GENETIC DIVERSITY ANALYSIS OF SWEET POTATO (*Ipomoea batatas* (L.) Lam.) BASED ON YIELD AND QUALITY TRAITS

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BY

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CERTIFICATE

This is to certify that the thesis entitled, "Genetic Diversity Analysis Of Sweet Potato (Ipomoea batatas (L) Lam.) Based On Yield And Quality Traits" submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of ***MASTER OF SCIENCE IN GENETICS AND PLANT BREEDING****, embodies the result of a piece of bona fide research work carried out by TANJINA RAHMAN, Registration number: 12-04850 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.*

I further certify that any help or source of information, received during the course of this investigation has duly been acknowledged.

Dated: June, 2018
Dhaka, Bangladesh

(Prof. Dr. Naheed Zeba)

Supervisor

I would like to dedicate

This thesis

To my

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SOME COMMONLY USED ABBREVIATIONS

Full Word	Abbreviation
Agricultural	*Agril.*
Agro-Ecological Zone	AEZ
and others	*et al.*
Bangladesh Bureau of Statistics	BBS
Biology	*Biol.*
Biotechnology	*Biotechnol.*
Botany	*Bot.*
Centimeter	cm
Cultivar	cv.
Date After Sowing	DAS
Degree Celsius	^{0}C
Etcetera	Etc
Exempli gratia (for example)	e.g.
Food and Agriculture Organization	FAO
Gram per liter	g/L
Hectare	ha
International	*Intl.*
Journal	*J.*
Muriate of Potash	MP
Newsletter	*Newsl.*
Pages	pp.
Physiology	*Physiol.*
Randomized Complete Block Design	RCBD
Research	*Res.*
Science	*Sci.*
Sher-e-Bangla Agricultural University	SAU
Species (Plural)	spp.
Square meter	m^2

GENETIC DIVERSITY ANALYSIS OF SWEET POTATO (*Ipomoea batatas* (L.) Lam.) BASED ON YIELD AND QUALITY TRAITS

By
TANJINA RAHMAN

ABSTRACT

An experiment conducted to study the genetic variability analysis based on different yield contributing and quality traits of sweet potato genotypes in Sher-E-Bangla Agricultural University, Dhaka-1207, Bangladesh during Rabi season (2017-2018). In case of morphological traits, analysis of variance revealed significant differences among all the genotypes for all the characters under study except vine internode length, vine internode diameter, above ground fresh weight per plant, storage root diameter, individual storage root weight and storage root fresh yield per plant. In qualitative traits, the analysis of variances showed significant mean squares for different characters indicated the presence of sufficient variation among the genotypes for all the characters except vitamin C. The significant positive correlation with yield (ton/ha) was found in above ground fresh weight per plant, storage root diameter, individual storage root weight, storage root fresh yield per plant and storage root fresh yield per plot at genotypic level and above ground fresh weight per plant, above ground fresh weight per plot at phenotypic level. In case of qualitative traits, the significant positive correlation with dry matter content was found in carbohydrate at genotypic and phenotypic level. Path coefficient analysis showed that Storage root fresh yield per plot had significant positive direct effect on yield. It had also significant positive correlation with yield. In case of qualitative traits, ash %, beta carotene, potassium, sodium and phosphorous content had direct positive effect on dry matter content % and carbohydrate had significant positive correlation with dry matter content %. The highest inter-cluster distance was observed between cluster I and III. Considering group distance and other agro-morphological and qualitative performance, genotypes G2 (SP002) and G5 (SP005) found the potential for future hybridization program in the response of increase nutrition and yield.

CHAPTER I

INTRODUCTION

Sweet potato (*Ipomoea batatas* (L.) Lam.) is a member of the family of morning-glory (Convolvulaceae), which is includes almost 55 genera and more than 1000 species (Girard *et al.*, 2017; Watson and Dallwitz, 2000). Sweet potato mainly originated from Central America and North-western parts of South America (Mandal, 2006; Lewthaite, 2004). In Africa, Asia and Latin America where sweet potato is considered as a staple food and it is extensively grown in these area. In addition to its nutritional advantages, the crop is facile to grow on less fertile soils, has a short growing season and is resistant to various biotic as well as abiotic constraints (Amoah, 2013; Islam, 2006). Sweet potato is ranked as the fifth crop because of its dry matter content but in terms of digestible energy production it is placed as the sixth and sometimes seventh crop (Kivuva, 2013; Thottappilly and Loebenstein, 2009). In developing countries where it is a good source of different nutrients and it plays a significant role in food security (Terry, 2008).

In Bangladesh, the total production of sweet potato has been increased from 92,479 to 104,000 MT in 2000 to 2016, respectively (FAOSTAT, 2017). Sweet potato production has been increased due to superior varieties and adaption of modern cultivation techniques by the farmers in Bangladesh. This crop can be grown as single crop but also can be grown in relay cropping, intercropping and in rotation with other crops. Sweet potato has recently received greater research-related attention due to its many agricultural advantages such as its adaptability to wide range of environmental conditions and its nutritional value as being an excellent source of carbohydrates, dietary fiber, sugars, proteins and different minerals.

Sweet potato is a crop of tropical and sub-tropical regions (Purseglove, 1968) and requires a warm humid climate (Mandal, 2006). Most cultivars do not flower and

even among the flowering genotypes because the duration and the intensity depends upon latitude, altitude, season and climate factors such as temperature, rainfall, sunlight (Samba, 2013; Mandal, 2006). The plant is an herbaceous perennial vine having alternate heart-shaped or palmately lobed leaves and medium-sized sympetalous flowers. The edible tuberous root is long and tapered, with wide ranges of skin colour such as yellow, orange, red, brown, purple, and beige. Its flesh colour ranges from beige through white, red, pink, violet, yellow, orange, and purple. Sweet potato varieties with white or pale yellow flesh are less sweet and moist than those with red, pink or orange flesh (Anonymous, 2016; Huaman, 1992).

Approximately one billion (795 million) people in developing countries suffer from hunger, malnutrition and poverty (FAO, 2015). However, over 3 billion people suffer from a different, sneakier form of hunger than the simple lack of sufficient quantities of foodstuffs referred to as micronutrient malnutrition or "hidden hunger" which is caused by a lack of food of sufficient dietary quality (Kennedy *et al*., 2003). There is an emergent recognition of Sweet potato as a cheap produce for combating food insecurity and micronutrient malnutrition worldwide (Hotz *et al*., 2012; Yamakawa and Yashimoto, 2002).

The UN population projection shows that the trend will continue until the end of this century when the global population will reach 10.8 billion or more (UN DESA, 2015). Young children, pregnant and lactating women are particularly at risk because they have a higher need for minerals and vitamins (Nabakwe and Ngare, 2004). In order to address the prevalent micronutrient deficiencies directly, the conventional approach is supplementation, food securing, dietary diversification and nutrition education (Laurie and Faber, 2008). Food based approaches to nutrition improvement are well documented worldwide (Nawiri *et al.,* 2012, Musinguzi *et al.,* 2006) and in such methods, choice of candidate crops is critical. Sweet potato is a logical choice for such interventions as the crop is

nutrient rich and widely cultivated ranking second after cassava in area (Boney *et al.,* 2014; FAOSTAT, 2012). Sweet potatoes are a nutritious food, low in fat and protein, but rich in carbohydrate. Both tubers and leaves are good sources of antioxidants (Teow *et al.,* 2007) fiber, zinc, potassium, sodium, manganese, calcium, magnesium, iron, and vitamin C (Antia *et al*., 2006).

The World Health Organization (WHO) reported that nearly 190 million preschool-aged children and about 19 million pregnant women mostly in Africa and South-East Asia, greatly affected by vitamin A deficiency (WHO, 2011). About 44–50 % of preschool children are affected by acute vitamin-A deficiency in South and Southeast Asia (Akhtar *et al.,* 2013). Among the South Asian countries, India has the highest prevalence of clinical and subclinical vitamin A deficiency, in preschool children the spread being as much as 62% (Suri and Kumar, 2015). In Bangladesh, approximately 20.5% the preschool-aged children is the prevalence of subclinical vitamin A deficiency, although in slum areas the prevalence is as high as 38.1% (Anonymous, 2013). Inadequate intake of vitamin A and essential minerals can lead to vitamin A deficiency that, in turn, may cause night blindness and undermine growth and immune function. As a results in increased risk of morbidity and mortality, largely from measles, diarrhea and respiratory infections (WHO, 2012; Sommer, 2011; WHO, 2011). Orange-fleshed sweet potato (OFSP) is an excellent source of the pro-vitamin A, β-carotene (Low *et al.,* 2007). A 125 g serving of boiled sweet potato can supply the daily requirement of vitamin A for preschool children and protect them from night blindness (USAID, 2015; Mitra, 2012). In addition to being rich in β-carotene, it contains great amounts of protein, fat carbohydrate, dietary fiber, other micronutrients and some phytonutrients (Mills *et al.,* 2009).

The amount of variability present in germplasm collections of a crop contributes toward breeding for better varieties. Analysis of genetic diversity of agro-morphological and nutritional traits is useful in selecting diverse parental

combinations, reliable classification of accessions, and for exact identification of variety. A study of the correlation between different quantitative and qualitative characters provides an idea of association that could be effectively exploited to formulate selection strategies for improving yield components. However, when more characters are involved in correlation study it becomes difficult to ascertain the traits which really contribute towards the yield. The path analysis under such a situation helps to determine the direct and indirect contribution of these traits towards the yield.

Considering the above facts, the present study was therefore undertaken in order to fulfill the following objectives:

To assess the magnitude of genetic divergence among the genotypes of sweet potato based on their agro-morphological and nutritional traits.

To study the correlation and path coefficient analysis for higher yield and nutrient contributing characters.

To provide farmers with better and superior genotype of sweet potato.

CHAPTER II

REVIEW OF LITERATURE

Sweet potato is the seventh most important food crop due to high nutritional values and adaptability to wide range environmental conditions (Rodriguez-Bonilla *et al.*, 2014; FAOSTAT 2011). Evaluation of genetic variability became an important issue due to its high demand for food and conservation of agricultural and genetic resources. In Bangladesh, the purpose of genetic diversity of sweet potato was less understood. Sweet potato is one of the under exploited of the developing countries major crops (Rees *et al.*, 2003). The need to identify local germplasm with desirable traits has been pointed out by the breeders. The accessions of the local gremplasm are better adapted in local environment than that of the exotic one (Rees *et al*., 2003).

According to Jones (1986) many sweet potato traits are quantitatively inherited. The phenotype of a quantitative trait occurs due to genotypic and environmental effect. Therefore, estimates of variability and its heritable components for the yield attributing characters available in the sweet potato germplasm are pre-requisite for high yield breeding program. Genetic-statistical methodologies are available that assists in selection of superior parents based on their combining ability and potentiality to produce promising segregating populations (Griffings, 1956).

It is necessary to find out the genetic makeup of important yield contributing characters and interrelations existing among them. In this investigation, attempt has been made to study genetic variability, heritability, genetic advance, correlation, path coefficient analysis and genetic divergence in sweet potato genotypes. A brief review of available literature pertaining to the present investigation in sweet potato has been presented in this chapter under the following headings.

2.1 Nomenclature of Sweet potato

Sweet potato (*Ipomoea batatas* (L.) Lam.) is an important staple crop of most tropic countries. It is mainly known for its vigorous growth, drought resistance and productivity with minimum inputs (Rahaman *et al.*, 2015). Globally sweet potato ranks seventh place after wheat, rice, maize, potato, barley and cassava (CIP, 2008). The largest sweet potato collection is maintained by CIP having about 4950 landraces, 21 wild varieties and six improved varieties (Anonymous, 2016). This gene bank was developed by the contribution of sweet potato germplasm all over the world.

2.1.1. Taxonomy of sweet potato

Sweet potato is a dicotyledonous root tuber crop belonging to the Convolvulaceae family. Sweet potato is distantly related to the potato (*Solannum tuberosum*) belonging to the nightshade Solanaceae family, both having the same order Solanales. In some parts of North America, the soft orange sweet potato is known as 'Yam' although it is botanically different from original Yam (*Dioscorea*). *Dioscorea* is monocot belonging to Dioscoreaceae family and native to Africa and Asia. In Argentina, Venezuela, Puerto Rico and the Dominican Republic, sweet potato is known as '*batata*'. In Maxico, Peru, Chile, Cantral America and Phillipines, sweet potato is called *camote* (Annonymous, 2016).

Sweet potato *(Ipomoea batatas (*L.) Lam.) was botanically described in 1753 by Linnaeus as *Convolvulus batatas,* but Lamarck, in 1791, re-classified the crop into the genus *Ipomoea* on the basis of the stigma shape and the surface of the pollen grains (Thottappilly and Loebenstein, 2009). Hence, the crop belongs to the family of Convolvulaceae, tribe of *Ipomoeae*, genus *Ipomoea*, sub-genus *Eriospermum*, section Eriospermum and species *batatas*. Therefore, the botanical name of sweet potato was changed to *Ipomoea batatas (L.) Lam.*

2.1.2. Morphology of sweet potato

The color of leaves and stem varies from green to dark purple due to presence of anthocyanin pigment (Laurie and Niederwieser, 2004). The general leaf outline varies from round to almost divided with the margins having no lateral lobes to deeply lobes. The shape and size of the storage root varies from round and long irregular or curved depending on the variety and environmental factors (Woofle, 1992). The skin color of sweet potato varies from white to dark purple and flesh color varies from white to orange depending on distributions (Laurie and Niederwieser, 2004). Sweet potato has an extended storage root which accumulates more edible components compared to tuber potato.

2.1.3. Origin and diversity of sweet potato

The exact origin of sweet potato is not well-known still now. According to historical evidences, it is assumed that sweet potato is originated from Central or South American lowlands. This crop probably have cultivated since 3000 BC in South American indigenous communities (Woofle, 1992). Therefore, it is believed to be originated from Yucatan Peninsula of Maxico and Orinoco river in Venezuela. Later sweet potato was spread by the explorers (Zhang *et al.*, 2004). In the 16th century it was introduced to Europe, Asia and later in Africa (Allemann *et al.*, 2004). The wild cultivated progenitors has not yet been identified. It is believed that the current cultivated hexaploid sweet potato varieties are the result of cross between tetraploide primitive and diploid weedy sweet potatoes (Sauer, 1993). It is possible to find out existence of wild hexaploid but according to the history, cultivars were independently domesticated in various regions. However, the origin of sweet potato is still under investigation.

Christopher Columbus brought sweet potatoes to Europe and Portuguese after his first voyage to the new world in 1942. By the 16th century, they were brought to the Philippines by Spanish explorers and to India, Africa, Indonesia and Southern Asia by the Portuguese. Around this same time, sweet potatoes began to be

cultivated in the southern Unites States, where they still remain a staple food in the traditional cuisine (Loebenstein and Thottappilly, 2009).

2.1.4. Economic aspect of sweet potato

Sweet potato cultivation can play an important role in context of food security in Bangladesh (Hossain and Siddique, 1985). Sweet potato is a highly nutritious food crop and gives higher and faster production under diverse agro-ecological conditions with minimal input (CIP, 2008). It has potentiality to combat malnutrition and poverty. Additionally, it has been recognized as highly valuable crop due to its calorie value per cultivated area (Scott *et al.*, 1992). High yield ability, drought tolerance, crude protein and palatability content has made this crop remarkable. Purple fleshed sweet potato contains more anthocyanine while the Orange one contains more beta-carotene. This two elements act as anti-oxidant which thought to prevent chronic heart disease and cancer (Teow *et al.*, 2007). Increased beta-carotene content (pro-vitamin A) and crude protein content is good for nutrition and health (Ukom *et al.*, 2009).

2.1.5. Cultivation of sweet potato

Warm days and nights are require for optimum sweet potato yield. It is sensitive to low temperature and grows best in tropical and warm temperate regions having sufficient water and sunlight. Well aerated, moderate to slightly acidic, sandy to sandy loam soil having ability to tolerate harsh and climate are favorable conditions of sweet potato (Van den Berg and Laurie, 2004).

Gibson *et al.* (2000) stated that landraces are adapted to their local areas and have developed resistance against local pests and diseases. However, in most cases, the landraces yield are low that reduces the overall sweet potato production (Allemann *et al.*, 2004). Similarly, Laurie *et al.* (2008) reported low yield and yield instability

due to the use of old landraces addressed by the resource-poor farmers. In Bangladesh, sweet potato can give satisfactory yield under adverse climatic and soil condition and under low or no use of external inputs (Githunguri and Migwa, 2004; Ndolo *et al.*, 2001; Carey *et al.*, 1999).

Cultivation of sweet potato crop is increasing every year. According to FAOSTAT (2017), the world production of sweet potato was 112,835,316 tons in 2017. Among it, about 78.68 million tons come from China and other Asian countries including Japan, Korea and Indonesia. In Bangladesh, 25,750 ha area was under sweet potato cultivation in 2017 while it was 40874 ha in 2000.

2.1.6. Constraints to Sweet potato Production

Despite the numerous potential uses and benefits of Sweet potato, the production of the crop is below the potential level in many parts of the world. Sweet potato has a yield potential of 20-50 t/ha of storage roots in the tropics (Çalifan *et al*., 2007). Sweet potato yield potential is yet to be realized in Bangladesh. These low yields are as a result of several socioeconomic, biotic and abiotic constraints. Socio-economic constraints in the production of Sweet potato include, poor post-harvest handling and storage facilities, lack of clean and poor seed distribution system, lack of processing skills and poor agronomic varieties (Njeru *et al*., 2004; Ames *et al*., 1996).

Several biotic constraints of sweet potato production in the temperate zones are alternaria blight, sweet potato virus disease (SPVD) (McGregor *et al.,* 2009) and root-knot nematodes (Grüneberg *et al*., 2009) and sweet potato weevil mostly found in tropics areas (Shonga *et al.*, 2013; Ehisianya *et al*., 2013). Moisture stress due to drought is becoming a major abiotic constraint to crop production worsened by climate change (Nakashima and Yamaguchi-Shinozaki, 2013). Soil moisture availability confirm the external water status at the boundaries of the plant (soil and air) and in the internal plant water status within the tissue of the plants.

Drought stress reduces photosynthesis and translocation of assimilates thus reduce the yield (Anjum *et al.*, 2011). However breeding drought tolerant varieties may ensure high yield production under conditions of limited water availability (Sorrells *et al.*, 2000).

2.2. Variability

Improvement of a crop mainly depends on the magnitude of genetic variability and the extent of heritable desirable characters. Sweet potato is a crop having wide range of variability in different agro-morphological characters like leaf shape, tuber skin colour, flesh part colour, tuber shape, time of maturity, resistance to disease and several other characters which can be exploited for the development of a desirable genotype. Existence of genetic diversity in a crop population and proper knowledge on this divergence is of great importance to breeders. Breeders can manipulate this divergence for improvement breeding of a crop. Hence, an attempt has been made to collect the background information on the amount of genetic variability present in sweet potato genotypes. This attempt can assist as a guideline to select parents as a donor in breeding program for proper utilization of the quality trait and development of the desirable varieties for various agro-ecological zones (AEZ) in Bangladesh. The effect of environment in expression of desirable traits also need to be taken into account. Burton (1952) suggested that co-efficient of variability together with heritability estimation will provide a landscape of genetic advance that can be obtained by selection process. Several works already has been done to find out wide range of genetic variability for characters of vine and tubers of sweet potatoes (Rao *et al.*, 1992; Vimala and Lakshmi, 1990; Kamalam, 1990; Kamalam *et al.*, 1977; Lowe and Wilson, 1975; Hayneys and Wholey, 1971; Jones *et al*, 1969; Mc Lean, 1955).

2.2.1. Phenotypic and Genotypic Variability

Variation is the occurrence of differences among the individuals due to the differences in their genetic composition and the environmental effect (Allard, 1960). Sweet potato has wide adaptability to harsh growth condition but still sensitive to environmental variation. The study of magnitude of variability of a crop species is important as it provides the basis for effective selection (Singh, 1993). Information on the nature and magnitude of genetic variability of a crop helps in designing effective crop breeding program for producing hybrids (Poehlman and Sleper, 1995). In crop improvement, plant breeder selects crop based on their phenotype and the effectiveness of the selection would largely depend on the proportion of the phenotypic variation that is due to the genotype (Amsalu, 1993). The genetic component of variation is important in crop improvement, since only this component is transmitted to the next generation (Singh, 1993). Phenotypic variation is the observable variation present in a character in population. It includes both genotypic and environmental components of variation and as a result, its magnitude differs under different environmental conditions (Singh 1993). Genotypic variation, on the other hand, is the component of variation, which is due to the genotypic differences among individuals within a population.

2.2.2. Morphological variability

Thirty two accessions of sweet potato were observed in which 5 and 27 accessions showed variability for morphological characters like type of leaf lobbing, petiole pigmentation, shape of the central leaves and root flesh colour (Wilckens *et al.* 1993). Choudhary *et al.* (2001) studied 21 morphological traits in sweet potato like nature of twining, vine pigmentation, vine growth rate, plant type, vine tip pubescence, vine inter node length and diameter, petiole pigmentation, petiole length, foliage color, axial leaf vein pigmentation, mature leaf shape, mature leaf size, flowering habit, flower colour , seed capsule setting, tuber neck length, tuber shape, tuber skin colour, tuber flesh colour, distribution of anthocyanin in tuber

flesh and latex production in tuber and they observed wide range of variations in these traits.

In a study by Kaledzi *et al.* (2010) on 40 accessions of sweet potato, they noticed variations among the different accessions in terms of the vine, leaf, petiole, root skin and flesh characteristics. Similarly Sreekanth *et al.* (2011) carried a preliminary yield trial with 230 clones selected from 1600 orange fleshed clones for morphological observations like leaf shape, emerging leaf colour, skin colour, flesh colour, weight of vine and weight of storage roots. They also observed that selection of a number of superior hybrid clones based on yield and yield contributing characters would provide a large gene pool for the recombination. Wadud *et al.* (2011) conducted an experiment on sweet potato genotypes on the basis of leaf, vine and tuber characters and concluded that leaf character varied from heart, tetra-lobbed to pent-lobbed, the vine and vine tip colour ranged from green, pink, pinkish green, light purple, deep purple to light pink, and the shapes of tuber were globulose, elliptical and fusiform respectively.

Vimala *et al.* (2011b) studied on 1600 orange fleshed sweet potato genotypes and observed wide range of genetic variation for skin colour of tuber (pink, purple and purple to light pink colour) and root flesh colour (orange, light orange, dark orange and creamy to yellow colour). Vimala *et al.* (2012) evaluated 1630 orange fleshed sweet potato genotypes and observed three types of leaf shapes like cordate (81.65%), slightly lobed (16.69%) and narrow lobed (1.66%) and emerging leaf colour ranged between green (92.5%) to purple (7.5%). In a study, Richardson (2012) evaluated six genotypes of sweet potato for tuber quality and found large variation in the leaf and tuber characteristics.

2.2.3. Quantitative variability

Kamalam (1990) conducted a trial with fifteen sweet potato cultivars and observed very high variability for some quantitative traits like vine length, vine thickness, number of branches, number of Tuber and tuber yield. Wilckens *et al.* (1993)

studied 32 accessions of sweet potato and observed that 5 and 27 accessions showed variability for growth habit and internode length respectively. Velmurugan *et al.* (1999) conducted experiment on nine clones of sweet potato on based on variation existing in quantitative characters during 90, 105 and 120 days after planting and the result showed that, clones with high number of tubers per vine gave higher mean value for tuber yield and highest variability was observed for weight of weevil free tubers, followed by weight of tubers per vine and number of weevil-free tubers per vine. Tsegaye *et al.* (2007) conducted a study on 30 sweet potato genotypes and revealed that there was significant variability among the genotypes for the characters like vine length, vine inter node length, vine inter node diameter, leaf area, above ground fresh and dry weight per plant, storage root number per plant, storage root length and diameter, individual storage root weight, harvest index per plant, storage root dry matter content and storage root fresh yield per plot.

Cavalcante *et al.* (2010) conducted an experiment on 9 clones and 2 varieties of sweet potato and revealed that, clones 6 and 11 presented the highest marketable root yield and clones 8, 14 and the “Rainha Prata” variety presented the highest phytomass yield on the shoot. Binu *et al.* (2011) studied the changes in dry matter content during 35 days of storage in 10 orange fleshed sweet potato clones at Central Tuber Crop Research Institute Thiruvanthapuram, Kerala and observed that gradual decreases in dry matter content from 24.1 to 25.5 %. Vimala and Hariprakash (2012) evaluated 250 hybrid progenies on the basis of vine, fresh yield per plant, fresh yield per plot, storage root and dry matter content and observed that the selection of a number of superior F1 clones for yield and other attributes would provide a large gene pool for the recombination to generate the promising variety of considerable value. Vimala *et al.* (2011a) conducted an experiment on 230 clones of orange fleshed sweet potato genotypes. They observed the morphological characters like leaf shape, emerging leaf colour,

weight of vine, skin colour, flesh colour and weight of storage root and reported that the selection of a number of superior hybrid clones for yield and other attributes would provide a large gene pool for the recombination from which the promising variety of considerable value could be generated. Vimala *et al.* (2011a) evaluated 42 orange fleshed sweet potato hybrids in upland and low land conditions for storage root yield and dry matter content (%) along with a control variety of Sree Kanaka and observed that root yield ranged from 3.0 - 20.0 t/ha in upland, 3.0- 30.0 t/ha in lowland condition and dry matter content varied from 18.5 to 29.2 %.

Neiva *et al.* (2011) evaluated fifteen sweet potato genotypes on the basis of vegetative and root characters. The evaluation of the vegetative part were carried out three months after planting and the roots were harvested nine months after planting and observed that, the characteristics of vegetative part showed highest significant difference among the clones. Pushpalata *et al.*(2011) evaluated 15 genotypes of sweet potato and recorded observations on vine length, vine weight per plant, neck length of tuber, tuber diameter, dry yield per plant and revealed that genotypes like IGSP.C-18, 440038, 440036 and IGSP.C-16 were superior than Sree Rethna in respect of tuber yield. Richardson *et al.* (2012) evaluated six genotypes of sweet potato for tuber yield and reported that the variety 'Six Weeks' (early maturity) produced high dry matter content and high marketable yield (25.5t/ha) followed by 'Antigua' (25.2t/ha). Vimala *et al.* (2012) studied on 1600 orange fleshed sweet potato genotypes and concluded that vine weight, root weight and harvest index varied according to the clone and environmental conditions.

2.2.4. Qualitative variability

Miller (1958) observed high carbohydrate and starch content, in different genotypes which may be due to variation in the genetic makeup of the genotype. Akkamahadevi *et al.* (1996) recorded highest starch content of 84.7 per cent on

dry weight basis in the clone Belgam local. Teshome *et al*. (2003) reported highest starch content in clone IGSP-9 (34.66%) and lowest in RNSP-1 (16.38%) under Coimbatore conditions. Sahu (2003) reported highest total soluble solids in genotypes IB-90-15-9 for Chhattisgarh plains. Vimala *et al.* (2009) evaluated 40 clones of orange fleshed sweet potato during different season like summer, kharif and rabi to find out the variability of carotenoids, β- carotene and observed that total carotenoid content ranged from 8.5-15.0 mg/100g fresh weight and β-carotene varied from 6.8-13.7 mg/100g fresh weight. Binu *et al.* (2011) studied the changes in carotenoid content during 35 days of storage in 10 orange fleshed sweet potato clones at Central Tuber Crop Research Institute, Thiruvanthapuram, Kerala and observed that significant variation in total carotenoids content (10.32-13.99 mg/100g fresh weight) and β-carotene (9.02-12.6 mg/100 g fresh weight) among the clones.

The crude protein content of sweet potato (Kjeldahl nitrogen × 6.25) generally ranges from 1.3% to > 10 % dwb (Bradbury *et al.,* 1985; Purcell *et al.,* 1978). However, substantial variation has been shown to exist. Ishida et al. (2000) reported 2.1% and 1.3% protein for *Koganesengan* and *Beniazuma* sweet potato cv., respectively. Diop (1998) reported 1.0–2.4% protein in sweet potato while Bovell-Benjamin *et al.* (2001) and Dansby and Bovell-Benjamin (2003a) reported protein contents ranging from 1 .2 ± 0. 05% to 1 .8% (fresh weight) for hydroponically grown sweet potatoes. Oboh *et al.* (1989) analyzed 49 varieties of sweet potato sold in Nigerian markets and reported protein contents between 1.4% and 9.4%. The protein contents of sweet potato roots from 16 cv. grown in Sri Lanka ranged from 3.0% to 7.2% on dry weight basis (dwb) (Ravindran *et al.,* 1995). Cambie and Ferguson (2003) reported 1.7% protein content for sweet potato while Gichuhi *et al.* (2004) reported 4.5%, 4.7%, and 9.0% protein (dwb) for cv. J6/66, Beauregard (commercial), and TU-82- 155. Bovell -Benjamin *et al.* (2004) observed a wide variation in the protein content of three cv. of sweet potato

with TU-82-155 containing almost twice as much protein (8. 7 ± 0.1%) on dwb as J6/66 (4.4 ± 0. 03 %) and Beauregard (4 . 7 ± 0.5%).

It has been argued that the mineral content of agricultural products varies with geographic location. Makki *et al.* (1986) reported that in two Egyptian sweet potato cv., the mineral in highest concentration was calcium followed by magnesium, iron, copper, zinc, and manganese. However, older data reported by Ekpenyong (1984) from FAO (1972) cited phosphorous as the mineral in highest concentration for sweet potatoes. The data indicated 56, 36, 0.9, 2.0, and 387-mg/100 g for phosphorus, calcium, iron, zinc, and manganese, respectively. Olaofe and Sanni (1988) reported potassium(3617 mg/100 g) as the most abundant mineral in sweet potato roots followed by magnesium (580 mg/100 g) and calcium (112 mg/100 g).Manganese, iron, copper, and zinc were present in low amounts of 8.8, 14.0, 1–5.0, and 3.0 mg/100 g, respectively.

Pushpalata *et al.* (2011) evaluated 15 genotypes of sweet potato and recorded observations on starch percentage, total sugar percentage, carbohydrate percentage and TSS of Sweet potato and revealed that genotypes like IGSP.C-18, 440038, 440036 and IGSP.C-16 were superior than Sree Rethna in respect of quality parameters. Vimala *et al.* (2011b) evaluated 42 orange fleshed sweet potato hybrids in upland and low land conditions for storage root yield along with a control variety of Sree Kanaka and observed that variety 106427-10 and 106035-9 possessed high β- carotene content (14.37 mg/100 g fresh weight) and dry matter content varied from 18.5-29.2%. Out of 42 hybrids studied, 22 hybrids possessed high β-carotene content (10-15 mg/100 g fresh weight).

2.3. PCV, GCV, Heritability and Genetic advance

Phenotype of an individual plant is decided by genetic composition and environment conditions in which it grows. Success of a breeder in changing and improving the heredity of a trait depends upon the degree of correspondence

between phenotypic and genotypic variations. Heritability is a measure that provides this information (Dabholkar, 1992). The principal uses of heritability estimates are: to determine the relative importance of genetic effects which could be transferred from parent to offspring, to determine which selection method would be most useful to improve the character and to predict gain from selection (Poehlman and Sleper, 1995). Heritability characterizes not only the character itself but also the population and the environment in which the character is studied (Falconer and Mackay, 1996; Roy, 2000). Heritability in broad sense or degree of genetic determination is proportion of total hereditary variance to phenotypic variance. The more useful estimate i.e. narrow sense heritability or degree of resemblance between relatives is ratio of additive genetic variance to phenotypic variance (Falconer, 1989). The most important function of heritability in the genetic studies of metric characteristics is its predictive role in expressing the reliability of phenotypic value as a guide to breeding value (Falconer, 1989). Genetic advance means improvement in the performance of selected lines over original population. Heritable variation can be determined with greater accuracy, when heritability is studied along with genetic advance (Swarup and Chaughale, 1962). High heritability with high genetic advance is associated with additive gene effects (Panse, 1957). On the contrary, non-additive gene effect (dominance or epistasis) is associated with characters exhibiting high heritability and low genetic advance.

The phenotypic and genotypic coefficients of variation (PCV and GCV) for length of vine, length of petiole, number of branches, length of internode and length to girth ratio of tubers, exposed very little differences indicating less influence of environment on these characters which suggested the presence of sufficient genetic variability and hence ample scope for effective selection (Singh *et al.*, 1998). Jones *et al.* (1969) observed high estimates of heritability for vine traits than root traits. Kasuhara *et al.* (1972) selected mother plants in breeding sweet

potato based on high heritability, estimates direct lateral tubers were higher than the other tuber categories. Jong (1974) suggested that the additive genetic variance was more important than the non-additive genetic variance in determining tuberous root weight and top weight in contrast to the number of tuberous roots where the main genetic variance was non-additive type. Singh and Mishra (1975) reported high heritability and high genetic advance for vine length. Thamburaj and Muthukrishnan (1976) observed high genetic advance and high heritability estimates for girth of tubers and number of tubers. Kamalam *et al.* (1977) reported high genetic advance for length of vine and number of tubers per plant and counting of high heritability for length of vine, number of tubers per plant, stem thickness, petiole length, skin colour, flesh colour and weight of tubers. They observed that the genotypic coefficient of variation was lower than the phenotypic characters like length of vine, length of petiole, number of tubers per plant, weight of vines per plant, weight of individual tubers. Length of vine and number of tubers showed very high degree of phenotypic and genotypic coefficients of variation. Saladaga (1981) observed that heritability for both root skin and flesh colours were very low. The estimates of heritability for tuber yield indicated that selection could be practiced on an individual plant basis.

Low heritability estimates were also observed for percentage weight loss and sprouting. Maluf *et al.* (1983) conducted an experiment on sweet potato to estimate the genetic variances and broad sense heritability of root and vine traits and revealed that the heritability estimates were high for vine length, number of inter nodes per vine and number of marketable roots. Negative estimates were observed for root yield, average weight per marketable root and mean inter nodal length. Lin (1983) evaluated fifteen cultivars of sweet potato and revealed that more than 65% of heritability observed in weight of dry matter, length of main stem, tuber weight, internodal length and yield. Tuber weight and number of large tubers showed very high genetic advance.

Dai *et al*. (1988) observed high heritability estimates for vine length and tuber weight. Chen *et al.* (1989) observed that tuber yield had high genotypic and phenotypic coefficient of variation. The broad sense heritability of tuber yield was relatively low and was non additive in sweet potato. Vimala and Lakshmi (1990) reported estimates of heritability high for tuber characters like tuber length, tuber weight and tuber girth and low for vine length.

Chen *et al.* (1995) conducted their studies on 30 sweet potato genotypes and observed that the genetic variation ranged from 20.03 to 37.65%. Studies conducted on 25 genotypes of sweet potato by Jain and Ganguli (1996) grown in Ranchi, during kharif revealed that vine length, number of branches, number of leaves and tuber yield showed high genotypic and phenotypic coefficients of variation whereas genotypic coefficient of variability ranged from 11.12 % (tuber length) to 39.07 % (number of branches). They also recorded high heritability estimates for vine length (96.05%), number of branches (90.0%), number of leaves (90.3%) and tuber yield (75.9%) and comparatively low for number of tubers (45.5%). Number of tubers, tuber width and tuber weight showed high genetic association with yield. Alam *et al.* (1998) studied on 15 genotypes of sweet potato and observed that the higher genotypic and phenotypic coefficients of variation were recorded for number of branches, tubers per plant, yield per plant, number of leaves and vine length. They also said that high heritability along with high or moderate genetic advances were recorded for all the characters except tuber length. Choudhary *et al*. (1999) conducted a study on fifty genotypes of sweet potato and found that a wide difference of phenotypic and genotypic co-efficient of variation was observed for the vine length and root yield and high heritability coupled with high genetic advance. Vimala and Lakshmi (1999) obtained low heritability estimates for vine length and high heritability estimates for tuber length, tuber weight, number of branches, tuber girth and vine weight indicating genetic variance was relatively more important than non-additive genetic variance

for these characters. Hossain *et al.* (2000) evaluated 30 genotypes of sweet potato and observed high phenotypic and genotypic coefficients of variation for number of tubers per plant, average tuber weight and tuber yield per plant. Estimates of heritability and genetic advance were highest for tuber yield per plant, average tuber weight and number of tubers per plant.

Sankari *et al.* (2001) evaluated fifteen genotypes of sweet potato and reported that the genotypic coefficient of variation was high for traits like yield of roots per vine, length of vine and girth of vine and observed high heritability coupled with high genetic advance for vine length, vine girth and yield of roots per vine. Teshome *et al.* (2004) studied 86 genotypes of sweet potato. They observed that characters *viz*., number of branches per plant, weight of single tuber, girth of tuber, and vine traits like length of tuber, length of vine, weight of foliage per plant, number of tubers per plant and weight of single tuber showed higher phenotypic and genotypic coefficient of variation with high heritability estimates. Sharma (2004) reported that the highest estimate of genetic advance as per cent of mean was obtained from tuber yield per plant, vine weight per plant, marketable tuber yield per plant, neck length of tuber, total soluble solids and vine length. Studies conducted on 30 genotypes of sweet potato by Tsegaye *et al.* (2007) revealed that the above ground fresh and dry weights, vine length, individual storage root weight, storage root fresh yield per plot, vine internodal length, storage root fresh yield per plant, leaf area and storage root number exhibited high genotypic coefficient of variation coupled with high heritability.

Gin *et al.* (2008) conducted a study on 30 genotypes of sweet potatoes and observed that GCV was highest for vine growth rate (65.38%) followed by vine internodal length (61.64%), number of tubers per plant (44.87%), tuber weight per plant (43.72%), petiole length (35.85%), single tuber weight (28.73%), tuber length (26.69%) and tuber diameter (20.26%). Shashikanth *et al.* (2008) conducted a study on 15 sweet potato genotypes and observed that the phenotypic and

genotypic coefficient of variations were found to be moderate to high for all the characters *viz.*, vine internodal length, fresh yield per plant, fresh yield per plot, number of branches per plant, number of leaves, total leaf area except length of vine. They also observed that high heritability with high genetic advance as percent over mean was for all the characters except leaf area. Choudhary and Mishra (2011) studied twelve genotypes of sweet potato and revealed that characters like vine length, number of tuber per plant and weight of tuber per plant exhibited high heritability coupled with high genetic advance. Thiyagu *et al.* (2013) conducted an experiment on 22 genotypes of sweet potato and revealed that high genotypic coefficients of variation along with high heritability were recorded for root length and leaf area.

2.4. Correlation and path-coefficient analysis in sweet potato

Correlation and path-coefficient are among the important analysis in crop improvement programs. The purpose of correlation and path-coefficient analysis are to describe the pattern of interrelationship among the various traits. It is useful to identify the degree of interrelationship of traits for direct and indirect selection for improve breeding program.

2.4.1. Correlation analysis

Correlation analysis is useful for selection of more complex and less heritable traits, such as yield, through selecting for traits that are highly correlated with yield, given that their heritability is high (De Araujo *et al*., 2002). Larger genotypic correlation coefficients indicate greater contribution of genetic factors and reduced effects of the environment (Iqbal *et al*., 2003). According to Martin and Rhodes (1983) significant correlations have direct implication on the progress of a selection program. Knowledge of the frequency of desired traits, and correlations among these, is helpful for direct/indirect selection and to develop

selection index (in mass or recurrent selection) to emphasize and develop the traits most desired.

Tsegaye *et al*. (2006) reported that in sweet potato clones, the genotypic correlation coefficients were lower than the phenotypic correlation coefficients among different sweet potato traits, 27 indicating the significant effects of the environment. The authors indicated the presence of high positive correlations between storage root yield and root diameter, harvest index (HI) and individual root weight per plant. On the other hand, storage root number had a significant negative correlation with storage root diameter and individual root weight implying that an increase in the number of roots per plant will result in competition between storage roots within a plant. This will result in many small sized roots (Tsegaye *et al*., 2006). In a study by Lin *et al*. (2007), significant positive correlations were found between above ground biomass, fresh root weight, storage root number; between storage root shape and above ground biomass and storage root weight; between skin colour and flesh colour of storage root and between starch content and amylase content. This suggests that above ground biomass can be used as an indicator for storage root yield (fresh weight and number).

Gasura *et al*. (2008) also found a positive correlation between yield and tuber number, while sugar content was negatively correlated with starch content. Protein content was positively correlated with dry matter content (Gasura *et al*., 2008). There exists a slight negative correlation between root dry matter and β-carotene contents of sweet potato (Cervantes-Flores *et al*., 2010; Chiona, 2009; Simonne *et al*., 1993), implying that the simultaneous improvement of the two traits is a challenge in sweet potato breeding for quality traits. Several studies indicated the existence of strong positive correlation between flesh colour and β-carotene content in sweet potato (Vimala and Hariprakash, 2012; Cervantes-Flores *et al*., 2010; Burgos *et al*., 2009; Mcharo and LaBonte, 2007). Therefore, root flesh

colour ranging from pale orange to dark orange may be used as an indicator of β-carotene content especially at the beginning of screening work where many progeny have to be evaluated. A colour chart developed by Burgos *et al*. (2009) can serve as a useful indicator to facilitate selection for high β-carotene content.

Gupta (1969) observed positive association of vine weight and vine length with tuber yield. Garica *et al*. (1970) reported that increase in orange colour of edible protein in sweet potato was positively correlated with carotene content. Wilson (1975) reported positive correlation between tuber weight and tuber shape. Huett *et al*. (1976) reported that tuber yield is positively associated with the harvest index and also said that high yielding genotypes generally had high harvest index. Pushkaran *et al.* (1976) observed that the root characters as a whole were more strongly correlated with the tuber yield than shoot characters. Thamburaj and Muthukrishnan (1976) resulted that tuber yield of sweet potato was highly and positively correlated with tuber width, length of tuber, petiole length and number of branches and negatively correlated with length of vine and inter node length.

Warid *et al.* (1976) observed that vine length was negatively correlated with yield, while root number and yield were positively correlated in all test cases. Kamalam (1977) observed that genotypic correlations were higher than the phenotypic correlations. She reported that the number of tubers had positive significant correlations with yield. However the length as well as weight of vine showed significant negative correlations with yield. Enyi (1977) observed that the highest yields were associated with earlier tuber initiation. Shikata (1980) conducted population studies on sweet potato and observed lack of correlation between root yield and starch content from his study. Saladaga *et al.* (1981) worked out correlations among yields and its components and observed that total yield was positively correlated with skin colour, leaf shape, stem length and diameter, internodal length and number of branches per stem. Bacusmo *et al*.

(1982) reported that leaf area index, crop growth rate, leaf angle of younger leaves, vine length, number of tuber per plant and mean root weight were positively correlated with root yield. Janssens (1982) claimed that tuber yield was positively correlated with average tuber weight and number of tubers per unit of ground area. Bhagsari and Harman (1982) revealed that yield is positively associated with the harvest index in sweet potato. Maluf *et al.* (1983) reported that the genotypic correlation between root and vine traits was low. Lin (1983) found that yield per plant was positively correlated with the yield per unit area, tuber dry weight, number of branches, number of large to intermediate tubers and the length of petiole and negatively correlated with stems per tuber value and drying percentage of the tubers. Bourke (1984) observed that tuber yield at the final sampling was very closely correlated with total dry weight per plant and number of tubers per plant. Yoshida (1985) in a study of correlation between successive yield tests for agronomic characters in sweet potato showed that correlation coefficients were generally higher at more advanced stages of selection. Naskar *et al.* (1986) revealed that in general genotypic correlations were higher than phenotypic correlations.

The characters like number of branches, girth of tubers and length of tubers were found to have high positive correlations with yield, where as the length of vine and intermodal length were negatively correlated with yield. Ibrahim *et al.* (1987) observed that the root characters as a whole were more strongly correlated to the tuber yield than shoot characters. Tiwari *et al.* (1987) reported a positive correlation of root yield with number of root per plant and average weight of root per plant. Gerpacio (1994) observed that tuber yield of sweet potato was highly and positively correlated with root size and dry matter percentage of tuber. Nanda (1994) reported that the marketable tuber yield was positively correlated with number of tuber per plant while, it had non-significant association with neck length. Kumar *et al.* (1996) observed that tuber yield of sweet potato was highly

and positively correlated with number of tubers, tuber width and weight of tuber. Rajesh Kumar Jain and Ganguli (1996) conducted their studies on 25 genotypes and reported that number of tubers, tuber width and tuber weight had high genetic association with yield. Alumira (1997) reported that various sink parameters i.e. number of tuber per plant, tuber length and fresh weight per tuber were positively correlated with tuber yield. Alam *et al.* (1998) studied on fifteen genotypes of sweet potato and revealed that characters *viz*., tubers per plant, tuber width and weight of individual tuber were positively correlated with yield while vine length had a negative significant association with yield at both genotypic and phenotypic levels. Parida *et al.* (1999) resulted that marketable tuber yield and numbers of tubers per plant were significantly positively correlated with tuber yield. Choudhary *et al.* (2001) evaluated fifty genotypes and revealed that the total tuber yield had highly significant and positive phenotypic correlation with petiole length and tuber girth.

Hossain et al. (2000) evaluated 30 sweet potato genotypes and revealed that root yield was positively and significantly correlated with root diameter, average tuber weight and number of tubers per plant. Pushpalata *et al.* (2011) studied on eight sweet potato clones and resulted that tuber weight and total plant weight were significantly and positively correlated with yield.

Sahu *et al.* (2003) studied on 24 genotypes of sweet potato and reported that tuber yield was positively and significantly correlated with biological yield per plant, tuber diameter and harvest index whereas Vine weight per plant had a positive correlation with vine length. Engida Tsegaye *et al.* (2006) conducted an experiment on 30 sweet potato genotypes and resulted storage root yield had positive and significant correlation with individual storage root weight, harvest index and storage root girth whereas number of storage roots per plant was negatively and significantly correlated with individual storage root weight and storage root girth. Shashikanth *et al.* (2008) reported that characters like tuber

diameter, starch and sugar content, tuber dry matter and fresh weight of vine are significantly and positively correlated with tuber yield. Li Yun Song *et al.* (2010) studied on 10 sweet potato genotypes and reported that the number of tuber per plant, number of branches per plant and number of green leaves per plant were significantly correlated with tuber yield. Choudhary and Mishra (2011) conducted their studies on 25 genotypes and revealed number of tubers per plant exhibited significant and positive correlation with marketable tuber yield. Tirkey *et al.* (2011) revealed that tuber yield showed significant positive correlation with vine weight at both genotypic and phenotypic level.

2.4.2. Path-coefficient analysis

Path-coefficient analysis was developed by Wright (1921), cited by Lynch and Walsh (1998), with the aim of interpreting the correlation between two variables in terms of hypothetical path of causality between the variables. The purpose of path-coefficient analysis is the quantification of the relative contributions of casual sources of variance and covariance once it is known that there is a certain degree of interrelatedness between the variables (Lynch and Walsh, 1998). It is a standard partial regression coefficient that measures the direct influence of one variable up on others, and permits the separation of the correlation coefficient into components of direct and indirect effects (Shimelis and Hugo, 2011).

Each correlation coefficient between a causal or independent variable and the response or dependent variable is partitioned. This provides components with a direct effect or path coefficient for the predictor variable and indirect effects, which involve the product of a correlation coefficient between two predictor variables with the appropriate path-coefficient in the path diagram (Shimelis, 2006; Diz. *et al*., 1994). Therefore, knowledge about both the direct and indirect effects of selecting for specific components can be attained by determining the inter-relationships among yield components and breeders can get a comprehensive understanding of the relationship among a set of traits and how each trait affects or

contribute to yield (Board *et al*., 1997; Akheter and Sneller, 1996; Diz. *et al*., 1994).

Storage root number also had a high positive direct effect on storage root yield per plant based on phenotypic and genotypic correlations. However, the negative indirect effect through individual storage root weight, i.e., -0.3856 and -0.4512 at phenotypic and genotypic levels, respectively, resulted in a low correlation coefficient among the two traits at both phenotypic and genotypic levels (Tsegaye *et al*., 2006). From this study it could be deduced that that although a character seems to have a positive direct contribution to yield, it may have an indirect negative influence on yield via another character that has a direct contribution to yield. Path-coefficient analysis therefore helps to understand those relationships and to identify the trait that best correlate with and influence root yield.

Lowe and Wilson (1975) observed that the tuber width was related to the mean tuber weight and yield. Tuber width appeared to be the most important determinant of yield in their investigation. Thamburaj and Muthukrishnan (1976) indicated that weight of the foliage contributed maximum direct effect on tuber yield and also reported that tuber yield of sweet potato had maximum positive direct effect on girth of tuber and number of tuber per vine. Kamalam *et al.* (1977) observed that tuber yield in sweet potato had direct influenced on number of tubers. They also suggested that the number of tubers per plant, length of petiole and to a lesser extent weight of vine should be the criteria for selection of a high yielding plant type in sweet potato. Lin (1983) revealed that number of branches had the direct effect on root yield per plant. Naskar *et al.* (1986) revealed that length of tubers showed maximum positive direct effect on yield. They also stated that selection based on characters like length of tubers, length of petiole and girth of tubers appeared to be most desirable for improving the yield in sweet potato. Ibrahim (1987) reported that root characters viz. tuber girth, number of tubers and tuber length showed higher path values than shoot characters and finally

concluded that in a breeding programme for yield, less importance may be given for shoot characters. Nanda (1994) reported that the direct effect on tuber yield was positive due to the characters *viz.*, tuber girth, tuber length, neck length of tuber and number of tuber per plant. Chen Feng Xiang (1995) studied on 30 sweet potato genotypes and observed that the high yielding genotypes having more roots, vigorous growth, heavy leaves and short vines. Kumar *et al.* (1996) indicated that tuber yield of sweet potato is influenced by the maximum positive direct effect on girth of tuber and weight of tuber. They noticed moderately high positive direct effect of number of branches on tuber yield. Rajesh Kumar Jain and Ganguli (1996) studied on 25 genotypes of sweet potato and revealed that the maximum direct effect (0.74) on tuber yield was through tuber weight. Tuber width, number of branches and number of tubers also had direct effects on tuber yield. Alam *et al.* (1998) studied on fifteen genotypes of sweet potato and resulted that tubers per plant and tuber width had maximum positive direct effect and the vine length had maximum negative direct effect on yield.

Parida *et al.* (1999) observed that marketable tuber yield and number of tubers per plant had direct influence on tuber yield. Choudhary *et al.* (2001) studied fifty genotypes of sweet potato and revealed that total tuber yield had direct effect on total tuber yield per plant and marketable tuber yield. Hossain *et al.* (2000) studied thirty sweet potato genotypes and concluded that average tuber weight and number of tubers per plant had positive direct effect on yield. Sahu *et al.* (2003) studied on 24 sweet potato genotypes and revealed that the number of marketable tubers had a direct positive effect on tuber yield whereas vine weight had positive indirect effects on tuber yield via tuber yield per plant and marketable tuber yield. Neck length of tuber, tuber length, tuber diameter, biological yield, harvest index, total soluble solids, dry matter content of foliage and dry matter content of tuber also exhibited positive indirect effects on tuber yield. Tsegaye *et al.* (2006) conducted study on thirty sweet potato genotypes and revealed that storage root yield had

direct effect on individual storage root weight, number of storage roots per plant and harvest index. Shashikanth *et al.* (2008) revealed that number of tubers had direct association with tuber yield. Li Yun Song *et al.* (2010) studied on 10 sweet potato genotypes and resulted that the characters of number of tubers per plant and number of green leaves per plant had important direct effect on sweet potato yield. Tirkey *et al.* (2011) revealed that marketable tuber yield, biological yield, tuber diameter and dry matter per cent of tuber, neck length of tuber, tuber length and vine had positive direct effect on tuber yield. Choudhary and Mishra (2011) studied on twelve sweet potato genotypes and concluded that number of tubers per plant exhibited had high significant direct effect on tuber yield.

CHAPTER III

MATERIALS AND METHODS

This chapter illustrates information concerning the methodology that was used in the execution of the experiment. The experiments were then divided into two parts viz. Experiment 1: Evaluation of sweet potato genotypes based agromorphological traits and Experiment 2: Evaluation of sweet potato genotypes based on nutritional analysis. The different steps of the experiments are stated here chronologically in section 3.1 and in 3.2 respectively.

3.1 Experiment 1: Evaluation of sweet potato genotypes based agro-morphological traits

It comprises a brief description of locations of experimental site, climate and soil, planting materials, land preparation, layout and design of the experiment, manuring and fertilizing, intercultural operations, harvesting, data collection procedure, statistical procedure etc., which are presented as follows:

3.1.1 Experimental site

The experiment was accomplished in the experimental field, Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh during the period from Mid November 2017 to April 2018. Location of the site is 23°74' N latitude and 90°35' E longitude with an elevation of 8 meters from sea level (Anonymous, 2004) in Agro-ecological zone of "Madhupur Tract"(AEZ-28) (Anonymous, 1988). The experimental site is shown in Appendix I (A and B).

3.1.2 Soil and climate

The area cover subtropical climate, which is characterized by high temperature, relative humidity and heavy rainfall in Kharif season (April-September) and relatively low rainfall associated with moderately low temperature during the Rabi season (October-March). Weather information regarding temperature, rainfall and

relative humidity persuade at the experimental site during the study period was presented in Appendix II. Soil of the experimental site belongs to the general soil type, Shallow red brown terrace soils under Tejgaon Series. Top soils were clay loam in texture. The pH ranged from 6.0- 6.6 and had organic matter 0.84%. Experimental area was flat which facilitated irrigation and drainage system easily. Soil samples from 0-15 cm depths were collected from experimental field. The analyses were done by Soil Resource and Development Institute (SRDI), Dhaka. Physicochemical properties of the soil are presented in Appendix III.

3.1. 3 Experimental materials

The experimental material consisted of 6 genotypes of advance generation of sweet potato collected from Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh for the research work. List of the genotypes is given in Table 1.

3.1.4 Design and layout of the experiment

The experiment was laid out and evaluated during Rabi season 2017-2018 in Randomize Complete Block Design (RCBD) that included 6 genotypes and 4 replications. The six genotype were planted each on a 4 m X 3 m plot size having 4 rows including 2 borders. The spacing between rows, plants, plots and replication was 60 cm, 50 cm, 50 cm and 50 cm respectively.

3.1.5 Plot and vine preparation

Plots were prepared by tillering 8 days before sowing. Fertilizing and watering were also done before sowing vines. Vine sowing of sweet potato was carried out on November 20, 2017 in the plots. Sweet potato vines were cut into pieces, each vine approx. 20-25 cm long with 3-4 nodes. Vine cuttings collected from the apical and middle portions are considered to have large number of sprouts and high yield of tubers in comparison with the cuttings from basal portion. Vines were sown in rows spaced at 50 cm apart, plots were watered regularly. Recommended cultural practices were taken up before and after sowing the vines.

Table 1. Name and origin of six sweet potato genotypes used in the present study

Sl. No.	Genotypes No.	Name/Acc No. (BD)	Source of collection
1	G1	SP006	Sher-e-Bangla Agricultural University, Dhaka,Bangladesh
2	G2	SP002	
3	G3	SP003	
4	G4	SP004	
5	G5	SP005	
6	G6	SP001	

3.1.6 Land preparation

The experimental plots were ploughed at 15-20 cm depth and brought into a fine tilth. The recommended dose of fertilizers and farm yard manures (FYM) application were done. Weeds and other stubbles were removed carefully from the experimental plot and leveled properly. The final land preparation was done on November 18, 2017.

3.1.7 Vine sowing

After preparing plots, the vines were cut into small pieces of 20-25 cm with 3-4 nodes. The vines were planted in 5-7 cm depth in 20 November, 2017. Vines were irrigated in the next day after sowing and later flood irrigation was provided via irrigation channels. Different stages of vine and harvesting of sweet potato plants from the experiment field is presented in Plate 1 and Plate 2.

Plate 1: Different stages of vine in the field.

Vine sowing in polybag

B. & C. Vine in the field

Plate 2: Harvesting of sweet potato

3.1.8 Manure and fertilizers application

Half Urea and half Muriate of Potash (MOP), total cow dung and total Triple Super Phosphate (TSP) were applied in the field during final land preparation. Remaining Urea and Muriate of Potash (MOP) were applied after five to six weeks of sowing with second earthing up. According to the fertilizer recommendation guide of BADC, 2012 Fertilizer dose 180:100:220 Kg/ha urea, TSP, Mop respectively. Well decomposed cow dung was calculated for each plot considering the dose of 1-hectare soil at the depth of 20 cm.

3.1.9 Intercultural operations

To ensure optimum plant density per plot, gap filling was done after one week of sowing. Necessary watering and intercultural operations were given as and when required. Weeding was performed in all plots as and when required to keep plants free from weeds. After 21 days of sowing earthing up was done. Second earthing up was done 21 days after the first one. Spilt portion of fertilizers was provided during second earthing up. Sevin dust and Furadan were given as protection of the vines.

3.1.10 Harvesting

All sweet potato verities were harvested in 10^{th} April, 2018. Harvesting from each plot was done by digging out carefully with spades or forks.

3.1.11 Data recording

Different biometric traits related to yield and its contributing characters were recorded *viz.* Vine length (cm), vine internode length (cm), vine internode diameter (cm), Leaf area index (cm^2), above ground fresh weight per plant (kg), storage root number per plant, storage root length (cm), storage root diameter (cm), individual storage root weight (kg), storage root fresh yield per plant (kg), harvest index (%), storage root fresh yield per plot (kg) and storage root fresh yield (ton/ha). Data were recorded in respect of the following parameters:

3.1.11.1 Vine length (cm)

During the final harvesting time, length of the vine was measured for five plants from cotyledonary node to the tip of the plant and the average was taken in cm.

3.1.11.2 Vine internode length (cm)

The ratio of total vine length to the number of nodes per vine gave the internodal length.

3.1.11.3 Vine internode diameter (cm)

The diameter of the vine was measured at middle part of the vine for 3 vines per plant with the vernier scale and expressed in cm.

3.1.11.4 Total Leaf area index (cm^2)

The length and width of middle leaves in the plant were recorded at its widest point along with the number of lobes per leaf at 2MAP. The leaf area per plant was computed adopting the linear measurement procedure and expressed in cm^2.

3.1.11.5 Above ground fresh weight/plant (kg)

The total weight of above ground fresh plant was recorded for five plants and the average was expressed in kilogram.

3.1.11.6 Number of roots per plant

The number of storage tubers of five plants was counted and the mean expressed as number of tubers per plant.

3.1.11.7 Root length (cm)

The length of the storage roots was measured with the scale and the mean was expressed in centimeters.

3.1.11.8 Root diameter (cm)

The maximum diameter of the tuber was measured at middle part of the tuber for 5 tubers per plant with the vernier scale and expressed in centimetres.

3.1.11.9 Individual storage root weight (kg)

The weight of ten Individual fresh roots from each plot was recorded and calculated the mean and expressed in kilograms.

3.1.11. 10 Root yield per plant (kg)

The total weight of all marketable roots obtained per vine was recorded for five plants and the average was expressed in kilograms.

3.1.11.11 Harvest index/plant (%)

Harvest index was calculated from the ratio of fresh yield to biological yield and expressed in percentage. It was calculated by using the following formula.

$$\text{HI (\%)} = \frac{\text{Economic yield (Fresh root yield)}}{\text{Biological yield (Fresh root yield + Above ground fresh plant yield)}} \times 100$$

3.1.11.12 Storage root fresh yield/plot (kg)

The mean weight of fresh roots from each plot was recorded and expressed in kilogram.

3.1.11.13 Storage fresh root (ton/Ha)

The mean weight of fresh roots from each plot was recorded and calculated the root yield per hectare and expressed in tons.

3.2 Experiment 2: Evaluation of sweet potato genotypes based on nutritional traits

It comprises a brief description of nutritional traits. The nutritional traits included moisture (%), dry matter (%), protein (%), lipid (%), fiber (%), ash (%), carbohydrate (%), sugar (g), beta carotene (g), vitamin c (g), calcium (g), magnesium (g), potassium (g), sodium (g) and phosphorus (g). Nutritional analysis was accomplished in the central laboratory of BARI (Bangladesh Agricultural

Research Institute). Gazipur, Dhaka, Bangladesh. Some moment captured during nutritional analysis is presented in Plate 3.




Plate 3: Different steps of nutritional analysis of sweet potato in laboratory.

3.2.1 Moisture (%)

Moisture content was measured by random sampling of three storage roots of a genotype from each plot and chopped into 2 mm thick strips. Fifty grams of the chopped samples in four replicates were oven-dried at 105°C until weight remained constant (AOAC, 2000). Percentage moisture was calculated as:

% Moisture = (Fresh weight - Dry matter) × 100

3.2.2 Dry Matter (%)

Dry matter content was measured by random sampling of three storage roots of a genotype from each plot and chopped into 2 mm thick strips. Fifty grams of the chopped samples in four replicates were oven-dried at 105°C until weight remained constant (AOAC, 2000). Percentage dry matter was calculated as:

% DM = (Dry meter / Fresh weight) × 100

3.2.3 Protein (%)

Protein contents were estimated from total N (nitrogen) analyzed by Kjeldahl method. Two gm of sweet potato flour was used for the analysis. Soluble protein was determined by using the BioRad protein assay reagent.

3.2.4 Lipid (%)

It was extracted from the tuber samples with Chloroform**:** Methanol **(**2**:**1**)** solution**.** Fat was determined from the extract by the method of Choudhury and Juliano **(**1980**)** by Chloroform, Methanol**.** About 4 g sweet potato dry powder was soaked with 100 mL of chloroform**:** methanol (2:1) mixture for overnight. Then the sample was filtered through Whatman filter paper No. 42 into a conical flask. The solvent was evaporated and transferred into a screw cap Pyrex test tube of known weight. Then the test tube was heated until the whole solvent was evaporated and dried completely under nitrogen. After that the weight of the test tube was taken again. The process was repeated until a constant weight was observed. Fat content was reported on a dry basis of the sample.

Calculation

Fat (%) = (Final weight of the test tube – Initial weight of the test tube) g×100
Weight of sample (g)

3.2.5 Fiber (%)

It was estimated by the method of the Association of Official Agricultural Chemists (AOAC, 1995). Sulphuric acid 0.26 N, Sodium hydroxide 0.30 N, Ethanol 95% reagents were used. About 2 g dry sample was taken into a 250mL beaker and 200 mL hot solution sulphuric acid (0.26 N) was added. Then placed the beaker on a pre-heated hot plate of the digestion apparatus and digested the sample for 30 minutes, rotating the beaker periodically to keep the solids or material from adhering to the sides. After digestion, the sample was filtered by a California modified Buchner funnel using a vacuum pump. The residues were washed with hot water until those were free from acid (Litmus paper used for that test). Transferred the residue (sample) backed into the beaker with 200 mL hot sodium hydroxide (0.30 N) solution. The beaker was placed on a preheated heater and digested the sample for 30 minutes as mentioned above. Then filtered the sample through California modified Buchner funnel and washed the residue with hot water until the washings were free from alkali (Litmus paper used for that test too). Finally, the residue was washed with alcohol (about 25 mL). Then the residue was transferred into a clean porcelain crucible and dried at 100^{o}C overnight. The crucible was transferred in desiccators and cooled at room temperature and weighed (W1). Then the residue was ignited in a muffle furnace at 600^{o}C for 30 min. After that the crucible was transferred into the desiccators and cooled at room temperature and weighed (W2).

Weight of the crude fiber = (W1 – W2) – Blank

Crude fiber (%) = $\frac{\text{Weight of the crude fiber}}{\text{Weight of the sample}} \times 100$

3.2.6 Ash (%)

Crude ash, which was obtained in a porcelain crucible, was completely poured over by an aqueous solution of hydrochloric acid HCI (1:1) in order to dissolve carbonates and separate silica (SiO_2) and evaporated in a sand bath. 10 cm^3 of 5% HCI helps to obtain a solution containing chlorides of analyzed elements and phosphoric acid (V). This solution was transferred to a volumetric flask (100 cm^3) and the silica was separated on a hard filter. Furthermore, the crucible was washed 3 times with deionized water, and the solution was transferred via the filter in order to remove chlorides and completed the volumetric flask (AOAC, 2000).

3.2.7 Carbohydrate (%)

A large number of analytical techniques have been developed to measure the total concentration and type of carbohydrates present in foods . The carbohydrate content of a food can be determined by calculating the percent remaining after all the other components have been measured:

% carbohydrates = 100 - %moisture - %protein - %lipid- ash%-fiber% - %mineral

3.2.8 Sugar (g)

The sugars are extracted in dilute ethanol; the solution is clarified with Carrez solutions I and II. After eliminating the ethanol, the sugars are determined before and after inversion by the Luff-Schoorl method.

3.2.9 Beta Carotene (g)

Beta-carotene content was determined spectrophotometrically as described by Imungi and Wabule (1990). Fresh peeled and unpeeled samples were initially homogenized using a blender.

Exact portions (2.00 g) in duplicates were weighed in a 50-ml extraction conical centrifuge tube and mixed with cold acetone (40 ml). The samples were

centrifuged for 60 seconds before filtering with suction through a Buchner funnel. The flask and residues were washed with acetone while receiving the washing in the funnel. The filtered residues were white in colour which indicated that all β-carotene had been extracted. Petroleum ether (40 ml) was put in a separator funnel. The resultant acetone extract was then added into the separator funnel. Distilled water was slowly added while letting it flow along the walls of the funnel. The mixture was not shaken to avoid formation of an emulsion. The two phases were allowed to separate and the lower aqueous acetone phase was discarded.

The resultant was washed first with distilled water (300 ml) and three times with distilled water (200 ml) to remove the acetone completely. The petroleum ether phase was collected in a 50-ml volumetric flask. The ethereal extract was made to pass through the funnel containing filter paper and anhydrous sodium sulphate. The washing solvent was also collected into the volumetric flask and the volume was made to the mark. The absorbance of the beta carotene ethereal extract was read at 450 nm in a UV/VIS spectrophotometer. Beta carotene content was calculated using the following formula:

$$\mu g/g = \frac{A \times Volume \times 10^4}{2592 \times Sample\ weight}$$

Where, A= Absorbance

3.2.10 Vitamin C (g)

Initially, three solutions were prepared as follows: solution 1: acid solution, prepared by solubilizing 15 g of metaphosphoric acid in 40 mL of glacial acetic acid and then adding 450 mL of distilled water, being stirred and filtered; solution 2: vitamin C solution, prepared by solubilizing 100 mg of vitamin C, previously dried, in 100 mL of the solution 1 in a volumetric flask (100 mL) and then, diluted 10 times in the same acid solution; solution 3: Tillman's solution, prepared by solubilizing 42 mg of sodium bicarbonate in 50

mL of distilled water, adding 50 mg of 2,6-dichlorophenol indophenol sodium salt was under stirring until total dissolution of the dye. Then, this solution was filtered and diluted in 200 mL of distilled water in a volumetric flask. In the standardization of Tillman's solution, 4 mL of the solution 2 was used together with 6 mL of the solution 1 in an Erlenmeyer flask, where 50 mL of distilled water was added. This solution was titrated with Tillman's solution (solution 3). A blank test was performed, replacing vitamin C solution (solution 2) by acid solution (solution 1) in order to calculate the Tillman's factor (F) according to equation 1

$$F = \frac{\text{Mass of vitamin C used in the tritation (mg)}}{\text{Volume of Tillman's solution used in tritation (mL)}} \qquad (1)$$

The titration of the solution was done by using 40 mL of filtered sample mixed with 40 mL of the solution 1. From this mixture it was taken 10 mL, which was then titrated with the Tillman's solution. The vitamin C content was calculated through the equation 2:

$$\text{Vitamin C content (mg per 100 mL)} = \frac{V \times F \times 100}{A} \qquad (2)$$

where, V is the Tillman's solution volume (mL) used in the titration, F is the Tillman's factor and A is the sample volume (mL)

3.2.11 Minerals (Calcium, Magnesium, Potassium, Sodium, Phosphorus)

In the dry weight of tubers were identified: general content of phosphorus, potassium, calcium, magnesium and sodium in a stock solution, which was obtained after the "dry" mineralization of tubers in a muffle furnace at 450°C. In such a prepared stock solution, the concentration of examined macronutrients was determined using ICP-AES method on an emission spectrometer with the inductively coupled plasma (argon) Optima 3200 RL, produced by the Perkin Elmer Company. For this purpose, the following wavelengths were used: for P – 214.914 nm; K –766.490 nm; Ca –315.887 nm; Mg –285.213 nm; Na –330.237 nm. Operating parameters of the camera were as follows: RF –1300 W, flow rate

of cooling argon –15 L min-1, auxiliary argon –0.5 L min-1, nebulizated argon –0.8 L min-1and the speed of sample loading –1.5 L min-1.

3.3 Statistical analysis

For each character the data were recorded and averaged to obtain mean data. Mean data of characters were subjected to multivariate analysis. Univariate analysis of the individual character was done for all characters under study using mean values (Singh *et al.* 1985) and was estimated using MSTAT-C computer program. Duncan's Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV%) were also estimated using MSTAT-C, the multivariate analysis was done by computer using the GENESTAT and Microsoft Excel 2016 software through four techniques *viz*. Principal Component Analysis (PCA), Principle Co-ordinate Analysis (PCO), Cluster Analysis and Canonical Vector Analysis (CVA).

3.3.1 Estimation of genotypic and phenotypic variances

Genotypic and phenotypic variances were calculated by the following formulae given by Johnson *et al*. (1955).

Genotypic variance, $\delta^2 g = \frac{MSG - MSE}{r}$

Where, MSG= Mean sum of square for genotype

MSE= Mean sum of square for error, and

r = Number of replication

b. Phenotypic variance, $\delta^2 p = \delta^2 g + \delta^2 e$

Where, $\delta^2 g =$ Genotypic variance,

$\delta^2 e$ = Environmental variance=Mean square of error

3.3.2 Estimation of genotypic and phenotypic co-efficient of variation

The genotypic and phenotypic co-efficient of variation in percent were computed by the following formula (Burton, 1952).

Genotypic co-efficient of variation (GCV%) = $\frac{\delta_g \times 100}{\bar{X}}$

Phenotypic co-efficient of variation (PCV%) = $\frac{\delta_p \times 100}{\bar{X}}$

Where, δ_g = Genotypic standard deviation

δ_p = Phenotypic standard deviation

$\bar{X}$ = Population mean.

The PCV and GCV values are ranked as low, medium and high (Shivasubramanian and Menon, 1973) and are mentioned below:

0-10% - Low

10-20% - Moderate

>20% - High

3.3.3 Estimation of heritability

Broad sense heritability was estimated by the following formula, suggested by Johnson *et al*. (1955)

h^2_b (%) = $\frac{\delta^2 g}{\delta^2 p} \times 100$

Where,

h^2_b= Heritability in broad sense

$\delta^2 g$ = Genotypic variance

$\delta^2 p$ =Phenotypic variance

Heritability values are catagorised as low, moderate and high (Robinson *et al.*, 1949) and are given below,

0-30% - Low

30-60% - Moderate

60% and above - High

3.3.4 Estimation of genetic advance

The genetic advance was estimated for different characters under selection by using the formula suggested by Johnson *et al.* (1955)

$$GA = \frac{\delta^2 g}{\delta^2 p} K.\ \delta_p$$

Where, GA= Genetic advance

δ_g^2 = Genotypic variance

δ_p^2 = Phenotypic variance

δ_p = Phenotypic standard deviation

K = Selection differential which is equal to 2.06 at 5% selection intensity

3.3.5 Estimation of genetic advance in the percentage of mean

Genetic advance in the percentage of the mean was calculated by the following formula given by Johnson *et al.* (1955).

Genetic Advance in the percentage of mean $= \frac{Genetic\ Advance}{Grand\ mean} \times 100$

Genetic advance as percent of the mean was classified as low, moderate and high (Johnson *et al*., 1955) and values are given below:

0-10% - Low

10-20% - Moderate

20% and above - High

3.3.6 Estimation of simple correlation co-efficient

Simple correlation co-efficient was estimated by the following formula (Clarke, 1980; Singh and Chaudhary, 1985).

$$r = \frac{\sum xy - \frac{\sum x . \sum y}{N}}{\sqrt{[\{\sum x2 - \frac{(\sum x)2}{N}\}\{\sum y2 - \frac{(\sum y)2}{N}\}]}}$$

Where,

$\sum$ = Summation

x and y are two variable correlated

N = Number of observations

3.3.7 Estimation of genotypic and phenotypic correlation co-efficient

The genotypic and phenotypic correlation co-efficient was estimated by the formula (Johnson *et al.*1955; Hanson *et al.* 1956).

Genotypic correlation (r_{gxy}) = $\frac{GCOVxy}{\sqrt{GVx.GVy}} = \frac{\sigma_{gxy}}{\sqrt{(\sigma^2_{gx}.\sigma^2_{gy})}}$

Where, σ_{gxy} = Genotypic co-variance between the traits x and y

σ^2_{gx} = Genotypic variance of the trait x

σ^2_{gy} = Genotypic variance of the trait y

Phenotypic correlation (r_{xy}) = $\frac{PCOVxy}{\sqrt{PVx.PVy}} = \frac{\sigma_{pxy}}{\sqrt{(\sigma^2_{px}.\sigma^2_{py})}}$

Where, σ_{pxy} = Phenotypic co-variance between the traits x and y

σ^2_{px} = Phenotypic variance of the trait x

σ^2_{py} = Phenotypic variance of the trait y

3.3.8 Estimation of path co-efficient analysis

Path co-efficient analysis was carried out according to the procedure employed by Dewey and Lu (1959) also quoted in Singh and Chaudhary (1985) using simple correlation values. In path analysis, correlation coefficient is partitioned into direct and indirect independent variables on the dependent variable.

In order to estimate direct and indirect effect of the correlated characters, say, xl, x2 and x3 yield y, a set of simultaneous equations (three equations in this example) are required to be formulated as shown below:

$r_{yx1} = P_{yxl} + P_{yx2} r_{xlx2} + P_{yx3} r_{x1x3}$

$r_{yx2} = P_{yxl} r_{x1x2} + P_{yx2} + P_{YX3} r_{x2x3}$

$r_{yx3} = P_{yxl} r_{x1x3} + P_{yx2} r_{x2x3} + P_{yx3}$

Where, r´s denotes simple correlation co-efficient and P´s denote path co-efficient (Unknown). P´s in the above equation may be conveniently solved by arranging them in matrix from.

Total correlation, say between x_1 and y is thus partitioned follows:

Pyx1= The direct effect of x1 via x_2 on y.

$P_{yx2}r_{x1x2}$= The indirect effect of x1 via x_2 on y.

$P_{yx3}r_{x1x3}$= The indirect effect of x1 via x_3 on y.

3.4 Multivariate analysis

Genetic diversity was estimated following Mahalanobis's (1936) generalized distance (D^2). Selection of parents in hybridization programme based on Mahalanobis D2 statistic is more reliable as requisite knowledge of parents in respect of a mass of characteristics is available prior to crossing. Rao (1952) reported that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a successful hybridization program. Statistical analysis such as Mahalanobis D^2 and Canonical Variate Analysis (CVA), which quantify the differences among several quantitative traits are an efficient method of evaluating genetic diversity. Mean data of each quantitative character were subjected to both univariate and multivariate analysis. Mean, range, co-efficient of variation (CV) and the correlation was estimated using MSTAT computer program. Multivariate analysis *viz*. Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CLU) and Canonical Variate Analysis (CVA) were done by using GENSTAT program.

3.4.1 Principle component analysis

Principle component analysis (PCA), one of the multivariate techniques, is used to examine the inter-relationship among several characters and can be done from sum of squares and product matrix for the characters. Therefore, principle component was computed from the correlation matrix and genotypes scores obtained from the first components (which has the property of accounting for the maximum variance) and succeeding components with latent roots greater than unity. The contribution of the different morphological characters towards divergence is discussed from the latent vectors of the first two principal components.

3.4.2 Principle co-ordinate analysis

The principal coordinate analysis is equivalent to PCA but it is used to calculate inter-unit distances. Through the use of all dimensions of P it gives the minimum distance between each pair of the N points using similarity matrix (Digby *et al*. 1989).

3.4.3 Cluster analysis (CA)

To divide the genotypes of a data set into some number of mutually exclusive groups clustering was done using non-hierarchical classification. In GENSTAT, the algorithm was used to search for optimal values of chosen criteria. Starting from some initial classification of the genotypes into the required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer can be found to improve the criterion, the algorithm switches to a second stage which examine the effect of swooping two genotypes of different classes and so on.

3.4.4 Canonical variate analysis (CVA)

Canonical Variate Analysis, complementary to D2 statistic, is a sort of multivariate analysis where canonical vectors and roots representing different axes of differentiation and the amount of variation accounted for by each of such axes respectively and derived. Canonical Variate Analysis computed linear combination of original variability that maximized the ratio between ground and within group variations, thereby giving functions of the original variables that could be used to discriminate between the groups. Thus in this analysis, a series of orthogonal transformation was done sequentially for maximizing the ratio of the groups to within-group variations.

3.4.5 Calculation of D^2 values

The Mahalanobis distance (D^2) values are calculated from transformed uncorrelated means of characters according to Rao (1952) and Singh and Chaudhury (1985). The D^2 values were estimated for all possible combinations between genotypes. In simpler form D^2 statastic is defined by the formula

$$D^2 = \sum_i^x d_i^2 = \sum_i^x (Y_i^j - Y_j^k) \qquad (j \neq k)$$

Where, Y= Uncorrelated variable (character) which varies from i=1 to x

X= Number of characters

Superscript j and k to Y = A pair of any two genotypes.

3.4.6 Computation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chaudhury (1985),

Average intra-cluster distance = $\frac{\sum D_i^2}{n}$

Where,

D_i^2 = the sum of distances between all possible combinations (n) genotypes included in a cluster.

n= number of all possible combinations between the populations in the cluster.

3.4.7 Computation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh and Chaudhury (1985) ,

Average inter-cluster distance = $\frac{\sum D_{ij}^2}{n_i \times n_j}$

$\sum D_{ij}^2$ = The sum of distances between all possible combinations of the populations in cluster i and j.

n_i = Number of populations in cluster i.

n_j= Number of populations in cluster j.

3.4.8 Cluster diagram

Using the values of intra and inter-cluster distances (D= $\sqrt{D^2}$), a cluster diagram, was drawn as suggested by Singh and Chaudhury (1985). It gives a brief idea of the pattern of diversity among the genotypes included in a cluster.

CHAPTER IV

RESULTS AND DISCUSSION

The experiment was conducted to perform the diversity analysis of different genotypes of sweet potato (*Ipomoea batatas* (L.) Lam.) using yield contributing and nutritional traits. This chapter comprises the presentation and discussion of the findings obtained from the experiment. The fruits were harvested when they began to change in shape and size and almost after four and half months of sowing. The data pertaining to thirteen characters have been presented and statistically analyzed with the possible interpretations given under the following headings:

4.1. Experiment 1: Evaluation of sweet potato genotypes based on agro-morphological traits

This part of the chapter opened the results and their interpretation in order to evaluation of sweet potato genotypes based on their morphological traits.

4.1.1 Genetic parameters

The analysis of variance indicated a significantly higher amount of variability present among the genotypes for all the characters studied except vine internode length (cm), vine internode diameter (mm), above ground fresh weight/plant (kg), storage root diameter (cm), individual storage root weight (kg) and storage root fresh yield/plant (kg) (Appendix V). The mean sum of squares of all the 13 characters is presented in Appendix V.

4.1.2 Genetic variability, heritability and genetic advance

The mean values for each character of all the genotypes are shown in Table 2. Performance of the genotypes is described below for each character. The extent of variation among the genotypes in respect of thirteen characters was studied and mean sum of square, coefficient of variation (CV), phenotypic variance (σ^2p), genotypic variance (σ^2g), phenotypic coefficient of variation (PCV), genotypic

Traits	GenMS	Min	Max	Mean	CV (%)	σ^2_g	σ^2_e	σ^2_P	GCV	ECV	PCV	h^2_b	GA	GA (% mean)
Vine length (inch)	337.0488**	70.92	99.16	85.98	18.26	30.1816	246.5039	276.6855	6.39	18.26	19.35	10.91	3.74	4.35
Vine internode length (cm)	1.4139	5.50	7.50	6.33	17.48	0.0633	1.2239	1.2872	3.98	17.48	17.92	4.92	0.11	1.82
Vine internode diameter (mm)	0.55	5.1	6.8	6.02	8.69	0.36	0.04	0.40	5.61	1.81	7.42	34.86	0.75	15.90
Leaf area index (cm2)	327.8299**	59.89	91.40	77.79	13.62	71.8471	112.2887	184.1358	10.90	13.62	17.44	39.02	10.91	14.02
Above ground fresh weight/plant (kg)	0.1702	1.63	2.28	2.11	16.62	0.0158	0.1229	0.1387	5.95	16.61	17.65	11.37	0.09	4.13
Storage root number/plant	3.3670*	6.00	7.00	6.50	28.23	0.9557	0.5000	1.4557	15.04	10.88	18.56	65.65	1.63	25.10
Storage root length (cm)	54.8185**	13.92	24.50	20.05	23.75	10.7145	22.6751	33.3896	16.33	23.75	28.82	32.09	3.82	19.05

Table 2. Estimation of genetic parameters in thirteen characters of six genotypes in sweet potato

Storage root diameter (cm)	1.8516	4.47	6.67	5.28	21.86	0.1737	1.3306	1.5043	7.89	21.85	23.23	11.54	0.29	5.52
Individual storage root weight (kg)	0.0990	0.20	0.74	0.49	57.29	0.0069	0.0782	0.0851	17.06	57.29	59.78	8.14	0.05	10.03
Storage root fresh yield/plant (kg)	0.1841	1.39	2.12	1.84	22.55	0.0038	0.1726	0.1764	3.36	22.58	22.83	2.17	0.02	1.02
Harvest index/plant (%)	59.4280**	45.16	49.08	46.50	16.58	17.6087	6.6020	24.2107	9.02	5.53	10.58	72.73	7.37	15.85
Storage root fresh yield/plot (kg)	213.8125**	40.92	64.53	57.73	8.72	62.8150	25.3675	88.1825	13.73	8.72	16.27	71.23	13.78	23.87
Storage root fresh yield (ton/ha)	33.5222**	22.00	31.67	28.39	8.60	9.1889	5.9556	15.1445	10.68	8.60	13.71	60.67	4.86	17.13

** Significant at 1% * Significant at 5%

MS = mean sum of square, σ^2 p = Phenotypic variance, σ^2g = Genotypic variance, σ^2e = Environmental variance, PCV = Phenotypic Coefficient of variation, GCV= Genotypic coefficient of variation and ECV= Environmental coefficient of variation, h^2_b = Heritability in broad sense, GA= Genetic advance.

coefficient of variation (GCV), heritability (h^2b), genetic advance (GA) and genetic advance in percent of mean presented in Table 2.

4.1.2.1 Vine length

The variance due to vine length showed that the genotypes differed higher significantly and ranged from 70.92 inch in G3 to 99.16 inch in G1 (Appendix IV). The genotypic variance and phenotypic variance for this trait were 30.1816 and 276.6855 respectively (Table 2). The PCV appeared to be higher than the GCV suggested influence of environment on the expression of genes controlling this trait.

The difference between the phenotypic coefficient of variation (19.35) and genotypic coefficient of variation (6.39) was high, which indicating dominant role played by the environment in the expression of this trait and was not desirable for the improvement of this crop. Jain and Ganguli (1996) reported high GCV and PCV for vine length. Similar findings were reported by Tsegaye *et al.* (2007) and Kamalam (1990). The heritability (10.91) estimates for this trait was low, genetic advance (3.74) was low and genetic advance in percent of the mean (4.35) were found low, revealed that this character was governed by non-additive gene and selection for this character would not be effective. Vimala and Lakshmi (1990) found similar results for vine length. Dai *et al.* (1988), Maluf *et al.* (1983) and Singh and Mishra (1975) found high heritability and high genetic advance for vine length. High heritability coupled with high genetic advance at percent of mean for vine length suggesting that this trait was highly heritable and there is a wide scope for improvement through selection of this trait.

4.1.2.2 Vine Internode length

Non-significant variation was found for vine internode length and it is ranged from 5.50 cm in G3 to 7.50 cm in G5 (Appendix IV). The phenotypic variance (1.2872) is higher than genotypic variance (0.0633) for this trait which advises significant influence of environment on the expression of genes. GCV and PCV were found

3.98 and 17.92 respectively in Table 2, which indicating dominant role played by the environment in the expression of this trait and wider gap between GCV and PCV implies that selection based upon phenotypic expression of this character wouldn't be productive for the improvement of sweet potato. Many author also found higher PCV than GCV (Wilckens *et al*. 1993 and Singh *et al*., 1998). The heritability (4.92) estimates for this trait is low, genetic advance (0.11) was very low and genetic advance in percent of the mean (1.82) was found low (Table 2), revealed that this trait was governed by the non-additive gene. Selection on the basis of this traits would not be effective.

4.1.2.3 Vine internode diameter

The studied genotypes showed non-significant difference for vine internode diameter. Maximum mean was found 6.8 mm in G6 and minimum mean was recorded 5.1 mm in G1 with mean value 6.02 mm (Appendix IV). The genotypic variance (0.36) was lower than phenotypic (0.40) variance. GCV (5.61) and PCV (7.42) were found lower indicating low variability among the genotypes (Table 2). GCV and PCV values were found close to each other, suggesting environmental influence is minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. The results of Singh *et al.*, (1998) supports the findings. The heritability estimates (34.86) for this trait was moderate suggesting delay selection of this trait to more advance generation. In contrast genetic advance (0.75) and genetic advance at per cent of mean (15.90) were found low and moderate respectively. High heritability and high genetic advance for this trait was found by Vimala and Lakshmi (1990) and Thamburaj and Muthukrishnan (1976).

4.1.2.4 Leaf area

High Significant differences were observed among the genotypes for leaf area which ranged from 91.40 cm^2 in G1 to 59.89 cm^2 in G4 with mean value 77.79

cm^2 (Appendix IV). Tsegaye *et al.* (2007) found similar significant variation for leaf area. The phenotypic and genotypic variance was observed 184.1358 and 71.8471, respectively (Table 2) with large environmental influence. The phenotypic co-efficient of variation (17.44) was higher than the genotypic co-efficient of variation (10.90), indicates that the apparent variation is not only due to genotypes but also due to the influence of the environment. Shashikanth *et al.* (2008) found moderate to high value for PCV and GCV for leaf area. The heritability estimates for this trait was moderate (39.02) with moderate genetic advance (10.91%) and moderate genetic advance in percent of mean (14.02%), revealed that this trait is heritable in next generations. Thiyagu *et al.* (2013) found high heritability but Shashikanth *et al.* (2008) found low heritability and genetic advance for this trait.

4.1.2.5 Above ground fresh weight per plant

Above ground fresh weight per plant in sweet potato showed non-significant difference where maximum value for the trait was found 2.28 kg in G3 and the minimum was recorded 1.63 kg in G5 with mean value 2.11 kg (Appendix IV). The phenotypic variance (0.1387) was higher than the genotypic variance (0.0158) revealing low environmental influence. The GCV and PCV were 17.65 and 5.95, respectively (Table 2) indicating existence of variability among the genotypes. Wider difference between GCV and PCV illustrates the trait as not viable as this trait is highly controlled by the environmental effect. Sreekanth *et al.* (2011) also showed that the PCV was higher than GCV for above ground fresh weight per plant. Tsegaye *et al.* (2007) also found significant variability for this trait. The heritability estimates for this trait was low (11.37), genetic advance was low (0.09) and genetic advance in per cent of mean (4.13) were found low, revealed that this trait was governed by the non-additive gene (Table 2). Selection on the basis of this traits would not be effective. High heritability and high genetic advance for this character was observed by Velmurugan *et al.* (1999).

4.1.2.6 Storage root number per plant

The maximum range for storage root number per plant was found 7.00 in G5 and the minimum was recorded 6 in both G1 and G4 with average number of 6.50 with significant difference (Appendix IV). The difference between genotypic (0.9557) and phenotypic (1.4557) variances indicate high environmental influence (Table 2). PCV (18.56) and GCV (15.04) was moderate, which indicated equal importance of additive and non-additive gene action (Table 2). Tsegaye *et al.* (2007) found high PCV and GCV value which does not support the findings. The heritability estimates for this trait was high (65.65), low genetic advance (1.63) and genetic advance at percent of mean (25.10) were found high, revealed that this character is less controlled by the environment, highly heritable and desirable for crop improvement. This character showed high heritability coupled with high genetic gain which is supported by Lin *et al.* (2007) and Velmurugan *et al.* (1999).

4.1.2.7 Storage root length

The storage root length was highly significant having maximum mean recorded 24.50 cm in G1 and the minimum was recorded 13.92 cm in G5 with mean value 20.05 (Appendix IV). The genotypic variance (10.7145) found smaller than phenotypic variance (33.3896) for storage root length (Table 2). GCV and PCV were moderate (16.33 and 28.82 respectively) and close to each other, proved that environment has little influence of the expression of this character and ensures presence of variation among the genotypes. Therefore selection based upon phenotypic expression of this character would be effective for the improvement of this crop. High GCV and PCV for average fruit weight were also noticed by Tsegaye *et al. (*2007) and Thiyagu *et al.* 2013). Moderate heritability (32.09) associated with moderate genetic advance at percent of mean (19.05) and low Genetic advance (3.82) was observed indicating scope for crop improvement and use of this highly heritable trait for selecting during crop improvement.

4.1.2.8 Storage root diameter

Non-significant variation was found for Storage root diameter and it is ranged from 4.47 cm in G5 and 6.67 cm in G2 (Appendix IV). The genotypic and phenotypic variance were 0.1737 and 1.5043 respectively. The GCV and PCV were 7.89 and 23.23 respectively (Table 2) indicating existence of variability among the genotypes. Wider difference between GCV and PCV illustrates the trait as not viable as this trait is highly controlled by the environmental effect. Tsegaye *et al*. (2006) showed that the PCV was greatest for this character which supports the present study. The heritability (11.54) estimates for this trait is low, genetic advance (0.29) was very low and genetic advance in percent of the mean (5.52) was found low, revealed that this trait was governed by the non-additive gene. Selection on the basis of this traits would not be effective.

4.1.2.9 Individual storage root weight

Individual storage root weight was found to be non-significant with mean of this trait was 0.49kg with a range of 0.20kg in G5 to 0.74kg in G2 (Appendix IV). The phenotypic and genotypic variance were 0.0851 and 0.0069 respectively indicating environmental control of the trait. Wherever, PCV (59.78) was higher than GCV (17.06), indicates that the apparent variation is not only due to genotypes but also due to the influence of the environment. Tsegaye *et al.* (2007) showed that the PCV was greatest for this character which support the present study. The heritability estimates for this trait was low (8.14), low genetic advance (0.05) and genetic advance at percent of mean (10.03) were found low, revealed that this character is greatly controlled by the environment.

4.1.2.10 Storage root yield per plant

The trait was found to be non-significant. The maximum range of storage root yield per plant was found 2.12kg in G6 and the minimum was recorded 1.39 in G5 with mean average of 1.84 kg (Appendix IV). The phenotypic and genotypic

variance were 0.1764 and 0.0038 respectively indicating environmental control of the trait. PCV (22.83) and GCV (3.36) indicating existence of variability among the genotypes. Observations done by Pushpalata *et al.* (2011) also supports the findings. The heritability estimates for this trait was very low (2.17), low genetic advance (0.02) and genetic advance at percent of mean (1.02) were found low, revealed that this character greatly controlled by environmental and improvement breeding is not effective by selection of this trait.

4.1.2.11 Harvest index per plant

The studied genotypes showed significant difference in case of harvest index (Table 2). Maximum was found 49.08% in G6 and the minimum was recorded 45.16% in G3 with mean value 46.50% (Appendix IV). The genotypic variance (17.6087) was lower than phenotypic (24.2107) variance explains presence of environmental effect. GCV (9.02) and PCV (10.58) were moderate and close to each other, suggesting equal additive and non-additive gene function and environmental influence has control upon the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this character would be non-effective for the improvement of this crop. Findings by Vimala *et al.* (2012) and Tsegaye *et al.* (2007) does not supports the observation as they found higher PCV and GCV for harvest index per plant. The heritability estimates for this trait was high (72.73), low genetic advance (7.37) and genetic advance at percent of mean (15.85) were found moderate, revealed that this character is less controlled by the environment, highly heritable and desirable for crop improvement.

4.1.2.12 Storage root fresh yield per plot

Significant variation was found for storage root fresh yield per plot and it is ranged from 40.92 kg in G5 to 64.53 kg in G4 with mean value of 57.73 kg (Appendix IV). Phenotypic variance (88.1825) higher than genotypic variance (62.8150) advised significant influence of environment on the expression of genes governing

the trait. Similar findings for storage root fresh yield per plot were also observed by Tsegaye *et al.* (2007) and Vimala and Hariprakash (2012). GCV and PCV were found moderate (13.73 and 16.27 respectively) implying similar importance of additive and non-additive gene action. Shashikanth *et al.* (2008) found similar result with moderate to high variability for this trait. The heritability estimates for this trait was high (71.23) with moderate genetic advance (13.78) and high genetic advance at percent of mean (23.87), indicating this trait serves wide scope for crop improvement.

4.1.2.13 Storage fresh root yield per hectare

Significant differences were observed among the genotypes for storage root fresh yield which ranged from 22.00 ton/ha in G5 and 31.67 ton/ha in G4 with mean value of 28.39 ton/ha (Appendix IV). The genotypic variance and phenotypic variance for this trait were 9.1889 and 15.1445 respectively. GCV and PCV were moderate (10.68 and 13.71 respectively) but the phenotypic variance appeared higher than the genotypic variance. The observations found by Tsegaye *et al.* (2007) and Vimala and Hariprakash (2012) were not similar. The heritability estimates for this trait was high (60.67), genetic advance was low (4.86) and genetic advance at percent of mean (17.13) was found moderate, revealed that this character has minimal environmental influence and selection for this character would be effective.

4.1.3 Correlation Co-efficient

Correlation studies along with path analysis provide a better understanding for the association of different characters with sweet potato tuber yield. Simple correlation was partitioned into phenotypic (that can be directly observed), genotypic (inherent association between characters) components as suggested by (Singh and Chaudhary, 1985). As we know yield is a complex product being influence by several inter-dependable quantitative characters. So selection may not be effective unless the other contributing components influence the yield directly

or indirectly. When selection pressure is applied for improvement of any character highly associated with yield, it simultaneously affects a number of other correlated characters. Hence knowledge regarding association of character with yield and among themselves provides guideline to the plant breeders for making improvement through selection with a clear understanding about the contribution in respect of establishing the association by genetic and non-genetic factors (Dewey and Lu, 1959). Phenotypic and genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype are given in Table 3 and Table 4.

4.1.3.1 Vine length

Vine length had significant positive correlation with vine internode length (1.000), above ground fresh weight per plant (1.000), storage root length (1.000), storage root diameter (1.000), individual storage root weight (1.000), storage root fresh yield per plant (1.000), storage root fresh yield per plot (0.895) and significant negative correlation with storage root number per plant (-1.000) and harvest index (-1.000) at genotypic level (Table 3). It had positive non-significant correlation with leaf area index (0.391), storage root yield per hectare (0.748) and negative non-significant correlation with vine internode diameter (-1.000) at genotypic level (Table 3). This character showed non-significant positive correlation with vine internode length (0.094), Leaf area index (0.276), above ground fresh weight per plant (0.276), storage root length (0.428), storage root diameter (0.351), individual storage root weight (0.237), storage root fresh yield per plant (0.393), (%), storage root fresh yield per plot (0.414), storage root fresh yield per hectare (0.353) and non-significant negative correlation with vine internode diameter (-0.113), storage root number per plant (-0.304) and harvest index (-0.030) at phenotypic level (Table 4). Gupta (1969) and Alam *et al.* (1998) observed positive correlation of this trait with storage root fresh yield which does support the present findings.

Table 3. Genotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of sweet potato

	VIL	VID	LAI	AGFWT	SRN	SRL	SRD	ISRWT	SRY	HI	SRYP	SRYH
VL	1.000**	-1.000	0.391	1.000**	-1.000**	1.000**	1.000**	1.000**	1.000**	-1.000**	0.895*	0.748
VIL		0.736	0.014	-1.000**	-1.000**	-1.000**	-0.361	-1.000**	-1.000**	-1.000**	-1.000**	-1.000**
VID			-1.000	-0.885*	-1.000**	-0.782	1.000**	-1.000**	0.256	-1.000**	-0.261	0.008
LAI				0.432	1.000**	1.000**	0.481	0.089	0.411	-1.000**	0.038	-0.105
AGFWT					-1.000**	1.000**	1.000**	1.000**	1.000**	-1.000**	1.000**	1.000**
SRN						-1.000**	-1.000**	-1.000**	-1.000**	-1.000**	-1.000**	-1.000**
SRL							0.808	0.821*	0.962**	-1.000**	0.785	0.773
SRD								1.000**	1.000**	-1.000**	0.883*	1.000**
ISRWT									1.000**	-1.000**	1.000**	1.000**
SRY										-1.000**	1.000**	1.000**
HI											-1.000**	-1.000**
SRYP												1.000**

VL-Vine length (inch), VIL- Vine internode length (cm), VID- Vine internode diameter (mm), LAI- Leaf area index (cm^2), AGFWT- Above ground fresh weight per plant (kg), SRN- Storage root number per plant, SRL- Storage root length (cm), SRD- Storage root diameter (cm), ISRWT- Individual storage root weight (kg), SRY- Storage root fresh yield per plant (kg), HI- Harvest index per plant (%), SRYP- Storage root fresh yield per plot (kg), SRYH- Storage root fresh yield (ton/ha)

Table 4. Phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotypes of sweet potato

	VIL	VID	LAI	AGFWT	SRN	SRL	SRD	ISRWT	SRY	HI	SRYP	SRYH
VL	0.094	-0.113	0.276	0.276	-0.304	0.428	0.351	0.237	0.393	-0.030	0.414	0.353
VIL		0.075	0.072	-0.313	-0.348	-0.496	-0.442	-0.792	-0.361	-0.062	-0.852*	-0.862*
VID			-0.542	-0.184	-0.203	-0.393	0.593	-1.000**	0.055	0.028	-0.180	-0.094
LAI				0.132	0.001	0.647	0.069	-0.033	0.102	-0.173	-0.013	-0.122
AGFWT					-0.254	0.686	0.537	0.829*	0.886*	-0.488	0.961**	0.936**
SRN						-0.265	0.181	0.253	-0.087	-0.006	-0.349	-0.407
SRL							0.418	0.556	0.460	-0.219	0.636	0.597
SRD								0.887*	0.700	0.224	0.472	0.482
ISRWT									0.829*	-0.167	0.778	0.799
SRY										0.753	0.830*	0.780
HI											-0.160	-0.248
SRYP												0.989**

VL-Vine length (inch), VIL- Vine internode length (cm), VID- Vine internode diameter (mm), LAI- Leaf area index (cm^2), AGFWT- Above ground fresh weight per plant (kg), SRN- Storage root number per plant, SRL- Storage root length (cm), SRD- Storage root diameter (cm), ISRWT- Individual storage root weight (kg), SRY- Storage root fresh yield per plant (kg), HI- Harvest index per plant (%), SRYP- Storage root fresh yield per plot (kg), SRYH- Storage root fresh yield (ton/ha)

4.1.3.2 Vine Internode length

Vine internode length showed significant negative association with above ground fresh weight per plant (-1.000), storage root number per plant (-1.000), storage root length (-1.000), individual storage root weight (-1.000), storage root fresh yield per plant (-1.000), harvest index (-1.000), storage root fresh yield per plot (-1.000), storage root fresh yield per hectare (-1.000) and non-significant negative correlation with storage root diameter (-0.361) at genotypic level (Table 3). It had positive non-significant correlation with vine internode diameter (0.736) and Leaf area index (0.014) at genotypic level (Table 3).It had showed significant negative association with storage root fresh yield per plot (-1.000), storage root fresh yield per hectare (-1.000) and non-significant negative association with above ground fresh weight per plant (-0.313), storage root number per plant(-0.348), storage root length (-0.496), storage root diameter (-0.442), individual storage root weight (-0.792), storage root fresh yield per plant (-0.361), harvest index (-0.062) and non-significant positive association with vine internode diameter (0.075), Leaf area index (0.072) at phenotypic level (Table 4).

4.1.3.3 Vine internode diameter

Vine internode diameter had highly significant negative correlation with above ground fresh weight per plant (-0.885), storage root number per plant (-1.000), individual storage root weight (-1.000), harvest index (-1.000) and significant positive correlation with storage root diameter (1.000) at genotypic level (Table 3). It had showed non-significant negative correlation with Leaf area index (cm^2), storage root length (-0.782), storage root fresh yield per plot (-0.261) and non-significant positive correlation with storage root fresh yield per plant (0.256), storage root fresh yield per hectare (0.008) at genotypic level (Table 3). It had showed significant negative association with individual storage root weight (-1.000) and non-significant negative association with Leaf area index (-0.542), above ground fresh weight per plant (-0.184), storage root number per plant (-

0.203), storage root length (-0.393), storage root fresh yield per plot (-0.180), storage root fresh yield per hectare (-0.094) and non-significant positive association with storage root diameter (0.593), storage root fresh yield per plant (0.055), harvest index (0.028) at phenotypic level (Table 4). A significant and positive correlation was observed by Saladaga *et al.* (1981) for this trait.

4.1.3.4 Leaf area index

Leaf area index had highly significant positive correlation with storage root number per plant (1.000), storage root length (1.000) and significant negative correlation with harvest index (-1.000) at genotypic level (Table 3). It had showed non-significant positive association with above ground fresh weight per plant (0.432), storage root diameter (0.481), individual storage root weight (0.089), storage root fresh yield per plant (0.411), storage root fresh yield per plot (0.038) and non-significant negative association with storage root fresh yield per hectare (-0.105) at genotypic level (Table 3). Leaf area index had non-significant positive correlation with above ground fresh weight per plant (0.132), storage root number per plant (0.001), storage root length (0.647), storage root diameter (0.069), storage root fresh yield per plant (0.102) and non-significant negative correlation with individual storage root weight (-0.033), harvest index (-0.173), storage root fresh yield per plot (-0.013) and storage root fresh yield per hectare (-0.122) at phenotypic level (Table 4).

4.1.3.5 Above ground fresh weight per plant

Above ground fresh weight per plant had highly significant positive correlation with storage root length (1.000), storage root diameter (1.000), individual storage root weight (1.000), storage root fresh yield per plant (1.000), storage root fresh yield per plot (1.000), storage root fresh yield per hectare (1.000) and significant negative correlation with storage root number per plant (-1.000), harvest index (-1.000) at genotypic level (Table 3). It had showed significant positive association with individual storage root weight (0.829), storage root fresh yield per plant

(0.886), storage root fresh yield per plot (0.961) and storage root fresh yield per hectare (0.936) and non-significant positive association with storage root length (0.686), storage root diameter (0.537) at phenotypic level (Table 4). It had also showed non-significant negative association with storage root number per plant (-0.254), harvest index (-0.488) at phenotypic level (Table 4). Tiwari *et al.* (1987) and Sahu *et al.* (2003) found high correlation of this trait with storage root fresh yield and vine length respectively.

4.1.3.6 Storage root number per plant

Storage root number per plant had highly significant and negative association with storage root length (-1.000), storage root diameter (-1.000), individual storage root weight (-1.000), storage root fresh yield per plant (-1.000), harvest index (-1.000), storage root fresh yield per plot (-1.000) and storage root fresh yield per hectare (-1.000) at genotypic level (Table 3). It had showed non-significant positive association with storage root diameter (0.181), individual storage root weight (0.253) and non-significant negative association with storage root length (-0.265), storage root fresh yield per plant (-0.087), harvest index (-0.006), storage root fresh yield per plot (-0.349) and storage root fresh yield per hectare (-0.407) at phenotypic level (Table 4). Lin *et al.* (2007) reported that storage root number per plant was positively correlated. On the other hand, Tsegaye *et al.* (2006) and Warid *et al.* (1976) reported that the storage root number per plant was negatively correlated with storage root diameter, vine length and individual root weight.

4.1.3.7 Storage root length

Storage root length showed significant and positive correlation with individual storage root weight (0.821), storage root fresh yield per plant (0.962) and significant negative association with harvest index (-1.000) and non-significant positive association with storage root diameter (0.808), storage root fresh yield per plot (0.785) and storage root fresh yield per hectare (0.773) at genotypic level (Table 3). It had showed non-significant positive correlation with storage root

diameter (0.418), individual storage root weight (0.556), storage root fresh yield per plant (0.460), storage root fresh yield per plot (0.636), storage root fresh yield per hectare (0.597) and non-significant negative correlation with harvest index (-0.219) at phenotypic level (Table 4). Naskar *et al.* (1986) and Thamburaj and Muthukrishnan (1976) reported that Storage root length had significant positive correlations with storage root yield. Kamalam *et al.* (1977) found negative correlation of this trait with yield.

4.1.3.8 Storage root diameter

This trait was found to be highly significant and positively correlated with individual storage root weight (1.000), storage root fresh yield per plant (1.000), storage root fresh yield per plot (1.000) and storage root fresh yield per hectare (1.000) and significant negative association with harvest index (-1.000) at genotypic level (Table 3). It had showed significant and positively correlation with individual storage root weight (0.887) and non-significant positive association with storage root fresh yield per plant (0.700), harvest index (.224), storage root fresh yield per plot (0.472) and storage root fresh yield per hectare (0.482) at phenotypic level (Table 4). Hossain et al. (2000) found high correlation of storage root diameter with storage root yield. Tsegaye *et al*. (2006) found negative correlation of this trait.

4.1.3.9 Individual storage root weight

High significance and positive correlation were found with storage root fresh yield per plant (1.000), storage root fresh yield per plot (1.000) and storage root fresh yield per hectare (1.000) and significant negative association with harvest index (-1.000) at genotypic level (Table 3). Individual storage root weight significance and positive correlation with storage root fresh yield per plant (0.829) and non-significant positive association with storage root fresh yield per plot (0.778) and storage root fresh yield per hectare (0.799) at phenotypic level (Table 4). Tsegaye *et al.* (2006) found negative significant correlation for this trait.

4.1.3.10 Storage root fresh yield per plant

This traits were found to be highly significant and positively correlated with storage root fresh yield per plot (1.000) and storage root fresh yield per hectare (1.000) and significant negative association with harvest index (-1.000) at genotypic level (Table 3). It had showed significant positive correlation with storage root fresh yield per plot (0.830) and non-significant positive correlation with harvest index (0.753), storage root fresh yield per hectare (0.780) at phenotypic level (Table 4). Sahu *et al.* (2003) and Lin (1983) found the similar result for this trait.

4.1.3.11 Harvest index per plant

Harvest index per plant had significant negative association with storage root fresh yield per plot (-1.000) and storage root fresh yield per hectare (-1.000) at genotypic level (Table 3) and non-significant negative association with storage root fresh yield per plot (-0.160) and storage root fresh yield per hectare (-0.248) at phenotypic level (Table 4). Tsegaye *et al.* (2006), Sahu *et al.* (2005) and Huett *et al*. (1976) found positive correlation for this trait.

4.1.3.12 Storage root fresh yield per plot

Storage root fresh yield per plot highly significant and positively correlated with storage root fresh yield per hectare (1.000, 0.989) at both levels (Table 3 and 4).

4.1.4 Path coefficient analysis

Path coefficient analysis is a means of measuring the direct and indirect effects of one variable through the other variables on the end product. Here yield (ton/ha) was considered as effect (dependent variable) and vine length (inch), Vine Internode length (cm), Vine internode diameter (mm), Leaf area (cm^2), Above ground fresh weight per plant (kg), Storage root number per plant, Storage root length (cm), Storage root diameter (mm), Individual storage root weight (g),

Storage root fresh yield per plant (kg), Harvest index per plant (%) and Storage root fresh yield per plot (kg) were treated as independent variables.

Wright (1921) developed the path coefficient analysis technique and later demonstrated by Deway and Lu (1959) facilitates the portioning of correlation coefficients into direct and indirect contribution of various characters on yield. It is standardized partial regression coefficient analysis. As such, it measures the direct influence of one variable upon other. Estimation of direct and indirect effect of path co-efficient analysis is presented in Table 5.

4.1.4.1 Vine length

Vine length had negative direct effect on yield (-0.012) which is contributed to result non-significant positive genotypic correlation with yield (0.748) It had positive non-significant effect on vine internode length (0.038), vine internode diameter (0.051), Leaf area index (0.038), above ground fresh weight per plant (0.085), storage root number per plant (0.047), storage root length (0.042), storage root diameter (0.050), individual storage root weight (0.044), storage root fresh yield per plant (0.064), harvest index (0.002) and storage root fresh yield per plot (0.298). Kamalam *et al.* (1977) and Naskar *et al.* (1986) suggested vine length as criteria for selection of a high yielding plant type in sweet potato as this trait has direct influence on tuber number and tuber yield. Alam *et al.* (1998) reported dissimilar result with the present study and they stated that this trait had negative direct effect on tuber yield.

4.1.4.2 Vine Internode length

Vine internode length had positive direct effect (0.061) on yield and negative correlation (-1.000) with yield. It had negative non-significant effect on vine length (-0.056), vine internode diameter (-0.123), Leaf area index (-0.063), above ground fresh weight per plant (-0.022), storage root number per plant (-0.078), storage root length (-0.062), storage root diameter (-0.015), individual storage root

weight (-0.079), storage root fresh yield per plant (-0.137), harvest index (-0.052) and storage root fresh yield per plot (-0.375). Sahu *et al.* (2003) and Nanda (1994) found positive direct effect of vine internode length on tuber yield.

Table 5. Path coefficient analysis showing direct and indirect effects of different characters on yield of sweet potato

Characters	Direct effect	Indirect effect												Genotypic correlation with yield
		VL	VIL	VID	LAI	AGFWT	SRN	SRL	SRD	ISRWT	SRY	HI	SRYP	
VL	-0.012		0.038	0.051	0.038	0.085	0.047	0.042	0.050	0.044	0.064	0.002	0.298	0.748
VIL	0.061	-0.056		-0.123	-0.063	-0.022	-0.078	-0.062	-0.015	-0.079	-0.137	-0.052	-0.375	-1.000**
VID	0.044	-0.013	-0.005		0.004	0.022	-0.012	-0.005	0.019	-0.003	0.005	-0.045	-0.004	0.008
LAI	-0.019	-0.010	0.010	-0.011		0.004	-0.003	0.005	0.015	0.002	0.004	-0.005	-0.094	-0.105**
AGFWT	-0.285	0.046	0.032	0.035	0.039		0.033	0.041	0.025	0.050	0.060	0.315	0.608	1.000**
SRN	-0.039	-0.107	-0.119	-0.109	-0.101	-0.074		-0.103	-0.115	-0.096	-0.162	-0.067	0.093	-1.000**
SRL	0.036	0.041	0.016	0.020	0.028	-0.098	0.035		-0.002	0.044	0.171	0.027	0.454	0.773
SRD	-0.001	0.094	0.059	0.078	0.093	0.041	0.098	0.092		0.110	0.183	0.072	0.080	1.000**
ISRWT	0.090	0.060	0.021	0.063	0.064	-0.064	0.079	0.065	-0.005		0.058	0.182	0.386	1.000**
SRY	0.475	0.050	0.041	0.053	0.052	0.036	0.043	0.054	0.032	0.052		-0.296	0.406	1.000**
HI	-0.540	-0.086	-0.082	-0.077	-0.081	0.114	-0.086	-0.081	-0.084	-0.088	0.240		-0.150	-1.000**
SRYP	0.983**	-0.012	-0.017	0.003	0.005	-0.186	0.015	0.004	0.003	0.012	0.155	0.035		1.000**

Residual Effect = 0.0425045

VL-Vine length (inch), VIL- Vine internode length (cm), VID- Vine internode diameter (mm), LAI- Leaf area index (cm^2), AGFWT- Above ground fresh weight per plant (kg), SRN- Storage root number per plant, SRL- Storage root length (cm), SRD- Storage root diameter (cm), ISRWT- Individual storage root weight (kg), SRY- Storage root fresh yield per plant (kg), HI- Harvest index per plant (%), SRYP- Storage root fresh yield per plot (kg), SRYH- Storage root fresh yield (ton/ha)

4.1.4.3 Vine internode diameter

Vine internode diameter had positive direct effect on yield (0.044) and it had also non-significant positive correlation with yield (0.008) at genotypic level. Vine internode diameter had positive indirect effect on Leaf area index (0.004), above ground fresh weight per plant (0.022), storage root diameter (0.019) and storage root fresh yield per plant (0.005). This trait had also negative indirect effect on vine length (-0.013), vine internode length (-0.005), storage root number per plant (-0.012), storage root length (-0.005), individual storage root weight (-0.003), harvest index (-0.045) and storage root fresh yield per plot (-0.004).

4.1.4.4 Leaf area index

Leaf area index had negative direct effect (-0.019) and negative significant correlation (-0.105) on yield. Leaf area index had positive indirect effect on vine internode length (0.010), above ground fresh weight per plant (0.004), storage root length (0.005), storage root diameter (0.015), individual storage root weight (0.002) and storage root fresh yield per plant (0.004). Leaf area index had negative indirect effect on vine length (-0.010), vine internode diameter (-0.011), storage root number per plant (-0.003), harvest index (-0.005) and storage root fresh yield per plot (-0.094).

4.1.4.5 Above ground fresh weight per plant

Above ground fresh weight per plant had negative direct effect on yield (-0.285) and it had positive significant correlation with yield (1.000). Above ground fresh weight per plant had positive indirect effect on vine length (0.046), vine internode length (0.032), vine internode diameter (0.035), Leaf area index (0.039), storage root number per plant (0.033), storage root length (0.041), storage root diameter (0.025), individual storage root weight (0.050), storage root fresh yield per plant (0.060), harvest index (0.315) and storage root fresh yield per plot (0.608).

4.1.4.6 Storage root number per plant

Storage root number per plant showed negative direct effect on yield (-0.039) and significant negative correlation with yield (-1.000). Storage root number per plant had positive indirect effects on storage root fresh yield per plot (0.093). It had negative indirect effects on vine length (-0.107), vine internode length (-0.119), vine internode diameter (-0.109), Leaf area index (-0.101), above ground fresh weight per plant (-0.074), storage root length (-0.103), storage root diameter (-0.115), individual storage root weight (-0.096), storage root fresh yield per plant (-0.162) and harvest index (-0.067).

4.1.4.7 Storage root length

Storage root length had direct positive effect (0.036) on yield and non-significant positive correlation with yield (0.773). Storage root length had positive indirect effect on vine length (0.041), vine internode length (0.016), vine internode diameter (0.020), Leaf area index (0.028), storage root number per plant (0.035), individual storage root weight (0.044), storage root fresh yield per plant (0.171), harvest index (0.027) and storage root fresh yield per plot (0.454). It had negative indirect effect on above ground fresh weight per plant (-0.098) and storage root diameter (-0.002). Sahu *et al.* (2003) and Nanda (1994) also reported positive direct effects on tuber yield.

4.1.4.8 Storage root diameter

Storage root diameter had negative direct effect (-0.001) on yield. It had also significant positive correlation with yield (1.000). Storage root diameter had positive indirect effect on vine length (0.094), vine internode length (0.059), vine internode diameter (0.078), Leaf area index (0.093), above ground fresh weight per plant (0.041), storage root number per plant (0.098), storage root length (0.092), individual storage root weight (0.110), storage root fresh yield per plant (0.183), harvest index (0.072) and storage root fresh yield per plot (0.080).

4.1.4.9 Individual storage root weight

Individual storage root weight showed positive direct effect (0.090) on yield. It had also significant positive correlation with yield (1.000). It had positive

indirect effect on vine length (0.060), vine internode length (0.021), vine internode diameter (0.063), Leaf area index (0.064), storage root number per plant (0.079), storage root length (0.065), storage root fresh yield per plant (0.058), harvest index (0.182) and storage root fresh yield per plot (0.386). It had negative indirect effect on above ground fresh weight per plant (-0.064) and storage root diameter (-0.005). This trait is supported by Tsegaye *et al.* (2006).

4.1.4.10 Storage root dry yield per plant

Storage root dry yield per plant had positive direct effect (0.475) on yield. It had also significant positive correlation with yield (1.000). This trait had indirect positive effect on vine length (0.050), vine internode length (0.041), vine internode diameter (0.053), Leaf area index (0.052), above ground fresh weight per plant (0.036), storage root number per plant (0.043), storage root length (0.054), storage root diameter (0.032), individual storage root weight (0.052) and storage root fresh yield per plot (0.406). It had also indirect negative effect on harvest index (-0.296).

4.1.4.11 Harvest index per plant

Harvest index per plant had negative direct effect (0.784) on yield. It had negative indirect effects on vine length (-0.086), vine internode length (-0.082), vine internode diameter (-0.077), Leaf area index (-0.081), storage root number per plant (-0.086), storage root length (-0.081), storage root diameter (-0.084), individual storage root weight (-0.088) and storage root fresh yield per plot (-0.150). It had also positive indirect effects on above ground fresh weight per plant (0.114) and storage root fresh yield per plant (0.240).

4.1.4.12 Storage root fresh yield per plot

Storage root fresh yield per plot had significant positive direct effect (0.983) on yield. It had also significant positive correlation with yield (1.000). This trait had also indirect positive effect on vine internode diameter (0.003), Leaf area index (0.005), storage root number per plant (0.015), storage root length (0.004), storage root diameter (0.003), individual storage root weight (0.012),

storage root fresh yield per plant (0.155) ant harvest index (0.035). It had also indirect negative effect on vine length (-0.012), vine internode length (-0.017) and above ground fresh weight per plant (-0.186).

4.5 Multivariate analysis

4.1.5.1 Principal component analysis (PCA)

Principal component analysis was calculated with six genotypes of sweet potato which gives Eigen values of principal component axes of coordination of genotypes with the first axes 50.32% of the total variation among the genotypes. First five Eigen values for five principal coordination axes of genotypes accounted for 100% variation showed in Table 6. Based on principal component scores I and II obtained from the Principal component analysis (Appendix VI), a two-dimensional scatter diagram (Z1-Z2) using component score I as X axis and component score II as Y axis was Constructed, which has been presented in Figure 1. The scatter diagram revealed that there were three apparent clusters and the genotypes were distantly located from each other, which indicated that considerable diversity existed among the genotypes.

4.1.5.2 Canonical variate analysis

Inter-cluster distances was compute by Canonical Variate Analysis (CVA). The intra and inter-cluster distance (D^2) values were shown in Table 7. When inter-cluster distances were higher than the intra- cluster distances, it's indicating broader genetic diversity among the genotypes of different groups. The highest inter-cluster distance was observed between lusters I and III (1.7856), followed by between clusters II and III (0.9989).

In contrast, the lowest inter-cluster distance was observed between cluster I and II (0.9407). However, the maximum inter-cluster distance was observed between the clusters I and III (1.7856) indicating genotypes from these two clusters if involved in hybridization may produce a wide spectrum of population. On the other hand, the maximum intra-cluster distance was found in cluster III (0.8361), which contained of 2 genotypes, while the minimum

distance was found in cluster II (0.0) that comprises 1 genotype. Inter and intra cluster distances were showed in Table 7. Cluster I consists of nearest cluster with D^2 values cluster II (0.9407) and farthest cluster with D^2 values III (1.7856) (Table 8). Cluster I consists of nearest cluster with D^2 values cluster II (0.9407) and farthest cluster

Table 6. Eigen values and yield percent contribution of 13 characters in 6 genotypes of sweet potato

Components	Eigen values	Percent variation	Cumulative % of Percent variation
I	6.542	50.32	50.32
II	2.857	21.98	72.30
III	1.655	12.73	85.03
IV	1.282	9.86	94.89
V	0.664	5.11	100.00
VI	0.000	0.00	100.00
VII	0.000	0.00	100.00
VIII	0.000	0.00	100.00
IX	0.000	0.00	100.00
X	0.000	0.00	100.00
XI	0.000	0.00	100.00
XII	0.000	0.00	100.00
XIII	0.000	0.00	100.00

Table 7. Intra (Bold) and inter cluster distances (D2) for 6 genotypes of sweet potato

I	**II**	**III**	
0.4142	0.9407	1.7856	**I**
	0	0.9989	**II**
		0.8361	**III**

Cluster	**Nearest with D^2 values**	**Farthest with D^2 values**
I	II (0.9407)	III (1.7856)

Table 8. The nearest and farthest clusters from each cluster between D2 values in sweet potato

II	I (0.9407)	III (0.9989)
III	II (0.9989)	I (1.7856)

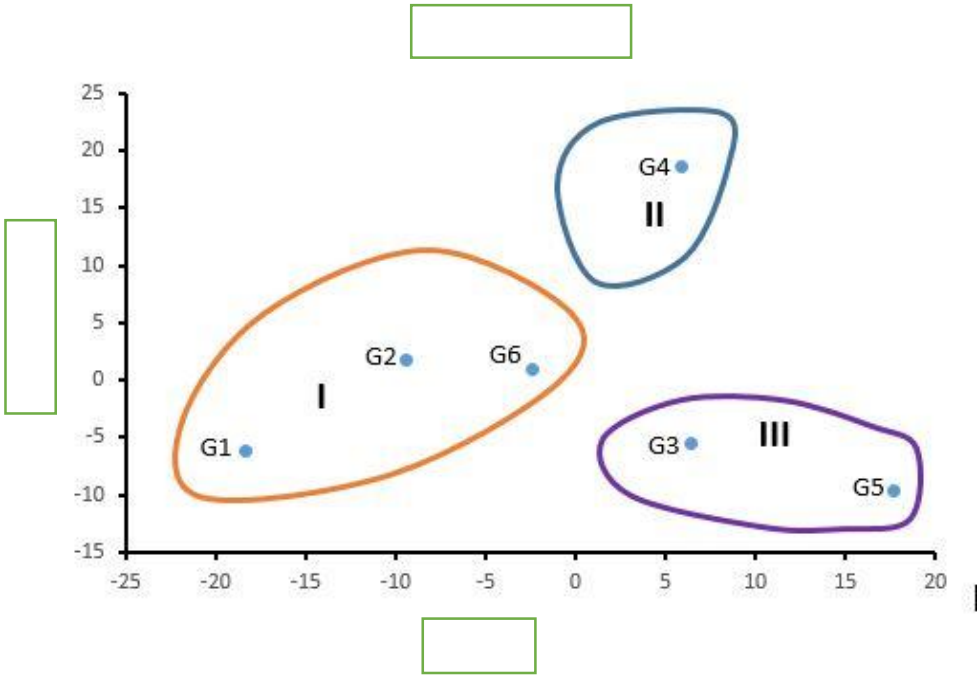


Figure 1. Scatter diagram of 6 sweet potato genotypes based on their principle component scores superimposed with clustering

with D^2 values III (1.7856) (Table 8). Cluster II consists of nearest cluster with D^2 values cluster I (0.9407) and farthest cluster with D^2 values III (0.9989). Cluster III consists of nearest cluster with D^2 values cluster II (0.9989) and farthest cluster with D^2 values I (1.7856). According to scatter diagram all the genotypes were apparently distributed into three clusters (Figure 2). It is occupied that higher amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. In the present study the maximum distance existence both cluster III and I at the same level. So the crosses between the genotypes belonging cluster III with cluster I might produce high heterosis. Also the crosses between genotypes from cluster III with I might produce high level of segregating population. So the genotypes belonging to cluster III and cluster I might be selected for future hybridization program.

4.1.5.3 Principal coordinate analysis (PCO)

Inter genotypic distances as (D^2) as attained by principal coordinate analysis (PCO) for all possible combinations between the couple of genotypes. Inter genotypic distances, as obtained from principal coordinate analysis showed that the highest distance was observed between the G2 and G5 (Table 9).The lowest distance was observed between the G4 and G6. The difference between the

highest and the lowest inter genotypic distance indicated the prevalence of variability among the 6 genotypes of sweet potato studied.

4.1.5.4 Non-hierarchical clustering

From covariance matrix the computations gave non-hierarchical clustering among six genotypes of sweet potato and grouped them into three clusters. The clustering pattern obtained coincided with the apparent grouping patterns performed by principal component analysis (PCA). So, the results obtained through PCA were confirmed by non-hierarchical clustering.

Composition of different clusters with their corresponding genotypes in each cluster is presented in Table 10. Cluster I had the maximum number of three

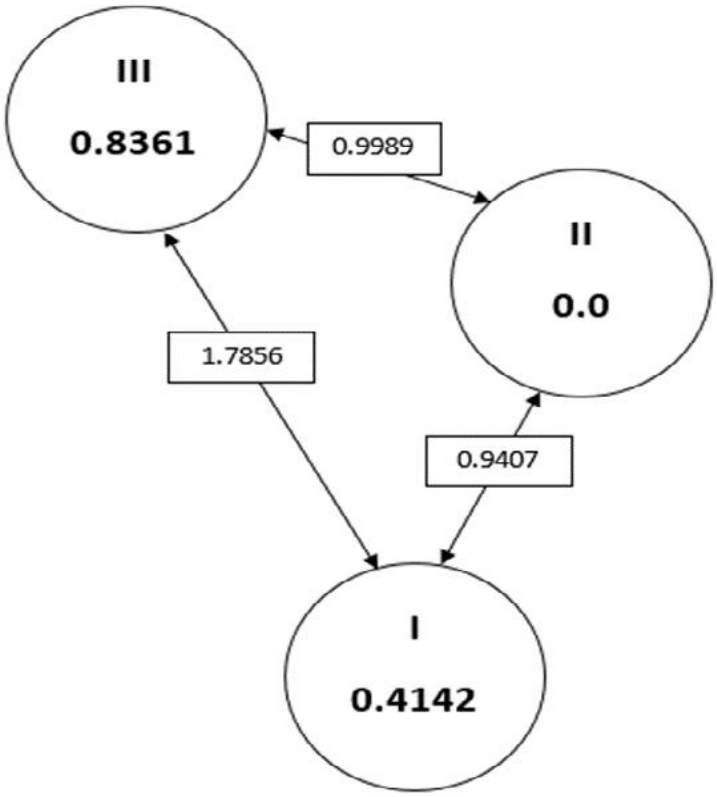


Figure 2. Intra and inter cluster distances (D2) of 6 genotypes of sweet potato

Table 9. Ten highest and ten lowest inter genotypic distance among six genotypes of sweet potato

10 highest inter genotypic distances				**10 lowest inter genotypic distances**			
Sl	Genotype	Genotype	Value	Sl	Genotype	Genotype	Value

	s	s	s		s	s	s
1	G5	G2	0.9618	1	G6	G4	0.3464
2	G5	G1	0.8401	2	G6	G2	0.3681
3	G5	G3	0.8361	3	G6	G3	0.3831
4	G5	G4	0.7969	4	G3	G2	0.3941
5	G6	G5	0.7083	5	G2	G1	0.4255
6	G4	G1	0.5703	6	G3	G1	0.4308
7	G4	G2	0.5087	7	G6	G1	0.449
8	G4	G3	0.4643	8	G4	G3	0.4643
9	G6	G1	0.449	9	G4	G2	0.5087
10	G3	G1	0.4308	10	G4	G1	0.5703

Table 10. Distribution of genotypes in different clusters

genotypes comprising G1 (SP006), G2 (SP002), and G6 (SP001) where cluster

Cluster	**Number of population**	**Genotypes**
I	3	G1, G2, G6
II	1	G4
III	2	G3,G5

II had the minimum one genotype G4 (SP004).

4.1.5.5 Cluster mean analysis

The cluster means of 13 different characters (Table 11) were compared and indicated considerable differences between clusters for all the characters studied. The maximum vine length were noticed in cluster I (93.84), whereas the minimum vine length were noticed in cluster III (75.58). The maximum vine internode length were observed in cluster III (6.50), whereas the minimum vine internode length in cluster II (5.97). The maximum vine internode diameter were noticed in cluster II (0.06), whereas the minimum vine internode diameter were noticed in cluster I and III (0.05). The maximum Leaf area index were noticed in cluster I (83.57), whereas the minimum Leaf area index were noticed in cluster II (59.89). The maximum above ground fresh weight per plant were noticed in cluster II (2.20), whereas the minimum above ground fresh weight per plant were noticed in cluster III (1.96). The maximum storage root number per plant was noticed in cluster III (6.83) and the minimum (6.00) in cluster II. Cluster I showed the highest storage root length (21.97) and cluster II showed the lowest (17.75). The highest storage root diameter were noticed in cluster I (5.68), whereas the minimum storage root diameter noticed in cluster III (4.78). The maximum individual storage root weight were noticed in cluster I (0.55), whereas the minimum individual storage root weight were noticed in cluster III (0.38). The maximum (1.97) and the minimum (1.64) storage root fresh yield per plant were observed in cluster I and III, respectively. The maximum harvest index was observed in cluster I (47.28), whereas the minimum harvest index was observed in cluster III (45.60). The maximum (64.53) and the minimum (50.83) storage root fresh yield per plot were noticed in cluster II and III, respectively. The maximum storage root fresh yield per hectare was observed in cluster II (31.67), whereas the minimum yield was observed in cluster III (25.83).

Parameters	I	II	III

VL	93.84	87.19	73.58
VIL	6.33	5.97	6.50
VID	0.05	0.06	0.05
LAI	83.57	59.89	78.09
AGFWT	2.18	2.20	1.96
SRN	6.44	6.00	6.83
SRL	21.97	17.75	18.32
SRD	5.68	5.07	4.78
ISRWT	0.55	0.53	0.38
SRY	1.97	1.87	1.64
HI	47.28	45.94	45.60
SRYP	60.07	64.53	50.83
SRYH	29.00	31.67	25.83

Table 11. Cluster mean values of 13 different characters of 6 genotypes of sweet potato

VL-Vine length (inch), VIL- Vine internode length (cm), VID- Vine internode diameter (mm), LAI- Leaf area index (cm^2), AGFWT- Above ground fresh weight per plant (kg), SRN- Storage root number per plant, SRL- Storage root length (cm), SRD- Storage root diameter (cm), ISRWT- Individual storage root weight (kg), SRY- Storage root fresh yield per plant (kg), HI- Harvest index per plant (%), SRYP- Storage root fresh yield per plot (kg), SRYH- Storage root fresh yield (ton/ha)

4.1.5.6 Contribution of characters towards divergence of the genotypes

The characters contribution towards the divergence obtained from principle component analysis is presented in Table 12. The character, which gave highest absolute magnitude for vector 1, was considered to be responsible for primary differentiation. Same as, the characters, which gave highest absolute magnitude for vector 2 was considered to be responsible for secondary differentiation. If same character given equal magnitude for both the vectors than the characters considered responsible for primary as well as secondary differentiation. In vector 1 (Z_1), the important characters responsible for genetic divergence in the axis of differentiation were vine internode length (0.3308), vine internode diameter (0.0344), storage root number per plant (0.1946). In vector 2 (Z_2), the second axis of differentiation vine length (0.0903), vine internode length (0.009), leaf area index (0.2412), above ground fresh weight per plant (0.0536), storage root length (0.254), storage root fresh yield per plot (0.0933) and storage root fresh yield per hectare (0.0683) were important because all these characters had positive signs.

On the other hand, vine length (-0.1712), leaf area index (-0.0439), above ground fresh weight per plant (-0.3806), storage root length (-0.2751), storage root diameter (-0.2605), individual storage root weight (-0.3476), storage root fresh yield per plant (-0.354), harvest index (-0.0851), storage root fresh yield per plot (-0.377) and storage root fresh yield per hectare (-0.3693) possessed the negative sign in the first axis of differentiation and vine internode diameter (-0.5516), storage root number per plant (-0.3713), storage root diameter (-0.3686), individual storage root weight (-0.2269), storage root fresh yield per plant (-0.1465) and harvest index (-0.4492) possessed negative signs in the second axis of differentiation that means these had minor role in the genetic divergence.

Table 12. Relative contributions of the 13 characters of 6 genotypes of sweet potato to the total divergence

Parameters	Vector-1	Vector-2
VL	-0.1712	0.0903
VIL	0.3308	0.009
VID	0.0344	-0.5516
LAI	-0.0439	0.2412
AGFWT	-0.3806	0.0536
SRN	0.1946	-0.3713
SRL	-0.2751	0.254
SRD	-0.2605	-0.3686
ISRWT	-0.3476	-0.2269
SRY	-0.354	-0.1465
HI	-0.0851	-0.4492
SRYP	-0.377	0.0933
SRYH	-0.3693	0.0683

VL-Vine length (inch), VIL- Vine internode length (cm), VID- Vine internode diameter (mm), LAI- Leaf area index (cm^2), AGFWT- Above ground fresh weight per plant (kg), SRN- Storage root number per plant, SRL- Storage root length (cm), SRD- Storage root diameter (cm), ISRWT- Individual storage root weight (kg), SRY- Storage root fresh yield per plant (kg), HI- Harvest index per plant (%), SRYP- Storage root fresh yield per plot (kg), SRYH- Storage root fresh yield (ton/ha)

4.1.5.7 Selection of genotypes as parent for hybridization program

Identification and selection of genetically diverse parents is an urgent step for hybridization program. Three factors (selection of specific variety from a cluster, choice of particular cluster and relative contribution of the character to the total divergence) should be considered for selecting parents for a breeding program (Chaudhary *et al.,* 1977). Thorough knowledge of genetic diversity of the crop is necessary for parental selection that maximizes genetic improvement (Rahman *et al*., 2011). So, in the present study genotypes were to be selected on the basis of specific objectives. From the crosses between genetically distance parents a high heterosis could be produced. Considering the magnitude of cluster mean and agronomic performance the genotype G2 (SP002) for the maximum storage root diameter, individual storage root weight from cluster I, G5 (SP005) for the minimum storage root length, storage root diameter, individual storage root weight, and storage root fresh yield per plant from cluster III. Therefore considering group distance and other agronomic performance G2 and G5 sweet potato genotypes may be suggested for future hybridization program.

4.2 Experiment 2: Evaluation of sweet potato genotypes based on nutritional traits

It comprises a brief description of nutritional traits. This part of the chapter opened the results and their interpretation in order to evaluation of sweet potato genotypes based on their nutritional traits.

4.2.1.1 Moisture

Significant differences were observed among the genotypes for moisture % which ranged from 65.6433 (G1) to 72.0500 (G6) with mean value 69.9378 (Table 13 and Appendix VII). The σ^2p and σ^2g was observed 6.6734 and 6.3085 respectively (Table 14). The PCV (3.69) and GCV (3.59) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement of sweet potato. The heritability estimates for this

Table 13. Analysis of variance for different quality characters in sweet potato genotypes

Character	Mean sum of square	
	Genotype (t-1=5)	Error (n-t=12)
Moisture	19.2903**	0.3182
Protein	1.0152**	0.0621
Lipid	0.1029**	0.0028
Fiber	0.3608**	0.0040
Ash	0.2073**	0.0124
Carbohydrate	25.0160**	0.0019
Sugar	5.6989**	0.2931
Beta Carotene	0.0017**	0.0000
Vitamin C	0.0000	0.0000
Calcium	0.0687**	0.0035
Magnesium	0.0183**	0.0008
Potassium	0.0447**	0.0001
Sodium	0.0045**	0.0002
Phosphorus	0.0132**	0.0001
Dry Matter	19.1950**	0.3107

** Significant at 1% * Significant at 5%

Table 14. Estimation of genetic parameters for fifteen qualitative characters in sweet potato

Traits	Mean	CV (%)	σ^2_g	σ^2_e	σ^2_P	GCV	ECV	PCV	h^2_b	GA	GA (% mean)
Moisture (%)	69.94	0.86	6.3085	0.3649	6.6734	3.59	0.86	3.69	94.53	5.03	7.19
Protein (%)	4.79	5.34	0.3166	0.0654	0.3820	11.75	5.34	12.90	82.88	1.06	22.03
Lipid (%)	0.44	9.45	0.0337	0.0018	0.0355	41.36	9.56	42.45	94.93	0.37	83.00
Fiber (%)	0.85	6.25	0.1193	0.0028	0.1221	40.78	6.25	41.25	97.71	0.70	83.03
Ash (%)	1.22	9.46	0.0647	0.0132	0.0779	20.85	9.42	22.88	83.06	0.48	39.14
Carbohydrate (%)	22.68	0.19	8.3380	0.0019	8.3399	12.73	0.19	12.73	99.98	5.95	26.22
Sugar (g)	7.42	6.42	1.8241	0.2265	2.0506	18.20	6.41	19.30	88.95	2.62	35.37
Beta Carotene (g)	0.06	4.50	0.0006	0.0000	0.0006	38.83	0.00	38.83	100.00	0.05	80.00
Vitamin C (g)	0.01	9.78	0.0000	0.0000	0.0000	0.00	0.00	0.00	0.00	0.00	0.00
Calcium (g)	1.25	3.79	0.0222	0.0022	0.0244	11.91	3.75	12.49	90.97	0.29	23.40
Magnesium (g)	0.65	4.71	0.0058	0.0009	0.0067	11.75	4.63	12.63	86.57	0.15	22.52
Potassium (g)	0.56	1.66	0.0149	0.0001	0.0150	21.83	1.79	21.90	99.33	0.25	44.81
Sodium (g)	0.23	6.50	0.0014	0.0002	0.0016	16.82	6.28	17.95	87.76	0.07	32.46
Phosphorus (g)	0.28	2.94	0.0044	0.0001	0.0045	23.69	3.59	23.96	97.76	0.13	48.26
Dry Matter (%)	30.06	1.99	6.2795	0.3564	6.6359	8.34	1.99	8.57	94.63	5.02	16.71

trait was high (94.53) with low genetic advance (5.03) over low genetic advance in percent of mean (7.19) (Table 14) revealed that this trait was governed by environmental effects selection would be ineffective.

4.2.1.2 Protein

The studied genotypes showed significant difference in case of protein % content (Table 13). Maximum was found 5.6333 in (G4) and the minimum was recorded 3.9667 in (G1) with mean value 4.7917 (Appendix VII). The σ^2g (0.3166) was lower than σ^2p (0.3820). GCV (11.75) and PCV (12.90) were also close to each other (Table 14) suggesting environmental influence is minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. The heritability estimates for this trait was high (82.88) with low genetic advance (1.06) over high genetic advance in percent of mean (22.03), revealed that this trait was governed by additive gene and selection is effective for protein content.

4.2.1.3 Lipid

The analysis of variance revealed highly significant differences among the genotypes with respect to lipid content (Table 13). The genotypic and phenotypic variance was observed 0.0337 and 0.0355, respectively for lipid content with environmental influence. The phenotypic co-efficient of variation (42.45) was higher than the genotypic co-efficient of variation (41.36), which indicated the presence of considerable variability among the genotypes for this trait. The heritability (94.93) estimates for this trait was high, genetic advance (0.37) was a very low and genetic advance in percent of the mean (83) was found high, revealed that this trait was governed by the additive gene and selection would be effective

4.2.1.4 Fiber

Significant differences were observed among the genotypes for fiber content which ranged from 0.5167 (G6) to 1.3333 (G2) with mean value 0.8472

(Appendix VII). The σ^2p and σ^2g was observed 0.1221 and 0.1193 respectively (Table 14). The PCV (41.25) and GCV (40.78) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement of sweet potato. The heritability estimates for this trait was high (97.71) with low genetic advance (0.70) over high genetic advance in percent of mean (83.03) (Table 14) revealed that this trait was governed by the additive gene and selection would be effective.

4.2.1.5 Ash

The analysis of variance revealed significant differences among the genotypes with respect to ash content (Table 13). The genotypic and phenotypic variance was observed 0.0647 and 0.0779, respectively for ash content with environmental influence. The phenotypic co-efficient of variation (22.88) was higher than the genotypic co-efficient of variation (20.85), which indicated the presence of considerable variability among the genotypes for this trait. The heritability (83.06) estimates for this trait was high, genetic advance (0.48) was a very low and genetic advance in percent of the mean (39.14) was found high, revealed that this trait was governed by the additive gene and selection would be effective.

4.2.1.6 Carbohydrate

Significant differences were observed among the genotypes for Carbohydrate % content which ranged from 20.0800 (G2) to 28.0200 (G1) with mean value 22.6847 (Appendix VII). The σ^2p and σ^2g was observed 8.3399 and 8.3380 respectively (Table 14). The PCV (12.73) and GCV (12.73) were same, indicating no environmental influence on this character that would be effective for the improvement of sweet potato. The heritability estimates for this trait was high (99.98) with low genetic advance (5.95) over low genetic advance in percent of mean (26.22) (Table 14) revealed that this trait was governed by the additive gene and selection would be effective.

4.2.1.7 Sugar

The studied genotypes showed significant difference in case of sugar content (Table 13). Maximum was found 9.4333 in (G3) and the minimum was recorded 5.5500 in (G4) with mean value 7.4156 (Appendix VII). The σ^2g (1.8241) was lower than σ^2p (2.0506). GCV (18.20) and PCV (19.30) were also close to each other (Table 14) suggesting environmental influence is minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. The heritability estimates for this trait was high (88.95) with low genetic advance (2.62) over high genetic advance in percent of mean (35.37), revealed that this trait was governed by additive gene and selection is effective for protein content.

4.2.1.8 Beta Carotene

Significant differences were observed among the genotypes for beta Carotene which ranged from 0.0337 (G4) to 0.1000 (G5) with mean value 0.0613 (Appendix VII). The σ^2p and σ^2g was observed 0.0006 and 0.0006 respectively (Table 14). The PCV (38.83) and GCV (38.83) were same, indicating no environmental influence on this character that would be effective for the improvement of sweet potato. The heritability estimates for this trait was high (100) with low genetic advance (0.05) over low genetic advance in percent of mean (80.00) (Table 14) revealed that this trait was governed by the additive gene and selection would be effective.

4.2.1.9 Vitamin C

The studied genotypes showed non-significant difference in case of vitamin-C content (Table 13). Maximum was found 0.0137 in (G2) and the minimum was recorded 0.0065 in (G1) with mean value 0.0093 (Appendix VII). Selection based upon this trait selection is ineffective.

4.2.1.10 Calcium

The studied genotypes showed significant difference in case of calcium content (Table 13). Maximum was found 1.4833 in (G4) and the minimum was recorded 1.0500 in (G5) with mean value 1.2647 (Appendix VII). The σ^2g (0.0222) was lower than σ^2p (0.0244). GCV (11.91) and PCV (12.49) were also close to each other (Table 14) suggesting environmental influence is minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. The heritability estimates for this trait was high (90.97) with low genetic advance (0.29) over high genetic advance in percent of mean (23.40), revealed that this trait was governed by additive gene and selection is effective for calcium content.

4.2.1.11 Magnesium

Significant differences were observed among the genotypes for magnesium which ranged from 0.5470 (G5) to 0.7503 (G4) with mean value 0.6483 (Appendix VII). The σ^2p and σ^2g was observed 0.0067 and 0.0058 respectively (Table 14). The PCV (12.63) and GCV (11.75) were close to each other, indicating minor environmental influence on this character that would be effective for the improvement of sweet potato. The heritability estimates for this trait was high (86.57) with low genetic advance (0.15) over high genetic advance in percent of mean (22.52) (Table 14) revealed that this trait was governed by additive gene and selection is effective.

4.2.1.12 Potassium

The studied genotypes showed significant difference in case of potassium content (Table 13). Maximum was found 0.7387 in (G5) and the minimum was recorded 0.4400 in (G4) with mean value 0.5586 (Appendix VII). The σ^2g and σ^2p was observed 0.0150 and 0.0149 respectively (Table 14). GCV (21.83) and PCV

(21.90) were also close to each other (Table 14) suggesting environmental influence is minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. The heritability estimates for this trait was high (99.33) with low genetic advance (0.25) over high genetic advance in percent of mean (44.81), revealed that this trait was governed by additive gene and selection is effective for potassium content.

4.2.1.13 Sodium

Significant differences were observed among the genotypes for sodium content which ranged from 0.1753 (G5) to 0.2727 (G4) with mean value 0.2251 (Appendix VII). The σ^2p and σ^2g was observed 0.0016 and 0.0014 respectively (Table 14). The PCV (17.95) and GCV (16.82) were also close to each other (Table 14) suggesting environmental influence is minor on the expression of the genes controlling this trait. The heritability estimates for this trait was high (87.76) with low genetic advance (0.07) over low genetic advance in percent of mean (32.46) (Table 14) revealed that this trait was governed by the additive gene and selection would be effective.

4.2.1.14 Phosphorous

The studied genotypes showed significant difference in case of phosphorous content (Table 13). Maximum was found 0.3467 in (G3) and the minimum was recorded 0.1810 in (G1) with mean value 0.2789 (Appendix VII). The σ^2g and σ^2p was observed 0.0044 and 0.0045 respectively (Table 14). GCV (23.69) and PCV (23.96) were also close to each other (Table 14) suggesting environmental influence is minor on the expression of the genes controlling this trait. So, selection based upon phenotypic expression of this character would be effective for the improvement of this crop. The heritability estimates for this trait was high (97.76) with low genetic advance (0.13) over high genetic advance in percent of

mean (48.26), revealed that this trait was governed by additive gene and selection is effective for phosphorous content.

4.2.1.15 Dry Matter

Significant differences were observed among the genotypes for dry matter content which ranged from 27.9500 (G6) to 34.3367 (G1) with mean value 30.0594 (Appendix VII). The σ^2p and σ^2g was observed 6.6359 and 6.2795 respectively (Table 14). The PCV (8.57) and GCV (8.34) were also close to each other (Table 14) suggesting environmental influence is minor on the expression of the genes controlling this trait. The heritability estimates for this trait was high (94.63) with low genetic advance (5.02) over high genetic advance in percent of mean (16.71) (Table 14) revealed that this trait was governed by the additive gene and selection would be effective.

4.2.2 Correlation Co-efficient

Correlation studies along with path analysis provide a better understanding of the association of different characters with yield. Simple correlation was partitioned into phenotypic (that can be directly observed), genotypic (inherent association between characters) components as suggested by (Singh and Chaudhary, 1985). Phenotypic and genotypic correlation coefficients among different pairs yield contributing characters for different genotypes of sweet potato are given in Table 15, Table 16 and Table 17.

4.2.2.1 Moisture

Moisture had significant negative correlation with carbohydrate (G= -0.959, P=-0.951) and dry matter (G=-1.000, P=-1.000) at both genotypic and phenotypic level (Table 16 and Table 17). It had non-significant positive association with protein, lipid, fiber, sugar, beta carotene, vitamin C, potassium, and phosphorus at both genotypic and phenotypic level (Table 16 and Table 17). It had also non-

significant negative association with ash, calcium, magnesium and sodium at both genotypic and phenotypic level (Table 16 and Table 17).

Table 15. Pearson correlation coefficients among different pair's characters for different genotype of sweet potato

	Protein	Lipid	Fiber	Ash	Carbohydrate	Sugar	B-Carotene	Vitamin C	Calcium	Magnesium	Potassium	Sodium	Phosphorus	Dry Matter
Moisture	0.2697	0.2884	0.2530	-0.0872	-0.9323**	0.5674*	0.4663	0.3630	-0.3459	-0.1819	0.4087	-0.2994	0.4399	-1.000**
Protein		-0.457	0.1575	0.4883*	-0.4808*	-0.2666	-0.3108	-0.3785	0.5963**	0.6207**	-0.3441	0.5052*	0.4173	-0.2678
Lipid			0.1917	-0.5381*	-0.1536	0.7789**	0.8037**	0.5345*	-0.8155**	-0.8970**	0.9429**	-0.9297**	0.5128*	-0.2892
Fiber				0.6097**	-0.4669	0.1386	-0.2631	0.2624	-0.086	-0.1625	0.0884	-0.2093	0.1235	-0.2528
Ash					-0.1787	-0.4410	-0.7831**	-0.2971	0.5972**	0.5661*	-0.6145**	0.4893*	-0.2272	0.0881
Carbohydrate						-0.4077	-0.2327	-0.3086	0.1602	0.0368	-0.2440	0.1617	-0.4569	0.9322**
Sugar							0.7701**	0.2194	-0.6400**	-0.6920**	0.7920**	-0.7299**	0.5138*	-0.5670*
β-Carotene								0.3868	-0.7737**	-0.7250**	0.9030**	-0.7792**	0.5475*	-0.4669
Vitamin C									-0.6297**	-0.5944**	0.5430*	-0.5576*	0.1637	-0.3625
Calcium										0.8389**	-0.8188**	0.8174**	-0.1789	0.3467
Magnesium											-0.8676**	0.9477**	-0.2914	0.1836
Potassium												-0.9085**	0.6217**	-0.4091
Sodium													-0.4004	0.3008
Phosphorus														-0.4389

Table 16. Genotypic (G) correlations among different pairs of qualitative traits for different genotype of sweet potato

	Protein	Lipid	Fiber	Ash	Carbohydrate	Sugar	Beta Carotene	Vitamin C	Calcium	Magnesium	Potassium	Sodium	Phosphorus	Dry Matter
Moisture	0.336	0.319	0.286	-0.081	-0.959**	0.614	0.480	0.432	-0.386	-0.236	0.411	-0.353	0.452	-1.000**
Protein		-0.493	0.161	0.553	-0.531	-0.245	-0.348	-0.323	0.707	0.708	-0.378	0.579	0.476	-0.334
Lipid			0.189	-0.639	-0.159	0.835*	0.848*	0.664	-0.933**	-0.997**	0.992**	-1.000**	0.527	-0.320
Fiber				0.647	-0.475	0.160	-0.258	0.330	-0.096	-0.143	0.096	-0.213	0.118	-0.286
Ash					-0.199	-0.445	-0.866*	-0.453	0.713	0.681	-0.691	0.660	-0.242	0.082
Carbohydrate						-0.442	-0.235	-0.373	0.170	0.043	-0.246	0.179	-0.462	0.958**
Sugar							0.863*	0.324	-0.817*	-0.753	0.863*	-0.840*	0.524	-0.618
β-Carotene								0.477	-0.822*	-0.809	0.914*	-0.841*	0.567	-0.480
Vitamin C									-0.781	-0.729	0.623	-0.739	0.196	-0.433
Calcium										1.000**	-0.899*	1.000**	-0.215	0.386
Magnesium											-0.939**	1.000**	-0.285	0.237
Potassium												-0.985**	0.630	-0.412
Sodium													-0.428	0.354
Phosphorus														-0.451

Table 17. Phenotypic (P) correlations among different pairs of qualitative traits for different genotype of sweet potato

	Protein	Lipid	Fiber	Ash	Carbohydrate	Sugar	Beta Carotene	Vitamin C	Calcium	Magnesium	Potassium	Sodium	Phosphorus	Dry Matter
Moisture	0.314	0.311	0.277	-0.083	-0.951**	0.604	0.476	0.408	-0.375	-0.219	0.411	-0.336	0.449	-1.000**
Protein		-0.482	0.161	0.531	-0.514	-0.246	-0.336	-0.342	0.676	0.679	-0.367	0.554	0.457	-0.312
Lipid			0.186	-0.608	-0.158	0.816*	0.839*	0.619	-0.911	-0.965**	0.982**	-0.990**	0.521	-0.311
Fiber				0.635	-0.473	0.151	-0.260	0.306	-0.100	-0.148	0.094	-0.209	0.118	-0.276
Ash					-0.193	-0.444	-0.839*	-0.397	0.672	0.643	-0.667	0.604	-0.237	0.084
Carbohydrate						-0.432	-0.234	-0.351	0.168	0.041	-0.245	0.173	-0.461	0.950**
Sugar							0.838*	0.280	-0.760	-0.735	0.847*	-0.809	0.521	-0.605
Beta Carotene								0.445	-0.812*	-0.782	0.911*	-0.821*	0.562	-0.476
Vitamin C									-0.727	-0.681	0.597	-0.675	0.184	-0.408
Calcium										0.969**	-0.880*	0.956**	-0.206	0.376
Magnesium											-0.917*	0.986**	-0.286	0.220
Potassium												-0.961**	0.628	-0.411
Sodium													-0.418	0.337
Phosphorus														-0.447

4.2.2.2 Protein

Protein had non-significant positive correlation with fiber, ash, calcium, magnesium, sodium and phosphorus at both genotypic and phenotypic level (Table 16 and Table 17). It had also non-significant negative correlation with lipid, carbohydrate sugar, beta carotene, vitamin C, potassium and dry matter at both genotypic and phenotypic level (Table 16 and Table 17).

4.2.2.3 Lipid

Lipid had significant positive correlation with sugar (G=0.835, P=0.816), beta carotene (G=0.848, P=0.839) and potassium (G=0.992, P=-0.982) at both genotypic and phenotypic level (Table 16 and Table 17). It had also significant negative association with calcium (G= -0.933), magnesium (G= -0.997, P= -0.965) and sodium (G= -1.000, P= -0.990) at both genotypic and phenotypic level (Table 16 and Table 17). It had non-significant positive correlation with fiber, vitamin C and phosphorus at both genotypic and phenotypic level (Table 16 and Table 17). It had also non-significant negative correlation with ash, carbohydrate and dry matter at both genotypic and phenotypic level (Table 16 and Table 17).

4.2.2.4 Fiber

Fiber had non-significant positive correlation ash, sugar, vitamin C, potassium, and phosphorous at both genotypic and phenotypic level (Table 16 and Table 17). It had also non-significant negative correlation with carbohydrate, beta carotene, calcium, magnesium, sodium, and dry matter at both genotypic and phenotypic level (Table 16 and Table 17).

4.2.2.5 Ash

Ash had significant negative association with beta carotene (G= -0.866, P= -0.839) at both genotypic and phenotypic level (Table 16 and Table 17). It had non-significant positive correlation with calcium, magnesium, sodium and dry matter at both genotypic and phenotypic level (Table 16 and Table 17). It had also non-

significant negative correlation with carbohydrate, sugar, beta carotene, vitamin C, potassium and phosphorus at both genotypic and phenotypic level (Table 16 and Table 17).

4.2.2.6 Carbohydrate

Carbohydrate had significant positive correlation with dry matter (G=0.958, P=0.950) at both genotypic and phenotypic level (Table 16 and Table 17). It had non-significant positive correlation with calcium, magnesium, and sodium at both genotypic and phenotypic level (Table 16 and Table 17). It had also non-significant negative correlation with sugar, beta carotene, vitamin C, potassium and phosphorus at both genotypic and phenotypic level (Table 16 and Table 17).

4.2.2.7 Sugar

Sugar had significant positive correlation with beta carotene (G=0.863, P=0.838) and potassium (G=0.863, P=-0.847) at both genotypic and phenotypic level (Table 16 and Table 17). It had also significant negative association with calcium (G= -0.817) and sodium (G= -0.840) at genotypic level (Table 16 and Table 17). It had non-significant positive correlation with vitamin C and phosphorus at both genotypic and phenotypic level (Table 16 and Table 17). It had also non-significant negative correlation magnesium and dry matter at both genotypic and phenotypic level (Table 16 and Table 17).

4.2.2.8 Beta carotene

Beta carotene had significant positive correlation with potassium (G=0.914, P=0.911) at both genotypic and phenotypic level (Table 16 and Table 17). It had also significant negative association with calcium (G= -0.822, P=-0.812) and sodium (G= -0.841, P= -0.821) at both genotypic and phenotypic level (Table 16 and Table 17). It had non-significant positive correlation with vitamin C and phosphorus at both genotypic and phenotypic level (Table 16 and Table 17). It had

also non-significant negative correlation with magnesium and dry matter at both genotypic and phenotypic level (Table 16 and Table 17).

4.2.2.9 Vitamin C

Vitamin C had non-significant positive correlation with potassium and phosphorus at both genotypic and phenotypic level (Table 16 and Table 17). It had also non-significant negative correlation with calcium, magnesium, sodium and dry matter at both genotypic and phenotypic level (Table 16 and Table 17).

4.2.2.10 Calcium

Calcium had significant positive correlation with magnesium (G=1.000, P=0.969), and sodium (G=1.000, P=0.956) at both genotypic and phenotypic level (Table 16 and Table 17). It had also significant negative association with potassium (G= -0.899, P= -0.880) at both genotypic and phenotypic level (Table 16 and Table 17). It had non-significant positive correlation with dry matter at both genotypic and phenotypic level (Table 16 and Table 17). It had also non-significant negative correlation phosphorous at both genotypic and phenotypic level (Table 16 and Table 17).

4.2.2.11 Magnesium

Magnesium had significant positive correlation with sodium (G=1.000, P=0.986) at both genotypic and phenotypic level (Table 16 and Table 17). It had also significant negative association with potassium (G= -0.939, P= -0.917) at both genotypic and phenotypic level (Table 16 and Table 17). It had non-significant positive correlation with dry matter at both genotypic and phenotypic level (Table 16 and Table 17). It had also non-significant negative correlation phosphorous at both genotypic and phenotypic level (Table 16 and Table 17).

4.2.2.12 Potassium

Potassium had significant negative association with sodium (G= -0.985, P= -0.961) at both genotypic and phenotypic level (Table 16 and Table 17). It had non-

significant positive correlation with phosphorous at both genotypic and phenotypic level (Table 16 and Table 17). It had also non-significant negative correlation with dry matter at both genotypic and phenotypic level (Table 16 and Table 17).

4.2.2.13 Sodium

Sodium had non-significant positive correlation with dry matter at both genotypic and phenotypic level (Table 16 and Table 17). It had also non-significant negative correlation with phosphorous at both genotypic and phenotypic level (Table 16 and Table 17).

4.2.2.14 Phosphorous

Phosphorous had non-significant negative correlation with dry matter at both genotypic and phenotypic level (Table 16 and Table 17).

4.2.3 Path Coefficient Analysis

The path coefficient analysis technique was developed by Wright (1921) and demonstrated by Deway and Lu (1959) facilitates the portioning of correlation coefficients into direct and indirect contribution of various characters on yield. It is standardized partial regression coefficient analysis. As such, it measures the direct influence of one variable upon other. Such information would be of great value in enabling the breeder to specifically identify the important component traits of yield and utilize the genetic stock for improvement in a planned way.

In path coefficient analysis the direct effect of a trait dry matter content % of plant and its indirect effect through other characters were computed and the results are presented in (Table 18).

4.2.3.1 Moisture

Moisture had negative direct effect (-0.824) on dry matter content % (Table 18) which is contributed to result significant negative genotypic correlation with dry

Table 18. Path analysis showing direct (bold) and indirect effects of qualitative traits by path analysis of sweet potato

	Moisture	Protein	Lipid	Fiber	Ash	Carbohydrate	Sugar	Beta Carotene	Vitamin C	Calcium	Magnesium	Potassium	Sodium	Phosphorus	Genotypic correlation with Dry matter content %
Moisture	**-0.824**	-0.101	-0.369	-0.459	-0.191	0.063	-0.325	0.355	0.298	0.169	0.378	0.097	-0.259	0.168	-1.000**
Protein	-0.811	**-0.178**	0.591	-0.187	0.109	0.200	0.193	-0.251	0.070	-0.279	-0.398	-0.038	0.386	0.259	-0.334
Lipid	-1.035	-0.024	**-0.230**	-0.442	-0.334	0.222	-0.550	0.560	-0.143	0.327	1.891	0.144	-0.773	0.068	-0.320
Fiber	-0.701	0.030	-0.135	**-0.513**	0.303	0.107	-0.005	-0.095	0.071	0.121	0.394	0.096	-0.070	0.112	-0.286
Ash	0.169	-0.204	0.593	-0.073	**0.877**	0.344	0.152	-0.734	-0.072	-0.421	-0.414	-0.268	0.303	-0.170	0.082
Carbohydrate	0.664	0.128	0.181	0.748	-0.369	**-0.194**	0.217	-0.181	0.001	-0.085	-0.028	-0.070	0.138	-0.192	0.958**
Sugar	-0.694	0.060	-0.886*	-0.241	-0.872*	0.949**	**-0.501**	0.702	-0.001	0.388	0.539	0.247	-0.530	0.222	-0.618
Beta Carotene	-0.384	0.026	-1.018	0.253	-0.670	0.420	-0.508	**0.735**	-0.072	0.367	0.648	0.199	-0.624	0.146	-0.480
Vitamin C	-0.031	-0.031	-0.031	-0.031	-0.031	-0.031	-0.031	-0.031	**-0.031**	-0.031	-0.031	-0.031	-0.031	-0.031	-0.433
Calcium	0.046	-0.167	0.992**	0.155	0.321	-0.363	0.378	-0.688	0.001	**-0.514**	-0.034	-0.256	0.596	-0.081	0.386
Magnesium	0.534	-0.168	0.048	0.245	0.240	-0.026	0.367	-0.653	0.003	-0.492	**-0.113**	-0.262	0.616	-0.104	0.237
Potassium	-0.292	-0.051	-0.210	-0.280	-0.456	0.389	-0.568	0.608	-0.143	0.311	0.778	**0.149**	-0.759	0.112	-0.412
Sodium	0.115	-0.054	0.151	0.423	0.222	-0.405	0.488	-0.633	0.070	-0.414	0.022	-0.214	**0.703**	-0.122	0.354
Phosphorus	-0.304	-0.113	-0.558	-0.158	-0.468	0.035	-0.272	0.431	0.001	0.104	0.554	0.183	-0.295	**0.410**	-0.451

Residual Effect = 0.0523321

matter content % (-1.000). Where it showed positive indirect effect with carbohydrate, sugar, vitamin C, calcium, magnesium, potassium and phosphorus. It had a negative indirect effect on protein, lipid, fiber, ash, sugar and sodium.

4.2.3.2 Protein

Protein had negative direct effect (-0.178) on dry matter content % (Table 18).). It had positive indirect effect on lipid, ash, carbohydrate, sugar, vitamin C, sodium and phosphorus. Negative indirect effect was also found on moisture, fiber, beta carotene, calcium, magnesium and potassium.

4.2.3.3 Lipid

Lipid had negative direct effect (-0.230) on dry matter content % (Table 18) which is contributed to result significant negative genotypic correlation with dry matter content% (-0.334). Where it showed positive indirect effect with carbohydrate, beta carotene, calcium, magnesium, potassium and phosphorus. It had a negative indirect effect on moisture, protein, fiber, ash, sugar, vitamin C and sodium.

4.2.3.4 Fiber

Protein had negative direct effect (-0.513) on dry matter content % (Table 18).). It had positive indirect effect on protein, ash, carbohydrate, vitamin C, calcium, magnesium, potassium and phosphorus. Negative indirect effect was also found on moisture, lipid, sugar, beta carotene and sodium.

4.2.3.5 Ash

Ash had positive direct effect (0.877) on dry matter content % (Table 18). It had positive indirect effect on moisture, lipid, carbohydrate, sugar and sodium. Negative indirect effect was also found on protein, fiber, beta carotene, vitamin C, calcium, magnesium, potassium and phosphorus.

4.2.3.6 Carbohydrate

Carbohydrate had negative direct effect (-0.194) on dry matter content % (Table 18) which is contributed to result significant positive genotypic

correlation with dry matter content % (0.958). It had positive indirect effect on moisture, protein, lipid, fiber, sugar, vitamin C and sodium. Negative indirect effect was also found on ash, beta carotene, calcium, magnesium, potassium and phosphorus.

4.2.3.7 Sugar

Sugar had negative direct effect (-0.194) on dry matter content % (Table 18). It had positive indirect effect on protein, carbohydrate, beta carotene, calcium, magnesium, potassium and phosphorus. Negative indirect effect was also found on moisture, lipid, fiber, ash, vitamin C and sodium.

4.2.3.8 Beta Carotene

Beta Carotene had positive direct effect (0.735) on dry matter content % (Table 18). It had positive indirect effect on protein, fiber, carbohydrate, calcium, magnesium, potassium and phosphorus. Negative indirect effect was also found on moisture, lipid, ash, sugar, vitamin C and sodium.

4.2.3.9 Vitamin C

Vitamin C had negative direct effect (-0.031) on dry matter content % (Table 18). It had negative indirect effect on moisture, protein, lipid, fiber, ash, carbohydrate, sugar, beta carotene, calcium, magnesium, potassium, sodium and phosphorus.

4.2.3.10 Calcium

Calcium had negative direct effect (-0.514) on dry matter content % (Table 18). It had positive indirect effect on moisture, lipid, fiber, ash, sugar, vitamin C and sodium. Negative indirect effect was also found on protein, carbohydrate, beta carotene, magnesium, potassium and phosphorus.

4.2.3.11 Magnesium

Magnesium had negative direct effect (-0.113) on dry matter content % (Table 18). It had positive indirect effect on moisture, lipid, fiber, ash, sugar, vitamin C and sodium. Negative indirect effect was also found on protein, carbohydrate, beta carotene, calcium, potassium and phosphorus.

4.2.3.12 Potassium

Potassium had positive direct effect (0.149) on dry matter content % (Table 18). It had positive indirect effect on carbohydrate, beta carotene, calcium, magnesium and phosphorus. Negative indirect effect was also found on moisture, protein, lipid, fiber, ash, sugar, vitamin C and sodium.

4.2.3.13 Sodium

Sodium had positive direct effect (0.703) on dry matter content % (Table 18). It had positive indirect effect on moisture, lipid, fiber, ash, sugar, vitamin C, magnesium and potassium. Negative indirect effect was also found on protein, carbohydrate, beta carotene, calcium, potassium and phosphorus.

4.2.3.14 Phosphorous

Phosphorous had positive direct effect (0.410) on dry matter content % (Table 18). It had positive indirect effect on carbohydrate, beta carotene, vitamin C, calcium, magnesium and potassium. Negative indirect effect was also found on moisture, protein, lipid, fiber, ash, sugar and sodium.

4.5 Multivariate analysis

4.1.5.1 Principal component analysis (PCA)

Principal component analysis was calculated with six genotypes of sweet potato which gives Eigen values of principal component axes of coordination of genotypes with the first axes 54.45% of the total variation among the genotypes. First five Eigen values for five principal coordination axes of genotypes accounted for 100% variation showed in Table 19. Based on principal component scores I and II obtained from the Principal component analysis, a two-dimensional scatter diagram (Z1-Z2) using component score I as X axis and component score II as Y axis was Constructed, which has been presented in Figure 3. The scatter diagram revealed that there were three apparent clusters and the genotypes were distantly

Table 19. Eigen values and yield percent contribution of fifteen qualitative characters in six genotypes of sweet potato

Components	Eigen values	Percent variation	Cumulative % of Percent variation
I	8.17	54.45	54.45
II	3.56	23.73	78.18
III	1.62	10.78	88.96
IV	1.01	6.74	95.70
V	0.65	4.30	100.00
VI	0.00	0.00	100.00
VII	0.00	0.00	100.00
VIII	0.00	0.00	100.00
IX	0.00	0.00	100.00
X	0.00	0.00	100.00
XI	0.00	0.00	100.00
XII	0.00	0.00	100.00
XIII	0.00	0.00	100.00
XIV	0.00	0.00	100.00
XV	0.00	0.00	100.00

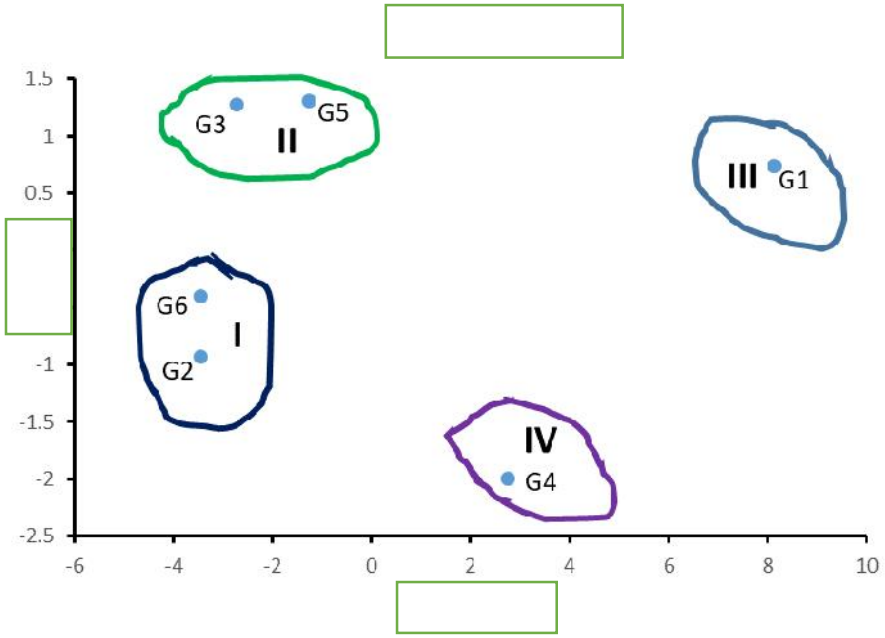


Figure 3. Scatter diagram of 6 sweet potato genotypes based on their principle component scores superimposed with clustering

located from each other, which indicated that considerable diversity existed among the genotypes.

4.1.5.2 Canonical variate analysis

Inter-cluster distances was compute by Canonical Variate Analysis (CVA). The intra and inter-cluster distance (D^2) values were shown in Table 20. When inter-cluster distances were higher than the intra- cluster distances, it's indicating broader genetic diversity among the genotypes of different groups. The highest inter-cluster distance was observed between lusters I and III (6.732), followed by between clusters II and III (5.329).

In contrast, the lowest inter-cluster distance was observed between cluster II and IV (1.115). However, the maximum inter-cluster distance was observed between the clusters I and III (6.732) indicating genotypes from these two clusters if involved in hybridization may produce a wide spectrum of population. On the other hand, the maximum intra-cluster distance was found in cluster II (0.505), which contained of 2 genotypes, while the minimum distance was found in both cluster III and IV (0.0) that comprises 1 genotype each. Inter and intra cluster distances were showed in Table 20. Cluster I consists of nearest cluster with D^2 values cluster II (1.715) and farthest cluster with D^2 values III (6.732) (Table 21). Cluster II consists of nearest cluster with D^2 values cluster IV (1.115) and farthest cluster with D^2 values III (5.329). Cluster III consists of nearest cluster with D^2 values cluster IV (4.327) and farthest cluster with D^2 values I (6.732). Cluster IV consists of nearest cluster with D^2 values cluster II (1.115) and farthest cluster with D^2 values III (4.327). It is occupied that higher amount of heterosis will be manifested in cross combination involving the genotypes belonging to most divergent clusters. In the present study the maximum distance existence both cluster III and I at the same level. So the crosses between the genotypes belonging cluster III with cluster I might produce high heterosis. Also the crosses between genotypes from cluster III with I might

Table 20. Intra (Bold) and inter cluster distances (D2) for 6 genotypes of sweet potato

I	II	III	IV	Cluster
0.485	1.715	6.732	2.801	**I**
	0.505	5.329	1.115	**II**
		0	4.327	**III**
			0	**IV**

Table 21. The nearest and farthest clusters from each cluster between D2 values in sweet potato

Cluster	Nearest with D^2 values	Farthest with D^2 values
I	**II** (1.715)	**III** (6.732)
II	**IV** (1.115)	**III** (5.329)
III	**IV** (4.327)	**I** (6.732)
IV	**II** (1.115)	**III** (4.327)

produce high level population. So the genotypes belonging to cluster III and cluster I might be selected for future hybridization program.

4.1.5.3 Principal coordinate analysis (PCO)

Inter genotypic distances as (D^2) as attained by principal coordinate analysis (PCO) for all possible combinations between the couple of genotypes. Inter genotypic distances, as obtained from principal coordinate analysis showed that the highest distance was observed between the G2 and G5 (Table 22).The lowest distance was observed between the G4 and G6. The difference between the highest and the lowest inter genotypic distance indicated the prevalence of variability among the 6 genotypes of sweet potato studied.

4.1.5.4 Non-hierarchical clustering

From covariance matrix the computations gave non-hierarchical clustering among six genotypes of sweet potato and grouped them into three clusters. The clustering pattern obtained coincided with the apparent grouping patterns performed by principal component analysis (PCA). So, the results obtained through PCA were confirmed by non-hierarchical clustering.

Composition of different clusters with their corresponding genotypes in each cluster is presented in Table 23. Both cluster I and cluster II had the maximum number of two genotypes comprising G2 (SP002), G6 (SP001), and G3 (SP003), G5 (SP005) respectively.

4.1.5.5 Cluster mean analysis

The cluster means of 15 different characters (Table 24) were compared and indicated considerable differences between clusters for all the characters studied. The maximum moisture were noticed in cluster I (71.87), whereas the minimum moisture were noticed in cluster III (65.64). The maximum protein content were observed in cluster IV (5.63), whereas the minimum protein in cluster II (5.97). The maximum lipid were noticed in cluster II

Table 22. Fifteen lowest to highest inter genotypic distance among 6 genotypes of sweet potato

Sl	Genotypes	Genotypes	Values
1	6	4	0.3464
2	6	2	0.3681
3	6	3	0.3831
4	3	2	0.3941
5	2	1	0.4255
6	3	1	0.4308
7	6	1	0.449
8	4	3	0.4643
9	4	2	0.5087
10	4	1	0.5703
11	6	5	0.7083
12	5	4	0.7969
13	5	3	0.8361
14	5	1	0.8401
15	5	2	0.9618

Table 23. Distribution of genotypes in different clusters

Cluster number	Genotypes	Number of populations
I	G2, G6	2
II	G3, G5	2
III	G1	1
IV	G4	1

Table 24. Cluster mean values of 15 different characters of 6 genotypes of sweet potato

Character	I	II	III	IV
Moisture	71.87	71.09	65.64	68.07
Protein	4.93	4.65	3.97	5.63
Lipid	0.35	0.66	0.38	0.25
Fiber	0.93	0.87	0.62	0.88
Ash	1.32	1.02	1.17	1.47
Carbohydrate	20.45	21.90	28.02	23.40
Sugar	7.28	8.93	6.51	5.55
Beta Carotene	0.06	0.09	0.05	0.03
Vitamin C	0.01	0.01	0.01	0.01
Calcium	1.26	1.11	1.26	1.48
Magnesium	0.68	0.57	0.65	0.75
Potassium	0.50	0.71	0.49	0.44
Sodium	0.24	0.18	0.24	0.27
Phosphorus	0.24	0.35	0.18	0.31
Dry Matter	28.13	28.92	34.34	31.93

(0.66), whereas the minimum lipid were noticed in cluster IV (0.25). The maximum fiber were noticed in cluster I (93), whereas the minimum fiber were noticed in cluster III (0.62). The maximum ash were noticed in cluster IV (1.47), whereas the minimum ash were noticed in cluster II (1.02). The maximum carbohydrate was noticed in cluster III (28.02) and the minimum (20.45) in cluster I. Cluster II showed the highest sugar (8.93) and cluster IV showed the lowest (5.55). The highest beta carotene were noticed in cluster II (0.09), whereas the minimum beta carotene noticed in cluster IV (0.03). The maximum calcium were noticed in cluster IV (1.48), whereas the minimum calcium were noticed in cluster II (1.11). The maximum (0.75) and the minimum (0.57) magnesium were observed in cluster IV and II, respectively. The maximum potassium was observed in cluster II (0.71), whereas the minimum potassium was observed in cluster IV (0.44). The maximum (027) and the minimum (0.18) sodium were noticed in cluster IV and II, respectively. The maximum phosphorous was observed in cluster II (0.35), whereas the minimum was observed in cluster III (o.18). The maximum dry matter were noticed in cluster III (34.34), whereas the minimum dry matter were noticed in cluster I (28.13).

4.1.5.6 Contribution of characters towards divergence of the genotypes

The characters contribution towards the divergence obtained from principle component analysis is presented in Table 25. The character, which gave highest absolute magnitude for vector 1, was considered to be responsible for primary differentiation. Same as, the characters, which gave highest absolute magnitude for vector 2 was considered to be responsible for secondary differentiation. If same character given equal magnitude for both the vectors than the characters considered responsible for primary as well as secondary differentiation. In vector 1 (Z_1), the important characters responsible for genetic divergence in the axis of differentiation were protein (0.1438), ash (0.2316), carbohydrate (0.1245), calcium (0.3292),

Table 25. Relative contributions of the 13 characters of 6 genotypes of sweet potato to the total divergence

Character	Principal Component	
	Vector-1	Vector-2
Moisture	-0.1888	-0.4067
Protein	0.1438	-0.42
Lipid	-0.334	0.0813
Fiber	-0.0415	-0.2618
Ash	0.2316	-0.2602
Carbohydrate	0.1245	0.4842
Sugar	-0.3034	-0.0891
Beta Carotene	-0.3198	0.0448
Vitamin C	-0.2383	-0.0139
Calcium	0.3292	-0.1203
Magnesium	0.3233	-0.1652
Potassium	-0.3402	0.0343
Sodium	0.3367	-0.0901
Phosphorus	-0.1799	-0.2339
Dry Matter	0.1891	0.4062

Magnesium (0.3233), sodium (0.3367) and dry matter (0.1891). In vector 2 (Z_2), the second axis of differentiation lipid (0.0813), carbohydrate (0.4842), beta carotene (0.0448), potassium (0.0343) and dry matter (0.4062) were important because all these characters had positive signs.

On the other hand, moisture (-0.1888), lipid (-0.334), fiber (-0.0415), sugar (-0.3034), beta carotene (-0.3198), vitamin C (-0.2383), potassium (-0.3402) and phosphorous (-0.1799) possessed the negative sign in the first axis of differentiation and moisture (-0.4067), protein (-0.42), fiber (-0.2618), ash (-0.2602), sugar (-0.0891), vitamin C (-0.0139), calcium (-0.1203), magnesium (-0.1652), sodium (-0.0901) and phosphorous (-0.2339) possessed negative signs in the second axis of differentiation that means these had minor role in the genetic divergence.

4.1.5.7 Selection of genotypes as parent for hybridization program

Identification and selection of genetically diverse parents is an urgent step for hybridization program. Three factors (selection of specific variety from a cluster, choice of particular cluster and relative contribution of the character to the total divergence) should be considered for selecting parents for a breeding program (Chaudhary *et al.,* 1977). Thorough knowledge of genetic diversity of the crop is necessary for parental selection that maximizes genetic improvement (Rahman *et al*., 2011). So, in the present study genotypes were to be selected on the basis of specific objectives. From the crosses between genetically distance parents a high heterosis could be produced. Considering the magnitude of cluster mean and agronomic performance the genotype G2 (SP002) for the maximum storage root diameter, individual storage root weight from cluster I, G5 (SP005) for the minimum storage root length, storage root diameter, individual storage root weight, and storage root fresh yield per plant from cluster III. Therefore considering group distance and other agronomic performance G2 and G5 sweet potato genotypes may be suggested for future hybridization program.

CHAPTER V
SUMMARY AND CONCLUSION

The present study was undertaken at Sher-e-Bangla Agricultural University Farm, Dhaka-1207, Bangladesh with six sweet potato genotypes during the period from Mid November 2017 to April 2018. Vine was prepared and sown to the main field in Randomized Complete Block Design (RCBD) with four replications. Data on various agro-morphological traits such as vine length (inch), vine Internode length (cm), vine internode diameter (mm), leaf area index (cm^2), above ground fresh weight per plant (kg), storage root number per plant, storage root length (cm), storage root diameter (mm), individual storage root weight per plant (kg), storage root fresh yield per plant (kg), harvest index per plant (%), storage root fresh yield per plot (kg), storage root fresh yield (ton/ha) were recorded. Data on various qualitative traits such as moisture (%), dry matter (%), protein (%), lipid (%), fiber (%), ash (%), carbohydrate (%), sugar (g), beta carotene (g), vitamin C (g), calcium (g), magnesium (g), potassium (g), sodium (g) and phosphorus (g).

In case of agro-morphological traits, analysis of variance revealed significant differences among all the genotypes for all the characters under study except vine internode length, vine internode diameter, above ground fresh weight per plant, storage root diameter, individual storage root weight and storage root fresh yield per plant. In case of qualitative traits, the analysis of variances showed significant mean squares for different characters indicated the presence of sufficient variation among the genotypes for all the characters except vitamin C.

Vine length showed highest range of variation in agro-morphological traits (99.16-70.92) that means wide range of variation present for this character. The carbohydrate content % showed highest range of variation in qualitative traits (20.0800-28.0200) that means wide range of variation present for this character.

Storage root number, harvest index, storage fresh root yield per plot and, storage fresh root yield per hectare in agro-morphological traits exhibit the highest value of heritability. In case of qualitative traits, all the characters under the present study exhibit the highest value of heritability except vitamin C.

Correlation coefficients among the characters were studied to define the association between yield and yield contributing components. In general, most of the characters showed the genotypic correlation co-efficient were higher than the corresponding phenotypic correlation co-efficient suggesting a strong inherent association between the characters under study. The significant positive correlation with yield (ton/ha) was found in above ground fresh weight per plant, storage root diameter, individual storage root weight, storage root fresh yield per plant and storage root fresh yield per plot at genotypic level and above ground fresh weight per plant, above ground fresh weight per plot at phenotypic level. In case of qualitative traits, the significant positive correlation with dry matter content was found in carbohydrate at genotypic and phenotypic level.

Path coefficient analysis showed that Storage root fresh yield per plot had significant positive direct effect (0.983) on yield. It had also significant positive correlation with yield (1.000). It also showed that vine internode length, vine internode diameter, storage root length, individual storage root weight and storage fresh root yield per plant had positive direct effect on yield. It also showed that above ground fresh weight per plant (1.000), storage root diameter (1.000), individual storage root weight (1.000) and storage fresh root yield per plant (1.000) had the positive correlation with yield. Its indicating selection would be more effective for these characters in crop improvement. In case of qualitative traits, ash %, beta carotene, potassium, sodium and phosphorous content had direct positive effect (0.877, 0.735, 0.149, 0.703, and 0.410 respectively) on dry matter content % and carbohydrate had significant positive correlation with dry matter content % (0.958).

In case of agro-morphological traits, genetic diversity of six sweet potato genotypes based on thirteen characters was measured through multivariate analysis. The six genotypes fell into three distant clusters. The highest inter-cluster distance was observed between lusters I and III (1.7856), followed by between clusters II and III (0.9989). In contrast, the lowest inter-cluster distance was observed between cluster I and II (0.9407). However, the maximum inter-cluster distance was observed between the clusters I and III (1.7856) indicating genotypes from these two clusters if involved in hybridization may produce a wide spectrum of population.

From the findings of the present study, the following conclusions could be drawn:

- In both agro-morphological and qualitative traits, technique of selection would be applied for desired characters such as vine length, leaf area index, storage root length, harvest index, storage root yield per plot and biochemical properties to develop high yielding varieties.

- In case of agro-morphological traits, wide range of genetic diversity existed among 6 sweet potato genotypes which were grouped into three clusters and most diverse genotypes were G2 (SP002) and G5 (SP005). That variability could be used for future breeding program of sweet potato in Bangladesh.

- In case of agro-morphological traits, highly significant positive association of fresh root yield was observed above ground fresh weight per plant, storage root diameter, individual storage root weight, storage root fresh yield per plant and storage root fresh yield per plot at genotypic level and above ground fresh weight per plant, above ground fresh weight per plot at phenotypic level. In case of qualitative traits, the significant positive correlation with dry matter content was found in carbohydrate at genotypic and phenotypic level. This results

suggested that fresh root yield and nutrition can be increased by improving these characters.

- In case of agro-morphological traits, storage root fresh yield per plot had significant positive direct effect on yield and above ground fresh weight per plant, storage root diameter, individual storage root weight and storage fresh root yield per plant had the positive correlation with yield. In case of qualitative traits, ash %, beta carotene, potassium, sodium and phosphorous content had direct positive effect on dry matter content % and carbohydrate had significant positive correlation with dry matter content %. This results suggested that tuber yield per plant and nutrition can be increased by improving these characters.

Based on the results of the study, the following recommendations may be drawn:

- Genotypes G2 (SP002) and G5 (SP005) could be included in future breeding program in the response of increase sweet potato yield.

- The genotypes of cluster I and II could be used as parents for the further breeding program to develop sweet potato variety.

REFERENCES

Akheter, M. and Sneller, C.H. (1996). Genotype by environment interaction and selection of early maturing soybean genotypes. *Crop Sci.* **36**: 883-889.

Akkamahadevi, B., Rao, P.N., Shrinivasan, C.N. and Bharti, P. (1996). Composition and cooking quality of five sweet potato varieties. *J. Root Crops***. 22**(2): 101-104.

Akhtar, S., Ahmed, A., Randhawa, M. A., Atukorala, S., Arlappa, N. and Ismail, T. (2013). Prevalence of vitamin A deficiency in South Asia: Cause, outcomes, and possible remedies. *J. Heal. Pop. Nutr.* **31**: 413-423.

Alam, S., Narzary, B.D. and Deka, B.C. (1998). Variability, character association and path analysis in sweet potato (*Ipomoea batatas* (L.) Lam.). *J. Agric. Sci.* **11**(1): 77-81.

Allard, R. (1960). Principles of plant breeding. John Willey and Sons Inc. New York. pp. 85-485.

Allemann, J., Laurie, S.M., Thiart, S. and Vorster H.J. (2004). Sustainable production of root and tuber crops (potato, sweet potato, indigenous potato, cassava) in southern Africa. *South African J. Bot*. **70**: 60-66.

Alumira, J.D. and Obara, C.M. (1997). Post-harvest consumption analysis of sweet potato in Kenya.

Ames, T., Smit, N.E.J.M., Braun, A.R., O'Sullivan J.N. and Skoglund, L.G. (1996). Sweet potato: Major pests' diseases and nutritional disorders. International Potato Center (CIP), Lima, Peru.

Amoah, R.S. (2013). The effects of ethylene of sweet potato storage. Phd thesis, Cranfield University. England. pp. 293.

Amsalu, A. (1993). Principles and methods of crop improvement. Teaching Material. Jimma, Ethiopia. pp. 183-188.

Anjum, S.A., Xie, X.L., Wang, M.F., Saleem, C. and Lei. W. (2011). Review: morphological, physiological and biochemical responses of plants to drought stress. *African J. Agric. Res.* **6**(9): 2026-2032.

Anonymous. (2016). Wikipedia. https://en.wikipedia.org/wiki/Sweet_potato

Anonymous. (2013). National Micronutrients Status Survey 2011–12. ICDDR. Bangladesh.

Anonymous. (2004). www.faostat.fao.org, FAO Static Division. Rome, Italy.

Anonymous. (1988). Crop Status Report. Christian Reformed Worlds Relief Committee, Bogra. pp. 124-127.

Antia, B.S., Akpan, E.J., Okon, P.A. and Umoren I.U. (2006). Nutritive and anti-nutritive evaluation of sweet potatoes (*Ipomoea batatas*) leaves. *Pakistan J. Nutr.*, **5**: 166- 168.

AOAC. (2000). Association of Official Analytical Chemists. Official Methods of Analysis, 17th edition. Washington, DC.

AOAC. (1995). Association of Official Analytical Chemists. Washington, DC.

Bacusmo, J.L. and Carpana, A.L. (1982). Morphological and agronomic traits associated with yield performance of sweet potato. *Annals. Tropi. Res.* **4**(2): 92-102.

Bhagsari, A.S. and Harman, S.A. (1982). Photosynthesis of photosynthate partitioning in sweet potato genotypes. *American J. Soc. Hort. Sci.* **32**: 107-506.

Binu, H., Vimala, B. and Nambisan, M. (2011). Variability of carotenoid and dry matter content in orange fleshed sweet potato during storage. *J. root crops.* **37**(2): 182-185.

Board, J.E., Kang, M.S. and Harville, B.G. (1997). Path analysis identify indirect selection criteria for yield of late planted soybean. *Crop Sci.* **37**: 879-884.

Boney, W., Yalu, A., Ramakrishna, A. and Deros, M. (2014). Genotypic variability estimates of agronomic traits for selection in sweet potato [*Ipomoea batatas* (L.) Lam.] poly crosses population in Papua New Guinea. *J. Plant Breed. Genet.* **2**(3): 131-136

Bourke, R.M. (1984). Growth analysis for four sweet potato Cvs. in Papua New Guinea. *Tropical agric.* **63**(3): 177-181.

Bovell-Benjamin, A.C., Bromfield, E., Pace, R., and Wang, B. (2001). Chemical and sensory characteristics of a hydroponic sweet potato during storage. Technical Paper 2001-01-2278. Society for Automative Engineers, Warrendale, PA.

Bovell-Benjamin, A.C., Gichuhi, P., Abdalla, M., Biswas, M., Bromfield, E., Alvarea, M., Kpomblekou, A.K., and Dean, D. (2004). Bulk ingredients from three cultivars of sweet potatoes: Composition and properties. Technical Paper 2004-01-2527. Society for Automative Engineers, Warrendale, PA.

Bradbury, J.H., Hammer, B., Nguyen, T., Anders, M., and Millar, J.S. (1985). Protein quantity and quality, and trypsin inhibitor content of sweet potato cultivars from the Highlands of Papua, New Guinea. *J. Agric. Food Chem.* **33:** 281–285.

Burri, B.J. (2011). Evaluating sweet potato as an intervention food to prevent vitamin A deficiency. *Compreh. Rev. Food Sci. Food Safety.* **10**(2): 118-130.

Burgos, B., Carpio, R., Sanchez, C., Paola, S., Eduardo, P., Espinoza, J. and Grüneberg, W. (2009). A colour chart to screen for high β-carotene in OFSP breeding. The 15th Triennial Symposium of the International Society for Tropical Root Crops (ISTRC), Lima. 2-6 November, 2009. ISTRC, Lima, Peru. pp. 47-52.

Burton, G.W. (1952). Quantitative inheritance in grasses. Proc. the sixth Intl Grassland Congr. **1:** 277-283.

Burton, W.G. and Meigh, D.F. (1971). The production of growth-suppressing volatile substances by stored potato tubers. *Potato Res.* **14(**2): 96-101.

Califan, M., Emin, C., Tahsin, S., Erkan, B., Elif, E. and Halis A. (2007). Growth, yield and quality of sweet potato (*Ipomoea batatas* (L.) Lam.) cultivars in the Southeastern Anatolian and East Mediterranean regions of Turkey. *J. Agric.* **31**: 213-227.

Carey, E.E. and Reynoso, D. (1999). Procedures for the evaluation of pathogen tested sweet potato clones **In:** Sweet potato Germplasm Management (*Ipomoea batatas*) Training manual. International Potato Centre, Lima, Peru pp. 170-186.

Carey E.E., Gichuki, S.T., Maisiba, G., Tana, P.O., Lusweti, C., Ngugi, J., Maina, D.K., Malinga, J., Omari, F., Kamau, J.W., Kihurani, A. and Ndolo, P.J. (1999). Sweet potato variety selection for Kenya: Food, feed and income: The International Potato Centre (CIP) and Kenya Agricultural Research Institute (KARI).

Cavalcante, M., Ferreira, P.V., Paixao, S.L., Costa, J.G., Pereira, R.G. and Madalena, J.A. (2010). Agronomic performance, genetic dissimilarity and parental selection of sweet potato for hybridization. *Revista Brasileira de Ciencias Agrarias.* **5**(4): 485-490.

Cervantes-Flores, J.C., Sosinski, B., Pecota, K.V., Mwanga, R.O.M., Catignani, G.L., Truong, V.D., Watkins, R.H., Ulmer, M.R. and Yencho, G.C. (2010). Identification of quantitative trait loci for dry-matter, starch, and β-carotene content in sweet potato. *Mol. Breed.* **28**: 201-216.

Chen, F.X., Chen, Y.Q., Yuan, Z.N. and Lin, W.X. (1995). Genetic parameter, correlation and path analysis of major quantitative traits of mass crossing generations in sweet potato. *J. Fujian Agric. Univ.* **24**(3): 257-261.

Chen, F.X., Xie, J.W. and Zhang, X.Z. (1989). Hereditary tendency of tuber yield, dry chip percentage and bacterial wilt resistance in sweet potato. *J. Fujian Agric. Univ*. **18**(2): 133-138.

Chiona, M. (2009). Towards Enhancement of β-carotene Content of High Dry Mass Sweet potato Genotypes in Zambia. PhD Thesis, University of KwaZulu-Natal, Pietermaritzburg. .

Choudhary, A.K. and Mishra, S.B. (2011). Character association and path analysis study in sweet potato (*Ipomoea batatas* (L.) Lam). *Environ. Ecol.* **29**: 435-438.

Choudhary, S.C., Kumar H., Nasar, S.K.T., Kumar, M. and Verma, V.S. (2001). Frequency distribution of morphological traits in sweet potato germplasm. *J. root crops.* **27**(1): 64-67.

Choudhary, S.C., Kumar, H., Verma, V.S. and Nasar, S.K.T. (1999). Genetic variability in sweet potato (*Ipomoea batatas* (L). Lam.). *J. Appl. Biol.* **9**(2): 146-148.

Choudhury, N.H. and Juliano, B.O. (1980). Effect of amylose content on the lipids of mature rice grain. *Phytochemistry*. **19**:1385

Chaudhary, B.D., Kakar, S.N. and Singh, R.K. (1977). Estimation of genetic parameters in barley (*Hordeum vulgare* L.). *Theol. Appl. Genet.* **49**(4): 153-156.

CIP. (2008). Centro International de la Papa. Sweet potato (*I. batatas).* www.cipotato.org/sweetpotato.

Clarke, G.M. (1980). Statistics and experimental design. 2nd Edition. Edward Arnold. London. pp 196.

Clark, C., John, C.R. and Bruce, S.W. (1983). Estimation of the coancestry coefficient: basis for a short-term genetic distance. *Genet.* **105**(3): 767-779.

Cambie, R.C. and Ferguson, L.R. (2003). Potential functional foods in the traditional Maori diet. Mutat. Res. pp.523–524.

Dabholkar, A.R. (1992). Elements of biometrical genetics. South Asia Books Publications, New Delhi. India. pp.431.

Dai, G.W. and Xie, Y.Z. (1988). Genetic parameters of quantitative trails and breeding strategy for high starch control and high yield in sweet potato. *J. Agric Sci.* **21**: 33-38.

Dansby, M.Y. and Bovell-Benjamin, A.C. (2003a). Production and proximate composition of a hydroponic sweet potato flour during extended storage. *J. Food Process Preserv*. **27:** 153–164.

De Araujo, M.R.A. and Coulman, B.E. (2002). Genetic variation, heritability and progeny testing in meadow brome grass. *Plant Breed.* **121**: 417-424.

Deshmukh, S.N., Basu, M.S. and Reddy, P.S. (1986). Genetic variability, character association and path coefficient of quantitative traits in Virginia bunch varieties of groundnut. *Indian J. Agric. Sci.* **56**: 816-821.

Dewey, D.R. and Lu, K. (1959). A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agron. J.* **51**(9): 515-518.

Digby, P.N., Gaiway and Lane, P. (1989). Genstat 5, A second course. Oxford Science Publication, Oxford. pp: 103-108.

Diop, A. (1998). Storage and processing of roots and tubers in the tropics. **In:** ‘‘Food and Agriculture Organization of the United Nations, Agro-Industries and Post-Harvest Management Service’’ (D.J.B. Calverley, ed.), pp. 38–50. Agricultural Support Systems Division. Food and Agriculture Organization, Rome, Italy.

Diz, D.A., Wofford, D.S. and Schank, S.C. (1994). Correlation and path-coefficient analyses of seed-yield components in pearl millet x elephant grass hybrids. *Theor. Applied Genet.* **89**: 112-115.

Ehisianya, C.N., Ukeh, D.A., Isah, M. D., Lale, N.E.S. and Umeozor, O.C. (2013). Field efficacy of neem seed oil and diazinon in the management of sweet potato weevil, *Cylas puncticollis* (Boh.) in south eastern Nigeria. *J. Plant Studies* **2**: 135-144.

Ekpenyong, T.E. (1984). Composition of some tropical tuberous foods. *Food Chem*. **15:** 31–36.

Engida, T. Nigussie, D. and Devakara E.V. (2007). Genetic variability for yield and other agronomic traits in sweet potato. *J. Agron.* **6**(1): 94-99.

Enyi, B.A.C. (1977). Analysis of growth and tuber yield in sweet potato. *J. Agric. Sci.* **88**(2): 421-430.

Falconer, D.S. and Mackay, T.F.C. (1996). Introduction to quantitative genetics, 4th ed. Longman, England. pp. 160 -161.

Falconer, D.S. (1989). Introduction to Quantitative Genetics, Longman Group Limited, England. pp. 48-263.

FAO. (2015). Food and Agriculture Organization. Myanmar floods deal major blow to country's agriculture.

FAO. (1995). Food and Agricultural Organization. ''Production Yearbook''. Rome, Italy.

FAO. (1972). Food and Agricultural Organization. Food composition tables for use in East Asia. US Department of Health, Education and Welfare.

FAOSTAT. (2017). Production Year Book. Food and Agriculture Organization of the United Nations, Rome, Italy. http://faostat.fao.rg

FAOSTAT. (2012). Food and Agriculture Organization Corporate Statistical Database. Global production and consumption of root and tuber. **In**: FAO corporate document repository. Report on the Inter-center review of root and tuber crops research in the CGIAR.

FAOSTAT. (2011). Food and Agriculture Organization of the United Nations. Available at http://faostat.fao.org

Garcia, E.H., Guerido, I.B. and Cahanap, A.C. (1970). The relation of carotene and starch content of 26 varieties of sweet potato (*Ipomoea botatas* (L.) Lam.). *Philippines J. Crop Sci.* **35**(34): 203-212.

Gasura, E., Mashingaidze, A.B. and Mukasa, S.B. (2008). Genetic variability for tuber yield, quality and virus disease complex traits in Uganda sweet potato germplasm. *African Crop Sci. J.* **16:** 147-160.

Gerpacio, S.C.M.T.L. and Chujoy, E. (1994). Heritability estimates of some root characters in sweet potatoes. *Philippines J. Crop Sci.* **19**(1): 27-32.

Gin, G., Devi, A.K.B. and Singh, N.B. (2008). Genetic variability and correlation studies in sweet potato. *Orissa J. Hort*. **36**(2): 73-76.

Gibson, R.W., Jeremiah, S.C., Aritua, V., Msabaha, R.P., Mpembe, I. and Ndunguru J. (2000). Sweet potato virus disease in Sub-Saharan Africa: Evidence that neglect of seedlings in the traditional farming system hinders the development of superior resistant landraces. *J. Phytopathol*. **148:** 441-447.

Girard, W.A., Grant. F., Watkinson, M., Okuku, H.S., Wanjala, R., Cole. D., Levin, C. and Low, J. (2017). Promotion of orange-fleshed sweet potato increased vitamin A intakes and reduced the odds of low retinol binding protein among postpartum Kenyan Women. *J. Nutr.* doi:0.3945/jn.116.236406.

Githunguri, C.M. and Migwa, Y.N. (2004). Performance, foliage and root yield of sweet potato clones from a preliminary yield trial at kiboko in semiarid eastern Kenya. NHFRCK atumani: Kenya Agricultural Research Institute.

Griffing, B.R.E. (1956). Concept of general and specific combining ability in relation to diallel crossing systems. *Australian J. Biol. Sci.* **9**(4): 463-493.

Grüneberg, W., Mwanga, R., Andrade, M. and Espinoza, J. (2009). Selection methods: breeding clonally propagated crops. **In**: S. Ceccarelli, E. P. Guimarães and E. Weltzien, (eds.) Plant breeding and farmer participation.

Gupta, S.K. (1969). Correlation studies in potato varieties (K-122). *Andhra Agric. J.* **14**: 2.

Hanson, C.H., Robinson, H.F. and Comstock, R.E. (1956). Biometrical studies of yield in segregating populations of Korean Lespedeza. *Agron. J.* ***48***(6): 268-272.

Hayneys, P.H. and Wholey, D.W. (1971). Variability in commercial sweet potatoes (*Ipomoea batatas* (L.) Lam) in Trinidad. *Expt. Agric*. **7:** 27-32.

Hotz. C., Loechl, C., Brauw, A., Eozenou, P., Gilligan, D., Moursi, M., Munhaua, B., Jaarsveld, P., Carriquiry, A. and Meenakshi, J.V. (2012). A large-scale intervention to introduce orange sweet potato in rural Mozambique increases vitamin A intakes among children and women. *Br. J Nutrit.* **108**: 163-176.

Hossain, M.D., Rabbani, M.G. and Mollah, M.L.R. (2000). Genetic variability, correlation and path analysis of yield contributing characters in sweet potato. *Pakistan J. Sci. Industrial Res.* **43**(5): 314-318.

Hossain, M.M. and Siddique, M.A. (1985). Sweet Potato. **In:** Production, Use and Improvement (in Bengali). H. Siddique (ed.). Bangladesh Agricultural University Campus, Mymensingh. p.112.

Huaman, Z. (1992). Systematic Botany and Morphology of the Sweet Potato Plant. Technical Information Bulletin-25. International Potato Centre (CIP), Lima, Peru. pp: 7-22

Huett, D.O. (1976). Evaluation of yield, variability and quality of sweet potato cultivars in subtropical. *Australian J. Expt. Agril. Animal Husbandry*. **12**: 9.

Ibrahim, K.K. (1987). Correlation, causation and predictability for yield in sweet potato (*Ipomoea batatas* (L.) Lam.). *J. Root Crops.* **13**(1): 21-24.

Imungi J.K. and Wabule M.N. (1990). Some chemical characteristics and availability of vitamin A and vitamin C from Kenyan varieties of papayas (*Carica papaya* L.). *Ecol. Food Nutr.* **24:** 115-120.

Iqbal, S., Mahmood, T., Ali, T.M., Anwar, M and Sarwar, M. (2003). Path coefficient analysis in different genotypes of soybean (*Glycine max* (L) Merril). *Pakistan J. Biol. Sci*. **6**: 1085-1087.

Islam, S. (2006). Sweet potato leaf: Its potential effect on human health and nutrition. *J. Food Science.* **71:** 13-21.

Janssens, M.J.J. (1982). Sweet potato improvement in Rwanda. In root crops in Eastern Africa proceeding of workshop. *I.D.R.C.* pp. 27-32.

Johnson, H.W., Robinson, H.F. and Comstock, R.E., (1955). Estimation of genetic and environmental variability in soybean. *Agron. J.* **47**: 477-483.

Johnson, R.W., Dixon, M.A. and Lee, D.R. (1992). Water relations of the tomato fruit during growth. *Plant Cell Environ*. **15**: 947-953.

Jones, A., Steinbauer, C.E. and Pope, D.T. (1969). Quantitative inheritance of ten root traits in sweet potato. *American J. Soc. Hort. Sci.* **94**: 271-275.

Jones, A., Steinbauer, C.E. and Pope, D.T. (1986). Quantitative inheritance of ten root traits in sweet potato. *American J. Soc. Hort. Sci.* **94:** 271-275.

Jong, S.K. (1974). General and specific combining ability in a diallele cross among six sweetpotato (*Ipomoea batatas* (L.) Lam.) clones. *Korean J. Breed.* **6**: 112-116.

Kaledzi, P.D., Ansong, E., Dapaah, U.K. and Timpo, G. (2010). Agromorphological characterization of sweet potato germplasm. *Ghana J. Hort*. **8:** 1-11.

Kamalam, P. (1990). Variation for quantitative traits in the first clonal generation of the open pollinated progenies of sweet potato. *J. Root Crops.* ISRC National Symposium. pp. 49-52.

Kamalam, P., Biradar, R.S., Hrishi, N. and Rajendran, P.G. (1997). Path analysis and correlation studies in sweet potato (*Ipomoea batatas* (L.) Lam.). *J. Root Crops*. **3**(1): 5-11.

Kamalam, P., Hrishi, N. and Rajendran, P.G. (1977). Genetic variability in open pollinated progenies of sweet potato. *J. Root Crops.* **3**(2): 13-23.

Kasuhara, M., Shikata, S. and Nimitome, H. (1972). Studies on selection of mother plants inbreeding sweet potato suitable for direct planting, characters of existing varieties, strain and mother plant selection. *Chugoku National Agric Expt. Station.* **21**: 65-87.

Kennedy, G., Natel, G., Shetty, P. (2003). The scourge of hidden hunger: global dimensions of micronutrient deficiencies. *Food Nutr. Agric*. **32**: 8-16.

Kivuva, B. (2013). Breeding sweet potato (*Ipomoea batatas* (L.) Lam) for drought tolerance in Kenya, Phd Thesis, University of KwaZulu Natal, Republic of South Africa. pp.198

Kumar, R., Jain, B.P. and Ganguli, D.K. (1996). Variability, character association and path analysis in sweet potato. **In:** Tropical tuber crops. Problems, prospects and future strategies. Oxford and IBH Publishing Co. Pvt. Ltd., New Delhi and Calcutta. **4**: 140-145.

Laurie, S.M. and Magoro M.D. (2008). Evaluation and release of new sweet potato varieties through farmer participatory selection. *African J. Agric. Res.* **3:** 672-676.

Laurie, S.M. and Faber, M. (2008). Integrated community based growth monitoring and vegetable gardens focusing on crops rich in â- carotene: Project evaluation in a rural community in the Eastern Cape, South Africa. *J. Sci. Food Agri.* **88**: 2093-2101.

Laurie, S.M. and Niederwieser, J.G. (2004). The sweet potato plant. **In:** Guide to sweet potato production in South Africa. J. G. Niederwieser. (ed.). Agricultural Research Council, South Africa, Pretoria. **1**: 7-14.

Lewthwaite, L.S. (2004). Storage root production in sweet potato (*Ipomoea batatas* (L.) Lam). Phd Thesis, Massey University, New Zealand. pp. 210.

Li, Y., Song, J.X., Deng, K.P. and Huang, T. (2010). Genetic effect of main agronomic characters of sweet potato in Guizhou. *Guizhou Agric. Sci.* **8**(10): 12-13.

Lin, K., Lai, Y., Chang, K., Chen, Y., Hwang, S. and Lo, H. (2007). Improving breeding efficiency for quality and yield of sweet potato. *Bot. Studies* **48:** 283-292.

Lin, P.S. (1983). Study on the heritability of the major characters in sweet potato and correlation between them. *J. Hort. Sci.* **5**(6): 12-16.

Loebenstein, G. and G. Thottappilly. (2009). The sweet potato, Springer science business media. Malden, USA.

Lowe, S.B. and Wilson, L.A. (1975). Yield and yield components of six sweet potato (*Ipomoea batatas*) cultivars. II. Variability and possible sources of variation. *Expt. Agric*. **11**(1): 49-58.

Low, J. W., Arimond, M., Osman, N., Cunguara, B., Zano, F. and Tschirley, D. (2007). A food-based approach introducing orange-fleshed sweet

potatoes increased vitamin A intake and serum retinol concentrations in young children in rural Mozambique. *J. Nutr*. **137:** 1320-1327.

Lush, J.L. (1943) Intra-sire correlations and regression of offspring on dam as a method of estimating heritability of characters. *Proc. American Soc. Animal Prod*. **33**: 293-301.

Lynch, M. and Walsh, B. (1998). Genetics and analysis of quantitative traits. sinauer associates, Inc. and W.H. Freeman and Company, Sunderland, USA.

Maluf, W.R., Miranda, J.E.C. and Ferreir, P.E. (1983). Broad sense heritability's of root and vine traits in Sweet potato. *Brazilian J. Genet.* **6**(3): 443-451.

Mahalanobis, P.C. (1936). On the generalized distance in statistics. *Natl. Inst. Sci. India.* **12**: 49-55.

Martin, F.W. and A.M. Rhodes. (1983). Correlations among characteristics of sweet potato roots, and intraspecific grouping. *Euphytica.* **32**: 453-463.

Mandal, R.C. (2006). Tropical root and tuber crops, Agrobios, India. pp.360.

Makki, H.M., Abdel-Rahman, A.Y., Khalil, M.K.M., and Mohamed, M.S. (1986). Chemical composition of Egyptian sweet potato. *Food Chem*. **20:** 39–44.

Mc Lean, T.F. (1955). Long vs. short vines in sweet potatoes. *Vegetable Growers News*. pp. 9.

McGregor, C.E., Miano, D.W., LaBonte, D.R., Hoy, M., Clark, C.A. and Rosa, G. J. M. (2009). Differential gene expression of resistant and susceptible sweet potato plants after infection with the causal agents of sweet potato virus disease. *J. American Soc. Hort. Sci.* **134**: 658-666.

Mcharo, M. and LaBonte, D. (2007). Genotypic variation among sweet potato clones for β-carotene and sugar content. Proceedings of the 13th International Society for Tropical Root Crops (ISTRC) Symposium, Arusha, Tanzania. 9-15 November, pp. 746-754.

Miller, J.C. and Gafer, A.K. (1958). A study of the synthesis of carotene in the sweet potato plant and root. *Proceed. American J. Soc. Hort. Sci.* **71**: 388-390.

Miller, J.C. and Tanksley, S.D. (1990). RFLP analysis of phylogenetic relationships and genetic variation in the genus *Lycopersicon*. *Theor. Appl. Genet*. **80**: 437-448.

Mills, J.P., Tumuhimbise, G.A., Jamil, K.M., Thakkar, S.K., Farlla, M.L., and Tanumihardjo, S. A. (2009). Sweet potato b-carotene bio-efficacy is enhanced by dietary fat and not reduced by soluble fiber intake in Mongolian gerbils. *J. Nutr.* **139:** 44-50

Mitra, S. (2012). Nutritional status of orange-fleshed sweet potatoes in alleviating vitamin A malnutrition through food based approach. *J. Nutr. Food Sci.* **2**: 160.

Musinguzi, E., Kikafunda, J.K. and Kiremire, B.T. (2006). Utilization of indigenous food plants in Uganda: A case study of south –western Uganda. *African J. Food Agric*. *Nutr. Dev*. **6**(2): 723-724

Nabakwe, E.C. and Ngare, K.D. (2004). Health and nutritional status of children in Western Kenya in relation to Vitamin A deficiency. *East African J. Pub. Heal.* **1**:1-8

Nakashima, K. and Yamaguchi-Shinozaki, K. (2013). ABA signaling in stress-response and seed development. *Plant Cell Rep.* **32**: 959-970.

Nanda, H.C. (1994). Correlation and path studies for yield and its components in rainfed sweet potato. *J. Root Crops*. **20**(2): 135-137.

Naskar, S.K., Ravindran, C.D. and Srinivasan, G. (1986). Correlation and path analysis in sweet potato. *J. root crops*. **12**(1): 33-35.

Nawiri, M.P., Nyambaka, H.N. and Murungi, J.I. (2012). Sundried cowpeas and Amaranthus leaves recipe improves ß-carotene and retinol in serum and hemoglobin concentration among preschool children. *European J. Nutr.* Doi: 10.1007/s00394-012-036-2

Ndolo, P.J., Micharo, T., Carey, E.E., Gichuki, S.T., Ndinya, C. and Malinga, J. (2001). Participatory on-farm selection of sweet potato varieties in western kenya. *African Crop Sci*. **1:** 41- 48.

Nedunchezhiyan, M., Naskar, S.K. and Byju, G. (2008). Performance of sweet potato (*Ipomoea batatas* (L.) Lam.) varieties under shaded and open field conditions. *Indian J. Agric. Sci.* **78**(11): 974-977.

Neiva, I.P., Andrade Junior, V.C., de Viana, D.J.S., Figueiredo, J.A., Mendonca Filho, C.V., Parrella, R.A., da C. and Santos, J.B. (2011). Morphologic characterization of sweet potato accesses from the germplasm bank of the Universidade Federal dos Vales do Jequitinhonha e Mucuri, Brazil. *Hort. Brasileira.* **29**(4): 537-541.

Njeru, R.W., Mburu, M.W.K., Cheramgoi, E., Gibson, R.W., Kiburi, Z.M., Obudho, E. and Yobera, D. (2004). Studies on the physiological effects of viruses on sweet potato yield in Kenya. *Annual Appl. Biol*. **145**: 71-76.

Oboh, S., Ologhobo, A., and Tewe, O. (1989). Some aspects of the biochemistry and nutritional value of the sweet potato (*Ipomoea batatas*). *Food Chem.* **31:** 9–18.

Olaofe, O. and Sanni, C.O. (1988). Mineral contents of agricultural products. *Food Chem.* **30:** 73–77.

Panse, V.G. (1957). Genetics of quantitative characters in relation to plant breeding. *Indian J. Genet. Plant breed.* **17**(2): 318-328.

Parida, A.K., Bera, M.K. and Nandi, S. (1999). Identification of parameters influencing sweet potato tuber yield under late planted rainfed condition. *Environ. Ecol.* **17**(4): 971-974.

Picha, D.H., (1987). Carbohydrate changes in sweet potatoes during curing and storage. *American J. Soc. Hort. Sci.* **112:** 89-92.

Poehlman, J.M. and Sleper, D.A. (1995). Breeding Field Crops, 4th ed. Iowa State University press. *puncticollis* (Boh.) in south eastern Nigeria. *J. Plant Stud.* **2**: 135-144.

Purcell, A.E., Walter, W.M. and Giesbrecht, F.G. (1978). Root, hill, and field variance in protein content of North Carolina sweet potatoes. *J. Agric. Food Chem*. **26:** 362–364.

Purseglove, J.W. (1968). Tropical crops: Dicotyledons Longman group limited, Longman house, Burnt Mill, Harlow, Essex, U.K.

Pushkaran, K., Sukumaran Nair, P. and Gopakumar, K. (1976). Analysis of yield and its components in sweet potato. *Agric. Res. J. Kerala*. **14**: 153-159.

Pushpalata, T., Kavita, A. and Krishna, T. (2011). Studies on orange fleshed Sweet potato for yield and quality traits. *Agric. Biol. Res*. **27**(1): 20-28.

Rahman, E.H.M.S., Mahmud, A.A., Hossain, M., Mohanta, H.C., Rahman, M. A., Khan, M.S.I. and Merideth, B. (2015). Field performance of sweet potato varieties in saline zone of Bangladesh. *Bangladesh Soc. Hort. Sci.* pp. 67.

Rahman, M.M., Rasul, M.G., Bashar, M.K., Syed M.A. and Islam, M.R. (2011). Parent selection for transplanted Aman rice breeding by morphological, physiological and molecular diversity analysis. *Libyan Agric. Res. Centre J. Int.* **2**: 26-28.

Rajesh, K., Jain, B.P. and Ganguli, D.K. (1996). Variability, character association and path analysis in sweet potato. Tropical tuber crops, problems, prospects and future strategies. Oxford and IBH Publishing Co. Pvt. Ltd., New Delhi and Calcutta. pp. 142-145.

Rao, C.R. (1952). Advanced statistical methods in biometrical research. John Willy and sons. New York. pp: 390.

Rao, P.V., Dora, D.K., Naskar, S.K. and Jagadev, P.N. (1992). Variability studies in sweet potato. *J. Root Crops*. **18**(2): 126-127.

Ravindran, V., Ravindran, G., Sivakanesan, R. and Rajaguru, S.B. (1995). Bio-chemical assessment of tubers from 16 cultivars of sweet potato (*Ipomoea batatas* L.). *J. Agric. Food Chem.* **43:** 2646–2651.

Rees, D. and Kapinga, R. (2003). Experiences from East Africa. **In:** Sweet potato post-harvest assessment. V. Q. Oirschot, (ed.). International Potato Center.

Richardson, V.A. (2012). Tuber quality and yield of six sweet potato varieties. Gladstone road agricultural centre crop research report. pp. 13.

Robinson, H. F., Comstock R. E. and Harvey P. M. (1949). Estimates of heritability and the degree of dominance in corrn. *Agron. J.* **41:** 353 - 359.

Rodriguez-Bonilla, L., Cuevas, H.E., Montero-Rojas, M., Bird-Pico, F., Luciano-Rosario, D. and Siritunga, D. (2014). Assessment of genetic diversity of sweet potato in Puerto Rico. *PloS One*. **9**(12): 116-184.

Roy, D. (2000). Plant breeding analysis and exploitation of variations. Narosa Publishing House, New Delhi. pp. 287.

Rubatzky, V.E. and Yamaguchi, M. (1997). Tomatoes, peppers, eggplants, and other solanaceous vegetables. In World Vegetables Springer US. pp. 532-576.

Sahu, G.D. (2003). Genetic variability, correlations and path analysis in sweet potato (*Ipomoea botatas* (L.) Lam.). M.Sc. (Ag.) Thesis. IGAU, Raipur.

Saladaga, F.A. (1981). Genetic variance, heritability and correlation for genetic characters of the sweet potato. *Annu. Trop. Res.* **41**(11): 406.

Samba, J.A. (2013). Flowering induction and cross compatibility studies for sweet potato (*Ipomoea batatas* L.) breeding. MS Thesis. Kwame Khurumah University of science and technology. Ghana.

Sankari, A., Thamburaj, S. and Kannan, M. (2001). Genetic variability in Sweet potato. *J. root crops*. **27**(1): 71-73.

Suri, S. and Kumar, D. (2015). Short article: Determination of subclinical vitamin A deficiency among children 1–5 years in a rural community of Jammu. *Indian J. Com. Health*. **27:** 263–269

Sauer. J (1993). The Historical Geography of Crop Plants: A Selected Roster. CRC Press, Boca Raton Scott, G.J., P.I. Ferguson and J.E. Herrera (eds.). Product Development for Root and Tuber Crops. Vol. III-Africa. Proceedings of the Workshop on Processing, Marketing, and Utilization of Root and Tuber Crops in Africa, held on October 26 to November 02.

1991 at International Institute for Tropical Agriculture (IITA), Ibadan, Nigeria. CIP, Lima, Peru. pp. 506.

Scott, G. J. and Ewell, P. (1992). ‘‘Sweet Potato in African Food Systems’’. International Potato Centre (CIP), Lima, Peru.

Sharma, G.P. (2004). Selection of ideal genotypes from open pollinated seedling population of sweet potato (*Ipomoea botatas* (L.) Lam.). M.Sc. (Ag.) Thesis. IGAU, Raipur.

Shashikanth, E., Patil, M.P., Madalageri, M.B. and Mulge, R. (2008). Genetic variability, heritability and genetic advance in sweet potato (*Ipomoea batatas* (L.) Lam.). *Environ. Ecol.* **26**(1A): 322-325.

Shikata, S. (1980). Studies use of random mating population in breeding sweet potato. Chugoku National agriculture experimental station. **28**: 48.

Shimelis, H. and Hugo, A. (2011). Determination of selection criteria for seed yield and seed oil content in Vernonia (*Vernonia galamensis*). *Indus. Crops Pro.* **33**(2): 436-439.

Shimelis, H.A. (2006). Associations of yield and yield components among selected durum wheats (*Triticum turgidum* L.). *South African J. Plant. Soil*. **23**(4): 305-309.

Shivasubramanian, S. and Menon, M. (1973). Heterosis and inbreeding depression in rice. *Madras Agril. J*. **60**: 1139.

Shonga, E., Gemu, M., Tadesse, T. and Urage, E. (2013). Review of entomological research on sweet potato in Ethiopia. *Discourse J. Agric. Food Sci.* **1**: 83-92.

Simonne, A.H., Kays, S.J., Koehler, P.E., and Eilenmiller. R.R. (1993). Assessment of β-carotene in sweet potato breeding lines in relation to dietary requirements. *J. Food Com. Anal.* **6**: 336-345.

Singh, B.D. (2009). Plant Breeding Principles and Methods, Kalyani Publisher, New Delhi, India.

Singh, R.K. and Chaudhury, B.D. (1998). Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi. pp: 304-307.

Singh, B.D. (1993). Plant Breeding, Principles and Methods. Kalayani Publishers, New Delhi. pp. 103-142.

Singh, R., Saxena, N.S., and Chaudhary, D.R. (1985). Simultaneous measurement of thermal conductivity and thermal diffusivity of some building materials using the transient hot strip method. *J. Appl. Physics*. **18**(1): 1.

Singh, R.K. and Chaudhary, B.D. (1985). Biometrical methods in quantitative genetic analysis. Kalayani Publisher, New Delhi, India.

Singh, R.K. and Choudhary, B.D. (1985). Biometrical methods of quantitative genetic analysis. *Haryana J. Hort. Sci*. **12**(2): 151-156.

Singh, T.R.P. and Mishra, D.N. (1975). Genetic variability in sweet potato (*Ipomoea batatas* (L.) Lam.). *Root crops*. Trivandram, India.

Sommer, A. (2011). Vitamin A deficiency disordered: origins of the problem and approaches to its control. *Ag. Bio. World*.

Sorrells, M.E., Diab, A. and Nachit, M. (2000). Comparative genetics of drought tolerance. **In**: C. Royo, M. Nachit, D. Fonzo, J.L. Araus, (eds.). Durum wheat improvement in the Mediterranean region: New Challenges, Zaragoza, Spain. pp. 191-201.

Sreekanth, A., Vimala, B., Binu, H. and Wolfgang, G. (2011). Morphological variability and tuber productivity in exotic orange fleshed Sweet potato. *Biol. Div. Con.* **4**(3): 1-7.

Swarup, B. and Chaughale, D.S. (1962). Studies on genetic variability in sorghum phenotypic variation and its heritability components in important characters towards yield. *Indian J. Genet. Plant breed.* **22**: 31-35.

Teow C.C., Truong, V.D., McFeeters, R.F., Thompson, R.L., Pecota, K.V. and Yencho, G.C. (2007). Antioxidant activities, phenolic and b-carotene contents of sweet potato genotypes with varying flesh colours. *Food Chemistry*. **103:** 829-838.

Terry, L.A. (2008). Health promoting properties of fruit and vegetables. CAB International MPG Book Group, Bodmin and King`s Lynn, UK.

Teshome, A., Veeranagavathathan, D. and Kannan, M. (2004). Genetic variability and correlation studies in Sweet potato. *Madras Agril. J.* **91**: 420-424.

Teshome, A., Veeraragavathatham, D. and Kannan, M. (2003). Evaluation of sweet potato (*Ipomoea batatas* (L.) Lam.) clones for high tuber yield, high starch and low sugar to substitute potato in cuisine. *J. Root Crops.* **29**(1): 41-46.

Thamburaj, S. and Muthukrishnan, C.R. (1976). Association of metric traits and path analysis in sweet potato (*Ipomoea batatas* (L.) Lam.). *Madras Agric. J.* **63**: 1-8.

Thiyagu, D., Rafii, M. Y., Mahmud, T. M. M., Latif, M. A., Malek, M. A. and Sentoor, G. (2013). Genetic variability of sweet potato (*Ipomoea batatas* (L.) Lam.) genotypes selected for vegetable use. *Madras Agril. J*. **11**(2): 340-344.

Thottappilly, G. and Loebenstein, G. (2009). The sweet potato. Doi: 10.1007/978-1-4020-9475-0-23 Kerala, India.

Tirkey, P.L., Chaurasia, J.S. and Sarnaik, D.A. (2011). Character association and path coefficient studies in sweet potato (*Ipomoea batatas* (L.) Lam.) genotypes. *J. Plant Dev. Sci*. **3**(1): 137-143.

Tiwari, J.P. (1987). Productivity potential of sweet potato (*Ipomoea botatas* (L.) Lam.). *J. Root Crops*. **13**: 95-101.

Tsegaye, E., Dechassa, N. and Sastry, E.D. (2007). Genetic variability for yield and other agronomic traits in sweet potato. *J. Agron.* **6**: 145-148

Tsegaye, E., Sastry, E.V.D and Dechassa, N. (2006). Correlation and path analysis in sweet potato and their implications for clonal selection. *J. Agron*. **5**: 391-395.

Ukom, A.N, Oijmelukwe, P.C. and Pokara, D.A. (2009). Nutrient composition of selected sweet potato (*Ipomoea batatas* (L.) Lam) cultivars as influenced by different levels of nitrogen fertilizer application. *Pakistan J. Nutri*. **8:** 1791-1795.

USAID. (2015). Orange-Fleshed Sweet Potatoes: Improving Lives in Uganda. Nutritious crop addresses critical vitamin A deficiency. USAID, 2015

UN DESA. (2015). United Nations Department of Environment and Social Affairs. World population prospects.

Van den Berg, A.A. and Laurie S.M. (2004). Cultivation Guide to sweet potato production in South Africa. **In:** J.G. Niederwieser, (ed.). Agricultural Research Council, Pretoria. **1:** 15-26.

Velmurugan, K., Thamburaj, S. and Kannan, M. (1999). Variability in the open pollinated progenies of sweet potato (*Ipomoea batatas* (L.) Lam) at three stage of harvest. *South Indian Hort.* **47**(6): 220-221.

Vimala, B. and Hariprakash, B. (2012). Variability of characters and dry matter content in the hybrid progenies of sweet potato. *Gene Conserve.* **10**(39): 65-86.

Vimala, B., Sreekanh, A., Hariprakash, B. and Wolfgang, G. (2012). Variation in morphological characters and storage root yield among exotic orange fleshed sweet potato clones and their seedling populations. *J. root crops.* **38**(1): 155-162.

Vimala, B., Sreekanth, A., Binu, H. and Wolfgang, G. (2011a). Variability in 42 orange fleshed sweet potato hybrids for tuber yield and carotene and dry matter content. *Gene Conserve.* **40**: 190- 200.

Vimala, B., Sreekanth, A., Binu, H. and Wolfgang, G. (2011b). Morphological variability and tuber productivity in exotic orange-fleshed sweet potato. *Bio. Diver. Conser.* **4**(3): 1-7.

Vimala, B., Kumari, B.R. and Nambisan, B. (2009). Seasonal variations of carotinoids in orange fleshed Sweet potato. *15th Triennial ISTRC symposium*. Central Tuber Crop Research Institute, Kerala, India.

Vimala, B. and Lakshmi, K.R. (1999). Evaluation of exotic seed population in sweet potato (*Ipomoea botatas* (L.) Lam.). In tropical tuber crops in food security and nutrition. **1**: 157-162.

Vimala, B. and Lakshmi, K.R. (1990). Heritability estimates in sweet potato. *J. Root Crops*. **4:** 35-38.

Wadud, M.A., Rabbani, M.G., Uddin, M.Z., Pramanik, M.E.A. and Rahman, M.M. (2011). Study on the morphological characteristics of sweet potato genotypes. *Intl. J. Sustainable Agric. Tech.* **7**(1): 5-9.

Warid, A., Boleid, D.W. and Kushad, M. (1976). Sweet potato clones adopted for Libyan Agriculture. *Plant breed.* **47**(12): 111-146.

Watson, I. and Dallwitz, M.J. (2000). The families of flowering plants. Descriptions, illustration, identification and information retrieval. Version 14th December.

Wilckens, E.R., Vidal, J.T., Hevia, H. F., Gutierrez, C.A.M. and Tapia, V.M. (1993). Exploration of the genetic variation in Chilean sweet potatoes (*Ipomoea batatas* (L.) Lam.) Vegetative morphology. *Agro-Ciencia*. **9**(2): 87-92.

Wilson, L.A. and Lowe, S.B. (1975). Yield and yield component of six sweet potato (*Ipomoea batatas*) cultivars contribution of yield components to tuber yield. *Expt. Agric*. **11**(1): 39-48.

Wingfield, H.L., Smith-Ryan, A.E., Melvin, M.N., Roelofs, E.J., Trexler, E.T., Hackney, A. C. and Ryan, E. D. (2015). The acute effect of exercise modality and nutrition manipulations on post-exercise resting energy expenditure and respiratory exchange ratio in women: a randomized trial. *Sports Medicine-Open*. **1**(1): 11.

WHO. (2012). Report: WHO technical consultation on vitamin A in newborn health: mechanistic studies. Geneva: World Health Organization.

WHO. (2011). Guidline: Vitamin A supplementation in infants and children 6–59 months of age. Geneva: World Health Organization.

Woolfe, J.A. (1992). Sweet potato: an untapped food resource. Cambridge Universal Press and the International Potato Centre (CIP). Cambridge, UK. pp. 1-643.

Wright, S. (1921). Correlation and causation. *J. Agril. Res.* **20**: 557-585.

Yamakawa, O. and Yoshimoto, M. (2002). Sweet potato as food material with physiological functions. *Acta. Hort*. **583**: 179-185.

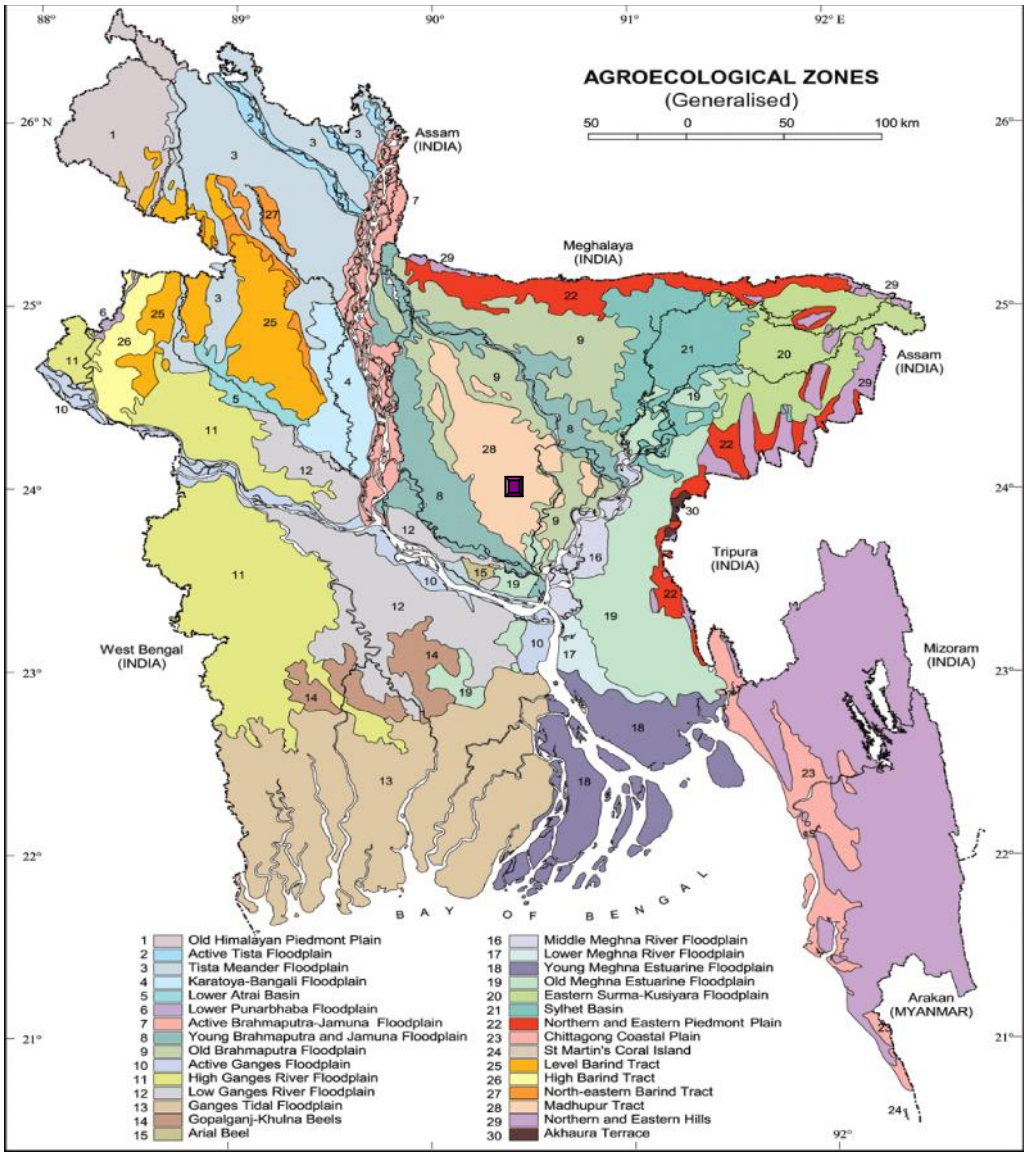
Yoshida, T. (1985). Correlation between successive yield tests for agronomic characters in sweet potato. *Japanese J. breed*. **35** (2): 204-208.

Zhang, D.P., Rossel, G., Kriegner, A. and Hijmans, R. (2004). AFLP assessment of diversity in sweet potato from Latin America and the Pacific region: Its implications on the dispersal of the crop. *Genet. Res. Crop Evol*. **51:** 115-120.

APPENDICES

Appendix 1. Map showing the experimental site under the study (A and B)

A. University location in Bangladesh



Experimental area under study

B. Experimental plot location at Sher-e-Bangla Agricultural University

Experimental area under study

Appendix II. Monthly average temperature, relative humidity and total rainfall of the experimental site during the period from December, 2017 to May 2018.

Month	Air temperature (°C)			Relative Humidity (%)	Rainfall (mm) (total)
	Maximum	Minimum	Average		
December, 2017	31	23	27	55	63.9
January, 2018	28	20	24	43	0
February, 2018	32	22	27	40	3.2
March, 2018	37	25	31	44	34.1
April, 2018	36	28	32	54	327.1
May, 2018	35	28	31.5	65	689.8

Source: Bangladesh Metrological Department (Climate and Weather division), Agargaon, Dhaka-1207.

Appendix III. Morphological, physical and chemical characteristics of initial soil (0-12cm depth) of the experimental pot

A. Physical composition of the soil

Soil separates	% Composition
Sand	36.90
Silt	26.40
Clay	36.66
Texture class	Clay loam

B. Chemical composition of the soil

SL No.	Soil characteristics	Analytical Data
01.	Organic carbon (%)	0.82
02	Total N(kg/ha)	1790.00
03	Total S(ppm)	225.00
04	Total P(ppm)	840.00
05	Available N (kg/ha)	54.00
06	Available P(kg/ha)	69.00
07	Exchangeable K (kg/ha)	89.00
08	Available S(ppm)	16.00
09	PH(1:2.5 soil to water)	5.55
10	CEC	11.23

Source: Central library, Sher-e-Bangla Agricultural University, Dhaka-1207

Appendix IV. Mean performance of various growth parameter and yield components of 13 characters of 6 genotypes of sweet potato.

Genotypes	VL	VIL	VID	LAI	AGFWT	SRN	SRL	SRD	ISRWT	SRY	HI (%)	SRYP	SRYH
G1	99.16	6.67	5.1	91.40	2.13	6.00	24.50	4.73	0.37	1.80	45.39	59.93	28.67
G2	93.51	6.17	6.3	80.61	2.22	6.67	23.92	6.67	0.74	1.99	47.38	61.11	30.00
G3	70.92	5.50	5.2	82.08	2.28	6.67	22.73	5.10	0.56	1.88	45.16	60.74	29.67
G4	87.19	5.97	6.4	59.89	2.20	6.00	17.75	5.07	0.53	1.87	45.94	64.53	31.67
G5	76.25	7.50	6.3	74.09	1.63	7.00	13.92	4.47	0.20	1.39	46.04	40.92	22.00
G6	88.85	6.17	6.8	78.69	2.19	6.67	17.50	5.63	0.53	2.12	49.08	59.17	28.33
Min	70.92	5.50	5.1	59.89	1.63	6.00	13.92	4.47	0.20	1.39	45.16	40.92	22.00
Max	99.16	7.50	6.8	91.40	2.28	7.00	24.50	6.67	0.74	2.12	49.08	64.53	31.67
Mean	85.98	6.33	6.02	77.79	2.11	6.50	20.05	5.28	0.49	1.84	46.50	57.73	28.39

VL= Vine length (inch), VIL = Vine internode length (cm), VID = Vine internode diameter (cm), LAI= Leaf area index (cm2), AGFWT= Above ground fresh weight/plant (kg), SRN= Storage root number/plant, SRL = Storage root length (cm), SRD=Storage root diameter (cm), ISRWT = Individual storage root weight (kg), SRY = Storage root fresh yield/plant (kg), HI=Harvest index/plant (%), SRYP =Storage root fresh yield/plot (kg), SRYH = Storage root fresh yield (ton/ha)

Appendix V. Analysis of variance and LSD of 13 yield and yield contributing characters of sweet potato

Sources of variation	df	VL	VIL	VID	LAI	AGFWT	SRN	SRL	SRD	ISRWT	SRY	HI	SRYP	SRYH
Genotypes	5	337.049**	1.414	0.000	327.830**	0.170	3.367*	54.819**	1.852	0.099	0.184	59.428**	213.813**	33.522**
Replication	3	199.834	0.834	0.000	48.897	0.154	3.167	21.917	17.934	0.233	0.035	53.581	86.169	17.556
Error	15	246.504	1.224	0.000	112.289	0.123	0.500	22.675	1.331	0.078	0.173	6.602	25.368	5.956

* Significant at 5% level of probability

** Significant at 1% level of probability

VL= Vine length (inch), VIL = Vine internode length (cm), VID = Vine internode diameter (cm), LAI= Leaf area index (cm2), AGFWT= Above ground fresh weight/plant (kg), SRN= Storage root number/plant, SRL = Storage root length (cm), SRD=Storage root diameter (cm), ISRWT = Individual storage root weight (kg), SRY = Storage root fresh yield/plant (kg), HI=Harvest index/plant (%), SRYP =Storage root fresh yield/plot (kg), SRYH = Storage root fresh yield (ton/ha)

Appendix VI. Z1-Z2 score of agro-morphological traits of six genotypes of sweet potato

Genotype number	PC1	PC2
G1	-18.358	-6.213
G2	-9.352	1.763
G3	6.467	-5.554
G4	5.946	18.649
G5	17.716	-9.608
G6	-2.419	0.962

Appendix VII. Mean performance of various qualitative components of 15 characters of 6 genotypes of sweet potato.

Genotypes	Moisture	Protein	Lipid	Fiber	Ash	Carbohydrate	Sugar	Beta Carotene	Vitamin C	Calcium	Magnesium	Potassium	Sodium	Phosphorus	Dry Matter
G1	65.6433	3.9667	0.3833	0.6167	1.1667	28.0200	6.5100	0.0480	0.0065	1.2600	0.6447	0.4877	0.2350	0.1810	34.3367
G2	71.6933	4.6667	0.4467	1.3333	1.4167	20.0800	7.1167	0.0480	0.0137	1.1800	0.6287	0.5400	0.2163	0.2340	28.3067
G3	71.2333	4.8667	0.6333	1.1833	1.3000	21.1283	9.4333	0.0767	0.0088	1.1667	0.5917	0.6780	0.1897	0.3467	28.7667
G4	68.0700	5.6333	0.2500	0.8833	1.4667	23.4000	5.5500	0.0337	0.0078	1.4833	0.7503	0.4400	0.2727	0.3137	31.9333
G5	70.9367	4.4333	0.6900	0.5500	0.7333	22.6700	8.4333	0.1000	0.0127	1.0500	0.5470	0.7387	0.1753	0.3430	29.0633
G6	72.0500	5.1833	0.2600	0.5167	1.2167	20.8100	7.4500	0.0613	0.0065	1.3400	0.7273	0.4673	0.2617	0.2550	27.9500
Min	65.6433	3.9667	0.2500	0.5167	0.7333	20.0800	5.5500	0.0337	0.0065	1.0500	0.5470	0.4400	0.1753	0.1810	27.9500
Max	72.0500	5.6333	0.6900	1.3333	1.4667	28.0200	9.4333	0.1000	0.0137	1.4833	0.7503	0.7387	0.2727	0.3467	34.3367
Mean	69.9378	4.7917	0.4439	0.8472	1.2167	22.6847	7.4156	0.0613	0.0093	1.2467	0.6483	0.5586	0.2251	0.2789	30.0594