} (Daba *et al*., 2012).

2.3 Nutritional Composition and Uses of Anchote

According to FAO (1998) report on root crops, or as often described, roots and tubers are the third largest carbohydrate food sources, although well behind cereals and sugarcane in total tons produced. The major contributors to root crops are potatoes, cassava (manioc), yams, sweet potatoes and taro. Minor crops such as chayote and yam beam are consumed in specific countries. Generally root crops contain 15-30% carbohydrate, 1-2% protein and less than 0.5% fat. The unexploited endemic root crop to Ethiopia anchote as well, is important crop in its uses i.e. as food, feed, economic and socio-cultural and medicine values (Abera, 1995).

Mostly, anchote is cultivated for the storage root organ which is the economic part (Abera, 1995). Storage root is rich in carbohydrate (21.2g/100g), protein (3.1g/100g) and minerals like calcium (119mg/100g), iron (1.8g/100g), ash (1.1g/100g) and fiber (1.7g/100g) (Abera, 1995).

The nutritional content of anchote parts (leaf, root and fruits) is variable. According to Desta (2011), anchote leaf contains more protein (34.5 - 53%) and phosphorous (37 - 85mg/100g) than tuberous root (4.6 - 16.4% and 8.38mg/100g) and fruit (10 - 36.4 % & 0.1-58mg/100g) while, the tuberous storage root contain more calcium (9.69 - 93mg/100g) and iron (11 - 89mg/100g) than leaf (6.48 - 109.2mg/100g Ca and 0-3.57mg/100g Fe) and fruit (95.95-124.4mg/100g Ca and 0 - 39mg/100g Fe). On the other hand, anchote fruit is known by its potassium (240.4-678.2mg/100g), magnesium (3.57-118mg/100 g) and zinc (0-5.45mg/100g) content. The top growing point of anchote plant (leaf) is considered as delicious dish in Dembi Dollo (Abera, 1995) and also some missioners in west Wollega used to consume its immature tender fruits (Amare, 2003). The nutritional content of anchote seed is not studied and its use as a food is not common in Ethiopia.

Habtamu (2011) as well reported appreciable quantity of carbohydrate, crude protein, crude fiber, calcium, magnesium, iron and low levels of anti-nutrients (Oxalate, tannin, and cynide)

except phytate in anchote storage root organ. He also pointed out that traditional processing method of anchote is very important as it increases fiber content and improves the bioavailability of zinc contained in the anchote storage roots. Further he confirmed, raw anchote root contains low anti-nutritional factors, except phytate and boiling anchote before peeling is preferable among consumers.

Amare (1985) as well stated anchote is good source of protein, carbohydrate, calcium and iron. He further stated that the high level of calcium content in anchote storage root organ may be due to alkaline soil conditions on which the crop is produced. Moreover, all parts of wild forms and cultivars of anchote are used as animal feed (Aschalew *et al.,* 2009). .Similarly, Sarwar *et al*. (1999) stated that, both roots and vines of sweet potato are either in fresh or dried form and fermented as silage used for animal feed. The roots basically represent a source of energy and leaves with vines are a source of protein in animal diets. Its tuberous root also supposed to be a potential raw material in starch production industry (Desta, 2011). This indication is useful in manipulation of the crop in food security program, for the reason that nothing is throwing away from the crop.

Apart from its food and feed values anchote has much medicinal worth. The traditional practitioners in the anchote were growing use different parts of anchote to treat different type of disease like; diabetes, gonorrhea, tuberculosis, asthma and cholesterol lowering (Amare, 1985; Abera, 1995). Similarly, Koller (2008) also stated, other *Coccinia* groups such as C. *grandis* and *C. indica* are widely used to treat gonorrhea, asthma, skin eruptions, and diabetes and eye diseases. Its higher calcium content makes the crop preferable among children, youth, aged persons, and those suffering from bone fracture and displaced joints (Abera, 1995).

The Oromo oral tradition teaches that anchote holds a very special place in the tradition and customs of the Oromo people (Abera, 1995). For the reason that, dish up of anchote during special occasions like wedding, circumcision, birthdays, *Meskel (*the finding of true cross*)* and

generally during feast has significant part in socio-cultural phases of the growers. Even the inclusion of anchote in the dish to be served at ritual ceremonies is considered to give status.

Anchote is served as *lanqaxa* (finely chopped anchote dish) which is the best dish that many people like or *mumura* (tuberous anchote are boiled, cut in to pieces and is larger than *lanqaxa* in size) with local butter and *kochkocha* (finely grinded ingredients of green pod of hot pepper and spices). Most women's in the crop growing area are an expert for its preparation (Abera, 1995), despite the fact that, the utilization mechanism of the crop is not well studied and documented.

Generally, preparations of anchote includes; the tuber is lifted, washed, boiled, peeled, cut into small pieces and mixed with ground pepper and salt. More elaborate preparations involve the addition of many spices and liberal amounts of butter. The spiced and buttered pieces are pounded and may be eaten alone or with "injera", locally prepared bread made from *Eragrostis tef* (Amare, 1985). Finally, it is obvious that farmers grow crops not only for home consumption but also for sale. With this regard anchote is amusing to generate income for small scale farmers (especially for women) and this is common mainly for any surplus product to barter what they unable to produce.

2.4 Breeding of Anchote

By tradition, anchote farm is considered as women's business, for the reason that, they play greater role in domestication, cultivation, selection and storage of the best genotypes for the next growing season than men (Abera, 1995). Outside its traditional improvement by women, BARC (2003/04) started to collect, characterize and evaluate anchote accessions to identify variability among anchote landraces thereby to utilize it in improvement program. But, it was unsuccessful because of poor seed maintenance. Therefore, strengthening the research on

variety development irrespective of yield, quality and any other agronomic characters are requesting instantaneous response.

2.5 Genetic Variability, Heritability and Genetic Advance

2.5.1 Genetic variability

Breeding progress is primarily determined by the magnitude, nature and inter-relations of genotypic and phenotypic variation in the various characters. An impending into the magnitude of variability is of greatest importance as it provides the basis for effective selection (Singh, 2005). This demand, partitioning of the overall variability into its heritable and non-heritable components with the use of suitable genetic parameters such as genetic coefficient of variation, heritability, genetic advance and correlation (Akinwale *et al.,* 2010). Besides, multivariate analysis methods are useful for characterization, evaluation and classification of plant genetic resources provided that many accessions are assessed for many characters of agronomic and physiological importance (Peeters and Martinelli, 1989).

The total variance of a given character is its genotypic variance and environmental variance (Falconer and Mackay, 1996). The total genetic variance is also known as variance of genotypic value (Dudley and Moll, 1969). Total genetic variance is further portioned into additive genetic variance, dominance genetic variance and epistatic genetic variance. The additive genetic variance, which is the variance of breeding values, is the important component. It determines the observable genetic properties of the population and the response of the population to selection (Dudley and Moll, 1969).

Genetic gains from phenotypic selection have been assessed for many plant species and environments and the progress has been varied (Volenec *et al.,* 2002). The most important factor influencing selection gains is the amount of available genetic variation for general adaptation and traits necessary for improved production under specific constraints (Vasal *et*

al., 1997). In agreement with this report, others also indicated that selection cannot create variability but can act on heritable variability already existing in the population (Singh and Chaudhary, 1985).

The choice of breeding methods for genetic improvement of a crop depends upon the nature and magnitude of genetic variability present (Singh and Chaudhary, 1985). Different mating designs are used in the estimation of genetic variability and other components of variance. On the contrary, without mating variability among inbred lines can be used as an estimation of genetic variability of a reference population (Dagne, 2010). Kisha *et al*. (1997) indicated that populations with greater genetic variance are expected to produce higher yielding transgressive sergeants than populations having lower genetic variance. The presence of genetic variation in a character is a must for any improvement in that character (Singh, 2003).

A large number of studies have been conducted on different crops to estimate genetic variability. Accordingly, Desta (2011) estimated the nature and magnitude of variability in morphological characters and nutritional contents among anchote accessions. He observed high (>20%) GCV and PCV for root yield number of seeds per fruit, fruit weight and leaf length.

Engida *et al.* (2007) also, estimated high (>20%) GCV and PCV for traits like vine length, vine internodes length, leaf length, number of storage root per plant, individual storage root weight and storage root fresh yield per plant in sweet potato. Similarly, genetic variability was assessed for eight parameters in 86 genotypes of sweet potato in India and high GCV and PCV was recorded for number of branches per plant, weight of single tuber, root diameter and root length. For all the characters studied, phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) indicating the influence of environment on the expression of these traits (Teshome *et al*., 2004).

Hossain *et al*. (2010) as well, conducted research on 58 cucumber genotypes and high (>20%) GCV and PCV for days to seed germination, vine length, petiole length, number of fruits per plant, average fruit weight, fruit length and fruit diameter. Similarly, Blessing *et al*. (2012) evaluated ten Nigerian pumpkin accessions and reported High (>20%) GCV and PCV were estimated for days to 50% emergence, fruit diameter and number of seeds per fruit.

Wide variability in 58 long type cucumber accessions was found for days to seed germination, vine length at harvest, petiole length and yield contributing characters namely, days to first male and female flowering, number of fruits per plant, average fruit weight, fruit length and fruit diameter (Hossain *et al*., 2010). The same authors reported highest GVC in fruit yield per plant, number of fruits per plant, fruit length, number of vines, average fruit weight and petiole length.

Balkaya *et al.* (2010) noted high GCV and PCV for fruit length, fruit diameter and fruit weight in winter squash seeds. Yadav *et al.* (2009) too, reported high genetic variability in 31 collections of cucumber and high GCV and PCV was identified for fruit weight and number of fruits per plant. Afangideh and Uyoh, (2007) and AbdEl-Salam *et al.,* (2010) noted same in cucumber and snake cucumber genotypes, respectively in Egypt.

2.5.2 Heritability in the broad sense

A quantitative measure, which provides information about the correspondence between genotypic and phenotypic variance, is heritability (Dabholkar, 1992). According to Falconer and Mackay (1996), the relative importance of heredity in determining phenotypic values is called the heritability of the character. The extent of contribution of genotype to the phenotypic variation for a trait in a population is ordinarily expressed as the ratio of genetic variance to the total variance, i.e., phenotypic variance, for the trait; this ratio is known as heritability (Singh, 2005). Thus heritability denotes the proportion of phenotypic variance that is due to genotype, i.e., heritable.

Estimates of heritability serve as a useful guide to breeders. The knowledge of the relative heritability of the various traits and their genotypic and phenotypic correlations can aid in designing of efficient breeding systems where many traits need to be improved simultaneously (Jones, 1986). The breeder is able to appreciate the proportion of variation that is due to genotypic (broad sense heritability) or additive (narrow sense heritability) effects, that is, the heritable proportion of variation in the first case, and the proportion of genetic variation that is fixed in pure lines in the latter case (Singh, 2005).

A broad sense heritability estimate based on various components of variance provides information on the relative magnitudes of genetic and environmental variation in the germplasm (Dudley and Moll, 1969). However, the type of gene action involved in the expression of a character has a significant role in determining heritability values. Characters that are controlled largely by genes acting in an additive fashion have higher heritability than characters governed by genes with large non-additive effects (Falconer, 1989). According to Dabholkar (1992), it is important to note that heritability is a property not only of the character being studied, but also the population being sampled and the environmental circumstances to which individuals have been subjected.

Studies have been conducted to estimate broad sense heritability for different traits in different crops. Accordingly, Engida *et al.* (2007) estimated high (>59%) heritability values for traits like vine length, vine internodes length, leaf area, above ground fresh and dry weights, number of storage root per plant, individual storage root weight and storage root fresh yield per plant. Teshome *et al*. (2004) as well estimated high heritability values for vine length and number of vines per plant in 86 genotypes of sweet potato of diverse origin in India. He also noted low (<40%) heritability value for number of tubers per plant. AbdEl-Salam *et al.,* (2010) noted high heritability value for number of fruits per plant and fruit length but, moderate (40-59%) heritability value for fruit diameter in snake cucumber genotypes.

2.5.3 Expected genetic advance

Genetic advance is a function of heritability of a trait, the amount of phenotypic variation, and the selection differential that the breeder uses (Kalloo, 1988). Heritability is not enough in predicting the effectiveness of selection unless otherwise it is considered along with genetic advance so that genetic advance is suggested to be used along with heritability estimates in predicting the resultant effect for selecting the best genotypes through characterizing into their character (Allard, 1999).

The genetic advance under selection will depend on the amount of genetic variability and the magnitude of the effects of environmental and interaction components of variability in masking the genetic effects. High heritability value could be obtained with accessions having small or large genetic variance but genetic progress would be larger with larger genotypic variance (Allard, 1960).

Thus, genetic gain is an important concept in quantitative genetics and plant breeding. It predicts changes in mean value of trait in a population due to selection. Maximum genetic gain through phenotypic selection can be obtained if heritability is high. Other component influencing genetic gain include level of phenotypic variation present in the population, the portion of the population selected as apparent for the next generation (selection intensity) and the duration of selection cycle. Genetic advance provides a prior quantitative estimate of the magnitude of the progress that could be achieved through selection (Falconer, 1989).

High heritability values together with high genetic advance was reported in sweet potato for the traits vine length, individual storage root weight, storage root number, vine internodes length, leaf area and storage root fresh yield per plant (Teshome *et al*. (2004; Engida *et al.* (2007)) .

Arunkumar *et al.* (2008) conducted an experiment in India, to study the genetic variability in F2 of BGDL x Hot Season cucumber. High variability were observed for number of branches per vine, average fruit weight, total number of fruits per vine and total fruit yield per vine. In addition high heritability coupled with relatively high genetic gain was noticed for vine length, number of nodes per vine, number of branches per vine, fruit length, fruit diameter, average fruit weight, total fruit yield per vine while, number of fruits per vine and fruit length recorded moderate heritability and genetic gain.

2.6. Correlation and Path Coefficient Analysis

2.6.1. Correlation coefficient

Correlation, indicated by correlation coefficient(r), is a measure of linear association between traits (Hallauer and Miranda, 1988). Correlation measures the degree of association, genetic or non-genetic, between two or more traits or it measures the mutual relationship between various plant characteristics and determines the component characters on which selection can be based for improvement in yield (Singh, 1993). The correlation between characters may arise from linkage or from developmental genetic interaction, with or without a purely phenotypic component (Simmonds, 1986). Genetic correlation is the association of breeding values (i.e., additive genetic variance) of the two characters (Falconer, 1989). Their coefficients provide a measure of genetic association between traits in order to identify the important traits to be considered in a breeding program whereas; phenotypic correlation is the observable correlation between two variables in a number of individuals of the population (Falconer, 1981). Both phenotypic and genotypic correlation coefficient measures the extent to which degree the same genes and closely linked genes cause co-variation in two different characters (Hallauer and Miranda, 1988). Genetic correlations inherently have large errors because of difficulties to avoid the directional effects of confounding factors on additive correlation estimates (Falconer, 1989).

Therefore, the degree of correlation among the characters is an important factor especially in economic and complex character like yield. When there is positive association of major yield characters, component breeding would be very effective but, when these characters are negatively associated, it would be difficult to exercise simultaneous selection for them in developing a variety (Nemati *et al*., 2009).

Plant breeders are interested in developing cultivars with improved yield and other desirable agronomic and phonological characters. In order to achieve this goal, the breeders had the option of selecting desirable genotypes in early generations or delaying intense selection until advanced generations (Puri *et al*., 1982). The selection criteria may be yield, or one or more of the yield component characters. However, breeding for high yield crops require information on the nature and magnitude of variation in the available materials, relationship of yield with other agronomic characters and the degree of environmental influence on the expression of these component characters.

Yield is quantitative trait and polygenically controlled thus, simultaneous improvement in yield components are essential for effective yield improvement (Bello and Olaoye, 2009). Meaning, selection on the basis of yield character alone is usually not very effective and efficient. However, selection based on its component characters could be more efficient and reliable (Muhammad *et al*., 2003). The knowledge of association between yield and its component traits and among the component parameters themselves can improve the efficiency of selection in plant breeding.

Many researchers reported the existence of traits correlation both at phenotypic and genotypic levels in different crops. Engida *et al. (2006*) reported that storage root yield is positively and significantly correlated with individual storage root weight and storage root diameter. Besides, he observed negative and significant correlation among number of storage roots per plant, individual storage root weight and storage root diameter indicating the presence of compensatory relationship between number of storage roots per plant and the latter two traits.

Teshome *et al*. (2004) also observed positive and significant correlation among storage root yield and storage root diameter, storage root length and number of vines per plant while, length of vine expressed negative and significant correlation with storage root yield. Thus, he concluded, selection based on weight of single tuber, tuber length and number of vines per plant can be effective for genetic improvement of sweet potato.

Blessing *et al*. (2012) also evaluated ten Nigerian pumpkin accessions during the 2007 and 2008 planting seasons to estimate characters association among some yield characters in randomized complete block design. He noted the number of seeds per fruit had a significant positive correlation with number of female flowers and the number of fruits per plant indicating increasing the number of female flowers would favors fruiting in pumpkin. The correlation coefficient revealed positive and highly significant association of yield per plant with fruit length, fruit diameter, average fruit weight and number of fruits per plant in long type cucumber genotypes (Hossain *et al*., 2010).

Aruah *et al.* (2010) as well, evaluated Nigerian accessions of *Cucurbita* species using quantitative and qualitative characters and reported that weight of harvested fruits had positive and significant relationships with number of fruits per plant, fruit diameter, fruit length, number of seeds per fruit, 100-seed weight and seed weight. Fruit yield was positively correlated with total number of fruits per vine, average fruit weight, fruit length, number of fruits per vine, fruit diameter, number of branches per vine, number of nodes per vine and vine length in cucumber plant (Arunkumar *et al.*, 2008).

2.6.2. Path coefficient analysis

Path coefficient is a standardized partial regression coefficient, which measures the direct influence of one trait upon another trait and permits the separation of correlation coefficients into components of direct and indirect effects (Dewey and Lu, 1959). It is most important to know the direct and indirect effect on yield component for selecting suitable genotypes for

improving the yield (Yadav *et al.,* 2010). Kang (1994) suggested that improvement of such complex trait (yield) could be handled through indirect selection i.e. selection for yield component trait or trait involved in the pathway leading to the formation of complex traits. He further stated, Path-coefficient analysis have been deemed more informative and useful than simple correlation coefficient. The residual effects (R^2) determine how best the causal factors account for the variability of the dependent factor. Storage root yield, the main goal of anchote breeding program, is also a complex quantitatively inherited traits and difficult to improve directly.

The Path coefficient analysis for sweet potato storage root yield revealed individual storage root weight, number of storage roots per plant and harvest index showed positive direct effect thus, can be used as selection criteria to increase storage root yield. Similarly, Ntawuruhunga *et al.* (2001) identified leaf area, storage root number, and storage root diameter and storage root weight as the main component for root yield showing highest direct effect in cassava genotypes. Path coefficient analysis explained fruit length, fruit diameter, average fruit weight and number of fruits per plant were directly contributed towards the yield per plant in cucumber genotypes Hossain *et al*. (2010). Blessing *et al*. (2012) also reported days to flowering, fruit diameter and number of seeds per fruit can be used as selection criteria to increase fruit yield in Nigerian pumpkins. Arunkumar *et al. (*2008) as well, reported that the maximum positive direct effect on yield was total number of fruits per vine, number of branches per vine, number of nodes per vine, vine length and days to first male flower whereas, negative and maximum direct effect on yield was observed for days to first female flower, number of good fruits per vine, fruit diameter, days to first fruit harvest, number of fruits per vine and fruit length.

2.7 Genetic Divergence

Diversity is expressed as genetic differences between species, sub species, varieties, population or individuals (Jarvis, 2000). The cause of high diversity among germplasm accessions of domesticated species is thus both environmental and man-imposed (Bekele, 1985). This is especially true in countries like Ethiopia where there are many nations and nationalities which in turn lead to high cultural diversity and this cultural versatility results selection of different crops at different localities as a source of food and for other applications. This variation in selection pressure finally, causes inherent variation among different populations of the same species. However, in Ethiopia, the genetic resources of traditional vegetables are to a large extent left to traditional process, although they are presumed to have high diversity (Dessalegn *et al.,* 1994).

Genetic diversity can be assessed among species, among population, within population and among individuals and sub dividing the variation into sub components may assist in genetic conservation (establishment of *insitu* conservation) and utilization (Bekele, 1996). Species with greater genetic diversity are more likely to be able to evolve in response to a changing environment than those with low genetic diversity. Population that lack genetic diversity may experience low fertility, high mortality among offspring, even in environment that are fairly suitable (Hunter, 1996). Studying the extent and patterns of distribution of genetic variation of a crop species is essential for effective utilization of germplasm in plant breeding programs, devising appropriate sampling procedure for germplasm collection and conservation, obtaining some collections for efficient germplasm management and elucidating the taxonomy, evolution and origin of the crop species (Keneni *et al*., 2007 ; Dangachew,2008).

Ethiopia is one of the eight centers of origin and diversity for many important crops in the world (IBC, 2001). Some of them are barley (*Hordeum vulgare*), finger millet (*Eleusine coracana*) and sorghum (*Sorghum bicolour*) from cereals; faba bean (*Vicia faba*), field pea (*Pisum sativum* including the endemic *var. abyssinicum*), chick pea (*Cicer arietinum*) and

grass pea (*Lathyrus sativus*) from pulses; Linseed (*Linum sativum*), niger seed (*Guizotia abyssinca*), safflower (*Carthamus tinctorius*) and sesame (*Sesamum indicum*) from oilseeds and anchote (*Coccinia abyssinica*), 'Oromo or Wollaita dinich' (*Plectranthus edulis*), and yams (*Dioscorea spp*.) from root and tuber crops.

Though scanty the information is, there are studies that demonstrated the existence of broad variations of some traits anchote (Desta, 2011) indicating it genetic diversity. These variations may occur due to diverse agro-ecological condition of the country together with the many millennia of cultivation of the crop under different socio-economic and cultural practices which could account for evolution of the highly diverse forms observed. Hence, genetic diversity in any given crop can be estimated either by Mendelian analysis of discreet (qualitative) morphological traits or statistical analysis of quantitative morphological traits along with eco-geographic information or both (Murty, 1976 ; Doggett, 1988).

Genetic diversity is essential to meet the diversified goals of plant breeding such as breeding for increasing yield, wider adaptation, desirable quality, and pest and disease resistance. Genetic divergence analysis estimates the extent of diversity existed among selected genotypes (Mondal *et al.* 2003). Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization.

Genetic divergence was studied for 26 genotypes of cassava and divergence analysis revealed great genetic diversity existing among the genotypes. Maximum magnitude of divergence was observed for number of branches per plant, tuber diameter, stem diameter, tuber length and number of tuber per plant (Bijaya *et al*., 2009). Similarly, Kabir et *al. (2009)* reported genetic divergence among 24 genotypes of pointed gourd. The D^2 analysis grouped the genotypes into five clusters and the clustering pattern of the genotypes under this study revealed the genotypes collected from the same location were grouped into different clusters. The inter cluster distance were large suggesting wider genetic diversity among the genotypes of different groups.

2.8 Cluster Analysis

Cluster analysis is multivariate statistical procedure whose primer purpose is to group individuals or objects based on the characteristics they possess, so that individuals with similar descriptors are mathematically gathered into the same cluster. The resulting clusters of individuals should then exhibited internal (within cluster) homogeneity and high external (between clusters) heterogeneity, thus if the classification is successful individuals within a cluster shall be closer when plotted geometrically and different cluster shall be farther apart (Cross *et al.,* 1995).

There are broadly two types of clustering methods: 1) Distance based method, in which a pair wise distance matrix is used as input for clustering analysis. The result can be visualized as a tree or dendrogram in which clusters may be identified, and 2) Model based method, in which observations from each clusters are assumed to be random draws from some parametric model, and inference about parameters corresponding to each cluster and cluster membership of each individual are performed jointly using maximum- likely hood or Bayesian method (Johnson and Wichern, 1992).

Another important aspect in cluster analysis is determining the optimal number of clusters or number of acceptable clusters. In essence, this involves deciding where to "cut" a dendrogram to find the true or natural group. An" acceptable cluster" is defined as group of two or more genotypes with a within-cluster genetic distance and between cluster distances greater than their within cluster distance of the two clusters involved (Mohammadi *et al.,* 2003).

In line with this many evidences were reported by many researchers. Aruah *et al.* (2010) reported two clusters in Nigerian accessions of *Cucurbita* species. Clustering based on

quantitative character, grouped the various accessions into two clusters. However, clustering based on the qualitative variations revealed a more realistic relationship by grouping the accessions into three distinct clusters that appeared to have some bearing with agro-ecology from which the accessions were collected. Balkaya *et al.* (2010) also noted 10 different groups among 115 populations of winter squash seeds.

2.9 Principal Component Analysis

Principal component analysis is a multivariate technique used for examining relationships among several quantitative variables (Crossa *et al.,* 1995). Principal component analysis can be used to derive a two dimensional scatter plot of individuals, such that the geometrical distance among them with minimal distribution. Aggregates of individuals in such a plot will show sets of genetically similar individuals (Warburton and Crossa, 2000).

Multivariate methods are useful for characterization, evaluation and classification of plant genetic resources when a large number of accessions are to be assessed for many characters of morpho–agronomic importance (Peetrs and Martinelli, 1989). Classification (grouping of entities with similar patterns) and ordination (description of spatial relationships among entities) used in such areas numerical taxonomy, plant breeding, genetic analysis and biochemistry to describe and analyze multivariate data sets (Crossa *et.al.,* 1995). Many of these multivariate techniques such as cluster analysis and principal component analysis have been used alone or in combination to study various aspects of diversity within crop germplasm (Rolf, 1992).

Although, it is easy to make analysis in a multivariable case, inference pertaining to their results is not an easy task. In cluster analysis, there are many distance measures and methods based on these measures. Depending on their distance measure or selected method, the results of cluster analysis could be different and this can lead researchers into uncertainty. That is

why, in recent years, principal component analysis mostly used. By this way, on the one hand, the number of variables is reduced; on the other hand, the correlation pattern between variables, which is negatively affecting the multi-variable analysis methods, can be removed. Furthermore, it is possible to derive detailed information from the plot of observations over the first two principal components. The resulting diagram can give the researcher an idea about the correctness and inferences of cluster analysis results (Bensmail *et al.,* 1997). This will allow visualization of the difference among the individual and identify possible groups. The reduction is achieved by linear transformation of the original variables into a new set of uncorrelated variables known as principal components. The first step in principal component analysis is to calculate Eagan values, which define the amount of total variation that is displayed on the principal component axes. The first principal component summarizes most of the variability present in the original data relative to all remaining principal components. The second explains most of the variability not summarized by the first principal components and uncorrelated with the first and so on.

Data on nutritional quality of fufu flour produced from 43 cassava varieties were analyzed using multivariate methods. The 1st, four principal components accounted for about 78% of the total variation (Nwabueze and Erch, 2009). Similarly, Ahmadizadeh and Felenji (2011) also reported the first three principal components explained 80.1% of the total variation among traits in potato. The first principal component exerted 38.3 percent and the second principal component were 66.3 percent of total variation between traits. The first principal component was more related to yield, tuber weight, dry weight percent, harvest index and biological yield. Principal component analysis in winter squash accessions revealed the first five principal component axes accounted for 65 % total variation. Major characters included in the principal components were fruit weight, fruit diameter and fruit length and the level of variation found in the collection showed the great potentiality of improving agronomic characters in winter squash (Balkaya *et al.*, 2010).

3. MATERIALS AND METHODS

3.1 Description of the study site

The experiment was conducted at Bako Agricultural Research Center (BARC), Oromia, Ethiopia. The experimental site is located 255 kilometer away in the west from Addis Ababa the capital city of Ethiopia. Its elevation is 1560m.a.s.l. and is situated at 9^{o} 6' N latitude and 37^{o}09' E longitude. The mean annual of eleven years rainfall is 1289 mm, while the mean minimum, maximum and average temperatures are 14^{o}C, 28^{o}C and 21^{o}C, respectively (Appendix 1). The climatic factors for the year 2011 are given in Appendix 2. The soil is dominantly reddish brown Nitosols. The physiochemical properties of the experiential site is clay loam (sand 37%, silt 24% and clay 39%), and 1.6% organic matter content and pH of 4.99 (BARC, 2004). Maize followed by sorghum, teff and other root crops including anchote are grown in the area.

3.2 Plant Material, Design and Management

3.2.1 Plant material

The study was carried out on 49 anchote germplasm accessions. The materials were kindly obtained from Debre Zeit Agricultural Research Center (DZARC) which were collected from four potential anchote growing areas of Amhara, Benshangul Gumuz, Oromia and SNNP regions (East Gojjam, Asosa, West Wollega, Kelem Wollega, East Wollega, Horro Guduru Wollega, Ilu-ababoora, Jimma, Kefa and Sheka zones) (Table 1).

Table 1. Lists of anchote germplasm accessions used in the current study

Accessions	Region /province of collection	Zone	Woreda/ district	Altitude (m.a.s.l.)
207984	B/ Gumuz	Asosa	Asosa	1400
DD	Oromia	Dembi Dollo	Gidda Gebo	2359
DD-1	Oromia	Dembi Dollo	Gidda Gebo	2359
223085	Oromia	East Wollega	Digga Leka	2200
223086	Oromia	East Wollega	Digga Leka	2200
223092	Oromia	East Wollega	Sibu Sire	1900
223093	Oromia	East Wollega	Sibu Sire	1900
223094	Oromia	East Wollega	Sibu Sire	1900
223096	Oromia	East Wollega	Guto Wayu	2100
223097	Oromia	East Wollega	Guto Wayu	2100
223098	Oromia	East Wollega	Guto Wayu	2100
223099	Oromia	East Wollega	Jimma Arjo	2560
223100	Oromia	East Wollega	Jimma Arjo	2560
223101	Oromia	East Wollega	Jimma Arjo	2560
DIGGA	Oromia	East Wollega	Digga	2123
KICHI	Oromia	East Wollega	Gute	1821
KUWE	Oromia	East Wollega	Sibu Sire	1987
SODDU	Oromia	East Wollega	Sibu Sire	1823
DIGGA-1	Oromia	East Wollega	Digga	2123
223096-1	Oromia	East Wollega	Guto Wayu	2320
223086-1	Oromia	East Wollega	Digga Leka	2180
KICHI-1	Oromia	East Wollega	Gute	1821
KUWE-1	Oromia	East Wollega	Sibu Sire	1987
223097-1	Oromia	East Wollega	Guto Wayu	2230

Cont…

Accessions	Region /province	Zone	Woreda	Altitude (m.a.s.l.)
DIGGA-2	Oromia	East Wollega	Digga	2123
90802-1	Oromia	H/G/ Wollega	A/Chomen	1980
90801	Oromia	H/G/ Wollega	A/ Chomen	1780
90802	Oromia	H/G/ Wollega	A/Chomen	1780
223108	Oromia	Ilu Ababoora	Ale	2150
223109	Oromia	Ilu Ababoora	Ale	2150
223110	Oromia	Ilu Ababoora	Ale	2150
223112	Oromia	Ilu Ababoora	Bedelle	1980
223108-1	Oromia	Ilu Ababoora	Ale	1920
223109-1	Oromia	Ilu Ababoora	Ale	2050
223104	Oromia	Jimma	Dedo	1800
223105	Oromia	Jimma	Dedo	1800
223113	Oromia	Jimma	Manna	1980
240407G	SNNP	Jericho Shekicho	Dacha	2150
240407B	SNNP	KefichoShekicho	Decha	2000
229702-1	Amhara	Misirak Gojam	Hulet Iju Enese	1890
220563	Oromia	West Shoa	Bako Tibe	1780
220563-1	Oromia	West Shoa	Bako Tibe	1750
223087	Oromia	West Wollega	Gimbi	2300
223088	Oromia	West Wollega	Gimbi	2300
223090	Oromia	West Wollega	Gimbi	2300
GM	Oromia	West Wollega	Gimbi/A/ Sena	2400
230566	Oromia	West Wollega	Gimbi	1820
223090-1	Oromia	West Wollega	Gimbi	2112
223087-1	Oromia	West Wollega	Gimbi	2165

3.2.2 Experimental design and management

This study was conducted during 2011 cropping season using 7 x 7 Simple Lattice Design described by Yates (1939) and seven incomplete blocks. Each entry was placed in five row plots of 2m long and 0.4m apart with a distance of 0.2m between plants in row as suggested by Girma and Hailu (2009). Trials were hand planted with two seeds per hill and latter tinned (at 4 weeks of planting) to one seedling per hill to get a total plant population of 125, 000 plants per hectare. The experimental plots were prepared well. Sowing was conducted on flat bed at five centimeter depth and covered with soil. Planting date was 21 June 2011. Fertilizer was applied as Diammonium Phosphate (DAP) and urea at the rate of 46kgN and 20kg P_2O_5. All recommended rate of P_2O_5 was applied at the time of planting while N was applied in split, half at planting and the remaining half at the start of vine growth forty five days after planting. Crop management practices such as weeding, cultivation etc were performed as per recommendation of Girma and Hailu (2009). The experiment was conducted under rainfed condition.

3.3 Data Collected

Data on 25 quantitative and 25 qualitative traits were recorded on plant basis with 10 plants from each accession by random sampling method and marked at early stage before the vines development. Data were recorded for quantitative (Table 2) and qualitative traits (Table 3) by adopting descriptors of cucurbits (ECPGR, 2008) and descriptors of sweet potato (IBPGR, 1991).

Table 2. Quantitative traits and description for data collection

No	Traits	Code	Description
1	Days to 50% emergence	DE	Date of 50% seed emergence from sowing date to the development of two true leaves.
2	Days to maturity	DM	When vines start to wither and most leaf are dropped
3	Petiole length (cm)	PEL	Petiole length (from the base to the insertion with the blade) were recorded from 10 randomly selected plants of three leaves in the middle portion of the main vine at harvesting
4	Leaf length (cm)	LL	Leaf length from (the basal lobes to the tip of the leaves) from 10 randomly selected plants for three leaves located in the middle portion of the main vine were recorded at harvesting and means was calculated
5	Internodes length(cm)	INL	Expression of three internodes length located in the middle section of the vine were recorded for randomly selected 10 plants at harvesting
6	Internodes Diameter(mm)	IND	Expression of three internodes diameter located in the middle section of the vine were recorded for randomly selected 10 plants at harvesting
7	Vine length	VL	Main vine length was computed from 10 randomly selected plants at harvesting
8	Vine number	VN	Number of vines per plants were recorded for 10 randomly selected plant at harvesting
9	Flower Length(cm)	FL	Fully opened flowers measured for 10 samples from top to bottom using ruler
10	Flower Width (cm)	FD	Width of the 10 sampled flower were measured using ruler
11	Fruit length(cm)	FRL	Length of the fruit measured for 10 randomly selected sample fruits from top to bottom using ruler
12	Fruit diameter (cm)	FRD	Width of the 10 sampled fruit were measured using a caliper
13	Fruit weight (g)	AFRW	10 randomly sampled fruits were weighed using a sensitive balance
14	Number of fruits per plant	NFRPP	Number of fruits per plant for 10 randomly selected plants were recorded at harvesting
15	Number of seeds per fruit	NSPF	Average number of seeds per fruit were recorded for 10 selected fruits at harvesting
16	100-seed weight	HSWt	The weight of 100 seeds of randomly sampled seeds
17	fruit yield per plant (kg)	AFRYPP	Ten sample plants fruit were measured using a sensitive balance (BP 16000-S) and the average were recorded
18	Root length(cm)	RL	Length of all roots from 10 randomly selected plants were measured using ruler and average root length was calculated top to bottom using ruler

cont…

No	Traits	Code	Description
19	Root diameter (cm)	RD	Diameter of all roots from 10 randomly selected plants were measured using a caliper and average root diameter was calculated
20	Average Root yield per plant (kg)	ARYPP	Tuberous roots of 10 sample plants were measured using a sensitive balance (BP 16000-S) and the average were recorded
21	Marketable root yield(t/ha)	MRY	Uninfected, under and over sized tuberous root was measured in kilogram per plot and converted to tones per hectare
22	Total root yield (t/ha)	TRY	The total storage root weight per 10 sampled plant were converted to tones per hectare
23	Number of roots per plant	NRPP	Number of roots per 10 sampled plant were counted
24	Number of sepal	NS	Number of sepal from three flowers of ten sampled plant were counted
25	Number of petal	NP	Number of petal from three flowers of ten sampled plant were counted

Table 3. Qualitative traits studied and their descriptions

No	Trait	Score	Description
1	Foliage green color intensity	1-3	1 = light green, 2 = green, 3 = deep green
2	Plant growth type	1-2	1 = determinate(main stem distinct with shortened internodes), 2 = indeterminate(long main stem)
3	Vine spreading nature or growth habit	1-2	1 = bushy, 2 = runner
4	Ground cover	3,5,7,9	3 = <50%low, 5 = 50-74%medium, 7 = 75-90%high, 9 = >90%total
5	Vine tip pubescence (degree of hairiness)	0,3,5,7	0 = absent, 3 = sparse, 5 = moderate, 7 = heavy
6	Flowering habit	0,3,5,7	0 = none, 3 = sparse, 5 = moderate, 7 = profuse
7	Flower color	1-6	1 = white, 2 = white limb with purple throat, 3 = white limb with pale purple ring and purple throat,4 = plea purple limb with purple throat, 5 = purple, 6 = yellow
8	Limb shape	3,5,7	3 = semi-satellite, 5 = pentagonal, 7 = rounded
9	Sepal shape	1,3,5,7,9	1 = ovate, 3 = elliptic, 5 = obviate, 7 = oblong, 9 = lance late
10	Sepal apex	1,3,5,7	1= acute, 3= obtuse, 5 = acuminate, 7 = caudate
11	Sepal color	1,2,3,5,6, 7,9	1 = green, 2 = green with purple edge, 3 = green with purple spots, 5 = green with purple areas, 6 = some green others purple, 7 = totally pigmented pale purple, 9 = totally pigmented dark purple
12	Sepal pubescence	0,3,5,7	0 = absent,3 = sparse,5 = moderate,7 = heavy
13	Color of stigma	1,5,9	1 = white,5 = pale purple, 9 = purple
14	Stigma exertion	1,3,5,7	1 = inserted,3 = same height as highest anther,5 = slightly exerted, 7 = exerted
15	Root shape	1-9	1 = round L/B ratio 1:1, 2 = round elliptic L/B ratio not >2:1, 3 = elliptic L/B ratio not >3:1, 4 = ovate-resemble longitudinal section of an egg 5 = obviate-inversely ovate(broadest at proximal end), 6 = oblong-almost rectangular outline L/B ratio about 2:1, 7 = long oblong-L/B ratio >3:1, 8 = long elliptic-elliptic outline with L/B ratio of more than 3:1, 9 = long irregular or curved

Cont …

No	Trait	Score	Description
16	Root surface and flesh defects	0-8	0 = absent, 1 = alligator like skin, 2 = veins, 3 = shallow horizontal constrictions, 4 = deep horizontal constrictions, 5 = shallow longitudinal grooves, 6 = deep longitudinal grooves, 7 = deep constrictions and deep grooves, 8 = others
17	Root cortex thickness	1,3,5,7,9	1 = very thin <1mm, 3 = thin 1-2mm, 5 = intermediate 2-3mm, 7 = thick 3-4mm
18	Root formation	1,3,5,7	1 = closed cluster, 3 = pen cluster, 5 = dispersed, 7 = very dispersed
19	Root cracking	0,3,5,7	0 = absent, 3 = few cracks, 5 = medium no. of cracks, 7 = many cracks
20	Latex production of root	3,5,7	3 = little, 5 = some, 7 = abundant
21	Oxidation of root	3,5,7	Amount of browning observed 5-10 seconds after roots cut cross sectionally; 3 = little, 5 = some, 7 = abundant
22	Predominant root flesh color	1-9	1 = white, 2 = cream, 3 = dark cream, 4 = pale yellow, 5 = dark yellow, 6 = pale yellow, 7 = intermediate orange, 8 = dark orange, 9 = strongly pigmented
23	Secondary root flesh color	0-9	0 = absent, 1 = white, 2 = cream, 3 = dark cream, 4 = pale yellow, 5 = dark yellow, 6 = pale yellow, 7 = intermediate orange, 8 = dark orange, 9 = strongly pigmented
24	Predominant root skin color	1-9	1 = white, 2 = cream, 3 = yellow, 4 = orange, 5 = pink, 6 = red, 7 = purple red, 8 = purple, 9 = dark purple
25	Secondary root skin color	0-9	0 = absent, 1 = white, 2 = cream, 3 = yellow, 4 = orange, 5 = pink, 6 = red, 7 = purple red, 8 = purple, 9 = dark purple

3.4. Statistical Analysis

3.4.1 Quantitative characters

3.4.1.1 Analysis of variance

Data of all traits were subjected to analysis of variance (ANOVA) based on simple lattice design. The difference between treatments means was compared using LSD at 5% probability level. The ANOVA for simple lattice design is given in Table 4 and stated as:

$$Yil(j) = \mu + ti + rj + rl(j) + eil(j)$$

Where, YIl(j) is the observation of the treatment i(i=1,…v,k^2), in the block l (l=1,..k) of the replication j(j=1,..,m); μ is constant common to all observations; ti is the effect of the treatment i; rj is the effect of the replication j; rl(j) is the effect of the block l of the replication j; eil (j) is the error associated to the observation Yil(j), where eil(j)≈N(0,S) independent.

Table 4. Analysis of variance skeleton for 7x7 simple lattice designs

Sources of variation	d.f.	Mean squares	Expected mean squares	f-value
Replication	$r-1$	MSr	$\sigma^2 e + r\sigma^2 p$	MSr/MSe
Block (adj.)	$r(g-1)$	MSb	-	-
Treatment (unadj.)	g^2-1	$MSg(unadj.)$	-	-
Interablock error	$(g-1)(rg-g-1)$	MSe	$\sigma^2 e$	-
Treatment (adj.)	g^2-1	$MSg(adj.)$	$\sigma^2 e + r\sigma^2 g$	$MSg(adj.)/MSe$
Total	$r(g^2-1)$	-	-	-

Where df= degree of freedom, r= number of replication and g=genotype/accession, SSr= sum square of replication, SSb= sum square of adjusted block, SSg (unadj.) = sum square of unadjusted treatment, SSe= sum square of interablock error, SSg (adj) = sum square of adjusted treatment, SST= sum square of total, MSr= mean square of replication, MSb= mean square of adjusted block, MSg= mean square of unadjusted treatment, MSe= mean square of error and MSg (adj) = mean square of adjusted treatment

3.4.1.2 Estimate of genotypic and phenotypic coefficient of variation

The phenotypic and genotypic variances and coefficient of variations were estimated as per the procedure suggested by Burton and De Vane (1953) as follows:

$$\sigma^2 g = \frac{(\sigma^2 e + r\sigma^2 g) - \sigma^2 e}{r} = \frac{MSg - MSe}{r}$$

Where; σ^2_g = Genotypic variance, σ^2_e= environmental variance

r= number of replication

MSg= mean square due to genotype (landraces)

MSe= mean square for error (environmental variance)

$$\sigma^2 p = \sigma^2 g + MSe$$

Where; σ^2_p = phenotypi$_c$ variance, σ2g = Genotypic variance and MSe = mean square for error

Genotypic coefficient of variation (GCV)

$$GCV = \frac{\sqrt{\sigma^2 g}}{\overline{X}} X100$$

Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sqrt{\sigma^2 p}}{\overline{X}} X100$$

Where; $\overline{x}$ = population mean of the character being evaluated (grand mean)

3.4. 1.3 Estimate of broad sense heritability (H^2) and genetic advance

Heritability in the broad sense for quantitative characters was computed using the formula suggested by Singh and Chaudhary (1985):

$$H^2 = \frac{\sigma^2 g}{\sigma^2 p} X100$$

Where, H^2= heritability in broad sense (in percentage)

Expected genetic advance (GA)

The genetic advance (GA) for selection intensity (K) at 5% was calculated by the formula suggested by Allard (1960) as:

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

Where; GA= expected genetic advance

K= selection differential (2.06 at 5% selection intensity)

σp = phenotypic standard deviation

Genetic advance as percent of mean (GAM) was computed to compare the extent of predicted genetic advance of different characters under selection using the formula:

$$GMA = \frac{GA}{\overline{X}} * 100$$

Where GA= Genetic Advance, X= population mean for the trait considered

3.4.1.4 Estimate of genotypic and phenotypic correlation

The character associations presented by correlation coefficient between different pairs of characters at the genotypic and phenotypic level were calculated from the genotypic, phenotypic and environmental covariance obtained by covariance analysis as shown in Table 5. Model of ANOVA for simple lattice design is:

$$Yil(j) = \mu + ti + rj + rl(j) + eil(j)$$

Table 5. Covariance variance analysis skeleton for 7x7 simple lattice designs

Source of variation	Degree of freedom	MSP	EMSP
Replication	$(r-1)$	$MS\,\mathrm{Pr}$	$\sigma^2 exy + g\sigma^2 rxy$
Genotype	$(g-1)$	$MSPg$	$\sigma^2 exy + g\sigma^2 rxy$
Error	$(r-1)(g-1)$	$MSPe$	$\sigma^2 exy$

Where MSP: mean sum product, EMSP: expected mean sum product, MSPr: mean sum product due to replication for characters x and y, MSPg: mean sum product due to genotypes for characters x and y, MSPe: mean sum product of environment (error) for characters x and y, and r = number of replications.

These covariance components were substituted in the following formula to calculate the genotypic and phenotypic correlation as described by Sharma (1998):

$$COVgxy = \frac{MSPg - MSPe}{r}$$

$$COVpxy = COVgxy + COVexy$$

Where; COVgxy = genotypic covariance between characters x and y

COVpxy = phenotypic covariance between characters x and y

COV (exy) = environmental covariance between characters x and y

The correlation was estimated using the formula suggested by Miller et al. (1958):

$$rp = \frac{P\,\mathrm{cov}\,x.y}{\sqrt{\sigma^2 px.\sigma^2 py}} \qquad rg = \frac{G\,\mathrm{cov}\,x.y}{\sqrt{\sigma^2 gx.\sigma^2 gy}}$$

Where; rg= genotypic correlation coefficient,

rp= phenotypic correlation coefficient

Pcovx.y and Gcovx.y are phenotypic and genotypic covariance between variables x and y respectively.

σ^2px and σ^2g x are phenotypic and genotypic variance for variable x, respectively

σ_p^2y and σ^2gy are phenotypic and genotypic variance for variable y, respectively

3. 4.1.5 Path coefficient analysis

In this analysis average root yield per plant was taken as the resultant (dependent) variable while the rest of the characters were considered as casual (independent) variables. The direct and indirect effect of the independent characters on average root yield per plant were estimated by the simultaneous solution of the following general formula suggested by Dewey and Lu (1959) and with statistical package developed by Doshi (1991):

$$rij = Pij + \sum rikPkj$$

Where r_{ij} = mutual association between the independent characters i(yield related trait) and dependent character, j (average root yield) as measured by the genotypic correlation coefficient, P_i is component of direct effect of the independent character(i) on the dependent character (j) as measured by the genotypic path coefficients: and $\sum r_{ik}P_{kj}$ = summation of components of indirect effects of a given independent characters (i) on the given dependent characters (j) via all other independent characters (k), whereas, the contribution of the remaining unknown characters are measured as a residual which is calculated as:

$$R_R = \sqrt{(1 - \sum Pij) - RIJ}$$

3. 4.1.6 Cluster analysis

Cluster analysis is a multivariate statistical analysis technique involving partitioning a set of objects into groups so that objects within a group are more similar and objects indifferent groups are more dissimilar (Crossa *et al.,* 1995). In agglomerative hieratical clusters methods start with the individual members and there are initially as many as cluster as individual members. The most similar individuals are first grouped and these initial groups are merged according to their similarities, as similarity decreases, all subgroups are fused into a single cluster as per the procedure of the Johnson and Wicher (1988). The 49 anchote accessions for 17 quantitative characters were clustered using the proc cluster of SAS with average linkage method of clustering strategy version 9.2 (SAS Institute, 2008) with grouped and sorted the accessions into clusters to form dendrogram. The number of cluster was determined by following the approach suggested by Copper and Milligan (1988) by the looking into three namely pseudo F, pseudo t^2 and the cubic clustering criteria (CCC). The number of cluster was decided where the CCC and pseudo F statistic combined with small value of the pseudo t^2 statistics and large pseudo t^2 statistics for the next cluster fusions.

3.4.1.7 Genetic divergence analysis

The genetic distances between clusters were estimated by Mahalanobis's D^2 statistics (1936) for the 17 quantitative characters and were analyzed using the procedure proc discrim of SAS version 9.2 (SAS institute, 2008). Mahalanobis (1936) developed this method to determine

divergence prevailing among population in terms of generalized group distance and the generalized distance between any two set of population is defined as:

$$D^2ij = (Ai - Aj)S^{-1}(Ai - Aj)$$

Where; D^2ij= total generalized distance between class i and j

(Ai-Aj)= difference in the mean vectors of i^{th} and j^{th} landraces, S^{-1} = var- covariance matrix of pooled error.

Testing the significance of D^2_{ij} values for pairs of clusters was tested using the calculated values of χ^2 (Chi-square) at 1% and 5% probablity level. The test was done aganist the tabulated values of χ^2 for 'p' degrees of freedom where p is the number of quantitative characters considered characters based on procedure suggested by Singh and Chaudhary (1985).

3.4.1.8 Principal component analysis

In Principal component analysis (PCA), the data were used to generate eigen values, the percentage of the variation accumulated by PCA and the load coefficient values which relate the values(eigen values are proportional to the amount of the total variation among the population that is associated with the axis). These principal components (PC) with eigen values > 1.0 were selected and those characters with load coefficent values >0.6 were considered highly relevant for that PC (Jeffers,1967 as cited in Balkaya *et al*., 2010). The principal component was derived as follows.

Suppose x^T = x1…xp is a p dimensional random variable with mean μ and covariance matrix $\sum$ Then

$$Yi = a1j$$

Yj= Y1, Y2, Yp are principal componente

aj^T = a1j…apj is a vector of constant (eigenvectors)

$$aj^T aj = \sum_{k-1}^{p} a^2 kj = 1$$

$$Var(Yi) = Var(a^T 1x = at1\sum a1$$

Where; X is a character (trait)

a is a character coefficient (eigenvector)

Y is principal component

Var (Y) is variance of Y

P is the number of character

J is the number of principal components. Important character in each principal component will be identified by using the formula suggested by Johnson and Wincher (1988)

X= trait coefficient divided by standard devotion of the respective Eigen values where, x>0.5 indicates the significant contribution of the trait in question.

3.4.2 Qualitative characters

3.4.2.1 Shannon- weaver diversity index (H') for qualitative trait

Genetic diversity index was estimated to measure the diversity of each qualitative trait employed in this study. The amount of genetic variation was determined using the Shannon – weaver diversity index, (H') which is calculated by the formula described by Jian *et al*. (1975) as follows:

$$H^{'} = -\sum(pi \ln(pi))$$

Where; pi= is the relative abundance of each trait

ln (pi) =is the natural; logarithm of each abundance,

Pi ln (pi) = is the relative abundance of trait, multiplied by the natural logarithm of the relative abundance (pi)

3.4.2.2 Cluster analysis

The qualitative characters were quantified by using appropriate scale (descriptors) of cucurbits (ECPGR, 2008) and descriptors of sweet potato (IBPGR, 1991). The associations among the 49 anchote accessions for 15 qualitative characters were examined by hieratical agglomerative cluster analysis of observations using proc clusters of SAS with average linkage method of clustering strategy (SAS institute, 2008).

4. RESULTS AND DISCUSSION

Forty nine *anchote* accessions were tested for yield and its related quantitative and qualitative traits. Range, mean, genotypic and phenotypic variance, genotypic (GCV) and phenotypic (PVC) coefficients of variation, heritability in broad sense (H^2), genetic advance as a percentage of mean (GAM%), genetic divergence, association studies and path coefficient analysis, principal component analysis for quantitative traits and Shannon weaver diversity indices (H') for qualitative traits were summarized and presented bellow.

4.1 Quantitative Characters

4.1.1 Variability assessments

4.1.1.1 Vegetative growth parameters

The analysis of variance showed highly significant ($P \leq 0.01$) differences among the tested accessions for most characters except days to maturity, flowering length and flowering width (Table 6). Characters like vine length, fruit length, fruit diameter, number of fruits per plant, average fruit weight, root length, root diameter, average root yield per plant, marketable root yield, and total root yield showed highly significant differences among anchote accessions. The variation observed for measured quantitative traits in this study were in agreement with the earlier findings of Desta (2011) who reported the significant difference among 36 *anchote* accessions and Engida *et al.* (2007) on 30 sweet potato genotypes, Hossain *et al*. (2010) on 58 cucumber genotypes, Blessing *et al*. (2012) on 10 pumpkin accessions, Balkaya *et al.* (2010) on 115 Winter squash, Yadav *et al.* (2009) on 31 collections of cucumber and AbdEl-Salam *et al.,* (2010) six snake cucumber genotypes.

Table 6. Analysis of variance (mean squares) for 22 characters of 49 *anchote* accessions grown at BARC (2011/12)

Sources of variation	Mean squares						R^2%	Efficiency in relative to RCBD
	Replication	Treatment		Block within replication	Error			
		Unadjusted	Adjusted		interablock	RCBD		
df	1	48	48	12	36	48	-	-
RD	1.760	1.770	1.610**	0.130	0.230	0.210	91.280	88.760
INL	6.230	3.490	3.000**	0.680	0.980	2.280	82.360	90.740
AFRYPP	0.000	0.020	0.010**	0.000	0.000	0.006	96.910	91.020
AFRWt	0.090	181.620	165.720**	14.390	15.320	15.090	94.150	98.480
HSWt	0.010	1.890	1.520**	0.050	0.050	0.050	97.890	98.960
VN	0.010	0.930	0.800**	0.010	0.010	0.460	99.180	100.000
FW	0.010	0.150	0.140ns	0.140	0.130	0.130	65.780	100.230
DM	2450.000	257.870	253.380ns	210.710	172.920	238.430	75.040	101.770
TRY	91.410	216.640	197.360**	18.790	14.250	15.380	95.430	101.820
ARYPP	0.010	0.010	0.010**	0.000	0.001	0.000	95.370	102.030
MRY	77.130	208.700	191.640**	19.850	14.630	15.930	95.150	102.200
RL	9.900	1.590	1.480**	0.800	0.570	0.630	82.350	102.600
DE	34.330	5.420	4.420**	2.140	1.500	3.860	85.560	102.930
NFRPP	0.000	6.230	5.020**	0.120	0.070	0.080	99.150	106.060
PEL	20.030	10.170	8.800**	1.880	1.300	5.880	92.990	106.370
FRD	0.030	0.070	0.050**	0.040	0.020	0.030	82.810	106.660
FRL	0.190	0.120	0.110**	0.050	0.030	0.030	86.580	107.630
FL	0.020	0.040	0.040ns	0.050	0.030	0.030	72.630	107.820
NSPF	110.370	468.660	364.560**	14.190	6.820	8.660	98.930	112.440
IND	0.000	0.010	0.010**	0.000	0.002	0.000	91.850	117.040
VL	135.580	2558.520	2048.220**	1075.880	424.270	587.170	89.890	120.200
LL	16.160	6.520	6.150**	2.630	0.900	1.330	91.760	127.260

Key: ** indicates highly significant at 0.01 probability level, ns: non significant RCBD: randomized complete block design, R^2: reliability of model df: degree of freedom , VN: Vine number, FW: Flower width(cm), DE: Days to 50% emergence, NFRPP: Number of fruits per plant, AFRYPP: Average fruit yield per plant (kg), TRY: Total root yield (tha^{-1}), HSWt: Hundred seeds weight(g), ARYPP: Average root yield per plant (Kg), MRY: Marketable root yield(tha^{-1}), RL: Root length(cm), AFRWt: Average fruit weight(g), FRD: Fruit diameter(cm), FRL: Fruit length(cm), NSPF: Number of seeds per fruit, FL: Flower length(cm), MD: Maturity date , RD: Root diameter (cm), INL: Internodes length(cm), LL: Leaf length (cm), VL: Vine length(cm), PEL: Petiole length(cm) and IND: Internodes diameter(mm)

On the other hand, analysis of variance did not indicate variation for quantitative characters such as maturity date, flower length (cm) and flower width (cm). Besides, three quantitative traits, i.e. number of roots per plant, number of sepal and petal per flowers remains the same for all accessions under study indicating narrow genetic base for those traits. The number of sepal and petal in *anchote* flower were five in all genotypes (Appendix 5a) and the finding is in agreement with Desta's (2011) report for 36 anchote genotypes. But, the number of roots per plant obtained in this study contradicted with the finding of Desta (2011); Daba *et al.* (2012) who reported three anchote storage roots per plant. For the reason that anchote is a tap rooted plant that thickens its tap root for storage root organ in the later stage of its development (mostly after 75 days of planting). It bears only one storage root organ per plant in all genotypes studied *i.e.* number of storage root per plant in anchote is one (Abera, 1995; Appendix 5b). However, when the soil is compact enough and hinders easy penetration of tap root the storage organ may develop a fork like structure on single root (Abera, 1995; Appendix 5c).

Range and mean values for 19 characters are shown in Table 7. The mean performance of the 49 anchote accessions for 19 traits is presented in Appendix 3. The mean storage root yield of anchote accessions ranged from 25 to 65.63 t ha^{-1} of which 40.82% of the accessions gave more storage root yield than grand mean (40.74tha^{-1}) indicating its greatest role to the total variability observed among anchote accessions.

From this finding, phenological characters like petiole length showed wide ranges of variation from 8.55 (for accession 223090-1) to 18.81cm (for accessions Kichi). The smallest mean minimum leaf length (9.39cm) were noted for accession 223086 while the highest mean maximum leaf length recorded for accession 223109-1(20cm). The smallest internodes length 8.78cm was recorded for accession 223108-1 while, highest 15.75cm for accession DD.

Accessions Kuwe and 223092 were recorded lowest (0.34 cm) mean minimum internodes diameter while, accession 223086 showed highest (0.86cm) internodes diameter. The lowest (163.24cm) mean minimum vine length were noted for accession 223104 whereas, highest

(332.49cm) mean maximum for accession 240407B. Finally, lowest (one) vine number were recorded for accession DIGGA-1 while, the highest vine number (4) were noted for the accessions GM, 223092, 223094, Kichi, 223086-1, 223093 and Kuwe-1. This finding is in line with the work of Desta (2011) on *anchote* and Engida *et al.* (2007) on sweet potato.

Fruit weight was also exhibited wide range of variation from 22.15g (for accession 223100) to 62.40g (for accession 223101). The lowest average fruit yield per plant was recorded for accessions 207984 (0.03kg) while the highest for accession 223101 (0.44kg). The lowest number of fruits per plant was recorded for accession 207984 (one) and the highest for accession 223100 (ten). Accession Kichi held the lowest number of seeds per fruit (20) while, accession 220563 highest numbers of seeds per fruit (84). Minimum hundred seed weight was recorded for accession 223096 (1.35g) while, Maximum by accession Kichi-1(5.65g) and. This is in agreement with the work of Abera (1995) and Desta (2011) on anchote accessions.

Storage root characters also showed wide range of variation among anchote accessions. Cognizant of this, the lowest storage root diameter (4.14cm) were recorded for accession 223090 whereas, the highest (8.89cm) for accession 223090-1. The smallest root length (7.62cm) and the largest (11.71cm) were recorded for accession 220563-1 and Kuwe respectively. The lowest mean value for accession GM and highest for accession Kichi for characters like average root yield per plant, marketable root yield and total root yield were ranged from 0.20 to 0.53kg, 24.83 to 64.75 t ha $^{-1}$ and 25 to 65.63 t ha $^{-1}$ respectively. This work is in line with the work of Desta (2011) in 36 anchote accessions.

Of all tested materials, based on mean values, the highest average fruit yield per plant (0.44kg) was noted for the accession 223101 which was collected from Jimma Arjo Woreda of Oromia whereas, the lowest average fruit yield per plant (0.03kg) was noted for accession 207984 which was collected from Asosa zone of Benishangul Gumuz (Appendix 3). On the contrary, of all tested materials the highest storage root yield (65.63tha-1) was obtained for accession Kichi which was collected from Gute Woreda of Oromia while, the lowest storage

root yield (25tha^{-1}) for accession 223090 which was collected from Gembi Woreda of Oromia.

Likewise, the differences between the minimum and maximum mean values for other characters such as seed emergence and maturation were also high indicating the availability of variation for improvement through selection. Accession 223112 took nine days to emerge/ germinate as compared to accessions Kichi-1, Digga, DD-1, DD, 240407B, 223108-1, 230566, 223101,223094,223086 and 207984 which took 14 days to emerge. In addition, early maturation (110days) was noted for accessions 223098, 908021-1, Kuwe-1, 220563 and 220566 harvested after 3-4 months while, late maturation (150days) for accessions 223105, 223113, 223086-1, 223087-1, DD and Kichi-1. The high storage root yielding anchote accession (Kichi followed by GM) has medium maturity period.

Generally, the average mean value for most characters was almost twice of the minimum mean value for most traits indicating, great opportunity to improve the various through selection to develop new varieties suitable for different agro- ecologies of the country and for different purposes.

Similarly, the overall earliness in maturity of anchote accessions of some region can also guide breeders to develop a variety which escape terminal low moisture stress by improving traits which correlate to days to maturity in the required direction. Finally, the variation in vegetative characters like leaf length and vine length as well, indicates the possibility to combat soil erosion problems by conserving moisture. Some of the variations observed for measured quantitative characters in the studies were in agreement with the findings of Desta (2011) in 36 anchote accessions, and Engida *et al.* (2007) in 30 sweet potato genotypes.

4.1.1.2 Genotypic and phenotypic variances and coefficient of variations

Genotypic and phenotypic variance ranging from 0.002 to 811.980 and 0.006 to 1236.250 respectively, were estimated for the traits considered in this study (Table 7). Thus, high

phenotypic variance values 1236.25, 185.69, 105.80, 103.14 and 90.40 were noted for characters like vine length, number of seeds per fruit, total root yield, marketable root yield and average fruit weight, respectively. In addition, high genotypic variance values of 811.98, 178.87, 91.56, 88.51 and 75.31 were noted for same characters.

According to Deshmukh *et al*. (1986) phenotypic and genotypic coefficient of variation values greater than 20% are considered as high whereas, values less than 10% are low and values between 10 and 20% as medium. Accordingly, high phenotypic coefficient of variation were noted for characters like average fruit yield per plant (35.777%), hundred seed weight (30.930%), number of seeds per fruit (28.790%), number of fruits per plant (27.820%), vine number (26.720%), marketable root yield (25.360%), average root yield per plant (22.470%), total root yield (25.350%) and average fruit weight (22.070%). Same characters showed high genotypic coefficients of variation, except vine number and average fruit yield per plant which showed medium genotypic coefficients of variation. In addition, medium (10-20%) phenotypic and genotypic coefficients of variation were obtained for the characters like petiole length (18.180 and 15.670%), internodes diameter (17.930 and 14.800%), vine length (15.310 and 12.400%), days to 50% emergence (15.030 and 10.560%), leaf length (14.900 and 12.860%), root diameter (14.820 and13.010%). Internodes length (13.880%), fruit length (10.490%) and root length (10.410%) showed medium values of PCV level only and vine number (13.86%), vine length (12.40) genotypic values signifying the existence of high genetic variability among *anchote* accessions.

Generally, the current finding revealed that, for all characters, estimates of phenotypic coefficients of variation were higher than genotypic coefficient of variation (Table 7), indicating the apparent variations in the accessions were not only genotypic but also environmental influence. This observation agrees with the earlier finding of Aina (2007) in cassava. However, phenotypic coefficients of variation and genotypic coefficients of variation in this study were close to one another for most characters, indicating the high contribution of genotypic variance to the expression of these characters than environmental variance and favors greater possibilities of improvement through selection. In line with this AbdEl-Salam *et al*., (2010) reported small difference for genotypic and phenotypic coefficients of variation

in fruit yield and fruit length of snake cucumber genotypes, enlightening that environmental effect were not great importance on these traits.

These high proportions of phenotypic and genetic variation along with high GCV and PCV indicating, genotype could be reflected by the phenotype and the effectiveness of selection based on phenotypic performance for these characters. Meaning, genetic variation can play important role in the inheritance of yield attributes in anchote and is an indication of high response to selection. The present finding is in line with the finding of Engida *et al*. (2007) in 30 sweet potato genotypes.

The present study is in agreement with the findings of AbdEl-Salam *et al*. (2005) in Snake cucumber genotypes. As opposed to this finding, Afangideh and Uyoh (2007) noted high (>20%) phenotypic and genotypic coefficients of variation in six cucumber genotypes for the traits like vine length, fruit length and average fruit yield.

This finding is also, in agreement with the work of Akinwale *et al*. (2010) in 43 cassava genotypes for the traits like root yield, plant height, root number and shoot weight and Desta (2011) as well reported same in 36 *anchote* accessions. Engida *et al.* (2007) too, reported high genotypic and phenotypic coefficients of variations in 30 sweet potato genotypes for the traits like root length, root diameter and root yield .

Finally, lower phenotypic coefficient of variation were recorded for fruit diameter (9.69%) likewise, lower genotypic coefficient of variation were recorded for traits like fruit length (7.97%), root length (6.93%), fruit diameter (6.18%), and internodes length (5.12%). These lower genotypic coefficient of variation values (<10%) traits indicates selection is not effective for such traits because of their narrower genetic variability.

Table 7. Estimates of range, mean, phenotypic ($\sigma^2 p$) and genotypic ($\sigma^2 g$) components of variances, phenotypic (PCV) and genotypic (GCV) coefficient of variability, broad senesce heritability (H^2), expected genetic advance (GAM) and genetic advance as a percentage of mean (GA %) for 19 characters of 49 *anchote* accessions at BARC (2011/12)

	Range			Genetic tools						
CH	Min	Max	Mean	$\sigma^2 g$	$\sigma^2 p$	GCV (%)	PCV (%)	H^2 %	GA	GAM (%)
DE	9.000	14.000	11.450	1.460	2.960	10.560	15.030	49.310	1.750	15.270
PEL	8.550	18.810	12.360	3.750	5.050	15.670	18.180	74.220	3.440	27.800
LL	9.390	20.000	12.600	2.630	3.530	12.860	14.900	74.510	2.880	22.880
INL	8.780	15.750	11.710	0.360	2.640	5.120	13.880	13.620	0.460	3.890
IND	0.330	0.850	0.430	0.004	0.006	14.800	17.939	68.067	0.108	25.152
VL	163.240	332.490	229.710	811.980	1236.250	12.400	15.310	65.680	47.570	20.710
VN	1.000	4.000	2.970	0.170	0.630	13.860	26.780	26.790	0.440	14.780
FRL	1.470	2.790	2.480	0.040	0.070	7.970	10.490	57.650	0.310	12.460
FRD	1.270	2.790	2.000	0.020	0.040	6.180	9.690	40.640	0.160	8.110
NFRPP	1.000	10.000	5.730	2.470	2.540	27.430	27.820	97.190	3.190	55.700
AFRWt	22.140	62.410	43.080	75.310	90.400	20.140	22.070	83.310	16.320	37.880
NSPF	20.000	85.000	47.040	178.870	185.690	28.430	28.970	96.330	27.040	57.480
HSWt	1.350	5.650	2.870	0.730	0.790	29.850	30.930	93.160	1.700	59.350
AFRYPP	0.030	0.440	0.250	0.002	0.008	17.889	35.777	25.000	0.046	18.425
RL	7.620	11.710	9.730	0.450	1.030	6.930	10.410	44.360	0.930	9.510
RD	4.130	8.890	6.430	0.700	0.910	13.010	14.820	77.060	1.510	23.520
ARYPP	0.200	0.520	0.330	0.005	0.006	20.328	22.473	81.818	0.125	37.878
MRY	24.820	64.750	40.050	88.510	103.140	23.490	25.360	85.810	17.950	44.830
TRY	25.000	65.620	40.740	91.560	105.800	23.490	25.250	86.540	18.340	45.010

Key: CH: character, GV: Genotypic Variance, PV: phenotypic variance, GCV: genotypic coefficient of variation, PCV: phenotypic coefficient of variation, H^2; broad sense heritability, GA: genetic advance, GAM: genetic advance as a percentage of mean, VN: Vine number, DE: Days to 50% emergence, NFRPP: Number of fruits per plant, AFRYPP: average fruit yield per plant (kg), TRY: Total root yield (tha^{-1}), HSWt: Hundred seeds weight(g), ARYPP: Average root yield per plant (Kg), MRY: Marketable root yield(tha^{-1}), RL: Root length(cm), AFRWt: Average fruit weight(g), FRD: Fruit diameter(cm), FRL: Fruit length(cm), NSPF: Number of seeds per fruit, RD: Root diameter (cm), INL: Internodes length(cm), LL: Leaf length (cm), VL: Vine length(cm), PEL: Petiole length(cm) and IND: Internodes diameter(mm)

4.1.1. 3 Heritability and genetic advance

The estimates of broad sense heritability are presented in Table 7. According to Singh (2001) heritability values greater than 80% are very high, values from 60-79% are moderately high, values from 40- 59% are medium and values less than 40% are low. Accordingly, very high heritability values were noted for quantitative characters like number of fruits per plant (97.190%), number of seeds per fruit (96.330%), hundred seed weight (93.160%), total root yield (86.540%), marketable root yield (85.810%), average fruit weight (83.310%) and average root yield per plant (81.818%) while root diameter (77.060%), leaf length (74.510%), petiole length (74.220%), internodes diameter (68.670%) and vine length (65.68%) showed moderately high heritability. Subsequently, medium heritability were recorded for the characters such as fruit length (57.65%), days to 50% emergence (49.31%), root length (44.36%), fruit diameter (40.64%) suggesting such characters were least affected by environmental modifications so that, selection based on phenotypic performance would be reliable. Low heritability were recorded for traits like vine number (26.790%), average fruit yield per plant (25.000%) and internodes length (13.620%). The environmental effect constitutes a major portion of the total phenotypic variation indicating management practice is better than selection to improve those traits.

In line with this finding , Akinwale *et al*. (2010) noted very high heritability values for the traits like root yield and plant height (but, moderately high in anchote) 43 cassava genotypes. Engida *et al.*(2007) as well, reported very high and moderately high heritability values for traits like root yield per plant, leaf length, vine internodes length, root length (but, low for anchote) and diameter in 30 sweet potato genotypes. Jones (1969) and Mok *et al*. (1997) too, noted very high heritability values for storage root yield per plant, root diameter, vine length, vine internodes length and vine internodes diameter in sweet potato genotypes.

As opposed to this finding AbdEl-Salam *et al*. (2010) found low heritability values for fruit yield per plant in cucumber genotypes. He also found moderately high heritability values for number of fruits per plant, fruit diameter and fruit length in snake cucumber genotypes collected from different regions of Egypt.

Genetic advance (GAM %) as percent of mean ranged from 3.89% for internodes length to 59.35 % for hundred seed weight (Table 7). Within these range, a relatively high genetic advance was observed for hundred seed weight (59.35%), number of seeds per fruit (57.48%), and number of fruits per plant (55.70%). Fruit diameter, root length and internodes length showed lowest genetic advance. Selection based on those traits with a relatively high GAM will result in the improvement of performance of genotypes for the traits. This low GAM arises from low estimate of phenotypic variance and heritability.

This result is in line with the work of Engida *et al.* (2007) who noted high genetic gain for traits like vine length, vine internodes length, vine internodes diameter, storage root length, storage root diameter, number of storage root per plant, individual storage root weight and root yield in 30 sweet potato genotypes. Akinwale *et al*. (2010) too, noted high genetic advance for the traits like plant height, root number and root weight in 43 cassava genotypes, Afangideh and Uyoh, (2007) in cucumber, AbdEl-Salam *et al*. (2010) in snake cucumber.

Estimate of genetic advance is more useful as a selection tool when considered jointly with high genotypic coefficients of variation and heritability values (Johnson *et al*., 1995). Accordingly, characters like hundred seed weight, number of seeds per fruit, number of fruits per plant, total root yield, marketable root yield, average fruit weight and average root yield per plant showed high genotypic coefficients of variation, heritability values and genetic gain indicating these characters are principally under genetic control (due to high additive gene effect) and selection for them can be achieved through their phenotypic performance. For traits with high heritability value but moderate value of genetic advance needs careful selection for such traits. Similarly, characters with high heritability values but low value of genetic advance may be governed by non additive gene action or high genotype by environmental interaction and used for development of hybrid varieties. Lower heritability values and genetic advance for internodes length implies most of the variations for these traits were environmental and such traits requires management practice than selection to improve the traits performance.

A trait with high heritability value but low GCV implies its improvement through early generation selection does not give the desired results. Under low GCV and heritability values direct selection for the trait may not be possible but through indirect selection of other secondary traits.

Generally, the high value for heritability and genetic advance of the characters in current study provide information for the existence of wider genetic diversity among anchote accessions and this offers high chances for improving several traits of the crop through simple selection.

4.1.2 Cluster analysis of anchote accessions with quantitative traits

Forty nine anchote accessions grouped into five different clusters (Table 8 and Figure 2). Clusters I and II contained the highest number of accessions (14) followed by cluster III and IV (10) and cluster V (1), respectively. The lowest number of accessions (1) was found in the clusters V. Quamruzzaman *et al. (*2011) reported similar in twenty local sponge gourd genotypes of Bangladesh, Masud *et al*. (1995) reported similar results in sweet gourd and Khan (2006) in pointed gourd. The clustering pattern of the accessions under this study revealed that the accessions collected from the same location were grouped into different clusters. The probable causes for the existence of related genotypes in different regions of origin were attributed to the unrestricted movement of anchote seeds from area to area by man as well as wild animals (Abera, 1995). It is in line with the finding of Khan (2006) in pointed gourd.

Anchote accessions collected from different areas such as Horro-Guduru Wollega (Abay Chomen Woreda), West Wollega (Gimbi and Aba-sena Woreda), East Wollega (Sibu Sire, Guto Wayyu, Jimma Arjo and Digga Leka), Kellem Wollega (Gidda Gebo), Ilu-Ababora (Ale) and West Shoa (Bako Tibbe) were grouped in cluster I.

Table 8.Distribution of accessions in to five clusters based on D^2 analysis for 49 *anchote* accessions tested at BARC (2011/12)

Cluster number	Accessions
I	90801, 220563-1*, 223110, 223097, 223109, KICHI, KUWE, DIGGA-2. DD-1, KICHI-1, 223086, 90802 , 223100 & 223096-1
II	DIGGA-2, SODDU, 223096, 223099, 223094, 223108, 223087-1, 230566, 223090, 223112, 223113, 223085 , 223088 & 220563*
III	207984, 223105, 90802-1, DD, 240407G, 223087, 223097-1, GM, 223090-1 & 223092
IV	223098, 223086-1, 223104, 223108-1, DIGGA, KUWE-1, 223093, 229702-1, 223101 & 223109-1
V	240407B

*Collection from Bako area

Likewise accessions collected from East Wollega (Digga Leka, Guto Wayyu, Jimma Arjo, Gute and Sibu Sire), West Wollega (Gimbi,), Ilu-Ababora (Bedele and Ale) and Jimma (Manna) were clustered together in cluster II. Accessions collected from Asossa, East Wollega (Guto Wayyu and Sibu Sire), Horo Guduru Wollega (Abay Chomen), West Wollega (Gidda Gebo), Jimma (Dedo), Keficho Shekicho (Dech), and West Wollega (Gimbi) were grouped in cluster III. Cluster IV includes accessions collected from east Wollega (Guto Wayu, Digga Leka, Sibu Sire and Jima Arjo Woreda), Jimma (Dedo) and west Wollega (Gimbi). The V cluster contains one accession (240407B) which was collected from Decha of Kefa and Sheka Zone. The present study indicating narrow genetic base for within cluster accessions while wide genetic bases for between clusters and these is useful for hybridization and simple selection programs.

The cluster means of different characters of 49 accessions of anchote are presented in Table 9. Cluster I was composed of 14 accessions. None of the 8 characters had the highest mean or the lowest mean value, fruit diameter (2.030cm) and number of seeds per fruit (62.350) had highest mean values while the lowest mean value for internodes length (11.338cm), internodes diameter (0.418cm), vine number (2.600) and root diameter (5.997cm) was found in cluster I. Cluster II comprising 14 accessions, the mean values of cluster II ranked first for internodes length (12.225cm), root diameter (7.093cm) and average root yield per plant

(0.381kg). Cluster III comprising 10 accessions had the highest cluster mean value for leaf length (13.724cm), vine number (3.3), fruit length (2.598cm), number of fruits per plant (6), average fruit weight (47.557g), hundred seed weight (3.195g), fruit diameter and average fruit yield per plant (0.289g). Prasad *et al.* (1993) also reported similar findings in cucumber. Cluster IV was composed of 10 accessions and the highest mean value was found for internodes diameter (0.455cm) but, the lowest in number of seeds per fruits. Cluster V was composed of one accession and had days to 50% emergence (14), petiole length (15.962cm), vine length (332.49cm) and root length (10.20cm) while, lowest for number of fruits per plant, average fruit weight, hundred seed weight, and average fruit yield per plant. Accessions of the cluster V had early maturation. Each clusters known by their highest mean value and it is helpful for easy selection of parents with the desired traits for hybridization or selection program.

Table 9. Mean value of 17 characters for the five clusters of 49 *anchote* accessions tested at BARC (2011/12)

CH	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5
DE	11.533	11.000*	11.600	11.385	14.000**
PEL	12.186*	11.725	12.655	12.543	15.962**
LL	12.097*	12.082	13.724**	12.658	13.316
INL	11.338*	12.225**	11.525	11.861	11.905
IND	0.418*	0.420	0.426	0.455**	0.443
VL	239.671	267.820	180.161*	219.124	332.490**
VN	2.600*	3.000	3.300**	3.115	3.000
FRL	2.535	2.386*	2.598**	2.400	2.453
FRD	2.030**	1.928*	2.076	1.958	2.021
NFRPP	5.616	5.570	6.003**	5.923	4.029*
AFRWt	42.026	43.293	47.557**	41.567	31.820*
NSPF	62.350**	41.641	47.166	34.256*	36.369
HSWt	2.753	2.585	3.195**	3.008	2.450*
AFRYPP	0.232	0.247	0.289**	0.239	0.125*
RL	9.630*	9.970	9.336	9.927	10.200**
RD	5.997*	7.093**	6.276	6.537	6.540
ARYPP	0.305	0.381**	0.283*	0.337	0.375

Key; *, **represents lowest and highest cluster mean values, respectively. CH: character, DE: days to 50% emergence , AFRYPP: average fruit yield per plant (Kg) PEL: Petiole length(cm), LL: Leaf length (cm), INL: Internodes length(cm), VL: Vine length(cm), VN: Vine number, FRL: Fruit length(cm), FRD: Fruit diameter(cm), NFRPP: Number of fruits per plant, AFRWt: Average fruit weight(g), NSPF: Number of seeds

per fruit, HSWt: Hundred seeds weight(g), RL: Root length(cm), RD: Root diameter (cm), ARYPP: Average root yield per plant (Kg),

Mahalanobis distance (D^2) of the five clusters of 49 *anchote a*ccessions based on 17 quantitative traits is presented in Table 10. Highly significant ($p<0.01$) inter cluster distance was observed between all clusters (I, II, III, IV) and clusters V while Significant ($p<0.05$) inter cluster distance between cluster I and III. The smallest and non significant inter cluster distance (14.224) was noted between clusters II and III while, large and highly significant inter cluster distance (273.968) was noted between cluster IV and V indicating anchote germplasm accessions among clusters are moderately divergent. Similarly, the highly significant inter cluster distances indicated high opportunity for obtaining transgressive sergeants.

Table 10. Average inter cluster divergence (D^2) value in 49 anchote accessions tested at BARC (2011/12)

Cluster	II	III	IV	V
I	23.748	32.413*	17.859	177.568**
II	-	14.224	49.323**	108.507**
III		-	82.988**	69.664**
IV			-	273.986**

*Significant at 0.05 (X^2) = 27.59 and ** Significant at $P<0.01$(X^2) =33.41

Souza and Sorrels (1991) pointed out that categorizing germplasm accessions into morphologically similar, more particularly genetically similar groups is useful for selecting parents for crossing. Falconer (1981) reported that genetic diversity has probably arisen through diversity in origin (geographical separation), ancestral relationship, gene frequency and morphology. These workers indicated that plants differing in either one or more of these factors would differ by significant number of genes. Singh and Chaudhary (1985) also reported divergence analysis is performed to identify the diverse genotypes for hybridization purpose so that genotypes grouped together are less divergent than genotypes which fall into different clusters; particularly clusters separated by the largest statistical distance (i.e. between cluster IV and IV followed by cluster I and V) show the maximum divergence.

4.1.3 Association studies

4.1.3.1 Correlation of yield with other traits

Phenotypic (r_p) and genotypic (r_g) correlation estimates of average root and fruit yield per plant as well as various characters were presented in Table 11 and Table 12, respectively. Average root yield per plant was positively and significantly ($P<0.01$) correlated both at phenotypic and genotypic level with root diameter and root length. Indicating accessions producing more root diameter and root length are high yielder. Conversely, average root yield per plant showed negative and highly significant correlation with fruit length (r_g=0.387) and fruit diameter (rg= 0.473) only at genotypic level indicating simultaneous improvement for root yield and fruit yield is ineffective. Similarly, average fruit yield per plant were positively and significantly correlated with number of fruits per plant and average fruit weight both at phenotypic and genotypic levels. Moreover, average root yield per plant had positive and significant association with vine length at genotypic level while, average fruit yield per plant had positive and significant association with leaf length (both at phenotypic and genotypic levels) and internodes length. This result is in agreement with work of Engida *et al.* (2006), Hossain *et al.* (2000) and Ravindran (2000) in sweet potato genotypes.

4.1.3.2 Correlation among other traits

4.1.3.2.1 Phenotypic correlation

Average fruit yield per plant had positive significant correlation with leaf length, number of fruits per plant and average fruit weight. Positive and highly significant correlation was noted between fruit length and fruit diameter. Average root yield per plant showed positive and highly significant correlation with root length and root diameter suggesting that, improvement aimed at any one of the character would lead to improvement in root yield. It is in line with the report of Afangideh and Uyoh (2007) in cucumber; AbdEl-Salam *et al*. (2010) in snake cucumber.

Table 11. Phenotypic (p_r) correlation coefficient of the 17 characters in 49 anchote accessions grown at BARC (2011/12)

CH	AFRYPP	PEL	LL	INL	IND	VL	VN	FRL	FRD	NFRPP	AFRW	NSPF	HSWT	RL	RD	ARYPP
DE	0.070	-0.213	0.071	0.031	0.260	-0.036	0.120	0.009	0.206	0.042	-0.011	-0.032	0.019	0.055	0.017	-0.009
AFRYPP	-	0.079	0.316*	0.255	0.004	-0.045	0.141	0.096	0.191	0.678**	0.619**	-0.071	0.166	-0.124	-0.048	0.099
PEL		-	0.226	0.071	-0.002	-0.058	-0.007	0.268	-0.022	-0.008	0.145	-0.066	0.159	-0.122	-0.114	0.064
LL			-	0.177	0.025	-0.196	-0.127	0.266	0.072	0.255	0.127	-0.342*	0.325*	-0.095	-0.074	-0.067
INL				-	-0.161	0.205	-0.026	0.090	-0.091	0.029	0.206	-0.202	0.033	0.175	-0.069	0.053
IND					-	0.025	0.131	-0.266	-0.144	0.104	-0.080	-0.213	-0.152	0.145	0.057	0.020
VL						-	-0.231	-0.095	-0.178	-0.024	-0.057	0.097	-0.196	0.159	0.042	0.250
VN							-	-0.199	-0.025	-0.109	0.334*	-0.176	0.171	0.159	-0.090	0.001
FRL								-	0.473**	-0.027	0.119	0.123	0.232	-0.204	-0.212	-0.219
FRD									-	0.068	0.167	0.115	0.171	-0.034	-0.178	-0.222
NFRPP										-	-0.036	0.019	0.169	-0.165	0.105	0.218
AFRW											-	-0.043	0.052	-0.144	-0.214	-0.181
NSPF												-	-0.032	-0.172	-0.223	-0.167
HSWt													-	-0.077	-0.346*	-0.159
RL														-	0.037	0.345*
RD															-	0.593**

Key: *, **: Significant at probability level of 0.05 (r = 0.281) and 0.01 values (r = 0.362), respectively CH: character, DE: days to 50% emergence , AFRYPP: average fruit yield per plant (Kg) PEL: Petiole length(cm), LL: Leaf length (cm), INL: Internodes length(cm), VL: Vine length(cm), VN: Vine number, FRL: Fruit length(cm), FRD: Fruit diameter(cm), NFRPP: Number of fruits per plant, AFRWt: Average fruit weight(g), NSPF: Number of seeds per fruit, HSWt: Hundred seeds weight(g), RL: Root length(cm), RD: Root diameter (cm), ARYPP: Average root yield per plant (Kg),

4.1.3.2.2 Genotypic correlation

Estimates of genotypic correlation coefficients between each pair of characters are presented in Table 12. Accordingly, positive and highly significant genotypic correlations were observed between days to 50% emergence and internodes diameter (r_g =0.416) and days to 50% emergence and root length (r_g =0.366) while, it had no significant correlation with the rest of characters.

The vegetative characters like any other non vegetative characters had either positive or negative association with each other or with other characters. Cogent of this, Petiole length showed positive and significant correlation with fruit length (r_g =0.303) and negative significant correlation with root length (r_g =0.299) whereas, it had no significant correlation with the rest of characters.

Positive and highly significant correlations were observed between leaf length and fruit length (r_g =0.429), leaf length and hundred seed weight (r_g =0.430). Besides, positive and significant correlation were observed between leaf length and internodes length (r_g =0.309) and leaf length and number of fruits per plant (r_g =0.312). Negative and highly significant correlation observed between leaf length and number of seeds per fruit (r_g =0.394) and root length (r_g=0.387). In addition, negatively significant correlation were observed between leaf length and vine length (r_g =0.334) while it had no significant correlation with the rest of characters studied.

Positive and significant correlation were observed between internodes length and root length (r_g =0.339), internodes length and average fruit weight (r_g =0.296), internodes length and vine length (r_g =0.289). Negative and significant correlation were observed between internodes length and internodes diameter (r_g =0.313) and fruit diameter (r_g =0.292). Similarly, Negative and highly significant correlation were observed between internodes diameter and fruit diameter (r_g =0.532) while, it had no significant correlation with other characters studied.

Positive and significant correlation were observed between vine length and average root yield per plant (r_g =0.321) also, negative and significant correlation were observed between vine length and number of vine (r_g =0.304) but it had no significant associations with the rest of characters. Similarly, vine number had positive and highly significant correlation with average fruit weight (r_g =0.387) but, it had no significant correlation with the rest of the characters.

Anchote fruit characters as well showed positive and negative genotypic correlation with the rest of the characters studied. Accordingly, negative and highly significant association were observed between fruit length and root length (rg=0.583), negative and highly significant correlation with average root yield per plant (rg=0.378), negative and significant correlation with root diameter (rg=0.296) and positive and significant correlation with fruit diameter (rg=0.308) but, it had no significant association with the rest of characters. Similarly, negative and highly significant correlation observed between fruit diameter and average root yield per plant (rg= 0.473), negative and significant correlation with root diameter (rg=0.296) but, it had no significant association with the rest of characters.

Alternatively, positive and highly significant correlation were observed between average fruit yield and number of fruits per plant (r_g =0.720) and average fruit weight (rg= 0.601), positive and significant correlation with leaf length (rg=0.335) and internodes length (r_g =0.316). Other fruit traits such as average fruit weight and number of seeds per fruit showed negative and significant association with root diameter (r_g =0.284 and 0.303 respectively) and the correlation between hundred seed weight and root diameter (r_g =0.484) were a little bit strong negative and highly significant.

All storage root traits under studies were showed positive and significant correlation with each other. For instance, positive and highly significant correlation were observed between average root yield per plant and root diameter (rg=0.858) whereas, positive and significant correlation were observed between average root yield per plant and root length (rg= 0.482) and between root length and root diameter (rg= 0.470).

Table 12. Genotypic (g_r) correlation coefficient of the 17 characters in 49 anchote accessions grown at BARC (2011/12)

	CH	DE	AFRYPP	PEL	LL	INL	IND	VL	VN	FRL	FRD	NFRPP	AFRW	NSPF	HSWT	RL	RD	ARYPP
DE		1	0.074	-0.253	0.077	-0.078	0.416**	-0.258	0.215	-0.061	0.094	0.09	-0.085	-0.08	0.02	0.366**	-0.01	0.004
AFRYPP			1	0.084	0.335*	0.316*	-0.002	-0.1	0.149	0.03	0.147	0.720**	0.601**	-0.059	0.168	-0.245	-0.021	0.088
PEL				1	0.226	0.091	-0.084	0.031	-0.002	0.303*	-0.159	-0.038	0.157	-0.076	0.166	-0.299*	-0.187	0.026
LL					1	0.309*	-0.143	-0.334*	-0.132	0.429**	0.118	0.312*	0.075	-0.394**	0.430**	-0.387**	-0.028	-0.17
INL						1	-0.313*	0.289*	-0.043	0.066	-0.292*	0.044	0.296*	-0.265	0.047	0.339*	-0.117	0.108
IND							1	-0.086	0.162	-0.532**	-0.256	0.106	-0.117	-0.248	-0.186	0.12	0.052	0.031
VL								1	-0.304*	-0.23	-0.218	-0.017	-0.12	0.074	-0.277	0.199	0.266	0.321*
VN									1	-0.268	-0.02	-0.136	0.387**	-0.181	0.178	0.214	-0.128	-0.002
FRL										1	0.308*	-0.087	0.046	0.175	0.271	-0.583**	-0.296*	-0.387**
FRD											1	0.041	0.056	0.135	0.193	-0.075	-0.297*	-0.473**
NFRPP												1	-0.055	0.013	0.169	-0.187	0.102	0.209
AFRW													1	-0.025	0.046	-0.227	-0.284*	-0.236
NSPF														1	-0.054	-0.207	-0.303*	-0.22
HSWt															1	-0.109	-0.484**	-0.165
RL																1	0.470**	0.482**
RD																	1	0.858**
ARYPP																		1

Key: *, **: Significant at probability level of 0.05 (r = 0.281) and 0.01 values (r = 0.362), respectively CH: character, DE: days to 50% emergence , AFRYPP: average fruit yield per plant (Kg) PEL: Petiole length(cm), LL: Leaf length (cm), INL: Internodes length(cm), VL: Vine length(cm), VN: Vine number, FRL: Fruit length(cm), FRD: Fruit diameter(cm), NFRPP: Number of fruits per plant, AFRWt: Average fruit weight(g), NSPF: Number of seeds per fruit, HSWt: Hundred seeds weight(g), RL: Root length(cm), RD: Root diameter (cm), ARYPP: Average root yield per plant (Kg),

Similarly, Aina *et al*. (2007) noted that root parameters such as medium-sized roots, number of roots and small sized roots were highly significantly correlated with root yield in cassava genotypes

Generally, average root yield per plant had positive and highly significant association with root diameter (rg=0.858) and root length (rg=0.482), and positive and significant correlation with vine length (rg=0.321) indicating root yield can be improved by improving root length and root diameter. Conversely, average root yield per plant showed negative and highly significant correlation with fruit yield traits such as fruit length (rg=0.387) and fruit diameter (rg= 0.473) indicating simultaneous improvement for root yield and fruit yield is ineffective.

From the estimate of genotypic correlation, about 28.35% of the total traits association showed significant, out of which 55% of them associated positively. This positive association could be resulted from the presence of common genetic elements or microenvironment (or both) that controls the characters to the same direction. Positive significant association due to the effect of genes can be the result of the presence of strong coupling linkage between their genes or the character may be the result of peliotropic genes that could control these characters in with the same direction (Kearsey and Pooni, 1996). Yet again, from the studies some characters showed negative and significant association among each other. Such negative correlation might be because of different genes or pleiotrphic genes that have dominance on the character may control the character in different direction (Kearsey and Pooni, 1996).

Therefore, selection for characters based on its close association (positive and negative) with other characters is very useful for simultaneous improvement of all the associated characters. On the other hand, for characters, manifesting negative association, simultaneous improvement of characters could be difficult and independent selection may have to be carried out to improve such characters (Sylva and Carvalcho, 1997). This finding is in line the work of Engida *et al*. (2006) in sweet potato, Akinwale *et al*. (2010) in 43 Cassava genotypes; Afangideh and Uyoh (2007) in cucumber and AbdEl-Salam *et al*. (2010) in snake cucumber.

From this finding it is possible to infer that, most of root yield and its related traits were negatively significantly correlated with fruit yield and its related traits indicating genotype that possesses high fruit yield tends to produce less root yield and the vice versa. This may also indicate the presence of competition between the shoot and storage root for photosynthate (as anchote storage root bulking overlap with anchote fruit setting stages) were make assimilate competition sever. Consistent with this finding Engida *et al.* (2006) reported the accumulation of assimilates in shoots results in reduction of accumulation of assimilates in sweet potato root storage. Similarly , in some sweet potato cultivars the shoot system served as an alternative sink for assimilate during early growth period and resulted in delayed storage root bulking (Wilson,1982).

In addition, even though it is a year trial in single location, there is an implication to combat lower storage root yielding accessions through breeding program by improving average root yield per plant, root length and root diameter since this traits have significant and positive correlation with each other. Likewise, there is an implication to combat lower fruit yielding accessions through breeding program by improving number of fruits per plant, average fruit weight and leaf length given that this traits have significant and positive correlation with each other. In line with this, Engida *et al.* (2006) noted the same on 30 sweet potato genotypes. Therefore, selection for characters based on its close association (positive and negative) with other characters is very useful for simultaneous improvement of all the associated characters. On the other hand, for characters, manifesting negative association, simultaneous improvement of characters could be difficult and independent selection may have to be carried out to improve such characters.

4.1.3.3 Path coefficient analysis

Results in Table 13 showed path coefficient analysis of all traits on average root yield per plant. Maximum positive direct effect on average root yield per plant was exerted by average fruit yield per plant (1.929). It had positive and non significant correlation with average root

yield per plant. The indirect effects via other traits were mostly negative. Hence the correlation coefficient it had with average fruit yield per plant was largely due to the direct effect. Leaf length, vine number, fruit length, fruit diameter, average fruit weight and number of seeds per fruit had negative direct effect and negative correlation coefficient. Internodes length, internode diameter, average fruit yield per plant and leaf length had negative direct effect and positive correlation coefficients. Hence the positive correlation coefficients were largely due to their respective indirect effects. As the direct effect and genotypic correlation between the two characters is positive thus it indicates true relationship and signifies the direct selection of this character in breeding program.

Root diameter had the second highest positive direct effect. The correlation it had with average root yield per plant was positive and its indirect effect through traits was mostly negligible. Hence, the correlation coefficient it had with yield was largely due to direct effect. Besides, the direct effect of days to 50% seedling emergence, petiole length and vine length were positive. The correlation coefficients these traits had with average root yield per plant were positive. Hence, the correlations the traits had been largely due to the direct effect. Similar findings have been reported by Engida *et al*. (2006) in sweet potato genotypes. As the direct effect as well as the genotypic correlation is positive, therefore, direct selection of this trait is recommended for obtaining higher yield.

Hundred seed weight had the third largest positive direct effect. The correlation it had with average root yield per plant was negative. This may be due to different environmental conditions and genetic background of breeding materials used. It is evident from the data that this character showed positive direct effect on average root yield per plant. This implies restricted simultaneous selection has to be followed; restrictions are to be imposed to void the undesirable indirect effects in order to make use of the direct effect of this trait.

The path analysis revealed the residual value of 0.21 which means the characters in the path analysis expressed the variability in average root yield by 79%.

Table 13. Estimate of direct (bold diagonal) and indirect effect (off diagonal) at genotypic level of 16 traits on average root yield per plant in 49 anchote accessions tested at BARC (2011/12)

CH	DE	AFRYPP	PEL	LL	INL	IND	VL	VN	FRL	FRD	NFRPP	AFRW	NSPF	HSWT	RL	RD	**rg**
DE	**0.223**	0.142	-0.046	-0.024	0.023	-0.240	-0.007	-0.027	0.030	-0.053	-0.111	0.104	0.012	0.005	-0.022	-0.005	**0.004**
AFRYPP	0.016	**1.929**	0.015	-0.103	-0.093	0.001	-0.003	-0.019	-0.015	-0.083	-0.885	-0.732	0.009	0.045	0.015	-0.010	**0.088**
PEL	-0.056	0.163	**0.184**	-0.069	-0.027	0.048	0.001	0.000	-0.148	0.090	0.047	-0.191	0.011	0.044	0.018	-0.089	**0.026**
LL	0.017	0.647	0.041	**-0.307**	-0.091	0.082	-0.009	0.017	-0.209	-0.067	-0.383	-0.091	0.058	0.115	0.023	-0.013	**-0.170**
INL	-0.017	0.610	0.017	-0.095	**-0.294**	0.181	0.007	0.005	-0.032	0.166	-0.055	-0.361	0.039	0.012	-0.020	-0.056	**0.108**
IND	0.093	-0.004	-0.015	0.044	0.092	**-0.577**	-0.002	-0.020	0.260	0.145	-0.130	0.143	0.036	-0.050	-0.007	0.025	**0.031**
VL	-0.058	-0.192	0.006	0.103	-0.085	0.050	**0.026**	0.038	0.112	0.124	0.021	0.147	-0.011	-0.074	-0.012	0.127	**0.321**
VN	0.048	0.287	0.000	0.041	0.013	-0.094	-0.008	**-0.126**	0.131	0.011	0.166	-0.472	0.026	0.048	-0.013	-0.061	**-0.002**
FRL	-0.014	0.058	0.056	-0.132	-0.019	0.307	-0.006	0.034	**-0.488**	-0.175	0.107	-0.056	-0.026	0.073	0.035	-0.141	**-0.387**
FRD	0.021	0.283	-0.029	-0.036	0.086	0.148	-0.006	0.002	-0.150	**-0.568**	-0.050	-0.068	-0.020	0.052	0.004	-0.142	**-0.473**
NFRPP	0.020	1.389	-0.007	-0.096	-0.013	-0.061	0.000	0.017	0.042	-0.023	**-1.229**	0.067	-0.002	0.045	0.011	0.049	**0.209**
AFRWt	-0.019	1.159	0.029	-0.023	-0.087	0.068	-0.003	-0.049	-0.022	-0.032	0.068	**-1.219**	0.004	0.012	0.013	-0.135	**-0.236**
NSPF	-0.018	-0.113	-0.014	0.121	0.078	0.143	0.002	0.023	-0.085	-0.077	-0.016	0.030	**-0.146**	-0.015	0.012	-0.145	**-0.220**
HSWt	0.005	0.324	0.030	-0.132	-0.014	0.107	-0.007	-0.022	-0.132	-0.110	-0.208	-0.056	0.008	**0.268**	0.006	-0.231	**-0.165**
RL	0.082	-0.473	-0.055	0.119	-0.100	-0.069	0.005	-0.027	0.285	0.043	0.230	0.276	0.030	-0.029	**-0.059**	0.225	**0.482**
RD	-0.002	-0.040	-0.034	0.009	0.034	-0.030	0.007	0.016	0.144	0.169	-0.125	0.346	0.044	-0.130	-0.028	**0.478**	**0.858**

** and * highly significant and significant, respectively, Residual effect =0.213, CH: character, DE: days to 50% emergence , AFRYPP: average fruit yield per plant (Kg) PEL: Petiole length(cm), LL: Leaf length (cm), INL: Internodes length(cm), VL: Vine length(cm), VN: Vine number, FRL: Fruit length(cm), FRD: Fruit diameter(cm), NFRPP: Number of fruits per plant, AFRWt: Average fruit weight(g), NSPF: Number of seeds per fruit, HSWt: Hundred seeds weight(g), RL: Root length(cm), RD: Root diameter (cm), rg = genotypic correlation coefficient

In line with this finding, Ntawuruhunga *et al.* (2001) reported the path analysis identified storage root diameter as the main component and showing highest direct effect in Cassava genotypes. As opposed to the present study path coefficient analysis for root yield in sweet potato also revealed that individual storage root weight, number of storage roots per plant and harvest index were the most important determinants of storage root yield (Engida *et al*., 2006). Besides, Aina *et al*. (2007) reported number of storage roots and medium-sized roots both contributed the largest influence on storage root yield in cassava and small-sized roots had a negative direct effect on root yield.

4.1.4 Principal component analysis (PCA)

Eigen values, percent of total variance, percent of cumulative variance and Eigen vectors for 17 quantitative characters in 49 *anchote* accessions results are given in Table 14. The first three principal components having egen values between 1.00 and 9.571 were extracted from the mean of 17 normalized quantitative traits of 49 *anchote* accessions. A variance of 56.30%, 28.50% and 8.60% were extracted from the first to the third components, respectively, and 93.50% of the total variance was explained by these three components and a total of 99.63% variation was extracted from the first six principal components. The cumulative variance of 93.50% by the first three axes with Eigen values of >1.0 indicates that the identified traits within these axis exhibited great influence on the phenotype of the landraces, and could effectively be used for selection among them.

The characters contributing more to the divergence are given greater emphasis for deciding on the cluster for the purpose of further selection and the choice of patterns for hybridization (Jagadev *et al*., 1991). Similarly, Nwabueze *et al. (*2011) reported cumulative variance of 90.90% for the first three axes in Cassava genotypes. Nwabueze and Anoruoh (2009) observed three principal components explained about 81.30% of the total variation in the functional properties of the cassava flours.

Table 14. Eigen values, total variance, cumulative variance and Eigen vectors for 17 characters in 49 *anchote* accessions tested at BARC (2011/12)

CH	PCA1	PCA2	PCA3
Days to 50% seedling emergence	0.544	0.578	-0.320
Petiole length	0.727	0.599	0.067
Leaf length	0.613	0.578	0.385
Internodes length	-0.546	-0.570	0.567
Internodes diameter	-0.752	0.203	0.068
Vine length	-0.728	-0.661	-0.135
Vine number	0.547	0.357	0.755
Fruit	0.804	0.586	-0.080
Fruit diameter	0.752	0.653	0.001
Number of fruit per plant	0.710	0.640	0.005
Average fruit weight	0.774	0.398	0.456
Number of seeds per fruit	0.482	0.199	-0.797
Hundred seed weight	0.730	0.611	0.217
Average fruit yield per plant	0.805	0.404	0.403
Root length	-0.834	-0.535	0.044
Root diameter	-0.405	-0.656	0.582
Average root yield per plant	-0.662	-0.708	0.188
Eigen value	9.571	4.845	1.462
Total variance (%)	56.300	28.500	8.600
Cumulative variance (%)	56.300	84.800	93.500

CH: character, PCA: principal component,

Afuape *et al.* (2010) as well reported a cumulative variance of 70.09% for the first three axes (56% variation for principal component one) in the evaluation of nine sweet potato genotypes and had found total root number, weight of total roots, weight of biomass, and biomass dry matter as the important traits that distinguished the elite materials they worked with. Yang (2008) reported the results of principal component analysis that showed cumulative ratio of contribution with the first four components total variation of 85.69%.

The variables with coefficients i.e. elements of Eigen vector of large absolute magnitude (close to unity) reflect a strong influence while those of small magnitude (near zero) reflect little influence for a particular variable (DeLacy and Cooper, 1990). Characters with higher coefficients (0.6) on the PC axes should be considered more important (Jeffery, 1967 as cited in

Balkaya *et al*., 2010). Accordingly, the first principal component which accounted for 56.30% of the total variability among anchote accessions were mainly due to the contrasting effects of discriminatory traits like average fruit yield per plant (0.805), fruit length (0.804), average fruit weight (0.774), fruit diameter (0.752), hundred seed weight (0.73), petiole length (0.727), number of fruit per plant (0.710), leaf length (0.613), average root length (-0.834), internodes length (-0.752) ,vine length (-0.728) and average root yield per plant (-0.662).

The contrasting effect of quantitative traits such as average root yield per plant (-0.708), vine length (-0.661), root diameter (-0.656), hundred seed weight (0.611), number of fruits per plant (0.64) and fruit diameter (0.653) contributed chiefly to the variation of principal component two (28.50%). Finally, the 8.60% variation for the third principal component were mostly due to variation contributed by contrasting effects of traits like number of seeds per fruit (-0.797) and vine number (0.755).

In line with this finding Mathew *et al.* (1986) reported that fruit weight per plant was the major contributor towards divergence in *Cucumis melo*. Masud *et al*. (1995) found that fruit weight was one of the important contributors to genetic divergence in sweet gourd. Khan (2006) observed that fruit weight, number of fruits per plant and weight of fruits per plant were the higher contributors to the divergence in pointed gourd.

4. 2 Qualitative Characters

4.2.1 Shannon-weaver diversity index (H') analysis

The percentage frequencies of the phenotypic classes of each character values are presented in Table 15. For all accessions, the percentage of frequencies of the phenotypic classes' values varied from 10% to 100%. Based on foliage green color intensity 20% of accessions had deep green, 60% had green and 20% had light green foliage color. Based on the potential of anchote vines ground cover, 30% of the accessions had high, 60% had medium and 10% had low ground

cover potential. With respect to vine tip pubescences (Appendix Plate 4) almost 50% of the accessions had no hairs on their vine tips, 10% of them had moderate and 40% had heavy hair.

Based on ering habit, 50% of accessions had moderate and profuse flowering habit each. In terms of limb shape, out of the 49 accessions smi-satellite (70%) was more common than pentagonal (10%) and rounded flower limb shape (20%). The most frequent sepal shape were lance late 80% of the accessions while, 10 of them had oblong and 10% and obviate each. Based on sepal apex 60%, 30%, and 10% of accessions had acute, obtuse and acuminate sepal apex, respectively. Fifty percent of accessions had no sepal pubescences, 40% sparse and 10% of the accessions hade moderate sepal pubescences

The storage root organ among anchote accessions is also diverse. Based on root shape, anchote accessions 20% of them possessed rounded, 60% ovate and 20% long irregular oblong or curved root shape (Appendix Plate 5). Similarly, based on root cortex thickness 70% of anchote accessions had thin root cortex (1-2mm) while 30% had intermediate root cortex (2mm-3mm). Abundant storage root latex production rate were recorded for 10% of the accessions studied, 70% of them showed some latex and 20% little latex production. The frequency of oxidation rate in anchote were low i.e. 80% of accessions showed little and 20% of them showed some oxidation. Finally, high diversity also observed in predominant root flesh color ranging from white (30%) and cream (60%) to intermediate orange (10%) of the studied anchote accessions. On the other hand, low diversity in anchote was observed for the qualitative traits root cracking and secondary root flesh color.

Shannon-Weaver diversity indices were calculated to compare phenotypic diversity among qualitative characters for accessions (Table 15). High value of H' indicates the existence of more descriptors states of equally common frequency class for individual trait and express diversity for that trait. Traits such as leaf color (H'=0.95), root shape (H'=0.95), vine tip pubescences (H'=0.94), sepal pubescences (H'=0.94), ground cover (H'=0.89), sepal apex

(H'=0.89), pre dominant root flesh color (H'=0.89), latex production rate (H'=0.80), flowering habit (H'=0.69), sepal shape (H'=0.63) and root cortex thickness (H'=61) showed

Table 15. Percentage of phenotypic class, value and estimates of diversity index (H') for 25 qualitative traits of 49 anchote accessions

Trait	State	Code	Freq.	%	H'
FC	Light Green	1	2	20	0.95
	Green	2	6	60	
	Deep Green	3	2	20	
PGH	Determinate	1	0	0	0.00
	Indeterminate	2	10	100	
VSN	Bushy	1	0	0	0.00
	Runner	2	10	100	
GC	<50%Low	3	0	0	0.89
	50-74%Medium	5	3	30	
	75-90%High	7	6	60	
	90% Total	9	1	10	
VTP	Absent,	0	5	50	0.94
	Sparse,	3	0	0	
	Moderate,	5	1	10	
	Heavy	7	4	40	
FH	None	0	0	0	0.69
	Sparse	3	5	50	
	Moderate	5	5	50	
	Profuse	7	0	0	
FLC	White	1	0	0	0.00
	White Limb With Purple Throat	2	0	0	
	White Limb With Pale Purple Ring	3	0	0	
	Plea Purple Limb With Purple Throat	4	0	0	
	Purple	5	0	0	
	Yellow	6	10	100	
SL	Semi-Satellite	3	7	70	0.80
	Pentagonal	5	1	10	
	Rounded	7	2	20	
SS	Ovate	1	0	0	0.63
	Elliptic	3	0	0	
	Obviate	5	1	10	
	Oblong	7	1	10	
	Lance Late	9	8	80	
SA	Acute	1	6	60	0.89
	Obtuse	3	3	30	
	Acuminate	5	1	10	
	Caudate	7	0	0	

FC: intensity of green foliage color, PGH: plant growth habit, VSN: vine spreading nature, VTP: vine tip pubescence, FH: flowering habit, FLC: flower color, SL: shape of limb, SS: sepal shape, SA: sepal apex

Cont…

Trait	State	Code	FRQ	%	H’
SC	Green	1	10	100	0.00
	Green With Purple Edge	2	0	0	
	Green With Purple Spots	3	0	0	
	Green With Purple Areas	5	0	0	
	Some Green Others Purple	6	0	0	
	Totally Pigmented Pale Purple	7	0	0	
	Totally Pigmented Dark Purple	9	0	0	
SP	Absent	0	5	50	0.94
	Sparse	3	4	40	
	Moderate	5	1	10	
	Heavy	7	0	0	
CS	White	1	0	0	0.00
	Pale Purple	5	0	0	
	Purple	9	10	100	
SE	Inserted	1	0	0	0.00
	Same Height As Highest Anther	3	0	0	
	Slightly Exerted	5	0	0	
	Exerted	7	10	100	
RS	Round	1	2	20	0.95
	Round Elliptic	2	0	0	
	Elliptic	3	0	0	
	Ovate	4	6	60	
	Inversely Ovate	5	0	0	
	Oblong	6	0	0	
	Long Oblong	7	0	0	
	Long Elliptic-Elliptic	8	0	0	
	Long Irregular or Curved	9	2	20	
RSD	Absent	0	0	0	0.00
	Alligator like skin	1	0	0	
	Veins	2	10	100	
	Shallow horizontal constrictions	3	0	0	
	Deep horizontal constrictions	4	0	0	
	Shallow longitudinal grooves	5	0	0	
	Deep longitudinal grooves	6	0	0	
	Deep constrictions and deep grooves	7	0	0	
	Others	8	0	0	
RCT	Very thin <1mm	1	0	0	0.61
	Thin 1-2mm	3	3	30	
	Intermediate 2-3mm,	5	7	70	
	Thick 3-4mm	7	0	0	

SC: sepal color, SP: sepal pubescence, CS: color of stigma, SE: stigma exertion, RS: root shape, RSD: root surface defect, RCT: root cortex thickness

Cont…

Trait	State	Code	FRQ	%	H’
RF	Closed cluster	1	0	0	0.00
	Pen cluster	3	0	0	
	Dispersed	5	0	0	
	Very dispersed	7	0	0	
	Single	9	10	100	
RC	Absent	0	9	90	0.32
	Few cracks	3	1	10	
	Medium	5	0	0	
	Many cracks	7	0	0	
LPR	Little	3	2	20	0.80
	Some	5	7	70	
	Abundant	7	1	10	
OR	Little	3	8	80	0.51
	Some	5	2	20	
PDRFC	White	1	3	30	0.89
	Cream	2	6	60	
	Dark cream	3	0	0	
	Pale yellow	4	0	0	
	Dark yellow	5	0	0	
	Pale yellow	6	0	0	
	Intermediate orange	7	1	10	
	Dark orange	8	0	0	
	Strongly pigmented	9	0	0	
SRFC	Absent	0	9	90	0.32
	White	1	0	0	
	Cream	2	0	0	
	Dark cream	3	0	0	
	Pale yellow	4	0	0	
	Dark yellow	5	0	0	
	Intermediate orange	6	1	10	
	Dark orange	7	0	0	
	Strongly pigmented	8	0	0	
PDRSC	White	1	10	100	0.00
	Cream	2	0	0	
	Yellow	3	0	0	
	Orange	4	0	0	
	Pink	5	0	0	
	Red	6	0	0	
	Purple red	7	0	0	
	Purple	8	0	0	
	Dark purple	9	0	0	

RF: root formation, RC: Root cracking, LPR: latex production rate, OR: oxidation rate, PDRFC: predominant root flesh color, SRFC: secondary root flesh color, PDRSC: predominant root skin color

Cont…

Trait	State	Code	FRQ	%	**H'**
SRSC	Absent	0	9	90	**0.32**
	White	1	0	0	
	Cream	2	0	0	
	Yellow	3	0	0	
	Orange	4	1	10	
	Pink	5	0	0	
	Red	6	0	0	
	Purple red	7	0	0	
	Purple	8	0	0	
	Dark purple	9	0	0	

SRSC: secondary root skin color

high phenotypic diversity except root cracking and secondary root flesh color H'=0.32 showed the lowest diversity (Table 15).Conversely, some qualitative traits lacks polymorphism i.e. for plant growth habit, vine spreading nature, flower color, sepal color, color of stigma, stigma exertation, root formation, root surface defect and predominant root skin color. In line with this finding Aruah *et al.* (2010) evaluated Nigerian accessions of *Cucurbita* species using 14 qualitative characters. These accessions were grown in Nigeria, in a randomized complete block design (RCBD) with three replications. The variations in qualitative characters showed higher discrimination with some implications on the genetic diversity and relationship among the accessions of *Cucurbita*.

4.2.2 Cluster analysis for qualitative characters

Cluster analysis based on 15 qualitative traits of anchote grouped the accessions into six clusters (Table 16). Cluster-I had the largest members of all clusters, 35 (77.77%) followed by cluster III, V, IV, and VI which had 4 (8.163%), 4 (8.163%) and 3 (6.122%). Cluster VI had only one accession (2.040 %). Accessions in cluster I were differentiated by the lowest mean values (Table 17) for qualitative traits like oxidation rate and secondary root flesh color. Cluster II comprising three accessions and it is known by having high cluster mean values for qualitative traits like secondary root skin color, storage root surface defect and oxidation rate while, lowest mean values for traits like vine tip pubescence and root flesh defect.

Table 16: Distribution of 49 anchote accessions over six clusters using qualitative characters

Cluster Numbers	Accessions
I	90802, 207984, 240407G, DIGGA-2, 223087, 223104, 223099, 90802-1, 223088, 223092, 223100, KICHI-1, 223094, 240407B, 223110, DIGGA-1, 223097-1, 223108-1, 220563, 223086, 223105, 223096,223101, KUWE, DIGGA, 223109, 90801, 229702-1, 223093, SODDU, KUWE-1, 223113, 223090, DD-1 & 223109-1
II	230566, 223090-1 & 223097
III	223085, KICHI, 220563-1 & 223096-1
IV	223098 & 223086-1
V	223108, GM, 223112 & DD
VI	223087-1

The mean of cluster II ranked first for sepal pubescence and predominant root flesh color while , lowest mean values for shape of limb, secondary root skin color, storage root surface defect and secondary root flesh defect. Cluster IV were known by highest mean values for foliage color, sepal apex ,predominant root skin color and root shape while, lowest mean value for trait sepal shape. The fifth cluster were showed highest mean values for trait flowering habit while, lowest mean cluster values for traits like leaf color, sepal apex, root cracking and latex production rate.

Finally, the sixth cluster were known by highest mean cluster values for characters such as vine tip pubescences , shape of limb, sepal shape and latex production rate while, lowest cluster mean values for traits like flowering habit, sepal pubescence, predominant root skin color, secondary root skin color, predominant root flesh color and root shape. Prasad *et al.* (1993) also reported similar findings in cucumber.

Table 17. Cluster means for qualitative traits

Traits	CI	CII	CIII	CIV	CV	CVI
Leaf Color	0.57	0.57	0.51	0.62**	0.37*	0.54
Vine Tip Pubescence	0.47	0.40*	0.45	0.55	0.48	0.60**
Flowering Habit	0.48	0.46	0.49	0.44	0.51**	0.41*
Shape of Limb	0.52	0.48	0.47*	0.48	0.55	0.67**
Sepal Shape	0.39	0.38	0.47	0.21*	0.37	0.48**
Sepal Apex	0.49	0.46	0.5	0.62**	0.41*	0.6
Sepal Pubescence	0.39	0.35	0.56**	0.43	0.46	0.00*
Predominant Root Skin Color	0.25	0.34	0.29	0.46**	0.29	0.00*
Secondary Root Skin Color	0.01	0.16**	0.00*	0.13	0.04	0.00*
Storage Root Surface Defect	0.25	0.47**	0.00*	0.06	0.29	0.37
Root Cracking	0.01	0.08	0.07	0.00*	0.00*	0.11**
Root Flesh Defect	0.03	0.00*	0.00*	0.25	0.31	0.34**
Predominant Root Flesh Color	0.03	0.14	0.18**	0.07	0.11	0.00*
Secondary Root Flesh Color	0.02*	0.06	0.24*	0.03	0.14	0.11
Latex Production Rate	0.42	0.63	0.3	0.56	0.22*	0.70**
Oxidation of Root	0.16*	0.28**	0.24	0.22	0.16	0.27
Root Shape	0.29	0.25	0.31	0.32**	0.29	0.25*

*and** indicates lowest and highest mean values

5. SUMMARY AND CONCLUSION

The progress of anchote improvement program depends on the choice of the material, the expectant of variability present and the knowledge of both quantitative and qualitative characters with storage root yield and among themselves. The present study comprises 49 *anchote* accessions that were collected from south and western parts of Ethiopia and evaluated at BARC with the objective of assessing the genetic variability and the character associations for 22 characters.

The analysis of variance showed the accessions were significantly different at ($p<0.01$) for all characters except days to maturity, flower length and width. The ranges of mean values for most of characters were large showing the existence of variation among the tested accessions. Phenotypic (PCV) and genotypic (GCV) coefficients of variation were high and medium for most of the characters. High PCV than GCV (but, with little difference) were observed for most characters indicating the existence of environmental variation. High PVC and GCV were observed for number of fruits per fruit, average fruit weight, number of seeds per fruit, hundred seed weight, average root yield per plant, marketable root yield and total root yield suggesting phenotypic selection is possible for such traits. The lowest PCV value was observed for fruit diameter which suggests the limitation of selection for this trait.

Very high heritability values were observed for number of fruits per plant, number of seeds per fruit, hundred seed weight, average root yield, marketable root yield and total root yield. Moderately high heritability values for root diameter, leaf length, petiole length, internodes diameter and vine length. Moderate heritability values were observed for days to 50% seedling emergence, fruit length, fruit diameter and root length suggesting such characters were least affected by environment modifications so that, selection based on phenotypic performance would be reliable.

The expected genetic advance as a percentage of mean varied between 59.35 % for trait hundred seed weight to 3.89% (internodes length). Quantitative traits like hundred seed weight, number of seeds per fruit, number of fruits per plant, average root yield per plant, total root yield, marketable root yield and average fruit weight had relatively high genetic advance as a percentage of mean. These characters with relatively high GAM allow the improvement of these characters through selection.

D^2 analysis on pooled mean of accessions classified 49 *anchote* accessions into five clusters, which makes them to be moderately divergent. There were statistically acceptable differences between most of the clusters. Maximum cluster distance was observed between cluster IV and V while minimum inter cluster distance were between cluster II and III suggesting broad genetic bases of the crop. Cluster II was distinguished by having high cluster mean values for root diameter and average root yield per plant which is the most important storage root yield components implies these accessions can be further used in storage root yield improvement.

Root yield per plant was positively and significantly correlated with root diameter and root length at both phenotypic and genotypic levels. It was negatively and significantly correlated with fruit length and fruit diameter at genotypic level. By selecting for these traits showing positive and significant correlation with average root yield per plant there is a possibility of increasing average root yield of anchote.

Path coefficient analysis based on average root yield per plant as a dependent variable revealed that average fruit yield per plant has positive strong direct effect. The correlation coefficient was also positive (though it is non-significant) between root yield per plant and average fruit yield per plant. Root diameter showed positive direct effect on average root yield per plant and it had positive and highly significant correlation with average root yield per plant. Thus, average fruit yield per plant and root diameter should get attention during storage root yield improvement in anchote for indirect selection of the crop.

In principal component analysis of 49 *anchote* accessions for 17 quantitative characters measured, the first three principal components with Eigenvalues greater than one explained 93.50% of the total variation. Quantitative traits such as fruit yield per plant, fruit length, average fruit weight, fruit diameter, hundred seed weight, petiole length, number of fruit per plant, leaf length, average root length, internodes length, vine length and average root yield per plant. This result further confirmed the presence of ample genetic diversity for use in improvement program. Hence, considerable emphasis should be given on these characters to increase root yield in anchote.

The percentage of frequencies of the phenotypic classes' values for all characters varied from 10% to 100%. Shannon-Weaver diversity indices (H') for qualitative traits showed polymorphism for most traits, implying the existence of a wide range of variation in *anchote* accessions.

The following conclusion can be drawn from the present study:

Average fruit yield per plant showed positive direct effect and positive non significant correlation, it will be a useful trait for indirect selection to increase average root yield. Root diameter as it showed moderately high heritability, relatively better GMA and positive correlation and direct effect on average root yield, this character may be included as a component of indirect selection. Generally the study confirmed the presence of diversity in anchote accessions and this could be exploited in the genetic improvement of the crop through hybridization and simple selection.

Future line of work

Germplasm considered in the present study represented collection from few woreda of anchote growing areas and these were some of accessions only tested at one location. It is however, necessary that the expression of different characters need to be studied with additional locations

and accessions. In such an effort confederation of yield and pest/disease reaction should receive due attention. Furthermore, genetic information for anchote especially at molecular level does not yet exist. Efficient utilization of *anchote* landraces for future breeding needs morphological diversity supported by molecular marker system.

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7. APPENDICES

Appendix Table 1. Eleven years (2001-2011) mean rain fall, field temperature and relative humidity and sunshine at BARC

Year	RF (mm)	Temperature ^{o}C		RH%	Sunshine (hrs)
		Min	Max		
2001	1354.20	14.00	28.00	61.57	5.13
2002	1040.90	13.70	28.90	58.76	4.90
2003	1395.10	14.70	28.60	56.06	4.67
2004	1161.30	13.20	28.70	58.23	4.85
2005	1258.20	13.50	29.70	60.55	5.05
2006	1365.10	14.20	28.10	57.82	4.82
2007	1287.40	13.70	26.50	55.96	4.66
2008	1527.60	13.60	28.60	56.28	4.69
2009	1035.80	12.30	28.70	49.35	4.11
2010	1338.00	13.40	27.90	55.59	4.63
2011	1425.30	13.20	28.40	60.47	5.04
Mean	1289.9	13.59	28.37	57.33	4.78

Appendix Table 2. Weather data of BARC in 2011 main cropping season

Weather	Jan.	Feb.	Mar.	Apr.	May.	Jun.	Jul.	Aug.	Sept.	Oct.	Nov.	Dec.	Total	mean
RF	15.90	2.00	58.80	68.10	222.20	295.00	224.10	294.60	131.30	53.20	60.10	0.00	1425.30	---
Min	12.00	11.00	14.30	14.80	15.20	15.10	14.60	14.90	14.90	12.60	12.30	10.50	162.20	13.19
Max	28.30	29.70	29.90	30.10	28.30	24.30	23.90	23.30	25.20	27.60	27.70	29.00	327.30	28.35
RH%	58.00	50.90	53.90	52.40	58.50	67.50	69.30	75.00	65.90	59.90	59.80	54.50	725.60	60.47
Sunshine	7.48	8.54	6.25	---	4.40	4.11	3.30	2.68	4.35	8.44	7.10	8.64	65.29	5.44

Appendix Table 3. Mean for 22 quantitative characters of 49 *anchote* accessions

Accessions	DE	DM	PEL	LL	INL	IND	VL	VN	FL	FW	FRL	FRD	NFRPP
90801	12	130	12.064	12.419	11.165	0.446	228.170	3	2.456	3.400	2.107	1.920	3
90802	12	125	12.000	11.887	11.285	0.417	236.010	3	2.291	3.250	2.670	2.356	3
207984	14	140	9.581	9.808	13.350	0.407	263.330	3	2.334	3.000	2.523	2.009	1
220563	12	110	10.050	10.934	9.555	0.357	233.250	3	2.587	3.400	2.621	2.066	4
223085	12	120	12.307	11.452	10.620	0.392	214.240	3	2.341	2.950	2.484	2.027	5
223086	14	145	10.549	9.389	8.800	0.855	220.950	4	2.378	3.300	1.625	1.831	6
223087	10	135	9.766	10.636	10.430	0.346	258.540	3	2.372	3.050	2.479	1.998	6
223088	12	130	12.034	10.786	11.775	0.361	219.380	3	2.259	3.150	2.434	2.017	5
223090	12	130	13.749	11.899	11.360	0.392	256.110	3	2.344	3.300	2.562	2.133	4
223092	10	135	8.735	10.100	11.320	0.332	272.430	4	2.287	3.100	1.475	1.986	6
223093	10	135	10.020	10.146	13.175	0.362	172.650	4	2.490	3.300	2.458	1.963	4
223094	14	120	11.031	10.224	11.415	0.387	234.860	4	2.244	2.950	2.611	2.089	5
223096	12	135	12.009	11.621	11.775	0.450	256.960	2	2.081	2.850	2.593	1.958	8
223097	10	135	13.580	11.638	11.095	0.421	217.090	3	2.425	3.050	2.656	1.985	2
223098	10	110	12.968	12.749	13.715	0.403	194.180	3	2.413	3.300	2.665	2.221	7
223099	12	120	13.363	12.062	10.920	0.423	251.710	3	2.447	2.950	2.628	2.122	8
223100	12	130	11.374	11.668	10.950	0.373	208.830	2	2.191	2.900	2.010	1.890	10
223101	14	130	14.069	18.669	12.840	0.474	167.950	3	2.043	2.800	2.699	2.067	7
223104	12	140	14.180	11.272	10.390	0.419	163.240	3	2.247	2.700	2.732	2.143	7
223105	10	150	13.388	12.094	11.740	0.432	265.450	2	2.384	3.250	2.558	1.957	5
223108	12	120	13.584	12.486	12.345	0.413	245.090	3	2.678	3.050	2.582	2.029	8
223109	10	130	13.217	13.091	12.530	0.423	214.990	3	2.253	2.750	2.625	2.015	6
223110	12	130	14.652	13.404	14.200	0.434	227.020	2	2.538	3.100	2.483	1.977	8
223112	9	120	15.328	13.410	12.570	0.444	256.440	2	2.481	3.200	2.500	1.955	6

DE: Days to 50% Emergence, MD: Maturity Date ,PEL: Petiole Length(cm), LL: Leaf Length (cm), INL: Internodes Length(cm), IND: Internodes Diameter(mm), VL: Vine Length(cm), VN: Vine Number, FL: Flower Length(cm), FW: Flower Width(cm), FRL: Fruit Length(cm), FRD: Fruit Diameter(cm), NFRPP: Number of Fruits per Plant

Cont…

Accessions	DE	DM	PEL	LL	INL	IND	VL	VN	FL	FW	FRL	FRD	NFRPP
223113	10	150	9.853	13.896	11.505	0.445	251.560	2	2.034	2.950	2.624	2.006	6
230566	14	110	11.064	12.414	11.395	0.449	241.750	2	2.387	2.950	2.507	2.067	7
220563-1	10	140	11.997	10.676	11.420	0.452	229.360	3	2.375	2.950	2.498	2.086	5
223086-1	10	150	15.508	13.307	11.215	0.444	204.200	4	2.319	2.950	2.632	2.064	6
223087-1	10	150	14.568	13.564	11.360	0.431	238.300	2	2.497	2.950	2.468	1.968	4
223090-1	10	115	8.553	11.943	9.480	0.452	275.340	2	2.132	3.100	2.596	2.174	7
223096-1	10	135	9.389	13.839	12.330	0.342	206.450	3	2.375	3.150	2.634	2.142	7
223097-1	12	140	12.869	12.909	12.190	0.462	269.970	3	2.228	3.050	2.597	1.829	6
223108-1	14	135	14.590	12.408	8.780	0.397	170.870	3	2.381	3.100	2.795	2.184	4
223109-1	12	130	9.743	20.000	10.500	0.440	175.180	3	2.319	2.750	2.626	2.024	6
229702-1	10	140	13.374	12.966	10.485	0.421	179.320	3	2.413	3.500	2.470	2.036	7
240407B	14	130	15.962	13.316	11.905	0.443	332.490	3	2.072	2.550	2.453	2.021	4
240407G	10	130	16.433	12.864	12.035	0.454	258.030	3	2.357	3.100	2.601	2.147	6
90802-1	10	110	14.159	13.840	14.135	0.424	269.640	3	2.100	2.750	2.438	1.915	6
DD	14	150	8.774	14.071	15.750	0.469	263.360	3	2.253	2.900	2.277	1.982	7
DD-1	14	125	9.920	12.544	11.240	0.469	220.650	4	2.406	3.050	2.580	2.127	7
DIGGA	14	130	11.278	12.766	12.185	0.392	192.270	3	2.144	3.050	2.646	2.062	6
DIGGA-1	10	130	11.049	13.073	11.585	0.433	232.310	1	2.288	2.800	2.340	1.759	5
DIGGA-2	10	130	13.766	12.563	13.055	0.485	219.680	3	2.235	2.900	2.454	1.346	4
GM	10	140	14.996	12.556	11.820	0.426	282.110	4	2.369	3.000	2.312	1.278	5
KICHI	10	140	18.812	15.607	12.105	0.396	222.530	4	2.113	2.950	2.550	2.136	8
KICHI-1	14	150	10.977	15.143	12.720	0.487	208.350	4	2.365	3.150	2.608	2.032	9
KUWE	10	130	12.763	12.571	12.580	0.331	224.540	3	2.219	3.000	2.371	1.973	3
KUWE-1	10	110	10.821	12.953	11.965	0.504	181.750	4	2.256	3.200	2.253	1.997	6
SODDU	10	130	10.807	11.750	10.600	0.471	227.090	3	2.250	4.350	2.401	1.894	6
Mean	11	131	12.360	12.600	11.707	0.430	229.714	3	2.315	3.065	2.480	1.999	6
CV%	10.70	9.64	8.52	7.52	8.88	8.59	8.96	3.40	6.93	11.57	6.82	7.46	4.66
LSD(0.05)	2.48	25.67	2.13	1.92	2.11	0.07	41.77	0.20	0.32	0.71	0.34	0.30	0.54

**: indicates highly significant, DE: Days to 50% Emergence, MD: Maturity Date ,PEL: Petiole Length(cm), LL: Leaf Length (cm), INL: Internodes Length(cm), IND: Internodes Diameter(mm), VL: Vine Length(cm), VN: Vine Number, FL: Flower Length(cm), FW: Flower Width(cm), FRL: Fruit Length(cm), FRD: Fruit Diameter(cm), NFRPP: Number of Fruits per Plant

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Accessions	AFRW	NSPF	HSWt	FRY	RL	RD	ARWPP	MRY	TRY
90801	43.120	37	2.450	0.130	9.495	6.075	0.295	36.740	36.875
90802	56.210	42	3.550	0.170	10.410	4.620	0.210	26.250	26.250
207984	30.840	43	2.550	0.030	10.810	6.540	0.310	38.400	39.450
220563	49.770	84	2.350	0.200	9.675	6.380	0.255	31.500	31.875
223085	35.160	83	2.300	0.175	9.350	7.105	0.320	39.750	40.000
223086	33.035	33	1.750	0.200	11.475	6.640	0.375	46.285	46.875
223087	35.170	48	2.650	0.210	9.210	6.350	0.275	34.250	34.375
223088	40.200	66	4.050	0.200	10.275	6.020	0.365	45.100	45.625
223090	53.570	65	4.000	0.210	8.695	4.135	0.200	24.825	25.000
223092	60.890	54	2.250	0.365	10.650	8.345	0.450	56.050	56.250
223093	40.840	75	2.400	0.165	11.050	6.510	0.310	38.750	39.250
223094	45.460	54	1.600	0.230	10.050	6.240	0.320	39.080	40.000
223096	42.270	66	1.350	0.340	9.110	7.035	0.310	38.450	38.750
223097	41.200	47	2.700	0.080	10.200	6.390	0.280	34.900	35.000
223098	49.730	57	2.800	0.345	9.450	4.990	0.245	30.500	30.625
223099	41.550	72	3.000	0.330	9.410	6.975	0.435	53.800	54.375
223100	22.145	46	2.750	0.220	8.675	6.885	0.315	39.250	39.375
223101	62.410	41	4.050	0.440	8.375	5.465	0.215	26.875	26.875
223104	57.505	57	4.150	0.400	8.775	6.945	0.310	38.650	38.750
223105	30.250	40	1.850	0.150	10.035	7.310	0.390	48.750	48.750
223108	35.875	48	4.950	0.290	9.060	5.890	0.340	41.750	42.000
223109	36.570	41	4.650	0.220	9.330	6.075	0.255	31.625	31.875
223110	43.140	32	1.900	0.345	11.525	6.695	0.490	60.645	61.250
223112	51.135	52	1.650	0.280	9.375	6.200	0.230	28.200	28.750
223113	29.820	64	1.950	0.180	10.475	5.850	0.320	40.000	40.000

AFRW: Average Fruit Weight (g), NSPF: Number of Seeds per Fruit, HSWt: Hundred Seeds Weight(g), TFRY: Total Fruit Yield (tha^{-1}), RL: Root Length(cm), RD: Root Diameter (cm), ARWPP: Average Root Weight per Plant (g), MRY: Marketable Root Yield(tha^{-1}) and TRY: Total Root Yield(tha^{-1})

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Accessions	AFRW	NSPF	HSWt	AFRYPP	RL	RD	ARYPP	MRY	TRY
230566	40.005	67	2.400	0.280	10.275	6.125	0.275	33.605	34.375
220563-1	48.050	38	1.500	0.240	7.620	6.650	0.210	25.000	26.250
223086-1	56.895	50	4.400	0.345	9.380	6.495	0.280	34.750	35.000
223087-1	32.050	58	2.750	0.130	8.750	4.320	0.260	32.000	32.500
223090-1	26.430	39	3.350	0.185	9.275	8.890	0.475	57.490	59.375
223096-1	54.925	30	3.450	0.385	10.075	6.070	0.390	46.875	48.750
223097-1	42.815	39	2.350	0.255	10.650	6.495	0.370	45.125	46.250
223108-1	47.800	49	2.850	0.195	8.460	6.405	0.300	36.550	37.500
223109-1	32.635	26	3.750	0.195	8.785	6.605	0.235	27.625	29.375
229702-1	37.935	60	3.800	0.285	9.000	5.875	0.290	36.250	36.250
240407B	31.820	36	2.450	0.125	10.200	6.540	0.375	46.250	46.875
240407G	54.860	38	2.450	0.330	9.425	6.800	0.360	43.625	45.000
90802-1	57.230	39	2.300	0.345	9.100	6.155	0.220	25.000	27.500
DD	51.210	39	3.150	0.360	10.245	7.505	0.455	53.875	56.875
DD-1	51.820	26	2.200	0.365	9.740	7.300	0.360	44.335	45.000
DIGGA	42.490	24	1.550	0.255	9.950	7.320	0.390	46.550	48.750
DIGGA-1	38.020	60	2.400	0.210	10.120	7.445	0.405	48.750	50.625
DIGGA-2	51.560	36	2.350	0.205	8.100	7.205	0.375	46.500	46.875
GM	43.230	38	2.950	0.240	10.300	6.540	0.505	62.490	63.125
KICHI	34.700	20	3.750	0.260	10.510	8.150	0.525	64.750	65.625
KICHI-1	39.870	35	5.650	0.340	10.600	4.355	0.220	27.250	27.500
KUWE	40.240	26	4.000	0.120	11.710	6.490	0.290	35.500	36.250
KUWE-1	47.330	33	2.200	0.260	10.130	6.145	0.250	31.125	31.250
SODDU	39.300	55	3.000	0.255	9.415	5.610	0.330	40.625	41.250
Mean	43.083	47	2.870	0.246	9.730	6.432	0.326	40.046	40.741
CV%	9.08	5.54	8.12	10.61	7.76	7.53	9.32	9.55	9.26
LSD(0.05)	7.937	5.294	0.473	0.053	1.531	0.982	0.061	7.757	7.654

AFRW: Average Fruit Weight (g), NSPF: Number of Seeds per Fruit, HSWt: Hundred Seeds Weight(g), AFRYPP: Average Fruit Yield per plant (kg), RL: Root Length(cm), RD: Root Diameter (cm), ARyPP: Average Root yield per Plant (g), MRY: Marketable Root Yield(tha^{-1}) and TRY: Total Root Yield(tha^{-1})

Appendix 4: Dendrogram showing grouping of 49 anchote accessions for quantitative and qualitative traits

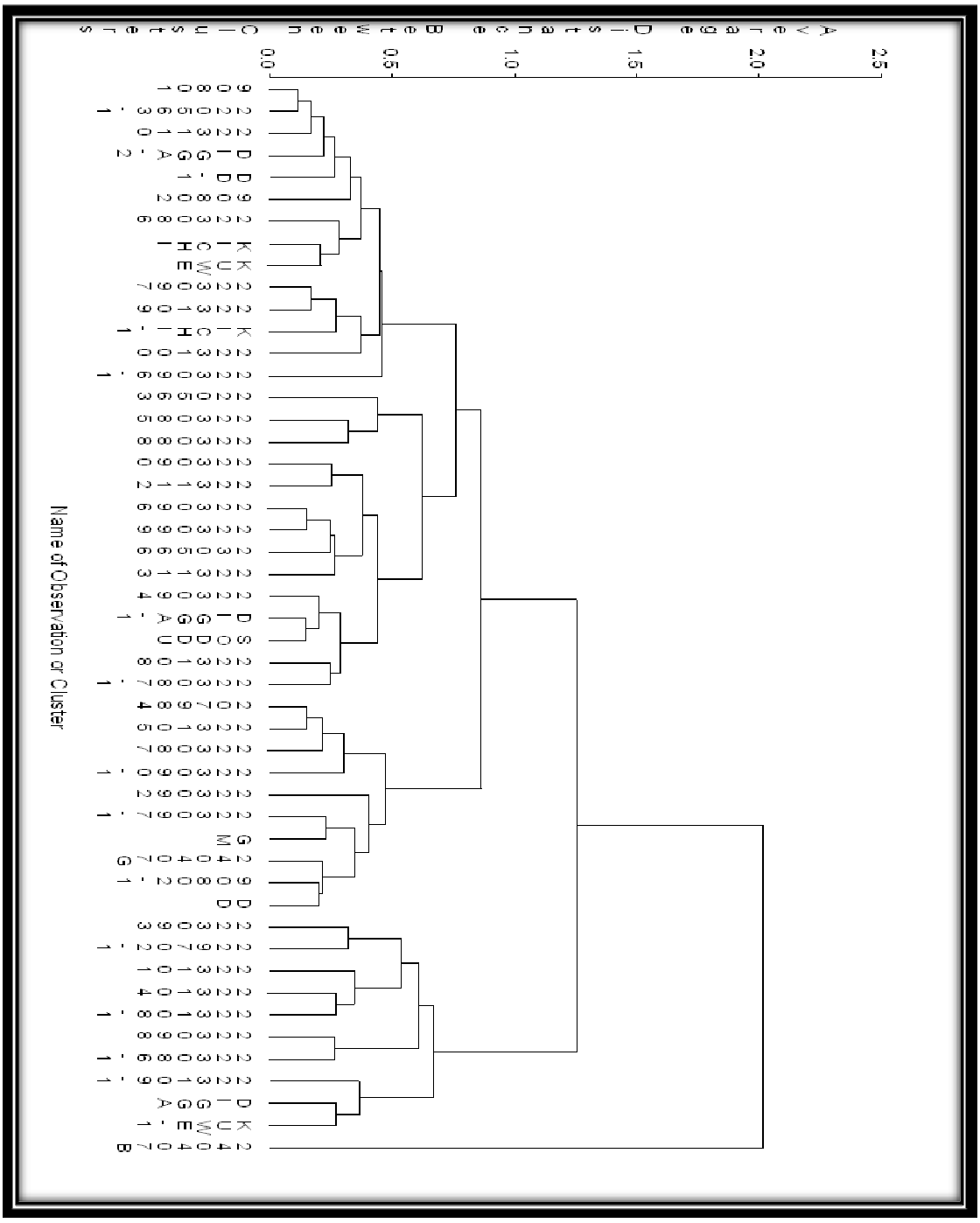

Fig. a: Dendrogram showing grouping of 49 anchote accessions in to 5 clusters based on 17 quantitative characters

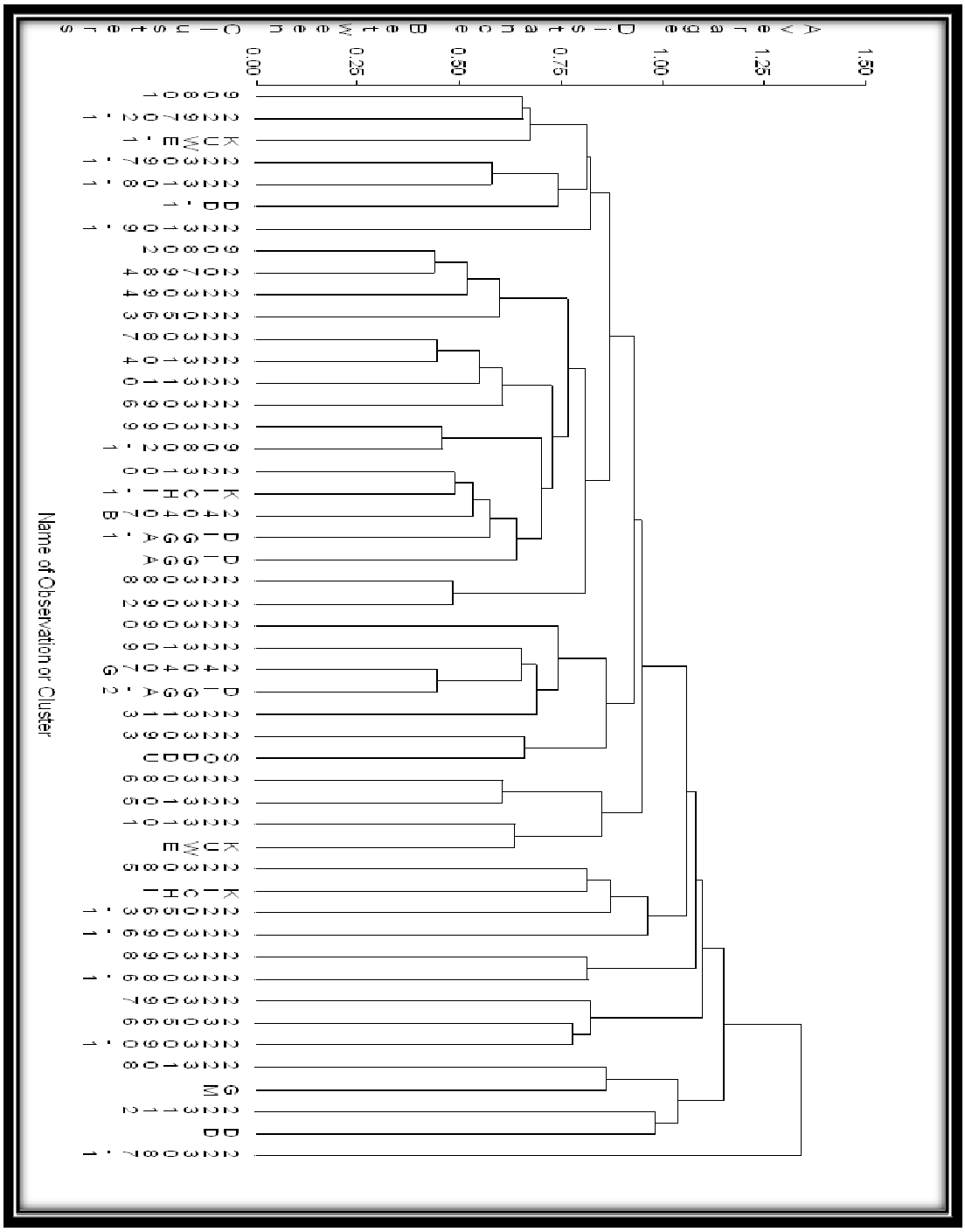

Fig.b : Dendrogram showing clustering of 49 *anchote* accessions based on seven qualitative characters

Appendix 5: Flowers, storage roots, vine tips of anchote

Plate a: Number of sepal and petal in anchote flower

Plate b: Typical anchote storage root per plant

Plate c: Anchote storage root fork

Appendix 5: cont..

Plate d: Vine tip pubescences

Plate e: Root shape