GENETIC DIVERSITY AND ASSOCIATION OF SEED YIELD AND RELATED TRAITS IN OKRA [*Abelmoschus esculentus* (L.) Moench] GENOTYPES

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Genetic Diversity and Association of Seed Yield and Related Traits in **Okra** [*Abelmoschus esculentus* (L.) Moench] **Genotypes**

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We hereby certify that we have read and evaluated this Thesis entitled**"Genetic Diversity and Association of Seed Yield and Related Traits in Okra** [*Abelmoschus esculentus* (L.) Moench] **Genotypes***"* prepared under our guidance by Fozia Yimam**.** We recommend that it be submitted as fulfilling the thesis requirement.

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As member of the Board of Examiners of the MSc Thesis Open Defense Examination, we certify that we have read and evaluated the thesis prepared by Fozia Yimam and examined the candidate. We recommend that the thesis be accepted as fulfilling the Thesis requirement for the Degree of Master of Science in Biology (Genetics).

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DEDICATION

I dedicate this thesis manuscript to my lovely mother Lubaba Seid and my father Yimam Tekaw, whose attitude is the central force for my success.

STATEMENT OF THE AUTHOR

By my signature below, I declare and affirm that this Thesis is my own work. I have followed all ethical and technical principles of scientific methods in the preparation, data collection, data analysis, and compilation of this Thesis. Any scholarly matter that is included in the Thesis has been given recognition through citation.

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BIOGRAPHICAL SKETCH

The author was born in 1994 at Ajibar town, South Wollo zone, Amhara National Regional state, Ethiopia. She attended her education starting from Primary up to Preparatory School in same town. She attended in Abiot Primary School from 2002 to 2009 and Ajibar Secondary and Preparatory School from 2010 to 2013.

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ACRONYMS AND ABBREVIATIONS

CLCA	Complete Linkage Cluster Analysis
GAM	Genetic Advance as Percent Mean
GCV	Genotypic Coefficient of Variation
H^2	Heritability in broad sense
IBPGR	International Board of Plant Genetic Resources
IPGRI	International Plant Genetics Resources Institution
MLCA	Median Linkage Cluster Analysis
MoANR	Ministry of Agriculture and Natural Resources
PCV	Phenotypic Coefficient of Variation
PER	Protein Efficiency Ratio
SAS	Statistical Analysis System
SLCA	Single Linkage Cluster Analysis
UPGMA	Unweighted Pair-Group Method with Arithmetic Means
UPGMC	Unweighted Pair-Group Method with Arithmetic Centroid
WPGMA	Weighted pair-Group Method with Arithmetic mean

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ABSTRACT

*Ethiopia is claimed as the likely center of origin for okra [Abelmoschus esculentus (L).*Moench*], but few studies were conducted to assess the diversity of the crop in the country. Moreover, no attempt has been made to assess the diversity of okra genotypes for seed yield and related traits though the crop is known for the production of quality edible oil. Therefore, this study was conducted with the objectives of assessing genetic variability among okra genotypes for seed yield and related traits, and to determine the association of traits. A total of 24 okra genotypes (14 and 10 from Ethiopia and other countries, respectively) were evaluated for 4 qualitative and 20 quantitative traits, at Dire Dawa in 2017. The field experiment was laid out in randomized complete block design (RCBD) with three replications. The results from analysis of variance revealed the presence of significant differences among genotypes for all quantitative traits. Moreover, the variation of genotypes for seed yield per hectare ranged from 122 to 3206 kg with mean seed yield of 1938.13 kg ha^{-1}. The 14 okra genotypes collected from Ethiopia had mean seed yield advantage of 43.08% over the introduced varieties. In addition, most of the okra genotypes from Ethiopia had higher mean values than introduced varieties for majority of the traits. The largest proportion of okra genotypes had desirable qualitative traits of green pod color, erects fruit position on stem and smooth pod. The phenotypic (PCV) and genotypic (GCV) coefficient of variations varied in the range between 8.35% to 57.70% and 5.44 to 49.20%, respectively. Heritability in broad sense (H^2) and genetic advance as percent of mean (GAM) ranged from 20.92 to 94 % and 5.13 to 91.94%., respectively. All the estimated variability components (GCV, PCV, H^2 and GAM) were high for all traits except days to first flowering, days to 50% flowering and days to maturity. Majority of the traits had positive phenotypic and genotypic correlations with seed yield per hectare. Moreover, the seed weight per pod followed by weight of dry pod per plant, stem diameter, internode length and plant height had positive and highly significant correlations with seed yield per hectare and had positive genotypic direct effect on the trait. Therefore, these traits could be considered in selection for high seed yield per hectare. The genetic distances of 24 okra genotypes ranged from 1.96 to 11.36 and the genotypes were grouped into seven distinct clusters. Cluster III (41.67%), I (20.83%) and V (16.67%) consisted of the largest proportion of genotypes while Cluster II, IV and VII consisted each of one genotype and Cluster VI consisted of two genotypes. Okra genotypes with high seed yield and high mean values for most of the traits were grouped in Cluster III and IV of all genotypes except the one obtained from Ethiopia. The introduced varieties tend to be grouped in the same clusters with lower genetic distance with others than genotypes obtained from Ethiopia. The results suggested the possibility of developing varieties for high seed yield through selection and/or crossing of distant genotypes collected from Ethiopia.*

Keywords: Direct effects, Genetic distance, Genetic variability, indirect effects, Path analysis.

1. INTRODUCTION

Okra [*Abelmoschu esculentus* (L.) Moench] is a species grouped under Malvaceae family (Linnaeus, 1753). Okra is cultivated as vegetable crop in tropical, subtropical and warm temperate regions of the world (Lim, 2012). There are two most popular hypotheses about the origin of the species. Some workers advocate the origin of the species is India (Masters, 1875; Zeven and Zukovsky, 1975; Ikram-ul *et al*., 2013) and others argue that it originated around Ethiopia (Benchasri, 2012; Reddy *et al.*, 2012). Many authors considered West Africa, India and Southeast Asia as the center of diversity (Charrier, 1984; Hammon and Van Sloten, 1989). However, Ethiopia was not considered as center of diversity and/or origin (IBGR, 1984). This might be due to little information available about the diversity of the crop from research conducted very recently (PGRC, 1995; Miheretu *et al*., 2014a, b; Muluken *et al*., 2015; 2016; Tesfa and Yosef, 2016).

Okra seed rich in both lysine and tryptophan amino acids which is comparable to that of soybean, but better than soybean in terms of protein efficiency ratio (PER) than soybean (Sanjeet et al., 2010; Adetuyi et al., 2012). (Protein Efficiency Ratio is the ratio of grams of body weight gain (in specified time) to the grams of protein consumed). The okra seed amino acids content is an adequate supplement to legume or cereal based diets (Ndangui *et al.,* 2010). Okra seed flour could be used to fortify cereal flour such as maize to increase protein, ash, oil and fiber content in the meal (Akingbala *et al.,* 2003; Adelakun *et al.,* 2008). Okra seeds are excellent source of zinc and pod are also rich in phenolic compounds (Cook *et al*., 2000). These properties, along with the high content of carbohydrates, proteins, glyco-protein, and other dietary elements enhance the importance of okra pod and seed foodstuff in the human diet (Manach *et al.,* 2005; Arapitsas, 2008). The oil content of the seed is quite high at about 40% (Anwar *et al*., 2011; Tripathi *et al*., 2011). The seed yields of okra are in the range of 500 to1000 kg/ha (Kumar *et al.,* 2013). Okra seeds oil is rich source of linoleic acid (23.6 to 50.65%), a polyunsaturated fatty acid essential for human nutrition, rich in palmitic acid (10.3 to 36.35%), and oleic acids (Jarret *et al*., 2011; Steyn *et al*., 2014). The potential for wide cultivation of okra for edible oil as well as for cake is very high (Sanjeet *et al*., 2010).

Okra is an important crop in most developing countries, covering approximately 4 % of the total vegetable consumption and contributes to satisfy the demand of vegetables besides nutritional requirements (Simonsma, 1982; Zobia *et al*., 2013). Ethiopia has favorable environment for the production of okra and the crop has a potential to play significant role to mitigate food insecurity and alleviate malnutrition in Ethiopia. But, there is no complete data on production area and productivity of okra in Ethiopia, although it is a traditional crop in southwestern, western and northwestern Ethiopia (Miheretu *et al*., 2014). The crop has been considered a minor crop and has not been given research attention. The first improved variety (Bamya-Humera) for tender fruit yield has been recommended for cultivation very recently in 2016 (MoANR, 2016).

Proper management of crop diversity can produce permanent gain in the performance of plant and high heritability of the traits gives a better opportunity for breeders to select directly for the traits of interest (Welsh, 1981). In all crops, knowledge of genetic diversity is a prerequisite to develop varieties or to identify parental lines to be used in combination breeding (Prakash *et al*., 2011). Characterization of okra is great importance for current and future genetic improvement programs of the crop (Shujaat *et al.,* 2014). However, few reports are available about the diversity of okra in Ethiopia for tender fruit yield and related traits (Muluken *et al*., 2015; 2016; Miheretu *et al*., 2014a, b; Tesfa and Yosef, 2016 and Anteneh, 2017). These studies indicated the existence of variations among okra genotypes collected from different parts of Ethiopia for seeds per pod, dry or mature pod weight and hundred seeds weight as tender fruit related traits. Most of the researchers in the world also studied seeds per pod and per plants as tender fruit yield related traits of okra and few research results are available on genetics of seed in okra (Oyetunde and Ariyo, 2015).

In crop improvement programs, selection is one of the major activities to identify genotypes with high yield in a given environment. However, direct selection for high yield is difficult because of its complex nature. Yield per unit area is the end product of components of several characteristics, which are polygenic in inheritance and highly influenced by environment. Therefore, information on correlations of yield and yield related traits of crops are useful to design appropriate selection criteria for the desired characters (Johanson *et al.,* 1955). Besides the study of phenotypic correlations, it is also necessary to generate information on genotypic

correlations of characters. This is because; correlations due to the genetic causes are mainly pleiotropic effects of genes and linkage between genes affecting two or more different characters and causes simultaneous variations in the characters (Singh, 1993; Falconer *et al.*, 1996). Nevertheless, selection for yield based on highly correlated characters becomes easy if the contribution of different characters to yield is quantified using path coefficient analysis (Dewey *et al.*, 1959). Many workers have studied the genotypic and phenotypic correlations of seeds per pod, seed yield per plant and hundred seeds weight of okra genotypes with tender fruit yield and pod yield related traits (Nwangburuka *et al*., 2012; Ahiakpa *et al.*, 2013; Miheretu *et al*., 2014a, b ; Abd-Allah, 2015; Muluken *et al*., 2015;2016; Pithiya *et al*., 2017). However, limited information is available on path analysis taking seed yield as dependent variable and other seed related traits as independent variables.

As discussed above, in Ethiopia, no research has been conducted to study the diversity of okra genotypes for seed yield per hectare and related traits, and little information is available about the heritability of seed yield per plant and the genetic advance that could be made. The genotypic and phenotypic correlations among seed yield and seed related traits are scarce and the direct and indirect effects of seed yield related traits on seed yield per hectare is not studied yet. Moreover, there is no information about the genetic diversity of okra genotypes from Ethiopia and other countries for seed yield and related traits except (Adekoya *et al*., 2014) and (Akinyele and Osekita, 2006) both from Nigeria done on correlation and path analyses of seed yield in okra [*Abelmoschus esculentus* (L.) Moench] and (Abd-allah, 2015) from Egypt done on Path coefficient analysis for some characters on fruit and seed yields of okra by used five genotypes.Therefore; this research was initiated with the general objective of assessing the genetic variability among indigenous and exotic okra genotypes for seed yield and seed related traits with the following specific objectives.

Specific objectives

- ✓ To assess genetic variability among okra genotypes for seed yield and related characters, and
- ✓ To determine the association of seed yield and related characters and the direct and indirect effects of characters on seed yield of okra

2. LITERATURE REVIEW

2.1. Taxonomy and Origin of Okra

Okra is known by many local names in different parts of the world. It is called lady's finger in England, gumbo in the United States of America, guino-gombo in Spanish, guibeiro in Portuguese and bhindi in India (Ndunguru and Rajabu, 2004; Sorapong Benchasr, 2012). In Ethiopia, it is called Kenkase (Berta), Andeha (Gumuz), Bamia (Oromic/Amharic). The term okra was used in English by the late 18th century (Arapitsas, 2008).

Okra at an earlier time was included in the genus Hibiscus. Later, it was designated to *Abelmoschus*, by Linnaeus (1773) which is different from the genus Hibiscus by the characteristics of the calyx: spatulate, with five short teeth, connate to the corolla and caduceus after flowering (Kundu and Biswas, 1973; Terrell and Winters 1974). Although about 50 species have been described, eight are most widely accepted (Borssum, 1966; IBPGR, 1990). There is significant difference in the chromosome number and ploidy levels in *Abelmoschus*. The lowest chromosome number known is 2n = 56 for *Abelmoschus angulosus* (Ford, 1938) and the highest are close to 200 for *Abelmoschus caillei* (Siemonsma, 1982). Even within *Abelmoschus esculentus*, chromosome numbers 2n=72, 108, 120, 132 and 144 are in regular series of polyploidy with n = 12 (Dutta and Naug, 1968).

Okra is believed to have originated in Africa and is currently being grown in most subtropical and tropical regions of the world (Tattanakorn and Kumarn 2004).There are two hypotheses concerning the geographical origin of *Abelmoschus esculentus*. Some scientists argue that one putative ancestor (*Abelmoschus tuberculatus*) is native to Northern India, suggesting that the species originated from this geographic area. On the basis of ancient cultivation in East Africa and the presence of the other putative ancestor (*Abelmoschus ficulneus*), others suggest that the area of domestication is Ethiopia or North Egypt, but no definitive proof is available today (Benchasri, 2012). The genus *Abelmoschus* is accepted to be of Asiatic origin, though opinions differ for the origin of *Abelmoschus esculentus* as India (Masters, 1875), Ethiopia (Vavilov, 1951; Decandolle, 1883), West Africa (Chevalier, 1940; Murdock, 1959), Tropical Asia

(Grubben, 1977) and Hindustani Centre of Origin chiefly India, Pakistan, Burma (Zeven and Zukovsky, 1975).

2.2. Growth and Development of Okra

Okra needs temperatures above 20°C for normal growth and development (Lamont, 1999; Abd El-Kader *et al*., 2010). Germination percentage and speed of emergence of okra plant are optimal at 30-35°C temperature (Akande *et al*., 2003; Dada and Fayinminnu, 2010). Flower initiation and flowering in okra are delayed with increasing temperatures (positive correlation between temperature and number of vegetative nodes). *Abelmoschus esculentus* is a short-day plant, but its wide geographical distribution (up to latitudes of 35-40°) indicates that cultivars differ markedly in sensitivity (Lamont, 1999; Abd ElKader *et al*., 2010). Okra tolerates poor soils, but prefers well-drained sandy loams, with pH 6-7, and a high content of organic matter (Lamont, 1999).

Okra is mainly propagated by seeds and has duration of 90-100 days. It is generally an annual plant and its stem is robust, erect, and variable in branching and varying from 0.5 to 4.0 meters in height. Leaves are alternate and usually palmately five lobed, whereas the flower is auxiliary and solitary (Tripathi *et al*., 2011). Okra plants are characterized by indeterminate growth. Flowering is continuous but highly dependent upon biotic and a biotic stress. The plant usually bears its first flower one to two months after sowing. The fruit is a capsule and grows quickly after flowering. Okra is furrow irrigated crop throughout the growing season. If the soil has good moisture at planting, the young seedlings will grow 3 to 5 inches before irrigation is needed. Heavy early irrigation tends to cool the soil and slow plant growth. The plants should not be water stressed for maximum yields. During the harvest period, every other row is irrigated leaving a dry furrow for pickers to walk on (Lamont, 1999).

The pods are ready for harvesting in about 45-60 days after seed sowings, depending up on varieties and season (Adetuyi *et al*., 2008). Fruits are harvested 4 to 6 days after the flower has opened, and the fruits are not fibrous (fruits 2 to 4 inches long). Mature fruits should be removed and discarded as they reduce the plant growth and decrease yield. Immature fruits of 8-9 cm long are ready for harvest. Harvesting is recommended at least every other day for size and quality (Adeniji and Peter, 2005). When harvested, okra pods rapidly lose moisture. This

causes the loss of pod quality. It is recommended that harvesting be conducted in the cooler parts of the day, mornings or evenings, and the harvested okra be kept as cool as possible. Avoid leaving the harvested okra in the sun for long periods (Moekchantuk and Kumar, 2004).

2.3. Economic Importance of Okra

Okra is an economically supportive vegetable crop grown in tropical and sub-tropical parts of the world (Habtamu *et al*., 2014). It is suitable for cultivation as a garden crop as well as on large commercial farms (Rubatzky and Yamaguchi, 1997). Okra is a multipurpose crop due to its various uses of the fresh leaves, buds, flowers, pods, stems and seeds (Mihretu *et al*., 2014). Immature okra fruits which are consumed as vegetables, can be used in salads, soups and stews, fresh or dried, fried or boiled (Ndunguru and Rajabu, 2004). Okra mucilage has medicinal applications when used as a plasma replacement or blood volume expander. The mucilage of okra binds cholesterol and bile acid carrying toxins dumped into it by the liver. The immature pods are also used in making pickle. The entire plant is edible and is used to have several food (Madison, 2008; Maramag, 2013).

Okra seeds are source of oil and protein. Its seeds have been used on a small scale for oil production. It can also be used as non-caffeinated substitute for coffee. Okra seeds may be roasted and ground to form a caffeine free substitute for coffee (Calisir, and Yildiz, 2005). Okra, which is currently grown mainly as a vegetable crop, has potential for cultivation as an essential oil seed crop because its seeds contain high amount of oil (20-40%) (Sorapong, 2012; MEF, 2013) .Okra seed is known to be rich in high quality protein especially with regards to its content of essential amino acids relative to other plant protein sources (Oyelade *et al*., 2003; National Academic Council, 2006). Okra seeds from Greece are a potential source of oil, with concentrations varying from 20% to 40% (Sorapong, 2012; MEF, 2013), depending on the extraction method. The oil mainly consists of linoleic acid (up to 47.4%) (Andras *et al*., 2005). Okra seed oil is a rich source of linoleic acid, a polyunsaturated fatty acid essential for human nutrition (Savello *et al*., 1980).

Okra seed is mainly composed of oligomeric catechins (2.5 mg/g of seeds) and flavonol derivatives (3.4 mg/g of seeds), while the mesocarp is mainly composed of hydroxycinnamic and quercetin derivatives (0.2 and 0.3 mg/g of skins). Pods and seeds are rich in phenolic

compounds with important biological properties like quercetin derivatives (Quercetin is a plant flavonol from the flavonoid group of polyphenols is found in many fruits, vegetables, leaves and grains) , catechin oligomers and hydroxycinnamic derivatives (Arapitsas, 2008). These properties, along with the high content of carbohydrates, proteins, glycol-protein, and other dietary elements enhance the importance of this foodstuff in the human diet (Manach *et al*., 2005; Arapitsas, 2008).

2.4. Characteristics of Okra Seed

Seed in Botany is a ripped fertilized Ovule that provides an important means of reproduction, dispersal, and serves as nutrition to seed eating animals and fungal colonies (Wicklow, 1995). However, in agriculture seed is defined as any plant part used to regenerate the next generation of a crop (Gardner *et al*., 1985).The seeds of Okra are normally sown at depths of 5–6 cm; hence, the germinating seeds are likely to encounter mechanical resistance when growing on the soil surface. Therefore, soil physical properties such as bulk density, water holding capacity, soil compaction play a great role in germination and emergence of seedling. Since germination and seedling development are the pioneer steps for crop growth, development and yield, study of germination indices and seedling quality has been shown to be highly indicative of subsequent performance of seed throughout the growing period (Khajeh-Hosseini, Lomholt, and Matthews, 2009).

Thick walls in some okra seeds delay germination. The seed coats are often hard and the embryo can be slow to develop during germination. Consequently, treatments to seed coats which overcome hard seededness are generally required for germination. Hard seed coat is reported as the major reason for okra seed dormancy (Egley and Elmore, 1987). Seeds at 13% moisture content tend to show little or no hard seededness.

2.5. Genetic Diversity

2.5.1. Crop Genetic Diversity

Crop diversity can be described as the degree of differentiation between or within species. Genetic diversity is a broad term encompassing all the variability occurring among different genotypes with respect to total genetic make-up of genotypes related to single species or

between species. Genetic diversity can be measured by counting the number of different gene in a gene pool (Bhandari *et al*., 2017). Crop genetic diversity can be viewed at different geographical scales or levels of analysis (Tiegist, 2010). The pattern and level of genetic diversity in a given gene pool can be measured in terms of genetic distance. Genetic distances are measures of the average genetic divergence between cultivars or populations and genetic similarity is the converse of genetic distance and it refers to the extent of genetic similarities among cultivars (Smith, 1984).

Genetic diversity is importance for selecting parents in combination breeding of different autogamous crops to obtain transgressive segregants (Pradip *et al*., 2010). Shujaat *et al*.(2014) suggested that genetic variations is an important feature to get together the diversified goals of plant breeding including higher and quality yield, resistance to diseases, and wider adaptations. In any breeding program, therefore, genetic diversity must be introduced periodically into the population to provide new recombination and selection potential (Welsh, 1981).

2.5.2. Basis of Crop Genetic Diversity

Genetic diversity is primarily a function of sexual recombination. During meiosis, homologous chromosomes undergo crossing over which results in appearance of several new recombination. Different phenomena affect the genetic diversity in plants. Evolutionary forces like selection, mutation, migration and genetic drift are the basis of crop genetic diversity. These basis acts as the cause of continuous changes in allelic frequency in the population and influence the genetic diversity of the crop plant (Bhandari *et al*., 2017). Artificial selection favors few alleles at the cost others resulting in increased frequency of selected alleles and also natural selection also affects the genetic diversity considerably. Directional and stabilizing selection decreases while disruptive selection increases the genetic diversity. This is because directional selection favors individuals at one extreme of a phenotypic distribution that are more likely to survive and reproduce in a particular environment. Whereas stabilizing selection tends to decrease genetic diversity for a particular gene because it eliminates alleles that cause a greater variation in phenotypes. In contrast, disruptive selection favors the survival of two or more different genotypes that produce different phenotype and the fitness values of a particular genotype are higher in one environment and lower in a different one.

Disruptive selection is likely to occur in populations that occupy diverse environments so that some members of the species survive in each type of environmental condition (Brooker, 2012).

Mating system of crop plants also affect genetic diversity. Inbreeding reduces while out breeding increases genetic diversity. Genetic drift can lead to loss of rare alleles thereby reduces genetic diversity. Gene flow is the phenomenon in which individuals migrate from one population to another population and the migrants are able to breed successfully with the members of the recipient population. Gene flow depends not only on migration, but also on the ability of the migrants' alleles to be passed to subsequent generations (Brooker, 2012). Gene flow within population increases the genetic diversity as new alleles are introduced (Osawaru *et al*., 2015). Mutation is also reported to increase genetic diversity. This process takes place in different condition such as in morphological, anatomical, biochemical features and smaller and gradual effects which accumulate over time and bring about changes. In addition to this mutation may also bring aberrations in several chromosomes. Smaller sub-lethal or non-lethal aberrations may bring the increment of genetic diversity (Bhandari *et al*., 2017).

2.5.3. Methods of Crop Diversity Analysis

Diversity analysis can be carried out using morphological, cytological, biochemical and molecular characterization methods. Morphological markers were used for diversity analysis and are still in use. It involves morphological characterization of different entries grown in the field and morphological characteristics are the strongest determinant of agronomic value and taxonomic classification of plant (Cholastova and Knotova, 2012). Morphological evaluations are direct, inexpensive, easy and do not require expensive technology. Morphological characterization suffers from the constraints of environmental-sensitivity as compared to other methods used for diversity analysis.

In okra, morphological characterization has been implemented by many researchers in many countries including the very recent works in Ethiopia. For instance, in India, Badiger *et al* (2017), Prakash (2017), Sing *et al*, (2017), Mallesh *et al* (2015), Akotkar *et al* (2010), Jindal *et al* (2010), Prakash and Pitchaimuthu (2010) and Somashekahr (2010) and in Nigeria, Bello and Aminu (2017), Olayiwola *et al*.(2015), Adekoya *et al*.(2014),

Nwangburka *et al*.(2012), in Gahana Oppong-Sekyere (2011) have been conducted morphological characterization. All the authors reported the presence of significant variation among the varied number of genotypes for most of the studied characters. In Ethiopia, Anteneh (2017), Tesfa and Yosef (2016), Muluken *et al*. (2016 a&b) and Miheretu *et al*. (2014 a&b) studied 25 to 58 okra genotypes from different regions of Ethiopia and reported wide range of variation for all the characters studied among genotypes. However, the above authors worked on genetic variability components for fruit yield and yield related traits of okra genotypes not worked on seed yield and related traits.

Cytological markers involves in the study of cytological features like chromosome size, secondary constriction in chromosomes, position of centromeres, arm ratio, constitutive heterochromatic patterns, banding characteristics (G, Q, R and N banding), DNA content, total genomic chromosome length, chromosome volume etc. Different cytological features have been applied to assess genetic diversity within and between species in maize, in potato, in lentil, in radish etc. However, these have limited application in genetic diversity analysis on account of their limited number and low resolution (Bhandari *et al*., 2017).

On the basis of cytogenetical observations in okra plant, Siemonsmo (1982) suggested that taxonomical classification at species level is much more complex with the massive morphological variation. The genus constitutes a polyploid complex ranging from 2n=56 to 2n=200. Charrier (1984) reported under the cytogenetic relationships among the species of *Abelmoschus* dividing the genus into three ploidy level, each with mitotic integrity: Ploidy level one 2n=56-72 (*Abelmoschus moschatus* subsp., *Abelmoschus tuberculatus, Abelmoschus ficulneus, Abelmoschus manihot -ssp. manihot Abelmoschus angulosus, Abelmoschus esculentus*); ploidy level two: 2n=108-144 (*Abelmoschus manihot -ssp. tetraphyllus, Abelmoschus esculentus*); ploidy level three: 2n=185-199 (*Abelmoschus caillei, Abelmoschus manihot var. caillei).* The existing taxonomical classifications at the speices level in the genus Abelmoschus are unsatisfactory. Detailed cytogenetical observations on Asian material of okra and related species are likely to provide more examples of the existence of amphidiploids in the genus (Siemonsma, 1982).

Biochemical markers are proteins produced by gene expression. Isozymes have different molecular forms of the same enzyme that catalyze the same reaction, are proteins. They are the products of the various alleles of one or several genes (Chawla 2004). Isozymes are used as biochemical markers in plant breeding and are common enzymes expressed in the cells of plants. The enzymes are extracted, and run on denaturing electrophoresis gels. This is a rapid method of assessing diversity and requires smaller amount of plant tissue as sample (Bhandari *et al*., 2017). Biochemical markers are superior to morphological markers because of the independent of environmental growth conditions. The only problem with isozymes in marker assisted selection is that most cultivars (commercial breeds of plants) are genetically very similar and isozymes do not produce a great amount of polymorphism and polymorphism in the protein primary structure may still cause an alteration in protein function or expression (Tiegist,2010).

Molecular markers are the method of choice for genetic diversity assessment on account of their hyper variability, better genomic coverage, high reproducibility, amenability to automation being neutral and free from environmental fluctuations (Bhandari *et al*., 2017). Molecular markers are functional related to the discovery of restriction enzymes (Smith and Wilcox 1970) and the polymerase chain reaction (PCR) (Mullis and Faloona, 1987) have created the opportunity to visualize the composition of organisms at the DNA level, and it is called genetic fingerprint (Kearsey and Pooni 1996). Molecular markers are superior to other forms of marker assisted selection because they are relatively simple to detect, abundant throughout the genome even in highly bred cultivars, completely independent of environmental conditions and can be detected at virtually any stage of plant development. Different kinds of molecular markers are available, such as RFLPs, RAPDs, AFLPs, SSRs and SNPs. They may differ in a variety of ways such as their technical requirements; the amount of time, money and labor needed; the number of genetic markers that can be detected throughout the genome; and the amount of genetic variation found at each marker in a given population (Bhandari *et al*., 2017).

In okra, molecular marker analysis currently applied by few researcher such as Yuan *et al.* (2014) asses genetic diversity by using inter simple sequence repeat (ISSR) markers, Ikram-ul-Haq *et al*. (2013) assess genetic diversity by using RAPD markers on 39 okra genotypes. Only

very recently those SSRs are developed and utilized in diversity studies in okra (Schafleitener *et al.*, 2013).

2.5.4. Estimation of Genetic Diversity using Statistical Tools

Multivariate statistics are used to assess the genetic diversity among different strains/varieties or entries of a species. These techniques are very important for theoretical basis to provide most reliable information about the real genetic distance of the genotypes (Sing and Pawar, 2005). Some of the multivariate techniques being used are explained as follow.

Metroglyph Analysis: a semi-graphical approach for displaying genetic diversity among a number of lines referred to as Metroglyph Analysis. This method represented each genotype by a circle of fixed radius called glyph with ray emanating from its periphery. The performance of genotypes is adjudged value of the index score of those genotypes. The score values determines by the length of ray which may be small, medium and long (Anderson, 1957).

D^2 Statistics: This technique also called Mahalanobis. It was developed by Mahalanobis .This technique reduces the number of comparisons among genotypes by classifying them to in different groups. Mahalanobis distance is a measure of distance between two points in the space defined by two or more correlated variables (Mahalanobis, 1936).

Genetic Distance: it was developed by Nei as a difference between two entities that can be described by allelic variation. This definition was later (1987) modified to extent of gene difference among populations that are measured using numerical values. Beumont *et al.* (1998) provide a more comprehensive definition for genetic distance as any quantitative measure of genetic difference at either sequence or allele frequency level calculated between genotypes, individuals and populations. Euclidean or straight line measure of distance is the most commonly used statistics for estimating genetic distance between individuals (genotypes or populations) by morphological data. Mohammadi and Prasama (2003) have described in different measures of genetic distance in detail.

Cluster Analysis: it depicts the pattern of relatedness between genotypes based on the evolutionary relationships or phenotypic performance and is used to group similar lines or

germplasm in one group and differentiate other groups. It is based on methods namely unweighted paired group method using arithmetic means (UPGMA), unweighted paired group method using centroid (UPGMC),weighted paired group method using arithmetic mean (WPGMA),Single Linkage (SLCA),Complete Linkage (CLCA) and Median Linkage (MLCA). UPGMA and UPGMC provide more accurate grouping information on breeding material in accordance with pedigrees (Bhandari *et al*., 2017).

Based on one or more methods, Muluken *et al*. (2015) analysis 25 okra genotypes and identified ten major clusters while Mihretu *et al*. (2014) investigate five divergent groups of 25 okra collections from two regions (Gambella and Asossa) of Ethiopia. Tesfa and Yosef (2016) were able to group 50 okra collections from four major production regions of Ethiopia into four major clusters. Anteneh (2017) studied 25 okra genotypes of which 11 and 14 genotypes were obtained from other countries and three geographic regions of Ethiopia, respectively. The genotypes were grouped into seven major clusters. He also indicated genotypes from same countries tend to be grouped in the same clusters. In general those authors cluster the okra genotypes based on morphological characters in fruit yield and yield related traits.

2.6. Genetic Variability Components

2.6.1. Genotypic and Phenotypic Variability

Variability refers to the presence of difference among the individuals of a population. The components of variability include phenotypic variation, genotypic variation, environmental variation, heritability, genetic advance etc. It is a known fact that genotypes within the species exhibit variation in different metric traits and components of yield. The genetic variation can only be useful for crop improvement with the help of partitioning variances. Plant breeders are able to determine the relative importance of genetic and environmental variances. Genetic variability is the existence of differences among individuals due to differences in their genetic composition and/or the environment in which they are raised (Allard, 1960; Falconer *et al.*, 1996). Genetic variability considered as important aspect which taken into account before planning for any breeding program. The success of any selection program depends largely upon the magnitude of genetic variability present in the population (Yadav *et al*., 2016).

The variation within each genotype is due to the environment that is two organisms with the same genotype may not necessarily be identical in color because nutrition, physiological state, and many other variables influence the phenotype**.** If the character expression of two individuals could be measured in an environment identical for both, differences in expression would result from genetic control and hence such variation is called genetic variation (Welsh, 1990; Falconer *et al.*, 1996). Information on the nature and magnitude of genetic variability present in a crop species is important for developing effective crop improvement program (Welsh, 1990; Dabholkar, 1999). Estimation of the magnitude of variation within genotype collections for important plant attributes will enable breeders to exploit genetic diversity more efficiently (Jahufer and Gawler, 2000).

The okra genotypes characterized showed a broad variation for most traits, which allows for the identification of promising accessions for okra breeding (Sekyere *et al*., 2011). Variability in okra species and found out that a large number of okra Variability in okra species and found out that a large number of okra characters such as pigment color and spines on the fruit surfaces are inherited in a simple fashion, suggesting that these characters are controlled by relatively few genes (Singh *et al*.,1974). The environment of an individual is the sum total of all factors other than the individual concerned. The various factors of environment are called biotic or abiotic depending up on their biological and/or non-biological nature (Welsh, 1990; Singh, 1993; Sharma, 1998).

The key for any success of any breeding program lies in the availability of genetic variability for desired traits (Heller, 1996). The phenotypic expression of the plant is mainly controlled by genetic makeup of plant and its interaction with environment. It is necessary to partition the observed phenotypic variability into its heritable and non-heritable components with suitable parameters (Robinson *et al*., 1949). Knowledge of genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful biometrical tools for understanding the extent of genetic variability in base population which is prerequisite (Badiger *et al*,.2017). In addition to this, Salesh *et al*. (2010), Bharathiveeraman *et al*. (2012), Nwangburuka *et al.* (2012) and Swati *et al*. (2014) reported that the high phenotypic and genotypic coefficient of variation is an indication of the less influence of environmental factors in the expression of traits and the higher possibility to

improve traits through selection breeding. Many researchers worked about the genetic variability of okra in different time and location and they reported there was a variation among okra genotypes.

In genetic variability study of okra Jindel *et al*. (2010); Somashkari *et al*. (2010); Mihretu *et al.* (2014) and Sing *et al*. (2017) reported the highest PCV and GCV values computed for number of branches per plant. In addition to this, Jindel *et al*. (2010) reported moderate values of PCV and GCV were observed for days to fruit picking, average fruit weight, plant height, internodes length, number of fruits per plant and low values of PCV and GCV were computed for fruit diameter and average fruit length. But node at which first flower appears had low GCV and moderate PCV values. Prakash and Pitchaimuthu (2010) reported low PCV and GCV for traits such as days to 50% flowering and days to 80% maturity, moderate PCV and GCV value for hundred seed weight, fruit length, fruit girth and stem girth and the rest all traits had high PCV and GCV values on 44 genotypes of okra collected from the IIHR, Bangalore, India.

Akotkar *et al*. (2010) and Somashkari *et al*.(2010) reported that plant height ,internodes distance and weight of fruits had moderate PCV and GCV values and high PCV and GCV values were calculated for fruit yield per plant. Besides, Akotkar *et al*. (2010) found that GCV and PCV were high for number of fruiting nodes; moderate for number of nodes on main stem and; and low for number of ridges per fruit, fruit diameter, fruit length and number of primary branches per plant during the evaluation of fifty genotypes of okra with eleven quantitative characters. Somashkari *et al*.(2010) reported high PCV and GCV values computed for number of fruits per plant, average fruit weight (g),moderate GCV and PCV in case of fruit length, number of nodes per plant, stem diameter, followed by lower GCV and PCV for days to 50% flowering, hundred seed weight.

Sibsankar *et al*. (2012) was investigated on eighteen genotypes of okra [*Abelmoschus esculentus* (L.) Moench] for the extent of genetic variability, heritability, correlation and path analysis among various morphological, reproductive and nutritional characters related to fruit yield over two growing seasons in eastern India observed PCV agreed closely with the GCV but the magnitude of PCV was higher than GCV for almost all the characters studied during both seasons which reflect the influence of environment on the expression of traits. High PCV

and GCV values were shown by fruit yield per plant, numbers of fruit per plant and plant height at flowering during both seasons. The remaining traits recorded moderate to low PCV and GCV estimates, indicating that selection for these characters will be less effective.

Koundinya *et al.* (2013); Mihretu *et al.* (2014) and Muluken *et al*. (2016) reported seed per pod were showed moderate PCV and GCV values. Besides, Koundinya *et al.* (2013) reported the estimates of PCV and GCV were moderate for plant height, internodes length, branches per plant, fruits per plant, test weight and fruit yield per plant indicating phenotypes reflected the genetic worth of the genotypes. Moderate PCV and low GCV values were observed for first fruiting node. Low PCV and GCV values were observed for stem diameter, days to first flowering, days to 50% flowering, days to first harvest, fruit length, fruit diameter and fruit weight. Mihretu *et al.* (2014) reported high values for both phenotypic and genotypic coefficient of variation for days to maturity, stem diameter, internodes length, fruit length, average fruit weight, fruit diameter, and number of internodes per plant, plant height and number of pod per plant whereas, days to emergency, and hundred seed weight had moderate GCV and high PCV value. In addition to this, number of ridge per pod had low GCV and moderate PCV and days to 50%flowering moderate GCV and PCV values calculated during the evaluation of 25 okra genotypes collected from south western Ethiopia.

Muluken *et al*. (2016) demonstrated that low PCV and GCV calculated for days to 50% emergence, internodes length. Whereas, days to first flowering, days to 50% flowering, days to maturity, stem diameter, number of internodes per plant, fruit diameter, fruit ridges, and 100 seed weight had medium values for both coefficient of variations. On the other hand, number of branches per plant, fruit length, fruit yield ha-1, number of mature pods per plant and fresh weight of mature pod per plant had high values (>20%) both PCV and GCV and the magnitude of the differences between the two were low. Anteneh (2017) reported low for all okra phenology and moderate GCV and PCV for fruit and growth traits as well as hundred seed weight and also reported high GCV and PCV for number of mature fruit per plant, mature fruit weight, dry pod weight and number of seeds per pod.

Sing *et al*. (2017) reported that the genotypic and phenotypic coefficient of variability were high for fruit width, internodes length, plant height, first flower production node and first fruit production node whereas, number of ridges per fruit, number of fruits per plant, yield per

plant and number of seeds per fruit, stem diameter, fruit length, hundred seed weight,50% flowering and fruit weight indicating the existence of limited variability in the genotypes evaluated for the traits showing low genetic variability in the genotypes stock studied.

Based on this information there was not sufficient information about the genetic diversity of okra genotypes related with seed yield and seed yield related traits only done on fruit yield and fruit yield related traits . So, this research focused on the genetic diversity of okra genotypes related with seed yield and seed yield related traits collected from Ethiopia and introduced from Indian and USA used as an experimental material.

2.6.2. Heritability and Genetic Advance

In general sense, heritability specifies the proportion of the total variability that is due to genetic causes, or the ratio of genotypic variance to the total variance. It is a good index of the transmission of characters from parents to their offspring (Falconer, 1960; Phani *et al*., 2015). Estimation of heritability serves as a useful guide to the breeder and also the breeder is able to appreciate the production of variation that is due to genotypic (broad sense heritability) or additive (narrow sense heritability) effects (Khanorkar and Kathiria, 2010). Whereas, genetic advance measures genetic gain under selection. Genetic advance is defined as the difference between the mean genotypic value of the selected lines and the mean genotypic values of the original population before selection (parental population) or it indicates that the potentiality of selection at a particular level of selection intensity. As Johnson *et al*. (1955a) suggested that both heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection (i) high heritability accompanied with high genetic advance indicates that most likely the heritability is due to additive gene effects and selection may be effective, (ii) high heritability accompanied with low genetic advance indicates non-additive gene action and selection for such traits may not be rewarding, (iii) low heritability accompanied with high genetic advance reveals that the characters is governed by additive gene effect .The low heritability is being exhibited due to high environmental effects, selection may be effective in such case and (iv) low heritability accompanied with low genetic advance indicates that the character is highly influenced by environmental effects and selection would be effective. The high heritability would be a close correspondence between the genotypic and phenotypic variations due to

relatively small contribution of the environment to the phenotype expression of the trait (Singh *et al.*, 1990).

In the study of heritability and genetic advance on okra genotype reported from Ethiopian Mihretu *et al.* (2014), Muluken *et al.* (2016) and Anteneh (2017) high heritability and genetic advance for plant height, number of primary branches per plant, fruit weight, and weight of mature pod per plant. Further this, Anteneh (2017) reported high values both heritability and genetic advance as percent mean for dry pod weight, number of seeds per pod and hundred seeds weight while Muluken *et al.* (2016) observed moderate heritability coupled with high genetic advance as percent mean or vice versa for these traits. All the above authors concluded that selection of high performing genotypes would be rewarding in traits that exhibited high heritability coupled with high GAM.

Akotkar *et al*. (2010) revealed that the estimates of heritability in broad sense were high for number of ridges per fruit followed by plant height and number of fruiting nodes and moderate for all the remaining character except number of primary branches and also high genetic advance was observed for number of fruiting nodes followed by fruit yield per plant, plant height, internodes distance and number of fruits per plant; and moderate for all the remaining character except number of primary branches. Prakash and Pitchaimuthu (2010) reported that all evaluated characters except stem girth had high heritability however, stem girth had moderate heritability and also reported high heritability coupled with high GAM were observed for almost all the characters studied, except for days to 50% flowering and days to 80% maturity, Moderate heritability with moderate to low genetic advance as percent of mean was recorded for internodes length and height of first flowering node. Somashkari *et al*. (2010) observed high heritability coupled with high genetic advance as percentage of mean (GAM) was computed for the characters plant height, number of branches per plant, average fruit weight, number of fruits per plant, fruit yield per plant in all the population.

Jindel *et al*. (2010) reported that heritability values were generally high for all the characters under study except for node at which first flower appears which registered moderate value; The highest value of GAM was obtained for number of primary branches per plant, total yield per plant and marketable yield per plant. Low values for GAM were observed for days to fruit picking, average fruit weight, plant height, internodes length, number of fruits per plant, fruit

diameter, average fruit length and node at which first flower appears. Estimates high H^2 coupled with high GAM obtained for number of branches per plant, total yield per plant .Presence of high heritability coupled with low genetic advance for days to fruit picking, average fruit weight, and plant height, and internodes length, number of fruits per plant, fruit diameter and average fruit length.

Mallesh *et al*. (2015) and Bello and Aminu (2017) observed the high heritability for plant height, fruit length and diameter and average fruit weight .Further this, Mallesh *et al*. (2015) observed the high heritability estimated for the character number of fruit per plant, number of ridge per fruit, number of seed per fruit and number of internodes and low for days to maturity. In addition to this high heritability (>60 %) coupled with high genetic advance (>20 %) as percent of mean was observed first flowering node, number of nodes per plant, number of fruits per plant, fruit yield per plant, average fruit weight, fruit length, fruit diameter, fruit yield per hectare, number of ridges on fruit surface, seed yield per fruit and number of seeds per fruit. Bello and Aminu (2017) noted a broad sense heritability of greater than 60 % was obtained for pod yield, days to anthesis. Fairly broad sense heritability estimate was observed for the number of primary branches. The least heritability value was obtained for the number of pod per plant and High heritability and genetic advance were observed for all the characters studied except days to anthesis and fresh pod diameter. As moderate heritability and high genetic advance were noted for the number of primary branches of okra, low heritability and high genetic advance estimates were detected for the number of pod per plant.

Sing *et al*. (2017) investigated all 15 evaluated characters of 100 genotypes shows high heritability. Moreover, that high heritability (>80 %) coupled with high genetic advance (>20 %) as percent of mean registered for plant height first flower producing node, number of ridges per fruit, internodes length ,fruit width, number of seeds per fruit, number of primary branches ,stem diameter and number of fruits per plant, Moderate heritability coupled with high genetic advance as per cent of mean was observed for first fruit producing node. High heritability coupled with moderate genetic advance as percent of mean was observed for fruit length, 100 seed weight and days to 50% flowering, high genetic advance as percent of mean coupled with moderate heritability was observed for marketable yield per plant and moderate

heritability coupled with low genetic advance as percent of mean was observed for fruit weight.

The above reviews indicates that in okra genotypes there was research conduct for estimation heritability and genetic advance as percent mean only on the number of seed per pod and seed yield per plant among seed yield and seed yield related traits

2.7. Correlation and Path Coefficient Analysis

2.7.1. Correlation Coefficient Analysis

Correlation coefficient is statistical measure which is used to find out the degree of relationship between two or more variables. The intensity of correlation between different variables is represented by r. The correlation coefficient, r ranges from -1 to 1.If r is -1, there is 100% correlation between two variables, but both vary in opposite direction (negative correlation). On the other hand, if r is +1, it implies perfect correlation (100%) where both traits vary in the same direction (positive correlation). If r=0 there is no correlation at all between two variables, that is the two variables are independent of each other or no correlation indicates that genes concerned are located far apart on the same chromosome or they are located on different chromosomes and also in plant genetics and breeding studies, correlated characters are of prime importance because of genetic causes of correlations through pleiotropic action or developmental interactions of genes and changes brought about by a natural or artificial selection (Singh, 1993; Falconer *et al.*, 1996; Sharma, 1998). At genetic level, a positive correlation occurs due to coupling phase of linkage and negative correlation arises due to repulsion phase of linkage of genes controlling two different traits. Both types of correlations may also stem from pleiotropy, i.e. developmental correlation.

The genotypic correlation coefficient between different characters pairs was similar in sign and nature to the corresponding phenotypic correlation coefficient (Akinyele and Osekita, 2006; Bello *et al*., 2006; Mehta *et al*., 2006; Rashwan, 2011 and Somashekhar et *al*., 2011). More significant genotypic association between the different pairs of characters than the phenotypic correlation means that there is strong association between those characters genetically, but the phenotypic value is lessened by the significant interaction of environment (Kumar and Reddy, 2016). Correlations between different characters of a crop plant may arise

either from genotypic factor or environmental factors. Environmental correlations arise from the effect of overall environmental factors and that varies at different environments. Correlations due to the genetic causes are mainly pleiotropic effects of genes and linkage (a phenomenon of genes inherited together) between genes affecting different characters. Pleiotropy is the property of a gene, which affects two or more characters; as a result it causes simultaneous variations in the two characters when the gene is segregants (Singh, 1993; Falconer *et al.,* 1996).

From a correlation study, Akinyele and Osekita (2006) reported Seed yield per plant showed significant positive correlation with number of pods per plant, height at flowering, pod width and weight of hundred seeds. Currently from similar countries Adekoya *et al.* (2013) reported positive and significant genotypic and phenotypic correlations of seed yield per plant with plant height, number of pods per plant, width of matured pod, weight of matured pods per plant and 100-seed weight in 20 okra genotypes evaluated for four seasons. In addition they reported that Correlation coefficients among characters varied among seasons and also days to flowering, number of pods per plant, length of matured pod, weight of matured pods per plant, number of ridges per pod, number of seeds per pod and 100 seed weight had significant genotypic correlations with seed yield per plant across the seasons. The correlation coefficient was showed positive and significant at both genotypic and phenotypic levels between seed yield per plant and number of seed and fruits per plant and it have highly significant associations of pod yield with fruit length, fruit width, fruit weight and total number of fruits per plant (Somashekhar *et al*., 2011).

Reddy *et al*. (2013) investigated on one hundred germplasm lines of okra [*Abelmoschus esculentus* (L.) *Moench*] during kharif season was observed plant height, fruit length, fruit width, fruit weight, total number of fruits per plant, number of marketable fruits per plant and total yield per plant had significant positive correlation at both phenotypic and genotypic level, while number of branches per plant, internodes length, days to 50% flowering, first flowering node and first fruiting node had significant negative correlation with marketable yield per plant. Mihretu *et al.* (2014) reported from Ethiopia days to 50% flowering and days to maturity with average fruit weight, fruit diameter and seed per pod had negative correlations at genotypic and phenotypic levels and also observed significant and positive phenotypic

association among stem diameter, internodes length, plant height and number of primary of branches. In addition to this positive and significant genotypic correlation of internodes length with stem diameter and number of primary of branches, and number of pods per plant with stem diameter and number of primary of branches.

Days to first flowering showed positive and significant phenotypic and genotypic correlation with days to 50% flowering and days to maturity and also days to 50% flowering were showed negative and significant phenotypic correlation with plant height, number of internodes, average number of dry pod per plant, weight of dry pod per plant, average dry pod weight, dry pod length and seed weight per pod and hundred seed weight. In addition to this positive and significant genotypic and phenotypic correlation among plant growth traits (plant height, stem diameter, number of branches per plant, number of internodes per plant and internodes length) and also observed plant height, stem diameter and number of internodes per plant with fruit diameter, fruit ridge had positive and significant phenotypic and genotypic correlation. Plant height and number of internodes per plant with number of seeds per pod, and number of branches per plant with number of mature pods per plant also had positive and significant phenotypic and genotypic correlation was reported by Muluken *et al*. (2015).

Abd-Allah (2015) observed highly significant and positive correlation of Seed yield had highly positively correlation with number of branches per plant, number of mature pods per plant, and number of seeds per pod. Meanwhile, number of seeds per pod was positively correlated with number mature pods per plant and highly positively correlated with number of branches per plant. Moreover, there were highly positive and negative correlation between number of mature pods per plant with number of branches per plant and plant height.

Kumar *et al.* (2016) also revealed that significantly positive correlation of fruit weight with fruit length, fruit width and total number of fruits per plant. Kumar and Reddy (2016) reported the correlation coefficient analysis of seventeen quantitative traits had strong association among growth, earliness and yield parameters of okra under study. Further, these traits also had significantly positive correlation with marketable pod yield and positive inter-correlation also among themselves.

Pithiya *et al*. (2017) reported number of fruits per plant and number of seeds per fruit showed highest positive and very high significant correlation with yield per hectare followed by 100-seed weight and plant height. Plant height and 100-seed weight showed positive and significant correlation with yield per hectare. Stem diameter showed negative and significant correlation with Number of leaves per plant, Fruit length and plant height with 100-seed weight and Seed yield per plant.

2.7.2. Path Coefficient Analysis

According to Wright (1921), path coefficient analysis provides a better knowledge of direct and indirect causes of associations and it permits a critical examination of the specific forces acting to produce a given correlation and measures the relative importance of each causal factor. This method was first used by Dewey and Lu (1959) in their analysis of seed yield in crested wheat grass. Since then several workers have applied this method for analysis of character association in various crops. In addition to this, the path coefficient analysis partitions the correlation in to direct and indirect effects and thus may be useful in choosing the characters that have direct and indirect effects on yield (Chandbalai *et al*.,2014) and also simultaneously captures the effects of intricate relationship among various traits under investigation. Information obtained from correlation coefficients can be enhanced by partitioning them into direct and indirect effects for a set of a priori cause -effect interrelationship, as has been demonstrated in various crops (Kang *et al*., 1983; Gravois & Helms, 1992; Gravois and McNew, 1993; Board *et al*., 1997; Murtadha *et al*., 2004).

In some conditions, correlation alone does not give the exact picture of direct and indirect effect of characters upon each other; thus, path coefficient analysis is preferable, since it can identify the direct and indirect causes of associations and can measure the relative importance of each (Sharma,1998).The path analysis is the portioning of the total correlation into direct and indirect effects of independent variable(s) on dependent variable (Nadarajian and Gunasekaran, 2005; Dabholkar, 1992; Singh and Chaudhary, 1977). If the variable/trait has positive correlation and the direct effect of the variable or trait is negative or negligible, the positive correlation of the trait is because of the indirect effects through other traits. In such situation, the indirect casual factors or traits are to be considered simultaneously for selection (Singh and Chaudhary, 1977). The residual effect determines how much best the causal factors

or dependent variables account for the variability of dependent variable (Dabholkar, 1992; Singh and Chaudhary, 1977).

Akinyele and Osekita (2006) were noted number of pods per plant had high positive direct effect on seed yield per plant. In addition, number of branches per plant had positive direct effect on seed yield per plant at genotypic level and Adeniji and Aremu (2007) were reported that plant height at maturity and seed per pod suggested using as selection indicators for seed yield improvement. In general no more researchers in Ethiopian as well as outside Ethiopian about path analysis of okra based on the central focus on seed yield per hectare as dependent variables and seed yield and related traits as independent variable.

3. MATERIALS AND METHODS

3.1. Description of the Study Area

The field experiment was conducted at Tony farm, research site of Haramaya University in Dire Dawa. The site (Tony farm) is 40 kilometers away from Haramaya University, 66 kilometers away from Harar and 518 kilometers away from Addis Ababa. Dire Dawa lies between latitude 9°36′N, 41°52′E and characterized by warm and dry climate with a relatively low level of precipitation. The altitude of Dire Dawa is 1260 meters above sea level (Hailay *et al*., 2004). The mean annual temperature of Dire Dawa is about 25.4^0C. The average maximum temperature of Dire Dawa is 31.4^0C, while its average minimum temperature is about 18.2^0C. The aggregate average annual rainfall is about 604 mm and the annual average humidity is 41.82 % (Levoyageur, 2012).

3.2. Experimental Materials

A total of 24 okra genotypes were evaluated of which 14 okra genotypes were collected from different okra growing regions of Ethiopia and the remaining 10 commercial varieties were introduced from India and USA. Four okra accessions each from northwestern, western and southwestern Ethiopia and one accession from northern Ethiopia were included which represents the four geographic regions of Ethiopia. Two (SOH 714 and SOH 701) are registered commercial varieties in Ethiopia introduced by companies and one commercial variety from USA was initially collected from North Africa. The other seven varieties were introduced from India for experiment purpose. The okra genotypes from Ethiopia were collected at different altitudes ranging from 490 to 1480 m.a.s.l. (Table 1).

Table 1. List of okra genotypes and their origins

No	Accession name /Codes	Regional State	Admistrative Zone	District	Altitude (m.a.s.l.)	Geographic Region
1	240204	B-Gumuz	Metekel	Mandura	1200	NWE
2	240207	B-Gumuz	Metekel	Dibate	1400	NWE
3	240784	B-Gumuz	Metekel	Dangur	1180	NWE
4	245162	B-Gumuz	Metekel	Pawe Special	1020	NWE
5	92203	Oromia	East Wellega	Diga Leka	1200	WE
6	242444	B-Gumuz	Asosa	Menge	1105	WE
7	242433	B-Gumuz	Asosa	Asossa	1480	WE
8	245157	B-Gumuz	Kemashi	SirbAbaye	870	WE
9	240609	Gambella	Zone 1	Gambella	730	SWE
10	240600	Gambella	Zone 2	Abobo	490	SWE
11	240586	Gambella	Zone 3	Akobo	490	SWE
12	240592	Gambella	Zone 2	Gog	630	SWE
13	Humera 01	Humera				NE
14	23793 (Bamaya-Humera)					Released variety
15	SOH 714					India
16	SOH 701					India
17	Mythri					India
18	Kiran					India
19	ArkaAnamica					India
20	NamdHari					India
21	Dhenu					India
22	Anoop					India
23	Arcanamica					India
24	Clemson Spineless					USA

B-Gumuz = Benishangul-Gumuz, NWE = northwestern Ethiopia, SWE = southwestern Ethiopia, WE = western Ethiopia, NE = northern Ethiopia and USA = United States of America.

3.3. Experimental Design

The field experiment was conducted in randomized complete block design with three replications. Each genotype was randomly assigned to a plot in each replication in the experimental field. Each plot consisted of 12 plants at spacing of 0.6 m between plants. The spacing between plots and between adjacent replications was 0.8 and 2 m, respectively. The

total plot size was 0.8 m x 7.2 m (5.76 m^2). Three seeds per hill was sown and thinned to one plant per hill when plants reached 3-4 leaves stage.

3.4. Experimental Management

The seeds of 24 genotypes were obtained from okra variety development project at Haramaya University. The seeds were harvested on 26 to 30 December in 2016 cropping season and kept in canvas bags after drying, and stored at ambient temperature for five months at Horticulture laboratory of Haramaya University.

Land was prepared using tractor and human labor. The soil was leveled to permit furrow irrigation. The rows were raised to increase soil surface area, aeration and drainage. The ridges were made according to the planting spacing's by hand. Okra seeds were placed at the depth of 5 cm. Furrow irrigation was applied throughout the growing season, once a week at emergence and every two weeks at flowering and pod production. On the cultivation process of okra different cultural practices was applied such as weeding, cultivation, and earthing-up. The dry pods from 5 plants in each plot leaving the two plants at both ends of the row were harvested to collect seed yield and seed yield related data. The dry pods from 5 plants in each plot by leaving the border plant at both ends of the rows was harvested to collect seed yield and seed yield related data.

3.5. Data Collection

International Plant Genetic Resources Institute (IPGRI, 1991) descriptor list for okra species were used to record data on quantitative and qualitative traits. Quantitative traits were recorded from five plants per row leaving the border plants grown at both ends of the row. From five randomly selected plants per row five dry pods from each harvest in each plot were used to record dry pod characters.

Days to seedling emergence (50%): refers to the time required in days for the shoot to emerge from the seeds above the soil. It was registered by counting the number of days from planting to the emergence of 50% of plant seedlings in each plot.

Days to first flowering: the number of days taken from the date of sowing to onset of first

flower appears on the plant in each plot.

Days to 50% flowering: refers to the time required in days for the okra plants to flower. It was recorded by counting the number of days from planting to flowering of 50% of plants in each plot.

Days to maturity: the number of days from emergence of seedling to the stage when 90% of the plants in a plot have reached physiological maturity.

Plant height (cm): the height of the plants from the ground surface to the tip of the main stem was measured in centimeter at the final harvest and the mean height of five plants was registered the mean plant height in centimeter for statistical analysis.

Stem diameter (cm): the diameter of the stem at the basal region was measured at the final harvest using a standard graduated scale Vernier caliper. The diameter of five plants was averaged to record the mean stem diameter in centimeter.

Number of branches per plant: average number of branches of five plants from each plot at last harvest was registered.

Number of internodes: the total number of internodes per plant was counted at final picking and average of five plants were calculated.

Internodes length (cm): the length of the internodes between the fifth and sixth node was measured at time of maturity before the first tender fruit harvest.

Number of dry pods per plant: the number of dry pods in each plot was counted and averaged over the sample plant

Weight of dry pods per plant (g): the dry pods of five plants in each plot were harvested, counted and weighed to estimate and registered weight of dry pods per plant.

Number of ridges per pod: number of ridges of five dry pods from each harvest in each plot was counted and the average was calculated to register as number of ridges per pod.

Average dry pod weight (g): five dry pods from each harvest in each plot that was used to measure pod length and width was weighed using sensitive balance and the average weight was calculated and recorded accordingly.

Dry pod length (cm): the length of five dry pods from each harvest in each plot was measured and the average length was calculated and recorded.

Dry pod width (cm): the width of five dry pods from each harvest in each plot was measured and the averages were registered.

Number of seeds per pod: the seeds of five dry pods from each harvest in each plot were extracted, counted, average number of seeds calculated and registered.

Seeds weight per pod (g): seeds extracted from five dry pods from each harvest in each plot were kept in oven for 24 hours at 78^0C after five days of sun drying under open air, then after seeds were measured and registered accordingly.

100 seeds weight (g):100 seeds extracted from five mature turned to dry pods (green color of pods changed to gray color) from each harvest in each plot was oven dried, weighed and registered.

Seed yield per plant (g): Seeds were extracted from the dry pods of five plants in each plot, kept in open air under sun for five days, oven dried as indicated above, weight of seeds were measured and the average seeds weight per plant registered accordingly.

Seed yield per hectare (kg): Seed yield per hectare was calculated from the mean seeds yield of plant in a plot.

Qualitative traits: were recorded as per the International Plant Genetic Resources Institute (IBPGRI, 1991) descriptor list for okra species.

Pod color: main color of the pods was observed at harvesting stage and described as 1) Green and 2) Red

Position of pods on main stem: the positions of pods on the main stem of the genotypes were observed and it was described in five distinct variations as 1) Erect 2) Intermediate 3) Horizontal 4) slightly falling and 5) Totally falling.

Pod pubescence: this was observed at harvest stage and described as 1) smooth and 2) rough.

Pod shape: was assessed from pods harvest stage and described as with shape scores of 1, 2, 3, 4, 12, 14 and 15, according to the descriptor (IBPGR, 1991)

3.6. Data Analysis

3.6.1. Analysis of Variance

The quantitative data was subjected to analysis of variance (ANOVA). The data registered as percentage were transformed into arcsin before they were subjected to analysis of variance ANOVA was computed with SAS statistical software (9.2) (SAS, 2008). Descriptive statistics was used to describe qualitative data. The comparison of mean performance of genotypes was conducted following the significance of mean squares using Tukey´s test at 5% probability level. The traits that exhibited significant mean squares in general ANOVA were further subjected to genetic analyses as per the description given in subsequent sub-titles.

3.6.2. Phenotypic and Genotypic Variability

The phenotypic and genotypic variability of each quantitative trait was estimated as phenotypic and genotypic variances and coefficients of variation. The phenotypic and genotypic coefficient of variation was computed using the formula suggested by Burton and de Vane (1953) as follows.

Genotypic variance ($\sigma^2 g$) $= \frac{Mg - Me}{r}$

Where, $\sigma^2 g$ = genotypic variance, M_g= mean square of genotype, M_e = mean square of error and r = number of replications.

Phenotypic Variance ($\sigma^2 p$) = $\sigma^2 g + \sigma^2 e$

Where, $\sigma^2 g$ = genotypic variance, $\sigma^2 e$ = environmental variance and $\sigma^2 p$ = phenotypic variance.

$$PCV = \left(\frac{\sqrt{\sigma_p^2}}{\bar{x}} \right) \times 100$$

$$GCV = \left(\frac{\sqrt{\sigma_g^2}}{\bar{x}} \right) \times 100$$

Where; PCV= phenotypic coefficient of variation, GCV= genotypic coefficient of variation and $\bar{x}$ = population mean of the character being evaluated.

3.6.3. Heritability and Genetic Advance

Broad sense heritability values were estimated using the formula adopted by Falconer and Mackay (1996) as follows:

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

Where, H^2 = heritability in broad sense, $\sigma^2 p$ = phenotypic variance and $\sigma^2 g$ = genotypic variance.

Expected Genetic Advance under Selection (GA)

Genetic advance in absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the genotypes was estimated in accordance with the methods illustrated by Johnson *et al*. (1955) as:

$$GA = K * SDp * H^2$$

Where, GA = Genetic advance, SDp = Phenotypic standard deviation on mean basis; H2 = Heritability in the broad sense and k = the standardized selection differential at 5% selection intensity (K = 2.063).

Genetic Advance as Percent of Mean (GAM)

Genetic advance as percent of mean was estimated as follows:

$$GAM = \frac{GA}{\bar{X}} X100$$

Where, GAM = genetic advance as percent of mean, GA = genetic advance and $\bar{X}$ = Population mean of the character being evaluate

3.6.4. Phenotypic and Genotypic Correlation Coefficient

Phenotypic (r_p) and genotypic (r_g) correlations between two traits were estimated using the formula suggested by Johnson *et al*. (1955) and Singh and Chaudhury (1985).

$$rpxy = \frac{COVpxy}{\sqrt{\sigma^2 px \,.\sigma^2 py}}$$

Where, $rpxy$= phenotypic correlation coefficient between character x and y

$COVpxy$ = phenotypic covariance between character x and y

$\sigma^2 px$ = phenotypic variance for character x

$\sigma^2 py$ = phenotypic variance for character y

$$rgxy = \frac{COVgxy}{\sqrt{\sigma^2 gx.\sigma^2 gy}}$$

Where; $rgxy$ = genotypic correlation coefficient between character x and y

$COVgxy$ = genotypic covariance between character x and y

$\sigma^2 gx$ = genotypic variance for character x

$\sigma^2 gy$ = genotypic variance for character y

The coefficient of correlation at phenotypic level was tested for significance by comparing the values of correlation coefficient with tabulated r-value at g-2 degree of freedom, where 'g' is number of genotypes. However, the coefficient of correlations at genotypic level was tested for the significance using the formula described by Robertson (1959).

$$t = \frac{(rgxy)}{SErgxy}$$

The calculated 't' value was compared with the tabulated't'' value at g-2 degree of freedom at 5% level of significance. Where, g= number of genotypes, rgxy=genotypic correlation

coefficient and SErgxy=standard error of genotypic correlation coefficient between character x and y which will be calculated as:

$$SE_{r_{gxy}} = \sqrt{\frac{(1-r^2)^2}{2H^2{}_x.H_y{}^2}}$$

Where: SErgxy=standard error of genotypic correlation coefficient between character x and y, H^2_x =Heritability value of character x and H^2y =heritability value of character y.

3.6.5. Path Coefficient Analysis

Based on genotypic and phenotypic correlations, path coefficient analysis which refers to the estimation of direct and indirect effects of the seed yield attributing characters (independent character) on seed yield (dependent character) was calculated based on the method used by Dewey and Lu (1959) as follows:

rij = Pij + Σrik pkj

Where, rij = mutual association between the independent character (i) and dependent character (j) as measured by the genotypic and phenotypic correlation coefficients. Pij = direct effect of the independent character (i) on the dependent variable (j) as measured by the genotypic path coefficients, and Σrikpkj = Summation of components of indirect effect of a given independent character (i) on a given dependent character (j) via all other independent characters (k).

The residual effect, which determines how best the causal factors account for the variability of the dependent factor yield, were computed using the formula;

$1=p^2R + \Sigma$ p ij rij

Where, p^2R is the residual effect and p ij rij is the product of direct effect of any variable and its correlation coefficient with yield.

3.6.6. Genetic Distance and Clustering

Genetic distance of 24 okra genotypes was estimated using Euclidean distance (ED) calculated from quantitative traits after standardization (subtracting the mean value and dividing it by the standard deviation) as established by Sneath and Sokal (1973) as follows:

EDjk = $\sqrt{\sum_{i=1}^{n}(Xij - Xik)^{\frac{2}{2}}}$ (Sneath and Sokal, 1973), Where;

EDjk = distance between genotypes j and k; xij and xik = phenotype trait values of the i^{th} character for genotypes j and k, respectively; and n = number of phenotype traits used to calculate the distance. The distance matrix from phenotype traits was used to construct dendrogram based on the Unweighted Pair-group Method with Arithmetic Means (UPGMA). The results of cluster analysis was presented in the form of dendrogram. In addition, mean ED was calculated for each genotype by averaging of a particular genotype to the other 23 genotypes.

4. RESULTS AND DISCUSSION

4.1. Analysis of Variance and Mean Performance

4.1.1. Phenology

The twenty four okra genotypes exhibited highly significant ($P<0.01$) differences for days to 50% seedling emergence, days to first flowering and days to 50% flowering. The genotypes also had significant ($P<0.05$) differences for days to maturity (Table 2). The results indicated that the presence of significant variations among genotypes for crop phenology might be giving a good opportunity for breeders to select genotypes of varied crop maturity. Muluken *et al.* (2016) and Mihretu *et al.* (2014) observed highly significant differences among okra genotypes for crop phenology in which the genotypes were collected from southwestern, northwestern and western Ethiopia. Tesfa and Yosef (2016) studied 50 okra accessions collected from four major production regions in Ethiopia and grouped accessions into early, medium and late for time of flowering and time of commercial harvest.

Mallesh *et al.* (2015) from India reported the existence of significant differences among 52 okra accessions for days to first flowering, days to first fruit set and days to first harvest. Badiger *et al.* (2017) and Singh *et al.* (2017) also reported the presence of significant variations among 12 and 108 okra genotypes, respectively, for days to first flowering, days to 50 % flowering and days to first harvest. In Nigeria, Nwangburuka *et al.* (2012) and Olayiwola *et al*. (2015) observed significant differences among 29 and 10 okra genotypes, respectively, for days to flowering.

Table 2. Mean squares from analysis of variance for phenology of 24 okra genotypes evaluated at Dire Dawa in 2017

Trait	Replication (2)	Genotype (23)	Error (46)	CV (%)
Days to 50% seedling emergence	5.39	36.123**	4.341	19.7
Days to 50% of flowering	24.94	74.13**	15.62	5.6
Days to first flowering	8.04	61.236**	9.905	5.1
Days to maturity	18.38	173.71*	96.84	10.6

*and**, significant at P<0.05 and P<0.01, respectively. Numbers in parenthesis represent degree of freedom for the respective source of variation.

The mean values of genotypes for crop phenology are presented in Appendix Table 1.The genotypes variations for days to seedling emergence and days to first flowering ranged from 7 to 20.67 and 54.02 to 79.18, respectively. The genotypes showed variations for days to 50% flowering and days to maturity in the range between 64.18 and 89.84 and 73.33 and 105.67, respectively. The seeds of 240600, 23793 (Bamya-Humera) and SOH701 showed significantly delayed emergence compared to the rest genotypes. The released variety Bamya-Humera (23793) had also significantly delayed flowering and maturity. In general, all other genotypes collected from Ethiopia except 92203 showed delayed maturity, and were on a pal with 23792. Five introduced commercial varieties (Dhenu, Namd Hari, Clemson spineless, SOH701 and SOH714) also had delayed maturity, and were on a pal with the released variety Bamya-Humera (23793). The other five introduced commercial varieties viz. Anoop, Mythri, Arcanamica, ArkaAnamica and Kiran showed early seedling emergence, flowering and maturity with non-significant difference among the mean values for each trait. Generally, okra genotypes collected from Ethiopia had delayed seedling emergence, flowering and maturity as compared to commercial varieties introduced from India and USA countries. Muluken *et al.* (2016) also reported delayed seed emergence, flowering and maturity for okra genotypes collected from Ethiopia than the two exotic (SOH 701) and (SOH 714) commercial varieties introduced from India.

Okra is mainly propagated by seeds a the plant usually bears its first flower one to two months after sowing and has maturity duration of 90 to100 days (Tripathi *et al.,* 2011). Sulikiri and Swamy Rao (1972) indicated that the first flower opened in okra 41 to 48 days after sowing

and the fruit is a pod and grows quickly after flowering. Badiger *et al.* (2017) reported 36 to 44 days to first flowering and 43 to 53 days to first harvest and Singh *et al.* (2017) observed 32 to 49 days to 50% flowering among 108 okra genotypes. Nwangburuka *et al.* (2012) and Olayiwola *et al*. (2015) studied okra collections from Nigeria and reported 44 to 58 days to flowering. Mihretu *et al.* (2014) observed 37 to 65 and 50 to101 days of first flowering and maturity, respectively, in 25 okra genotypes collected from southwestern Ethiopia, while Muluken *et al.* (2016) observed 53 to 62 and 84 to 104days of first flowering and maturity, respectively, in genotypes collected from three geographic regions of Ethiopia and two introduced okra varieties.

4.1.2. Plant Growth Characteristics

The okra genotypes had highly significant ($P<0.01$) differences for all growth traits except for internodes length that exhibited significant ($P<0.05$) differences (Table 3). Mihretu *et al.* (2014) and Muluken *et al.* (2016) also observed significant variations among okra genotypes for plant height, stem diameter, number of branches and internodes length. Badiger *et al.* (2017), Singh *et al.* (2017) and Prakash *et al.* (2017) from India reported significant differences among okra genotypes for plant height and number of branches. In addition, Singh *et al.* (2017) for stem diameter and Prakash *et al.* (2017) for internodes length reported the presence of significant differences among genotypes. Nwangburuka *et al.* (2012) and Olayiwola *et al*. (2015) reported significant differences among okra genotypes collected from Nigeria for number of branches, plant height at flowering and at the end of harvest.

Table 3. Mean squares from analysis of variance for growth traits of 24 okra genotypes evaluated at Dire Dawa in 2017

Trait	Replication(2)	Genotype (23)	Error(46)	CV%
Plant Height (cm)	100.38	1312.1**	218.6	11.9
Stem Diameter (cm)	0.01	0.32713**	0.08653	16
Number of branches per plant	0.12	9.7079**	0.3609	13.6
Number of internodes per plant	1.70	231.227**	4.469	8.5
Internode Length (cm)	0.06	5.3552*	0.5775	12.4

*and**, significant at P<0.05 and P<0.01, respectively. Number in parenthesis represented degree of freedom for the respective source of variation.

The highest and significantly different mean values for plant height (175.2 cm), stem diameter (2.67cm) and internodes length (8.99cm) were registered for 245162, 242433 and 240207, respectively, But 240586 and 240784 for plant height, 240204 for stem diameter and 92203 and 240586 for internodes length also had highest mean values without significant difference from the above three genotypes with three traits. The two genotypes, 245162 (47.82) and 242433 (9.36) had significantly highest number of internodes and number of branches, respectively. In contrast, Mythri for plant height (89.2 cm) and Humrea 01 for number of branches (1.91) while 23793 for number of internodes (7.77) and Dhenu for internodes length (4.44) had the lowest mean values (Appendix Table 2).

The 14 okra genotypes collected from Ethiopia showed more variations for all growth traits as compared to 10 commercial varieties introduced from other countries (Appendix Table 2). It was reported that there was wide range of variations for growth traits of okra genotypes collected from different regions of Ethiopia (Mihretu *et al.*, 2014; Muluken *et al.*, 2016; Tesfa and Yosef, 2016).Besides the existence of wide range of variations in growth traits, Muluken *et al.* (2016) also reported that the okra genotypes collected from Ethiopia were more vigorous than the two registered commercial varieties introduced from India.

Tripathi *et al.* (2011) indicated that okra is an annual plant with robust stem, erect growth with variable branching that grows to 0.5 to 4.0 meters in height. Singh *et al.* (2017) evaluated 108 okra genotypes in India and the genotypes had 55.2 to 160 cm, 13.2 to 29 mm and 4.18 to

19.24 cm of plant height, stem diameter and internodes length, respectively, while the genotypes had 2 to 7 number of branches. Badiger *et al.* (2017) also reported 89.07 to 125.83 cm and 3.13 to 6.23 cm of plant height and internodes length, respectively, for 12 okra genotypes evaluated in Bangalore, India. Olayiwola *et al*. (2015) reported plant height at flowering in the range between 40.1 and 99.6 cm and mean values ranged from 1.93 to 3.56 for number of branches in 10 okra accessions evaluated over two years in southwestern Nigeria.

4.1.3. Dry Pod, Seed Yield and Seed Related Traits

The genotypes exhibited highly significant ($P<0.01$) difference for all dry pod, seed yield and seed yield related traits (Table 4). Anteneh (2017) evaluated 14 and 11 okra genotypes obtained from Ethiopia and other countries, respectively, and he reported the presence of significant difference for number of pod per plant, average weight of pod per plant, number of seeds per pod, hundred seed weight, fruit length and width. Muluken *et al*. (2016) also reported significant differences for pod characters, number of seeds per pod and hundred seed weight among 23 and 2 okra genotypes collected from Ethiopia and India, respectively. This study result was in agreement with the finding of Salesh *et al*. (2010) who reported highly significant differences among okra genotypes for fruit diameter, average fruit weight, average fruit length and number of fruits per plant. Nwangburuka *et al.* (2012) also found significant variation among okra genotypes for number of seeds per pod, number of fruit per plant and 100 seed weight.

Table 4. Mean squares from analysis of variance for dry pod, seed yield and seed related traits of 24 okra genotypes evaluated at Dire Dawa in 2017

Trait	Replication(2)	Genotype (23)	Error(46)	CV%
Average number of dry pod per plant	4.92	83.37**	10.79	17.8
Weight of dry pod per plant(g)	1004.44	352934**	39259	30.1
Number of ridge per pod	0.55	3.1697**	0.1607	5.9
Average weight of dry pod (g)	7.99	773.84**	36.21	18.3
Dry pod length (cm)	0.75	21.548**	2.04	12.9
Dry pod width (cm)	0.00	0.68062**	0.03226	10.3
Number of seed per pod	16.87	1552.5**	152.4	15.1
Seed weight per pod (g)	0.31	9.3477**	0.9845	20.8
Hundred seed weight	0.12	3.7667**	0.2132	8.3
Seed yield per plant (g)	1282.90	5145.4**	613	26.6
Seed yield per hectare (kg)	61864.44	2233195**	266036	26.6

*and **significant at P<0.01. Number in parenthesis represents degree of freedom for the respective source of variation.

The mean values for average number of dry pod per plant, weight of dry pod per plant and number of ridge per pod ranged from 3.53 (Humera 01) to 24.73 (ArkaAnamica), 175.9(g) (Humera 01) to 1518.9(g) (ArkaAnamica) and 5.17 (Mythri) to 8.46 (245162), respectively. The genotypes had mean values ranged from 12.55 (SOH714) to 83.93g (Dhenu), 5.24 cm (Arcanamica) to 16.29 cm (240609) and 0.66 cm (Humera 01) to 2.65cm (240586) for average dry pod weight, dry pod length and dry pod width respectively. The 14 okra genotypes collected from Ethiopia showed wide variation for number of ridge per pod and dry pod width. However, for the rest pod characters, introduced commercial varieties had relatively higher variation (Appendix Table 3).

Jindal *et al*. (2010) evaluated 12 okra genotypes in India and reported the presence of significant variation among genotypes for fruit characters. The authors reported in the range

between 5.33 and 8.70g, 1.46 cm and 1.96 cm, and 9.73 and 12.53 cm for average fruit weight, fruit diameter, fruit length, respectively, and 17 to 27 for number of fruit per plant. Mishra (2014) evaluated 33 okra genotypes in India and he found 11.79 to 17.62cm, 6.78 to 5.78 cm and 12.33 to 23.39g for fruit length, fruit diameter, fruit weight, respectively, and 16.26 to 23.55 for number of fruit per plant. Shivaramegowda *et al*. (2016) also reported that 36 okra genotypes showed wide variation for number of fruit per plant, fruit weight and fruit length in which the variation ranged from 10.13 to 23.26, 9.60g to 20.86g and 9.23 cm to 16.09 cm, respectively. They also observed fruit girth variation of among okra genotypes in the range between5.32 and 7.36 cm. Saleem *et al*. (2017) evaluated 25 okra genotypes in Pakistan and they reported 10.8 to 14.8 cm, 5.0 to 5.8 cm and 17.0 to 25.9 for fruit length, fruit girth and fruits per plant, respectively, while the range was 10.5 to 14.3g for fruit weight.

The highest and significantly different mean values for number of seed per pod (110.17), seed weight per pod (7.09g) and 100seed weight (7.01g) were registered for 245162, 240207, and 240586, respectively. The genotypes had mean values for seed yield per plant ranged from 5.86 to and 153.89g and seed yield per hectare ranged from 122 to 3206 kg ha^{-1}in which the lowest and highest seed yields were obtained from Humera 01 and 240204, respectively. The okra collections from Ethiopia had extreme variation for all seed yield and seed yield related traits (Appendix Table 3). The variation among genotypes for seed yield per plant and related traits was also reported by other researchers in Ethiopia (Mihretu *et al*., 2014, Muluken *et al*., 2016 and Tesfa and Yosef, 2016). This suggested that the higher chance of improving seeds yield through selection among okra genotypes collected from Ethiopia to produce high amount of edible oil and for other purpose such as seeds as a substitute for coffee, protein source etc. Abd-allah (2015) from Egypt, reported variation among five okra genotypes for number of seed per pod, 100 seed weight and seed yield per hectare in the range between 74.6 and 86.3, 4.52 and 5.18g and 1549.9 and 1918.4 kg ha^{-1}, respectively.

4.2. Qualitative Traits

The largest proportion of genotypes had green pod color (70.83%), erect pod position (58.33%), smooth pod pubescence (62.5%) and number 3 pod shape (29.17%) as per IPGRI (1991) descriptors for okra (Appendix Figure 1). Small proportion of genotypes had red pod color (8.33%), slightly falling pod position (4.17%), hairy pod (37.5%) and number 7, 9, 10

and 14 pod shape each 4.17% (Figure 1a-b, Appendix Table 5). The 14 okra genotypes collected from Ethiopia were distributed in all categories of four qualitative traits. All commercial varieties of other countries except ArkaAnamica and Dhenu had green pod color. Only ArkaAnamica, Dhenu and Clemson had intermediate and horizontal position while other commercial varieties had erect pod position whereas SOH701, SOH714 and Dhenu had rough pod pubescence while all others had smooth pod (Appendix Table 5).

Muluken (2015) observed 72% of the 25 genotypes produced green fruits while 28% displayed green yellow fruits. He also reported that 68% of genotypes had fruits positioned erect and 32% bore fruits positioned intermediate fruit on main stem, while 56 and 44% of the genotypes had smooth fruit and rough fruit, respectively. In his study, he observed that 28, 32 and 12% of the accessions had fruit shape of score '3', '4' and '12', respectively, as per IPGRI (1991) descriptors for okra. Anteneh (2017) also reported that 84% and 16% of the 25 genotypes had fruits positioned erect and intermediate on the main stem, respectively. He also observed 4 (16%) and 21 (84%) genotypes had red and green pod color, respectively, in which all introduced varieties had green pod color.

Oppong-Sekyere *et al* (2011) observed that 72% of okra accessions produced green fruits while others had green-with-red-spotted fruits, dark green to black fruits and green to yellow-fruits. AdeOluwa and Kehinde (2013) also reported three distinct fruit color of green (42.85%), purple (48.57%) and green yellow (8.57%).Ahiakpa (2012) observed yellowish green fruit color was the most predominant whereas green and green with red patches were least observed among okra accessions. Oppong-Sekyere *et al.* (2011) reported 60, 20 and 12% of the okra accessions had intermediate, erect and horizontally fruit position, respectively. Adeoluwa and Kehinde (2013) observed only erect (60%) and horizontal (40%) fruit position and downy (80%), rough (14.29%) and prickly (5.71%) fruit pubescence. Ahiakpa (2012) observed most of the okra genotypes had fruits at erect position on main stem and very few genotypes had pendulous and horizontal positioning of fruits on main stem. Oppong-Sekyere *et al.* (2011) and Ahiakpa, (2012) observed that the majority of okra accessions with smooth fruits and few genotypes with slightly rough and downy to little hairs.

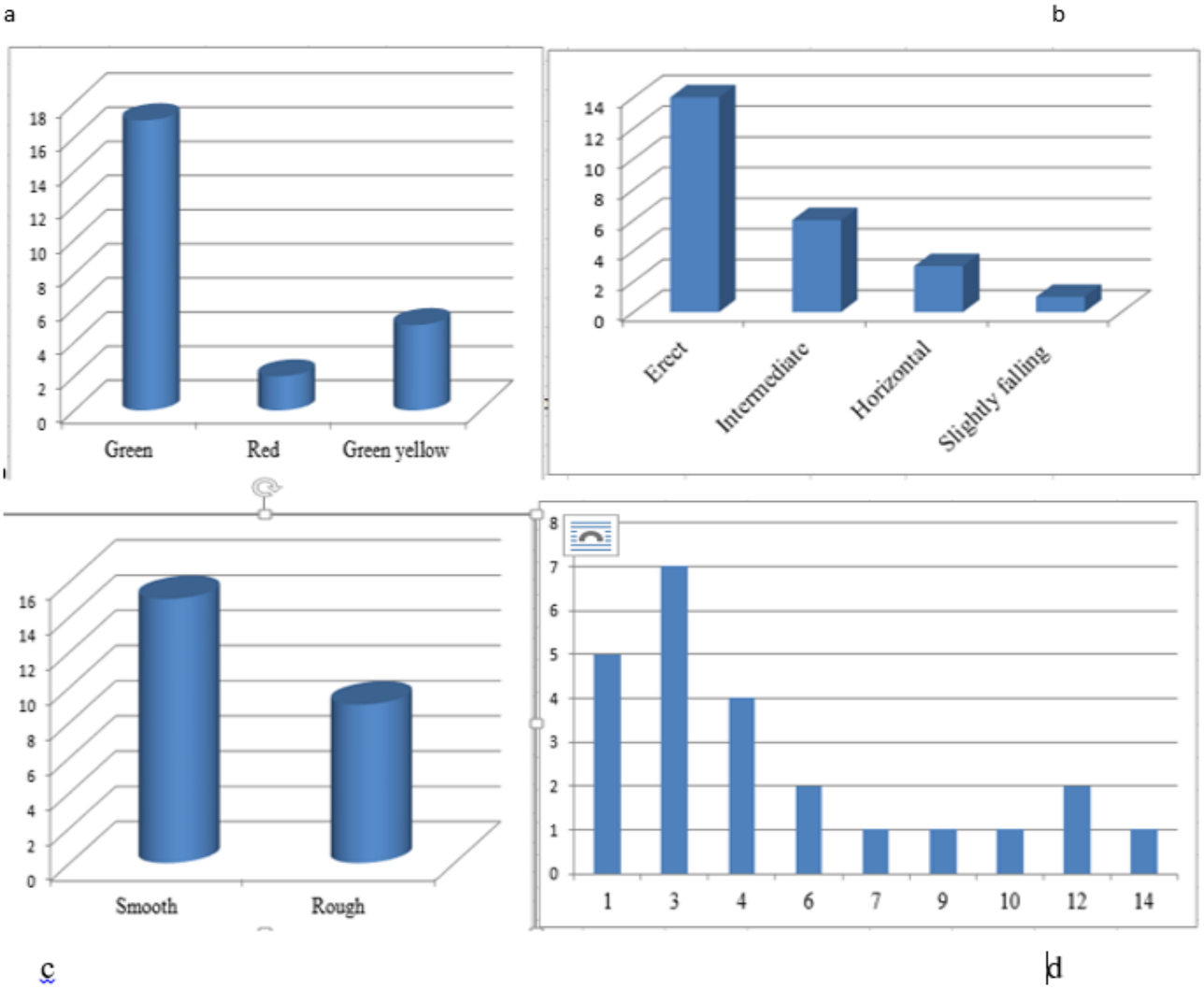

Figure 1. Distribution 24 okra genotypes into different categories of four qualitative traits; a= Pod color, b= pod position, c= pod pubescence, d= pod shape

4.3. Estimates of Variability Components

4.3.1. Phenotypic and Genotypic Variations

The estimated phenotypic (PCV) and genotypic (GCV) coefficient of variations for 20 quantitative traits of okra genotypes are presented in (Table 5). The phenotypic and genotypic coefficients of variation ranged from 8.35% to 57.70% and 5.44 to 49.20%, respectively. The crop phenology (days to first flowering, days to 50% flowering and maturity) had less than 10% both for PCV and GCV. Dry pod weight per plant followed by average dry pod weight, seed yield per plant and seed yield per hectare had higher GCV and PCV.

According to Sivasubramanian and Madhavamenon (1973), PCV and GCV can be categorized as low (<10%), moderate (10-20%) and high (> 20%). Correspondingly, low PCV and GCV values were computed for phenology traits (days to first flowering, days to 50% flowering and maturity) and moderate values for both PCV and GCV were calculated for plant height and number of ridges per pod. Stem diameter and hundred seed weight showed moderate values of GCV with relatively high values of PCV. All other traits had high PCV and GCV values >20%. The difference between the values of PCV and GCV was low (<5%) for majority of the traits. This suggested that most of the traits were less influenced by environmental factors and selection based on phenotypic expression of the genotypes could be applied as breeding method to improve the traits. Salesh *et al*. (2010), Bharathiveeraman *et al*. (2012), Nwangburuka *et al.* (2012) and Swati *et al*. (2014) suggested that the high phenotypic and genotypic coefficients of variation is an indication of the less influence of environmental factors in the expression of traits and the higher chance to improve the traits through selection breeding.

Muluken *et al*.(2016) reported low GCV and PCV for days to emergence, and internodes length and moderate GCV and PCV for days to first flowering, 50% flowering and maturity, stem diameter, number of internodes, fruit diameter, number of ridges on fruits, number of seeds per pod and hundred seeds weight. The authors also indicated that both GCV and PCV were high for plant height, number of branches, number of matured fruit per plant, and dry pod weight. Anteneh (2017) estimated values of GCV and PCV as low for all okra phenology, moderate for hundred seed weight, fruit and growth traits and high values for number of mature fruit per plant, mature fruit weight, dry pod weight and number of seeds per pod. Mihretu *et al.* (2014) reported high values of PCV and GCV for number of branches per plant.

Prakash and Pitchainthu (2010), Somashkari *et al*. (2010), Thirupathi *et al*. (2012), Koundinya *et al*. (2013) and Sing *et al*. (2017) for days to 50% flowering and Jindel *et al*. (2010), Sibsankar *et al*. (2012), Koundinya *et al*. (2013) and Mallesh *et al*. (2015) for days to first flowering reported low values of PCV and GCV in varied number of okra genotypes. Prakash and Pitchainthu (2010) also reported low values of PCV and GCV for days to maturity in 44 okra genotypes, while moderate values for stem diameter and hundred seed weight and high values for internodes length, number of seeds per pod and average fruit weight. Akotkar *et al*.

(2010), Jindel *et al*. (2010) and Somashkari *et al*. (2010) observed moderate values for PCV and GCV for plant height. Sing *et al*. (2017) reported moderate values of GCV and PCV for stem diameter and number of ridge per pod while high values for fruit width, number of branches per plant and internodes length. Somashkari *et al*. (2010) and Jindel *et al*. (2010) also reported high values of GCV and PCV for number of branches per plant.

4.3.2. Estimates of Heritability and Genetic Advance

Estimates of heritability in broad sense (H^2) and genetic advance as percent of mean (GAM) for 20 quantitative traits of okra genotypes are presented in Table 5. The heritability values ranged from 20.92% to 94.42 %. As suggested by Johnson *et al.* (1955a), heritability values are categorized as low (<30%), moderate (30-60%) and high (>60%). Based on this classification, days to maturity (20.92%) had low heritability, while days to 50% flowering (55.53%) and stem diameter (48.10%) had moderate heritability. The majority of the traits (17 out of 20) had high values of heritability.

Muluken *et al*. (2016) reported high heritability for all traits except low H^2 was estimated for internodes length, moderate for days to emergence, number of internodes, number of seeds per pod and hundred seeds weight. Anteneh (2017) also observed high H^2 for all traits of 25 okra genotypes except moderate H^2 for days to emergence and days to first flowering. Mihretu *et al.* (2014) also reported that the high heritability estimates for fruit diameter, fruit weight, plant height, number of branches per plant and fruit length.

Akotkar *et al*. (2010), Mallesh *et al*. (2015) and Sing *et al*. (2017) reported that the estimates of heritability in broad sense were high for plant height, fruit diameter, fruit length and number of ridge per pod. In addition, Mallesh *et al*. (2015) high heritability for number of seeds per pod and Sing *et al*. (2017) for number of seeds per fruit, hundred seed weight and number of branches per plant had high heritability values in okra genotypes. Akotkar *et al*. (2010), Prakash and Pitchainthu (2010) and Jindal *et al.* (2010) observed high H^2 for internodes length. In addition, Prakash and Pitchainthu (2010) reported high heritability for average weight of dry pod weight, number of seeds per pod and 100 seed weight and Jindal *et al.* (2010) also indicated high heritability for average weight of dry pod and number of branches. Somashkari *et al*. (2010) for plant height, number of branches per plant, and number of ridges

on pods, and Bello and Aminu (2017) for plant height, days to anthesis, pod length, pod diameter and pod mass observed high heritability.

Table 5. Genetic variability components for 20 traits of 24 okra genotypes evaluated at Dire Dawa in 2017

Trait	Mean	GCV (%)	PCV (%)	H^2 (%)	GAM (5%)	Difference between PCV & GCV
Days to 50%emergence	10.58	30.76	36.52	70.93	53.44	5.76
Days to first flowering	61.25	6.75	8.49	63.34	11.09	1.74
Days to 50% of flowering	70.94	6.23	8.35	55.53	9.57	2.12
Days to maturity	93.07	5.44	11.89	20.92	5.13	6.45
Plant height (cm)	124.54	15.33	19.39	62.51	25	4.06
Stem diameter (mm)	1.84	15.43	22.24	48.1	22.07	6.81
Number of branches per plant	4.42	39.96	42.21	89.62	78.05	2.25
Number of internodes per plant	25.01	34.77	35.78	94.42	69.69	1.01
Internodes length (cm)	6.14	20.55	23.99	73.39	36.32	3.44
Average number of dry pods per plant	18.42	26.7	32.1	69.16	45.8	5.4
Weight of dry pods per plant (g)	657.24	49.2	57.7	72.7	86.54	8.5
Number of ridges per pod	6.78	14.77	15.9	86.19	28.28	1.13
Average dry pod weight (g)	32.85	47.74	51.13	87.16	91.94	3.39
Dry pod length (cm)	11.06	23.06	26.43	76.12	41.51	3.37
Dry pod width (mm)	1.75	26.63	28.55	87.01	51.25	1.92
Number of seeds per pod	81.77	26.42	30.43	75.38	47.32	4.01
Seed weight per pod (g)	4.77	35.01	40.73	73.9	62.1	5.72
Hundred seed weight (g)	5.6	19.45	21.13	84.75	36.94	1.68
Seed yield per plant (g)	93.03	41.78	49.54	71.14	72.7	7.76
Seed yield per hectare (kg)	1938.13	41.78	49.54	71.14	72.7	7.76

PCV=Phenotypic Coefficient of Variation, GCV=Genotypic Coefficient of Variation, H^2=Heritability in broad sense, GA=Genetic advance, GAM=Genetic Advance as Percent of Mean

The genetic advance as percent of mean was estimated in the range between 5.13 and 91.94%. According to Johnson *et al*. (1955a) the range of genetic advance as percent mean are classified as low (<10%), moderate (10-20%) and high (>20%). Accordingly, all the traits had high GAM at 5% selection intensity except for days to 50% flowering and days to maturity on the other hand days to first flowering exhibited low and moderate GAM, respectively. In agreement with the current study results, Mihretu *et al.* (2014b), Muluken *et al*. (2016) and Anteneh (2017) reported high values of genetic advance values for all okra traits except for few traits. Muluken *et al*. (2016) observed low and moderate GAM for days to emergence and hundred seeds weight, respectively, and Anteneh (2017) low and moderate GAM for all phenology traits.

The importance of considering both the genetic advance and heritability of traits was suggested than considering them separately was suggested in how much progress can be made through selection (Johnson *et al.*, 1955). In this study, high heritability was coupled with high GAM for all traits except for days to 50% flowering and days to maturity. Whereas moderate heritability was coupled with high GAM for stem diameter and high heritability was coupled with moderate GAM for days to first flowering. The results suggested selection of high performing genotypes is possible to the improvement of all traits except for days to 50% flowering and days to maturity. The high heritability would be a close correspondence between the genotypic and phenotypic variations due to relatively small contribution of the environment to the phenotype expression of the trait (Singh *et al.*, 1990). Heritability estimates along with genetic advance provides better information than each parameter alone and it is also an expression of additive gene action (Sibsankar *et al*., 2012). Phani *et al*. (2015) suggested that selection based on phenotypic performance of genotypes would be effective to improve the traits for which high genetic advance as per cent of mean coupled with high heritability estimates since such situation is an indication of strong influence of additive gene action.

In agreement with the current study results, Mallesh *et al*. (2015), Chandramouli *et al*. (2016) and Sing *et al*. (2017) reported high heritability (>60 %) coupled with high genetic advance (>20 %) as percent of mean for plant height, number of ridges per fruit, fruit width, number of seeds per fruit, number of branches per plant, stem diameter and number of fruits per plant.

Parkash and Pitchamuth (2010) reported high heritability coupled with high GAM for almost all the characters studied, except for days to 50% flowering and days to 80% maturity. Jindal *et al*. (2010) reported high heritability coupled with high GAM for number of branches per plant and Somashkari *et al*. (2010) for plant height, number of branches per plant, average fruit weight, and number of fruits per plant also reported high heritability that coupled with high GAM. Mihretu *et al.* (2014), Muluken *et al.* (2016) and Anteneh (2017) from Ethiopia also reported high heritability and genetic advance for plant height, number of primary branches per plant, fruit weight, and weight of mature pod per plant. In addition, Anteneh (2017) observed high values of H^2 and GAM for dry pod weight, number of seeds per pod and hundred seeds weight while Muluken *et al.* (2016) observed moderate H^2 coupled with high GAM or vice versa for these traits. All the authors concluded that selection of high performing genotypes would be rewarding in traits that exhibited high H2 coupled with high GAM.

4.4 Phenotypic and Genotypic Correlation Coefficient

4.4.1. Phenotypic and Genotypic Correlation Coefficient of Seed yield with other Characters

Seed yield per hectare showed positive and highly significant (P<0.01) correlation with plant height, number of branches, number of internodes, internodes length, number of dry pod per plant, number of ridge per pod, dry pod width, number of seeds per pod, seed weight per pod and hundred seed weight both at the genotypic and phenotypic levels. Of which internodes length and seed weight per pod had lowest (rp=0.59**& rg=0.56**) and highest (rp=0.94**& rg=0.91**) correlation coefficient, respectively, both at genotypic and phenotypic levels. Seed yield per hectare also showed positive and significant (P<0.05) genotypic and phenotypic correlations with stem diameter and weight of dry pod per plant (Table 6). The presence of significant correlation of these traits with seed yield per hectare both at genotypic and phenotypic levels indicated prime importance of these traits in selection program to identify okra genotypes with high seed yield. Phenotypic correlation (r_p) measures the extent to which the two observed characters are linearly related while genotypic correlation (r_g) measures the extent to which degree the same genes or closely linked genes cause co-variation

(simultaneous variations) in two different characters (Singh and Chaudhary, 1977; Falconer *et al.*, 1996; Sharma, 1998).

Adekoya *et al.* (2013) reported positive and significant genotypic and phenotypic correlations of seed yield per plant with plant height, number of pods per plant, width of matured pod, weight of matured pods per plant and 100-seed weight in 20 okra genotypes evaluated for four seasons. Abd-Allah (2015) observed highly significant and positive correlation of seed yield with number of branches per plant, number of mature pods per plant, and number of seeds per pod. Akinyele and Osekita (2006) from Nigeria also reported that number of pods per plant had the highest genotypic correlation coefficient with seed yield. The findings of these researchers were in agreement with the current study results imply that these traits possessed greater practical values for selection of okra genotypes for high seed yield.

Seed yield per hectare had negative and significant ($P<0.05$) correlation with days to emergence, days to first flowering and days to 50% flowering at phenotypic level. However, these traits had negative correlation with seed yield but it was non-significant at genotypic level. Days to maturity and dry pod length showed positive and significant ($P<0.05$) association with seed yield at phenotypic level (Table 6). The presence of negative correlation indicated the associated traits are in opposite direction and selection of genotypes for high performance of one trait leads to the reduction of performance in the other traits. Therefore, it is important to give attention to phenology of the crops in the process of the selection of okra genotypes for high seed yield. Akinyele and Osekita, (2006); Nwangburuka *et al*. (2012) and Ahiakpa *et al.*(2013) also suggested that negative association of traits was difficult or practically impossible to improve through simultaneous selection of those traits. The sign of genetic correlations between two characters can either facilitate or impede selection progress and $r = 0$ or non-significant carries the implication of no correlation between the two characters (Singh and Chaudhary, 1977; Falconer., 1996; Sharma, 1998).

4.4.2. Estimate of Correlation Coefficients among other Characters

The phenology traits (days to emergence, days to first flowering, days to50% flowering and days to maturity) showed significant association among them both at genotypic and phenotypic levels except the genotypic correlation between days to emergence and days to

maturity was positive but non-significant. The genotypic correlation of phenology traits with growth traits of okra was non-significant except the genotypic correlation of days to emergence with number of internodes per plant (r_g=-0.49*) and days to maturity with stem diameter (r_g=0.46*) showed negative and positive significant genotypic association, respectively (Table 6). At the phenotypic level, days to emergence with plant height and number of branches per plant, number of internodes per plant with days to emergence, days to first flowering and days to 50% flowering had negative and significant association. Internodes length with all phenology traits, days to first flowering and days to maturity with stem diameter and number of branches per plant as well as days to maturity with plant height had positive and significant phenotypic correlations. All phenology traits showed non-significant genotypic correlation with pod and seed traits. However, dry pod width with days to 50% flowering and days to maturity with number of seeds per pod and seed weight per pod had positive and significant phenotypic correlations.

In agreement with this study results, Muluken *et al*. (2015) reported that days to first flowering showed positive and significant phenotypic and genotypic correlation with days to 50% flowering and days to maturity. They also indicated days to 50% flowering had negative and significant phenotypic correlation with plant height, number of internodes, and average number of dry pod per plant, weight of dry pod per plant, average dry pod weight, dry pod length and seed weight per pod and hundred seed weight. Mihretu *et al.* (2014) also reported positive and significant association among phenology traits of okra. However, days to 50% flowering and days to maturity with average fruit weight, fruit diameter and seed per pod had negative correlations at genotypic and phenotypic levels. In addition, the two phenology traits had negative phenotypic correlation with plant height and negative genotypic association with fruit weight, and hundred seed weight. It has been also reported that days to 50% flowering had significant negative correlation with branches per plant and fruit length (Ahamed *et al*., 2015). The negative correlation of these traits to other growth, pod and seed traits suggested selection for earliness has negative effect on growth, pod and seed traits. Negative and significant correlations of traits with one another both at phenotypic and genotypic levels will make difficult the simultaneous selection and improve traits (Akinyele and Osekita, 2006).

Number of branches and number of internodes per plant had positive and significant correlations with plant height; stem diameter at genotypic and phenotypic levels. Number of branches with internodes per plant at both levels had positive and significant correlation coefficient. Plant height with stem diameter and internodes length showed positive and significant association at phenotypic level. However at genotypic level plant height with stem diameter had showed positive and non-significant correlation. Most of growth traits (plant height; stem diameter, internodes length, number of branches and number of internodes per plant) showed positive and significant association with number of ridges per pod, dry pod width, number of seeds per pod, seed weight per pod and hundred seeds weight at both levels except stem diameter with hundred seeds weight at genotypic level and stem diameter with number of branches at both levels showed positive but non-significant correlation coefficient. On the other hand, number of internodes with dry pod length and dry pod weight had negative and significant phenotypic correlation. In addition to this, plant height, internodes length and number of branches with dry pod length and dry pod weight showed negative and significant phenotypic association.

The positive and significant genotypic and phenotypic correlation among plant growth traits (plant height, stem diameter, number of branches per plant, number of internodes per plant and internodes length) has been reported (Muluken *et al*., 2015). The authors also indicated that plant height, stem diameter and number of internodes per plant with fruit diameter and fruit ridge had positive and significant phenotypic and genotypic correlation. Plant height and number of internodes per plant with number of seeds per pod, and number of branches per plant with number of mature pods per plant also had positive and significant phenotypic and genotypic correlation. Mihretu *et al.* (2014) also found significant and positive phenotypic association among stem diameter, internodes length, plant height and number of primary of branches. They also investigated positive and significant genotypic correlation of internodes length with stem diameter and number of primary of branches, as well as number of pods per plant with stem diameter and number of primary of branches. Reddy *et al*. (2013) reported that plant height had significant positive correlation with internodes length and number of fruits per plant. Kumar and Reddy (2016) reported the presence of positive and significant phenotypic correlation among plant height, number of branches per plant and internodes

length and these traits had also positive and significant phenotypic correlation with number of fruits per plant, fruit length and fruit weight.

Hundred seeds weight and seeds weight per pod showed positive and significant genotypic and phenotypic correlations with all pod and seed traits except the genotypic association was positive and non-significant in seeds weight per pod with dry pod weight per plant, dry pod length and dry pod weight and hundred seeds weight with dry pod weight and number of seeds per pod. Positive and significant genotypic and phenotypic association was observed between dry pod weight per plant with dry pod length, and dry pod width with number of seeds per pod. Number of dry pod and dry pod weight per plant with number of ridges and number of seeds per pod, while number of dry pod with dry pod width as well as dry pod weight per plant with dry pod length and weight showed positive and significant phenotypic correlations.

Pithiya *et al*. (2017) reported pod length with hundred seeds weight and hundred seeds weight with seed yield per plant exhibited significant and positive genotypic correlation. They also indicated that seed yield per plant and number of seed and fruits per plant had positive and significant genotypic and phenotypic correlation coefficients. Highly significant associations of pod yield with fruit length, fruit width, fruit weight and total number of fruits per plant was reported (Somashekhar *et al*., 2011), Kumar *et al.* (2016) also found significant positive correlation of fruit weight with fruit length, fruit width and total number of fruits per plant. Muluken *et al*. (2015) found that the existence of positive and significant genotypic and phenotypic correlations of fruit length with fruit weight, matured pod weight and hundred seeds weight, fruit diameter with matured pod per plant and dry pod weight as well as number of seeds per pod and hundred seeds weight. The authors also indicated that number of ridges with mature pod, dry pod weight and number of seeds per pod and dry pod weight with number of seeds per pod showed positive and significant correlations at both levels.

Table 6. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficient among seed and seed related traits of 24 okra genotypes

	DE	DF	D50%F	DM	PLH	SD	NBPP	NIPP	IL	ANDP
DE		0.50**	0.68**	0.30^{ns}	-0.28^{ns}	0.03^{ns}	-0.24^{ns}	-0.49*	0.06^{ns}	-0.03^{ns}
DF	0.56**		0.94**	0.74**	-0.02^{ns}	0.27^{ns}	0.06^{ns}	-0.28^{ns}	0.21^{ns}	-0.17^{ns}
D50%F	0.77**	0.97**		0.71**	-0.08^{ns}	0.29^{ns}	-0.03^{ns}	-0.37^{ns}	0.17^{ns}	-0.15^{ns}
DM	0.49*	0.83**	0.77**		0.27^{ns}	0.46*	0.26^{ns}	0.01^{ns}	0.25^{ns}	-0.08^{ns}
PLH	-0.29*	-0.01^{ns}	-0.07*	0.51**		0.26^{ns}	0.71**	0.73**	0.43*	0.24^{ns}
SD	-0.01^{ns}	0.34*	0.40*	0.86**	0.28*		0.62**	0.43*	0.03^{ns}	0.08^{ns}
NBPP	-0.25*	0.08*	0.00^{ns}	0.44*	0.77**	0.73**		0.66**	0.34^{ns}	0.27^{ns}
NIPP	-0.51**	-0.31*	-0.41*	0.03^{ns}	0.78**	0.49*	0.67**		0.08^{ns}	0.38^{ns}
IL	0.06*	0.23*	0.19*	0.33*	0.48*	0.03^{ns}	0.35*	0.09*		0.33^{ns}
ANDP	-0.02^{ns}	-0.23*	-0.19*	-0.18*	0.21*	0.05^{ns}	0.29*	0.41*	0.33*	
WtDP	-0.25*	-0.38*	-0.36*	-0.51**	0.02^{ns}	-0.01^{ns}	0.07*	0.33*	-0.06*	0.57**
NRPP	-0.19*	0.05^{ns}	0.07*	0.55**	0.86**	0.74**	0.73**	0.62**	0.61**	0.37*
ADPW	-0.16*	-0.27*	-0.22*	-0.42*	-0.23*	0.03^{ns}	-0.21*	0.01^{ns}	-0.24*	0.01^{ns}
DPL	-0.44*	-0.24*	-0.24*	-0.22*	-0.18*	-0.05^{ns}	-0.22*	0.15**	-0.25*	0.31*
DPW	-0.13*	0.09*	0.13*	0.46*	0.68**	0.50**	0.62**	0.46*	0.67**	0.51**
NSPP	-0.23*	-0.03^{ns}	-0.05^{ns}	0.51**	0.62**	0.80**	0.66**	0.54**	0.37*	0.18*
SWPP	-0.37*	-0.16*	-0.16*	0.29*	0.76**	0.58**	0.73**	0.67**	0.60**	0.55**
100SW	-0.31*	-0.21*	-0.19*	-0.13*	0.48*	0.09*	0.40*	0.45*	0.54**	0.67**
SYP	-0.24*	-0.16*	-0.16*	0.24*	0.66**	0.49*	0.66**	0.70**	0.59**	0.77**

*, *and ns, significant at P<0.01, P<0.05 and non-significant, respectively. DE=days to emergency, DF=days to first flowering, D50%F =days to 50% flowering, DM=days to maturity, PLH=Plant height, SD=Stem diameter, NBP=Number of branches, NIP=Number of internodes per plant, IL=Internodes length, ANDP=Average number of dry pod per plant, WtDP=Weight of dry pod per plant, NRP=Number of ridge per pod, ADPW=Average dry pod weight, DPL=Dry pod length, DPW=Dry pod width, NSP=Number of seed per pod, SWE=Seed weight per pod, HSW=Hundred seed weight.

Table 6 Continue

	WtDP	NRPP	ADPW	DPL	DPW	NSPP	SWPP	100SW	SYP
DE	-0.22^{ns}	-0.17^{ns}	-0.14^{ns}	-0.37^{ns}	-0.12^{ns}	-0.21^{ns}	-0.31^{ns}	-0.28^{ns}	-0.21^{ns}
DF	-0.31^{ns}	0.03^{ns}	-0.24^{ns}	-0.21^{ns}	0.08^{ns}	-0.02^{ns}	-0.14^{ns}	-0.20^{ns}	-0.12^{ns}
D50%F	-0.30^{ns}	0.04^{ns}	-0.19^{ns}	-0.22^{ns}	0.10^{ns}	-0.05^{ns}	-0.15^{ns}	-0.18^{ns}	-0.13^{ns}
DM	-0.31^{ns}	0.33^{ns}	-0.27^{ns}	-0.20^{ns}	0.30^{ns}	0.32^{ns}	0.17^{ns}	-0.10^{ns}	0.16^{ns}
PLH	0.07^{ns}	0.77**	-0.19^{ns}	-0.14^{ns}	0.62**	0.55**	0.68**	0.44*	0.63**
SD	0.04^{ns}	0.60**	0.06^{ns}	0.01^{ns}	0.43*	0.65**	0.49*	0.09^{ns}	0.42*
NBPP	0.07^{ns}	0.69**	-0.19^{ns}	-0.20^{ns}	0.61**	0.62**	0.68**	0.39^{ns}	0.62**
NIPP	0.32^{ns}	0.60**	0.01^{ns}	0.13^{ns}	0.45*	0.52**	0.63**	0.43*	0.65**
IL	-0.04^{ns}	0.57**	-0.23^{ns}	-0.21^{ns}	0.61**	0.33^{ns}	0.54**	0.50**	0.56**
ANDP	0.58**	0.33^{ns}	0.03^{ns}	0.32^{ns}	0.48*	0.19^{ns}	0.50**	0.61**	0.77**
WtDP		0.20^{ns}	0.78**	0.53**	0.21^{ns}	0.10^{ns}	0.34^{ns}	0.49*	0.47*
NRPP	0.23*		0.04^{ns}	0.02^{ns}	0.82**	0.80**	0.90**	0.55**	0.80**
ADPW	0.79**	0.05^{ns}		0.58**	-0.05^{ns}	0.04^{ns}	0.12^{ns}	0.22^{ns}	0.04^{ns}
DPL	0.54**	0.01^{ns}	0.59**		0.13^{ns}	0.07^{ns}	0.25^{ns}	0.42*	0.22^{ns}
DPW	0.19*	0.86**	-0.08*	0.12*		0.54**	0.86**	0.77**	0.80**
NSPP	0.07*	0.87**	0.00^{ns}	0.04^{ns}	0.55**		0.78**	0.18^{ns}	0.67**
SWPP	0.33*	0.98**	0.08*	0.24*	0.89**	0.77**		0.75**	0.91**
100SW	0.51**	0.58**	0.21*	0.44*	0.79**	0.17*	0.76**		0.72**
SYP	0.43*	0.88**	0.01^{ns}	0.20*	0.84**	0.68**	0.94**	0.75**	

*, *and ns, significant at P<0.01, P<0.05 and no-significant, respectively. DE=days to emergency, DF=days to first flowering, D50%F =days to 50% flowering, DM=days to maturity, PLH=Plant height, SD=Stem diameter, NBP=Number of branches, NIP=Number of internodes per plant, IL=Internodes length, ANDP=Average number of dry pod per plant, WtDP=Weight of dry pod per plant, NRP=Number of ridge per pod, ADPW=Average dry pod weight, DPL=Dry pod length, DPW=Dry pod width, NSP=Number of seed per pod, SWE=Seed weight per pod, HSW=Hundred seed weight.

4.5. Path Analysis

The correlation coefficients of seed yield with tested traits were significant. This implies the importance of partitioning the correlation coefficients into direct and indirect effects on seed yield, so as to determine the selection criteria for seed yield improvement. In this study, using seed yield per hectare as dependent variable and the other eighteen characters as casual variables, the path coefficient analysis was studied both at genotypic and phenotypic level and illustrated in Table 7and 8 respectively.

4.5.1 Genotypic Path Coefficient Analysis of Seed Yield with other Characters

Seed weight per pod, weight of dry pod per plant, stem diameter, internodes length and plant height had positive and highly significant genotypic correlation with seed yield per hectare. These traits also exerted positive direct effect on seed yield per hectare. Lenka and Mishra (1973) rated the direct and indirect effects into negligible (0.00-0.09), low (0.10-0.19), moderate (0.20-0.29), high (0.30-1.00) and very high (>1.00). Based on these rates, seed weight per pod (1.0624) had exerted very high positive direct effect, while weight of dry pod per plant (0.7665) and stem diameter (0.3134) had exerted high positive direct effect on seed yield per hectare. Internodes length (0.2549) and plant height (0.1859) had exerted moderate and low positive direct effects on seed yield per hectare, respectively. They contributed low and positive indirect effect through each other and via average dry pod weight.

Number of internodes per plant, average number of dry pod per plant and dry pod width had positive significant genotypic correlation with seed yield per hectare but had negative and negligible direct effect ($\leq$ -0.0042) on seed yield. These traits had positive and highly significant genotypic correlation with seed yield per hectare was due to the high and positive indirect effect through seed yield per hectare. All traits that exhibited positive and significant genotypic correlation with seed yield per hectare had also high positive indirect effect through seed weight per pod. Moreover, all traits that exhibited positive and significant genotypic correlation regardless their negative or positive direct effect on seed yield had high and positive indirect effect through seed weight per pod. The results of genotypic path analysis showed that seed weight per pod, weight of dry pod per plant, stem diameter, internodes length and plant height had practical importance in selection of okra genotypes for high seed yield per hectare.

Akinyele and Osekita (2006) reported that number of pods per plant had high positive direct effect on seed yield per plant. In addition, number of branches per plant had positive direct effect on seed yield per plant at genotypic level which is in agreement with the current study results. The current results are also in agreement with results of path analysis reported by Adeniji and Aremu (2007) that plant height at maturity and seeds per pod had positive direct effect on seed yield per plant.

Number of branches, number of ridges per pod, and hundred seeds weight showed highly significant genotypic correlation with seed yield per hectare but these traits had negative and moderate direct effect on seed yield per hectare. Similarly number of internodes per plant, average number of dry pod and dry pod weight had highly significant genotypic association with seed yield per hectare, however, these traits had negative but negligible direct effect on seed yield per hectare. The highly significant genotypic association of all these traits was due to the low to high positive indirect effects through one or more traits of the positive direct effect of seed yield per hectare.

The correlation coefficient indicates the association of variables which is the total effect that does not show the direct effect and indirect effects of variables. The path analysis is the portioning of the total correlation into direct and indirect effects of independent variable(s) on dependent variable (Singh and Chaudhary, 1977; Dabholkar, 1992; Nadarajian and Gunasekaran, 2005). If the variable or trait has positive correlation and the direct effect of the variable or trait is negative or negligible, the positive correlation of the trait is because of the indirect effects through other traits. In such situation, the indirect casual factors/traits are to be considered simultaneously for selection (Singh and Chaudhary, 1977). Therefore, the seed weight per pod, weight of dry pods per plant, plant height, stem diameter and internodes length need to be considered simultaneously. This is because the positive indirect effects of these traits were the cause of positive and significant genotypic correlation of number of branches, number of ridges per pod, hundred seeds weight, number of internodes per plant, average number of dry pod and dry pod weight with seed yield per hectare.

Residual effect in the present study was 0.080 (Table 7) showing that 91.92% of the variability in seed yield was explained by the component factors. The remaining 8.07% is explained by other traits not considered in this study.

Table 7. Estimates of direct and indirect effect of different traits on seed yield at genotypic level in 24 okra genotypes tested at Dire Dawa 2017.

	DE	DF	D50%F	DM	PLH	SD	NBPP	NIPP	IL
DE	**0.1043**	-0.0524	-0.0318	0.0234	-0.0521	0.0087	0.0559	0.0018	0.0163
DF	0.0520	**-0.1051**	-0.0440	0.0588	-0.0028	0.0843	-0.0131	0.0010	0.0528
D50%F	0.0712	-0.0993	**-0.0465**	0.0565	-0.0146	0.0907	0.0067	0.0013	0.0429
DM	0.0308	-0.0780	-0.0332	**0.0793**	0.0508	0.1437	-0.0606	0.0000	0.0640
PLH	-0.0292	0.0016	0.0037	0.0216	**0.1859**	0.0799	-0.1632	-0.0027	0.1095
SD	0.0029	-0.0283	-0.0135	0.0364	0.0474	**0.3134**	-0.1431	-0.0016	0.0084
NBPP	-0.0254	-0.0060	0.0014	0.0209	0.1322	0.1954	**-0.2295**	-0.0024	0.0861
NIPP	-0.0512	0.0298	0.0170	0.0009	0.1365	0.1340	-0.1506	**-0.0037**	0.0213
IL	0.0067	-0.0218	-0.0078	0.0199	0.0799	0.0103	-0.0775	-0.0003	**0.2549**
ANDP	-0.0028	0.0180	0.0068	-0.0065	0.0444	0.0243	-0.0620	-0.0014	0.0833
WtDP	-0.0228	0.0326	0.0139	-0.0247	0.0126	0.0139	-0.0158	-0.0012	-0.0099
NRPP	-0.0172	-0.0036	-0.0021	0.0263	0.1439	0.1869	-0.1595	-0.0022	0.1456
ADPW	-0.0148	0.0250	0.0090	-0.0214	-0.0355	0.0176	0.0436	-0.0001	-0.0583
DPL	-0.0381	0.0225	0.0103	-0.0155	-0.0257	0.0041	0.0455	-0.0005	-0.0542
DPW	-0.0124	-0.0081	-0.0044	0.0240	0.1148	0.1350	-0.1394	-0.0016	0.1562
NSPP	-0.0216	0.0026	0.0024	0.0257	0.1025	0.2045	-0.1431	-0.0019	0.0851
SWPP	-0.0328	0.0144	0.0069	0.0136	0.1262	0.1537	-0.1569	-0.0023	0.1388
100SW	-0.0291	0.0205	0.0085	-0.0078	0.0823	0.0270	-0.0884	-0.0016	0.1271

Residual factor=0.0807

DE =days to emergency, DF=days to first flowering, D50%F=days to 50% flowering, DM=days to maturity, PLH=Plant height, SD=Stem diameter, NBP=Number of branches, NIP=Number of internodes per plant, IL=Internodes length, ANDP=Average number of dry pod per plant, WtDP=Weight of dry pod per plant, NRP=Number of ridge per pod, ADPW=Average dry pod weight, DPL=Dry pod length, DPW=Dry pod width, NSP=Number of seed per pod, SWE=Seed weight per pod, HSW=Hundred seed weight

Table 7. Continued

	ANDP	WtDP	NRPP	ADPW	DPL	DPW	NSPP	SWPP	100SW	rg
DE	0.0005	-0.1673	0.0441	0.0895	-0.0351	0.0048	0.0385	-0.3342	0.0753	-0.21^{ns}
DF	0.0031	-0.2379	-0.0091	0.1497	-0.0206	-0.0031	0.0046	-0.1455	0.0527	-0.12^{ns}
D50%F	0.0027	-0.2287	-0.0120	0.1214	-0.0212	-0.0038	0.0097	-0.1584	0.0490	-0.13^{ns}
DM	0.0015	-0.2385	-0.0887	0.1696	-0.0188	-0.0121	-0.0603	0.1825	0.0267	0.16^{ns}
PLH	-0.0043	0.0517	-0.2067	0.1199	-0.0133	-0.0248	-0.1027	0.7212	-0.1193	0.63**
SD	-0.0014	0.0340	-0.1593	-0.0353	0.0013	-0.0173	-0.1215	0.5209	-0.0233	0.42*
NBPP	-0.0049	0.0529	-0.1856	0.1194	-0.0190	-0.0244	-0.1161	0.7261	-0.1038	0.62**
NIPP	-0.0069	0.2420	-0.1605	-0.0092	0.0129	-0.0179	-0.0966	0.6708	-0.1158	0.65**
IL	-0.0059	-0.0298	-0.1526	0.1436	-0.0204	-0.0246	-0.0622	0.5787	-0.1344	0.56**
ANDP	**-0.0180**	0.4460	-0.0872	-0.0204	0.0303	-0.0194	-0.0353	0.5359	-0.1650	0.77**
WtDP	-0.0105	**0.7665**	-0.0544	-0.4921	0.0512	-0.0084	-0.0194	0.3651	-0.1308	0.47*
NRPP	-0.0059	0.1561	**-0.2672**	-0.0233	0.0016	-0.0329	-0.1497	0.9562	-0.1487	0.80**
ADPW	-0.0006	0.6004	-0.0099	**-0.6283**	0.0554	0.0019	-0.0065	0.1224	-0.0582	0.04^{ns}
DPL	-0.0057	0.4092	-0.0044	-0.3628	**0.0960**	-0.0052	-0.0123	0.2697	-0.1125	0.22^{ns}
DPW	-0.0087	0.1601	-0.2191	0.0297	0.0124	**-0.0402**	-0.1003	0.9130	-0.2080	0.80**
NSPP	-0.0034	0.0799	-0.2148	-0.0220	0.0063	-0.0216	**-0.1863**	0.8237	-0.0478	0.67**
SWPP	-0.0091	0.2635	-0.2405	-0.0724	0.0244	-0.0345	-0.1444	**1.0624**	-0.2023	0.91**
100SW	-0.0110	0.3720	-0.1474	-0.1358	0.0401	-0.0310	-0.0330	0.7973	**-0.2695**	0.72**

DE =days to emergency, DF=days to first flowering, D50%F=days to 50% flowering, DM=days to maturity, PLH=Plant height, SD=Stem diameter, NBP=Number of branches, NIP=Number of internodes per plant, IL=Internodes length, ANDP=Average number of dry pod per plant, WtDP=Weight of dry pod per plant, NRP=Number of ridge per pod, ADPW=Average dry pod weight, DPL=Dry pod length, DPW=Dry pod width, NSP=Number of seed per pod, SWE=Seed weight per pod, HSW=Hundred seed weight

4.5.2 Phenotypic Path Coefficient Analysis of Seed Yield with other Characters

The phenotypic correlation coefficient computed between seed yield per hectare and other traits showed the presence of significant association except the average dry pod weight with seed yield which had positive and non-significant correlation. This implies the importance of partitioning the correlation coefficients into direct and indirect effects on seed yield per hectare, so as to determine the selection criteria for seed yield improvement in okra. The results of path analysis at phenotypic level are presented in Table 8. Seed weight per pod had very high (1.7939) positive direct effect with seed yield followed by average number of dry pod per plant, dry pod width, and number of internodes per plant which had high positive direct effect (0.2965 to 0.9434) on seed yield per hectare. Days to first flowering and internodes length had moderate (0.2332) and low (0.1442) positive direct effect on seed yield per hectare, respectively. All these traits had positive and significant phenotypic correlation with seed yield per hectare except average dry pod weight and days to first flowering.

Seed weight per pod had also positive and very high indirect effect via dry pod width and average number of dry pod per plant as well as positive moderate indirect effect through number of internodes per plant. Average number of dry pod per plant, dry pod width, and number of internodes per plant had also moderate and positive indirect effect via each other except the first two traits which had positive and low indirect effect via number of internodes per plant. Similarly internodes length via seed weight per pod and through average number of dry pod per plant and dry pod width had also very high and positive indirect effect on seed yield per hectare, respectively.

Hundred seeds weight had very high (-1.4093), and number of seeds per pod and weight of dry pod per plant had high (-0.876 and -0.7394, respectively) negative direct effects on seed yield per hectare though the phenotypic correlation coefficient of these traits with seed yield per hectare was positive and significant. One or more of these traits also exerted low to very high negative indirect effect on seed yield per hectare via the traits that exhibited positive and direct effects on seed yield. Other traits, viz. plant height, stem diameter, number of branches per plant had negligible positive direct effect though these traits exhibited positive and significant phenotypic correlation with seed yield per hectare. Dry pod length showed positive and significant phenotypic correlation with seed yield per hectare but had negative and negligible direct effect.

The phenotypic correlation of days to 50% flowering and days to emergence with seed yield per hectare was negative significant and the traits had also moderate (-0.1283) and negligible (-0.0697) negative direct effect on seed yield, respectively.

In this study, the results of path coefficient analysis showed that seed weight per pod followed by average number of dry pod per plant, dry pod width, number of internodes per plant and internodes length could be used as selection criteria for high seed yield per hectare in okra genotypes. Besides positive and highly significant correlation of these traits with seed yield per hectare, the traits had very high to moderate positive direct effect except that it is low for internodes length. If the correlation coefficient between causal factor and the effect is almost equal to its direct effect, the correlation explains the true relationship and the direct selction through these trait will be effective (Singh and Chaudhary, 1977).

Mihretu *et al.* (2014) and Muluken *et al*. (2015) reported the positive and significant phenotypic correlations among seeds per pod, number of pods per plant, fruit length and width. In this study the seed weight per pod, average number of dry pod per plant and dry pod width having positive and significant phenotypic correlations with seed yield per hectare also exhibiting very high to moderate direct effect suggested that the association between these traits is perfect and contributed much for the observed seed yield per hectare in 24 okra genotypes. This suggestion is supported by many authors (Singh and Chaudhary, 1977; Dabholkar, 1992; Nadarajian and Gunasekaran, 2005). In support of the current study results, Akinyele and Osekita (2006) also reported that high positive direct effects of number of pods per plant on seed yield in okra. Alake *et al.* (2012) also reported number of pods per plant exhibited a high positive direct effect on pod yield of okra.

Residual effect from phenotypic path analysis was 0.079 (Table 8), indicating that all the traits included in the study explained high percentage of variation (92.07%) in seed yield per hectare in okra and other factors not included in the study can explain only 7.9%. The residual effect determines how much best the causal factors or dependent variables account for the variability of dependent variable (Dabholkar, 1992; Singh and Chaudhary, 1977).

Table 8. Estimates of direct and indirect effect of different traits on seed yield at phenotypic level in 24 okra genotypes at Dire Dawa 2017

	DE	DF	D50%F	DM	PLH	SD	NBPP	NIPP	IL
DE	**-0.0697**	0.1315	-0.0989	-0.0519	-0.0061	0.0004	-0.0092	-0.1527	0.0085
DF	-0.0393	**0.2332**	-0.1240	-0.0877	-0.0002	-0.0251	0.0028	-0.0915	0.0325
D50%F	-0.0538	0.2253	**-0.1283**	-0.0812	-0.0014	-0.0296	-0.0001	-0.1215	0.0276
DM	-0.0341	0.1929	-0.0983	**-0.1060**	0.0108	-0.0639	0.0162	0.0093	0.0480
PLH	0.0201	-0.0018	0.0085	-0.0541	**0.0211**	-0.0210	0.0284	0.2302	0.0692
SD	0.0004	0.0789	-0.0511	-0.0913	0.0060	**-0.0742**	0.0270	0.1467	0.0038
NBPP	0.0174	0.0177	0.0005	-0.0465	0.0163	-0.0543	**0.0369**	0.1976	0.0498
NIPP	0.0359	-0.0719	0.0526	-0.0033	0.0164	-0.0367	0.0246	**0.2965**	0.0131
IL	-0.0041	0.0526	-0.0246	-0.0353	0.0101	-0.0020	0.0127	0.0270	**0.1442**
ANDP	0.0012	-0.0531	0.0242	0.0195	0.0044	-0.0039	0.0107	0.1218	0.0481
WtDP	0.0175	-0.0888	0.0466	0.0542	0.0003	0.0008	0.0025	0.0966	-0.0083
NRPP	0.0131	0.0106	-0.0085	-0.0586	0.0181	-0.0547	0.0268	0.1848	0.0880
ADPW	0.0113	-0.0627	0.0282	0.0446	-0.0048	-0.0024	-0.0077	0.0023	-0.0348
DPL	0.0309	-0.0561	0.0304	0.0231	-0.0038	0.0035	-0.0079	0.0442	-0.0354
DPW	0.0087	0.0206	-0.0165	-0.0488	0.0143	-0.0370	0.0228	0.1366	0.0971
NSPP	0.0161	-0.0081	0.0058	-0.0537	0.0130	-0.0591	0.0245	0.1616	0.0531
SWPP	0.0256	-0.0363	0.0201	-0.0307	0.0161	-0.0431	0.0269	0.1980	0.0871
100SW	0.0217	-0.0484	0.0247	0.0134	0.0102	-0.0068	0.0147	0.1321	0.0783

Residual factor= 0.079

DE =days to emergency, DF=days to first flowering, D50% F=days to 50% flowering, DM=days to maturity, PLH=Plant height, SD=Stem diameter, NBP=Number of branches, NIP=Number of internodes per plant, IL=Internodes length, ANDP=Average number of dry pod per plant, WtDP=Weight of dry pod per plant, NRP=Number of ridge per pod, ADPW=Average dry pod weight, DPL=Dry pod length, DPW=Dry pod width ,NSP=Number of seed per pod, SWE=Seed weight per pod, HSW=Hundred seed weight.

Table 8 Continued

	ANDP	WtDP	NRPP	ADPW	DPL	DPW	NSPP	SWPP	100SW	rp
DE	-0.0161	0.1856	0.0318	-0.1381	0.0327	-0.0654	0.2025	-0.6587	0.4384	-0.24*
DF	-0.2148	0.2816	-0.0077	-0.2301	0.0178	0.0461	0.0304	-0.2790	0.2926	-0.16*
D50%F	-0.1780	0.2684	-0.0113	-0.1878	0.0175	0.0669	0.0399	-0.2809	0.2711	-0.16*
DM	-0.1737	0.3781	-0.0939	-0.3596	0.0161	0.2400	-0.4436	0.5188	0.1780	0.24*
PLH	0.1968	-0.0121	-0.1459	-0.1939	0.0132	0.3540	-0.5411	1.3695	-0.6780	0.66**
SD	0.0497	0.0077	-0.1251	0.0275	0.0034	0.2596	-0.6970	1.0426	-0.1287	0.49*
NBPP	0.2748	-0.0498	-0.1236	-0.1781	0.0159	0.3232	-0.5810	1.3072	-0.5623	0.66**
NIPP	0.3875	-0.2408	-0.1058	0.0068	-0.0110	0.2403	-0.4773	1.1980	-0.6277	0.70**
IL	0.3149	0.0428	-0.1036	-0.2064	0.0182	0.3512	-0.3227	1.0837	-0.7660	0.59**
ANDP	**0.9434**	-0.4183	-0.0623	0.0105	-0.0232	0.2647	-0.1589	0.9786	-0.9415	0.77**
WtDP	0.5337	**-0.7394**	-0.0395	0.6796	-0.0400	0.0969	-0.0595	0.5997	-0.7196	0.43*
NRPP	0.3464	-0.1720	**-0.1698**	0.0451	-0.0010	0.4500	-0.7654	1.7512	-0.8211	0.88**
ADPW	0.0116	-0.5876	-0.0089	**0.8552**	-0.0438	-0.0434	-0.0018	0.1491	-0.2905	0.01^{ns}
DPL	0.2965	-0.4009	-0.0023	0.5075	**-0.0739**	0.0603	-0.0370	0.4345	-0.6177	0.20*
DPW	0.4789	-0.1374	-0.1465	-0.0712	-0.0085	**0.5215**	-0.4814	1.5973	-1.1095	0.84**
NSPP	0.1711	-0.0502	-0.1484	0.0017	-0.0031	0.2866	**-0.8760**	1.3774	-0.2338	0.68**
SWPP	0.5146	-0.2472	-0.1658	0.0711	-0.0179	0.4644	-0.6726	**1.7939**	-1.0644	0.94**
100SW	0.6303	-0.3775	-0.0989	0.1763	-0.0324	0.4106	-0.1453	1.3550	**-1.4093**	0.75*

DE =days to emergency, DF=days to first flowering, D50% F=days to 50% flowering, DM=days to maturity, PLH=Plant height, SD=Stem diameter, NBP=Number of branches, NIP=Number of internodes per plant, IL=Internodes length, ANDP=Average number of dry pod per plant, WtDP=Weight of dry pod per plant, NRP=Number of ridge per pod, ADPW=Average dry pod weight, DPL=Dry pod length, DPW=Dry pod width ,NSP=Number of seed per pod, SWE=Seed weight per pod, HSW=Hundred seed weight.

4.6. Genetic Divergence Analysis

4.6.1. Genetic Distances among Okra Genotypes

The genetic distances of 276 pair of genotypes is presented in Appendix Table 6. The genetic distance of for all possible pairs of 24 okra genotypes ranged from 1.96 to 11.36 with the mean, standard deviation and coefficient of variation of 5.85, 1.97 and 33.75%, respectively (Table 9).The highest genetic distances (Euclidean distance) was computed between the released okra variety, 23793 (Bamya-Humera) and 245162 (11.36) followed by between Humera 01 and 245162 (11.28) and between Humera 01 and 240207 (10.69). Whereas, the lowest genetic distances (Euclidean distance) was estimated between Anoop and Mythri (1.96) followed by between 240207 and 240586 (2.07) and between ArkaAnamica and Kiran (2.2) (Appendix Table 6). Generally, 43 (15.58%) pair of genotypes had genetic distances ≤3.88, 110 (39.86%) pair of genotypes had genetic distances between 3.89-5.85, 74 (26.81%) pairs of genotypes had genetic distance between the interval 5.86 to 7.83 while 40 (14.49%) pair of genotypes had genetic distances between 7.84 to 9.79 and 9(3.26%) pair of genotypes had genetic distance ≥9.79 (Figure 2, Appendix Table 6).

The released variety Bamya-Humera (23793) and Humera 01 both collected from northern Ethiopia had higher genetic distances with genotypes collected from other regions and introduced varieties. The genetic distances among the introduced varieties were lower than genetic distances among genotypes collected from Ethiopia ranged from 1.96 to 10.01. This showed that there is a higher chance of improving seed yield and seed related traits through selection and/or hybridization of okra genotypes from different okra growing regions of Ethiopia. Mulukn *et al*. (2015) reported that Ethiopian okra collections exhibited wide genetic distances in the range between 5.16 and 11.14 while introduced varieties had 5. 32. Anteneh (2017) estimated genetic distances of all possible pairs of 25 okra genotypes in which the genetic distance ranged from 3.1 to 12.6 with 7.2, 2 and 27.85 mean, standard deviation and coefficient of variation, respectively. He also reported that the highest genetic distance was observed between okra collections from Ethiopia and introduced commercial varieties from other countries while the lowest genetic distance was estimated between introduced commercial varieties.

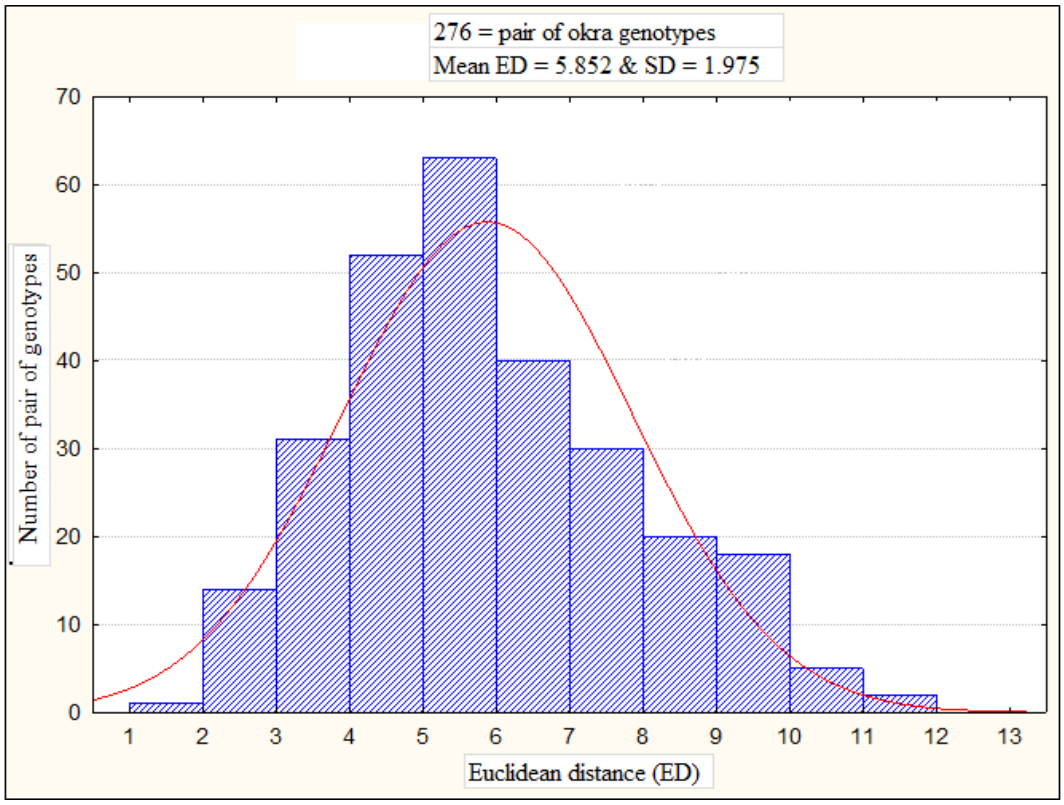

Figure 2.Distribution of 276 pair of okra genotypes into different categories of Euclidean distances

The mean genetic distance of each okra genotype to other 23 genotypes was calculated to have information about the most distant and closest genotypes (Table 9). Depending on the mean Euclidean distance, 23793 (8.86) followed by Humera 01 (8.56) and Arcanamica (7.34) were the most distant genotypes to others, whereas Clemson (4.7) followed 240592 (4.82) and 245157 (4.91) were found the closest to other genotypes. Generally, eight (33.33%) genotypes, four each obtained from Ethiopia and other countries had mean genetic distance of ≥5.85 (overall mean distances of genotypes). However, only two okra genotypes collected from Ethiopia had significantly highest mean genetic distance of >7.82 (overall mean distances of genotypes + standard deviation). The result suggested the presence of considerable number of distant okra genotypes to others that could be used in crossing program.

It is believed that the distant parental lines are producing heterotic hybrids. Genetic distance is

important for selecting parents in combination breeding of different autogamous crops to obtain transgressive segregants (Pradip *et al.,* 2010). .Shujaat *et al*.(2014) suggested that genetic variations is an important feature to get together the diversified goals of plant breeding including higher yield, resistance to diseases, quality of the yield and wider adaptations. Mihretu *et al*. (2014a) also suggested that crossing of genotypes not genetically diverse or with little genetic diversity might not give higher heterotic value in F_1 and narrow range of variability in the segregating F_2 population.

Table 9. Range and mean Euclidean distance of 24 okra genotypes estimated from 20 quantitative traits as evaluated at Dire Dawa in 2017

Genotype	Minimum	Maximum	Mean	SD	CV (%)
Anoop	1.96	10.01	6.2	1.81	29.26
Arcanamica	4.05	9.68	7.34	1.51	20.6
ArkaAnamica	2.2	9.45	5.62	1.56	27.74
Clemson spinless	2.43	8.54	4.78	1.62	33.92
Dhenu	3.93	9.78	6.2	1.32	21.29
Kiran	2.2	9.08	5.66	1.62	28.6
Mythri	1.96	9.05	5.85	1.8	30.71
NamdHari	2.39	8.27	5.67	1.59	28.06
SOH701	2.61	7.62	5.03	1.22	24.16
SOH714	3.16	7.41	5.35	1.17	21.8
23793 (Bamya-Humera)	6.71	11.36	8.86	1.22	13.74
Humera 01	5.96	11.28	8.56	1.51	17.69
92203	2.82	9.62	5.23	1.84	35.09
240204	2.85	10.6	5.53	2.25	40.66
240207	2.07	10.69	5.82	2.36	40.49
240586	2.07	10.6	5.66	2.26	39.9
240592	2.43	8.39	4.82	1.68	34.87
240600	2.61	8.24	5.9	1.19	20.25
240609	2.47	9.46	5.12	1.79	34.97
240784	2.71	8.7	5.06	1.81	35.78
242433	3.15	9.94	5.8	1.83	31.65
242444	3.71	8.12	5.16	1.07	20.77
245157	2.71	9.78	4.91	1.94	39.46
245162	3.13	11.36	6.33	2.35	37.04
Overall	1.96	11.36	5.85	1.97	33.75

4.6.2. Clustering of Genotypes

The Euclidean distance matrix of 276 pair of genotypes estimated from seed yield and seed yield related traits was used to construct dendrograms based on the Unweighted Pair-group methods with Arithmetic Means (UPGMA). Accordingly, the 24 okra genotypes were grouped into seven distinct clusters (Figure 3).Cluster III consisted of 10 genotypes (41.67%) including one commercial introduced variety while Cluster II, IV and VII contained each one genotype. Cluster I and V consisted of five (20.83%) and four (16.67%) genotypes, respectively. Cluster I was constructed by the commercial varieties introduced from India while Cluster V was consisted of two genotypes each obtained from Ethiopia and India. Cluster VI consisted of two okra genotypes obtained from Ethiopia and India.

Muluken *et al*. (2015) studied 25 okra genotypes and identified ten major clusters while Mihretu *et al*. (2014) reported five divergent groups of 25 okra collections from two regions (Gambella and Asossa) of Ethiopia. Tesfa and Yosef (2016) were able to group 50 okra collections into four major clusters which were obtained from four major production regions of Ethiopia. Anteneh (2017) studied 25 okra genotypes of which 11 and 14 genotypes were obtained from other countries and three geographic regions of Ethiopia, respectively. The genotypes were grouped into seven major clusters. He also indicated genotypes from same countries tend to be grouped in the same clusters which was in agreement with the current study results that a total of 6 (60%) out of 10 introduced varieties from India were grouped separately into two clusters.

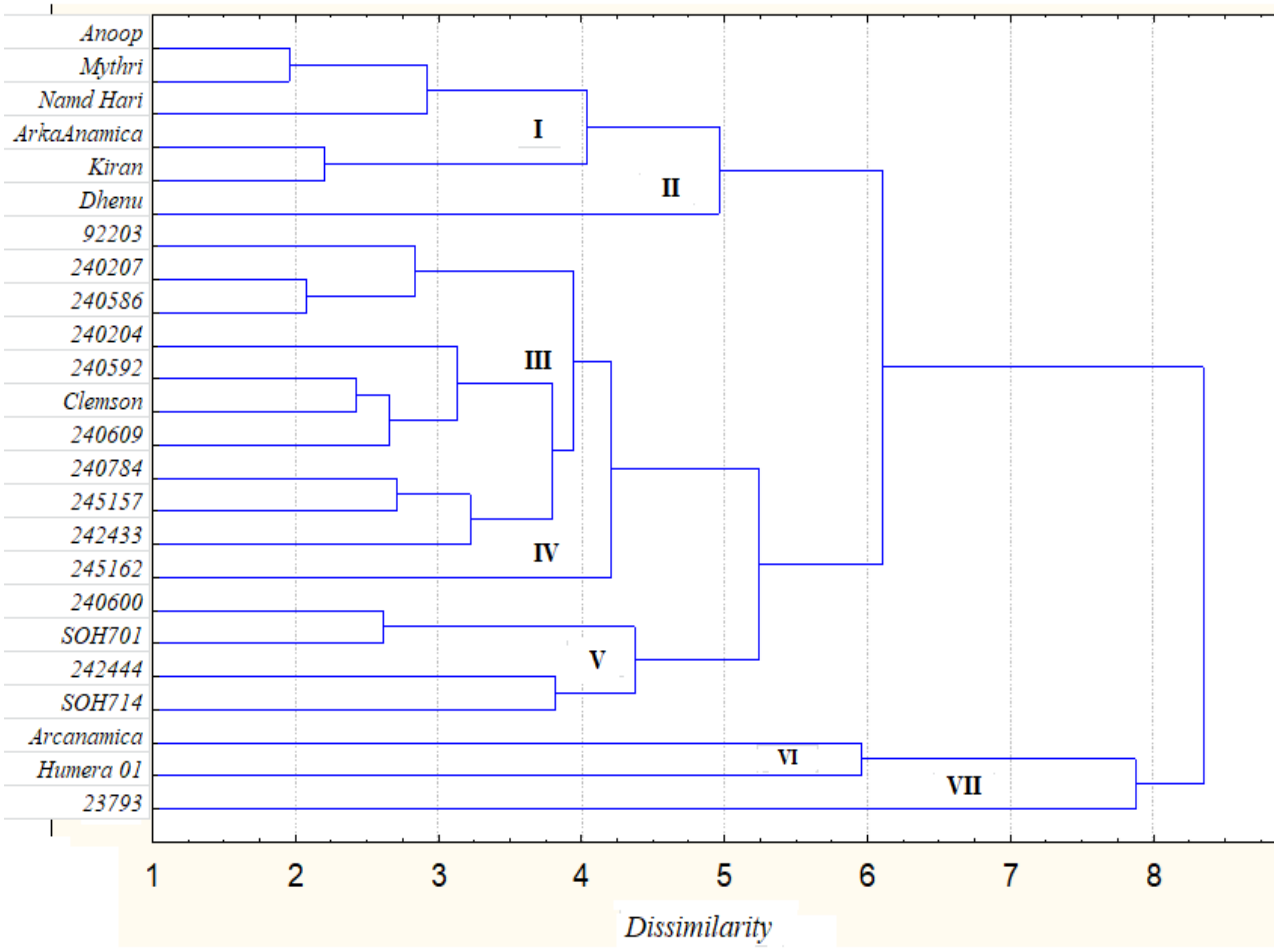

Figure 3. Dendrogram depicting dissimilarity of 24 okra genotypes by Unweighted Pair group Method with Arithmetic Means (UPGMA) clustering method from Euclidean distances matrix estimated from 20seed yield and seed related traits.

4.6.3. Cluster Mean Analysis

The mean values of the seven clusters for 20 seed yield and seed related traits were presented in Table 10.The unique features of Cluster III and IV were by having higher mean values than the overall mean values of genotypes for all traits including for seed yield except the former cluster for average pod weight, dry pod weight and days to 50% emergence and flowering and the latter cluster for days to 50% emergence, days to first and 50% flowering. This suggested the higher chance of developing varieties through selection and further evaluation of genotypes from these two clusters. Cluster I, V, VI and VII were distinguished by having lower mean values for all traits including seed yield than overall mean values of genotypes for all traits except the clusters had mean values greater than over all mean values only for 2 to 4 traits. Cluster II had higher mean values than overall mean values of genotypes for stem diameter, number of branches per plant, number of internodes per plant, weight of dry pod per plant, number of ridge per pod and average dry pod weight. The cluster also had higher mean values than overall mean values of genotypes for dry pod length and width, number of seed per pod, seed weight per pod and hundred seed weight. However, this cluster had lower mean values than overall mean values of genotypes for the rest of the traits including seed yield.

According to the mean analysis of clusters, selection of genotypes from Cluster III and IV is possible to obtain genotypes with highest seed yield and other desirable traits. It is suggested also to make cross among the two cluster members and genotypes from Cluster II to combine desirable traits in hybrids and searching better performing varieties in subsequent segregating generations. Mihretu *et al.* (2014a), Muluken *et al.* (2015) Tesfa and Yosef (2016) and Anteneh (2017) also reported that some of the clusters constructed by okra genotypes obtained from Ethiopia that had higher mean values for desirable traits including seeds per pod and hundred seed weight.

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Table 10.Cluster mean values for 20 quantitative traits of 24 okra genotypes evaluated at Dire Dawa in 2017

	Cluster						
Trait	I	II	III	IV	V	VI	VII
Days to 50% emergence	9.47	10.33	9.03	8.33	14.58	10.83	17.67
Days to first flowering	57.92	57.69	61.65	60.46	61.22	60.84	79.18
Days to 50%flowering	67.32	69.02	70.68	69.80	72.72	69.85	89.84
Days to maturity	84.00	90.00	96.00	95.00	94.09	93.34	105.67
Plant height (cm)	102.76	121.60	137.62	175.20	118.38	111.00	106.70
Stem diameter(cm)	1.49	2.21	2.02	1.94	1.76	1.71	1.79
Number of branches per plant	2.52	4.80	5.92	5.13	3.92	2.81	2.93
Number of internodes per plant	20.90	26.20	29.61	47.82	19.56	19.78	7.77
Internodes length (cm)	5.32	4.44	7.00	6.32	6.04	4.51	6.80
Number of dry pod per plant	21.40	12.09	19.99	22.05	19.53	5.68	11.69
Weight of dry pod per plant (g)	1006.04	1150.20	656.73	886.00	370.75	199.80	257.40
Number of ridge per pod	5.72	7.38	7.58	8.46	6.44	5.47	5.87
Average dry pod weight (g)	45.70	83.93	28.99	33.83	18.61	26.44	24.91
Dry pod length (cm)	13.29	14.79	11.08	12.81	9.38	6.68	9.69
Dry pod width (cm)	1.35	1.76	2.15	1.92	1.68	0.88	1.52
Number of seed per pod	60.81	83.43	97.70	110.17	77.93	66.66	42.79
Seed weight per pod(g)	3.51	5.66	6.13	7.01	4.48	1.46	2.10
Hundred seed weight (g)	5.56	6.47	6.15	6.18	5.36	2.95	4.99
Seed yield per plant(g)	77.85	67.97	122.28	153.55	88.07	10.81	25.19
Seed yield per hectare (kg)	1621.80	1416.00	2547.70	3199.00	1834.75	225.00	525.00

5. SUMMARY AND CONCLUSION

Ethiopia is claimed as the likely center of origin for okra, however, the crop contribution to food and nutrition security in the country is negligible which is produced as traditional crop in some parts of the country. The crop is not only known for high nutritious tender fruits used as vegetable but it is known to produce seeds with reasonably high oil content with high proportion of desirable fatty acids (oleic and linoleic acids). But there was no attempt to characterize okra genotypes from Ethiopia for seed yield and seed yield related traits. Therefore, this study was conducted with the objectives of assessing genetic variability among okra genotypes for seed yield and related traits, to determine the association of seed yield and seed yield related traits and to estimate the direct and indirect effects of traits on seed yield of okra. The field experiment was conducted in randomized complete block design (RCBD) with three replications at Dire Dawa in 2017.

The research result revealed the presence of highly significant ($P<0.01$) differences among okra genotypes for all quantitative traits. The seed yield per hectare ranged from 122 to 3206 kg with mean seed yield of 1938.13 kg ha^{-1}. The mean seed yield of 14 okra genotypes collected from different regions of Ethiopia was 2216.14 kg ha^{-1}while the 10 commercial varieties introduced from two countries had 1548.9 kg ha^{-1}. This indicated that the genotypes collected from Ethiopia had seed yield advantage of 43.08% over the introduced varieties. Besides, most of okra genotypes collected from Ethiopia had higher mean values than introduced commercial varieties for majority of the traits. The results showed the higher chance of developing okra varieties for high seed yield through selection of okra genotypes collected from Ethiopia.

The largest proportion of okra genotypes had green pod color and erects fruit position on stem and smooth pod. The okra genotypes collected from Ethiopia had wide variation for pod shape more than the introduced commercial varieties from other countries. However, the introduced varieties were early flowering and maturity than the genotypes collected from Ethiopia. The okra genotypes having green pod color and fruit at erect position on stem are desirable characteristics for the production of tender fruit since the green color is preferable by the consumers to use as vegetable and the erect position protect fruits not to have contact to ground during the development of fruits.

The phenotypic (PCV) and genotypic (GCV) coefficient of variations of the 20 seed yield and seed related traits of okra genotypes varied in the range between 8.35% to 57.70% and 5.44 to

49.20%, respectively. Heritability in broad sense (H^2) and genetic advance as percent of mean (GAM) ranged from 20.92% to 94 % and 5.13 to 91.94%., respectively. All the estimated variability components (GCV, PCV, H^2 and GAM) were high for all traits except days to first flowering, days to 50% of flowering, days to maturity in which the values of two or more components were categorized under low or moderate. In addition, the values of PCV and GCV were moderate for plant height and GCV was moderate for stem diameter and hundred seeds weight. The differences between the values of PCV and GCV were <5%. This showed that most of the traits except the three phenology traits were highly heritable which showed the expression of the traits was more of the function of genetic factor.

The genotypic correlation coefficient between seed yield per hectare and most of other traits was positive and significant except days to emergence, days to first flowering, days to 50% flowering, days to maturity, average dry pod weight and dry pod length. The phenotypic correlation coefficient between seed yield per hectare and all traits except average dry pod weight was significant in positive and negative direction. Among the traits; seed weight per pod and internodes length had positive direct effects on seed yield per hectare at phenotypic and genotypic levels. Moreover, the seed weight per pod followed by weight of dry pod per plant, stem diameter, internodes length and plant height had very high to low positive genotypic direct effects on seed yield per hectare. These traits also exerted very high to low positive indirect effects through other traits on seed yield at genotypic level. Therefore, these traits will have practical importance in selection of okra genotypes for high seed yield per hectare.

The genetic distances of 24 okra genotypes ranged from 1.96 to 11.36 with the mean, standard deviation and coefficient of variation of 5.85, 1.97 and 33.75%, respectively, in which most of the higher genetic distances were computed between okra genotypes collected from Ethiopia. In contrast most of the genetic distances among the introduced okra varieties were low. A total of 43 (15.58%) pair of genotypes had genetic distances $\leq$3.88, 110 (39.86%) pair of genotypes had genetic distances between 3.89-5.85,74(26.81%) pairs of genotypes had genetic distance between the interval 5.86 to 7.83 while 40 (14.49%) pair of genotypes had genetic distances between 7.84 to 9.79 and 9(3.26%) pair of genotypes had genetic distance $\geq$9.79 . Eight (33.33%) genotypes, four each obtained from Ethiopia and other countries had mean genetic distance of >5.85 (overall mean distances of genotypes). However, only two okra genotypes collected from Ethiopia had significantly highest mean genetic distance than overall mean distances of genotypes (>7.82).

Dendrograms constructed based on the Unweighted Pair-group Methods with Arithmetic Means (UPGMA) from Euclidean distance matrix of 276 pair of genotypes was capable to group the 24 okra genotypes into seven distinct clusters. Cluster III, I and V consisted of 10 (41.67%), 5(20.83%) and 4 (16.67%) genotypes, respectively, while Cluster II, IV and VII consisted of each one genotype. Majority of commercial varieties introduced from India (6 out of 9 or 66.67%) constructed two separate clusters without mix of okra genotypes from Ethiopia and USA. Cluster III and IV which consisted of 10 okra genotypes from Ethiopia and one okra variety from USA had mean values greater than the overall mean values of genotypes for all traits except the former cluster for average pod weight, dry pod weight and days to 50% emergence and flowering and the latter cluster except days to maturity. Therefore, it is possible to develop variety (ies) for high yield through further evaluation and selection of genotypes from these two clusters.

Generally, the research results indicated, i) the presence of wide variations among okra genotypes for seed yield and related traits, ii) most of the traits except phenology of the crop had high heritability, genotypic and phenotypic correlations with seed yield, iii) the okra genotypes collected from Ethiopia had higher seed yield per hectare and other desirable traits than introduced commercial varieties, and iv) the okra genotypes collected from Ethiopia had high genetic distances among them and between introduced commercial varieties, and v) most of genotypes with high seed yield were grouped into two clusters. These major results suggested that the presence of high chance to develop varieties either through selection and/or hybridization to be made within the okra collection from Ethiopia. However, this research was conducted for one season and at one location, the research was not deal with determination of seed oil content, oil yield per unit area, and fatty acids composition.

Therefore, it is recommended to conduct replicated evaluation of genotypes over varied locations and seasons, which also deal with determination of seed oil content, oil yield per unit area, and fatty acids composition.

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7. APPENDIX

Appendix Table 1. Mean values of 24 okra genotypes for phenology traits evaluated at Dire Dawa in 2017

Genotype	Days to 50% Emergency	Days to first Flowering	Days to50% Flowering	Days to Maturity
92203	11^{bcd}	58.9^{b-f}	68.57^{cde}	84^{cde}
240204	8.33^{c-f}	63.41^{bc}	72.08^{bc}	102.67^{ab}
240207	8.33^{c-f}	62.23^{b-e}	70.89^{cd}	97.67^{abc}
240586	10.67^{b-e}	59.16^{b-f}	70.16^{cde}	92.67^{a-d}
240592	7.33^{ef}	63.35^{bc}	71.68^{bcd}	105.67^{a}
240600	20.67^{a}	63.51^{bc}	77.84^{b}	97^{a-d}
240609	7^{f}	61.96^{b-e}	69.96^{cde}	94^{a-d}
240784	11.33^{bc}	62.87^{bcd}	70.53^{cde}	97^{a-d}
242433	10.33^{b-f}	63.3^{bc}	72.3^{bc}	95.67^{a-d}
242444	9.33^{c-f}	60.05^{b-e}	70.39^{cde}	89.67^{a-d}
245157	7.67^{def}	59.73^{b-e}	68.73^{cde}	90.67^{a-d}
245162	8.33^{c-f}	60.46^{b-e}	69.8^{cde}	95^{a-d}
23793(BamyaHumera)	17.67^{a}	79.18^{a}	89.84^{a}	105.67^{a}
Humera 01	13.33^{b}	63.82^{b}	74.16^{bc}	99.67^{abc}
Mean	10.81	63.00	72.64	96.22
SD	4.00	4.98	5.49	6.06
CV (%)	37.04	7.90	7.56	6.30
Range	7 -20.67	58.9 -79.18	68.57 -89.84	84 -105.67
Anoop	8^{c-f}	54.02^{f}	64.35^{e}	73.33^{e}
Arcanamica	8.33^{c-f}	57.86^{def}	65.53^{de}	87^{b-e}
ArkaAnamica	10.67^{b-e}	59.98^{b-e}	70.31^{cde}	87.67^{b-e}
Dhenu	10.33^{b-f}	57.69^{ef}	69.02^{cde}	90^{a-d}
Kiran	10.33^{b-f}	59.9^{b-e}	67.9^{cde}	86.67^{b-e}
Mythri	8.33^{cf}	57.18^{ef}	64.18^{e}	81de
Namd Hari	10^{b-f}	58.52^{c-f}	69.85^{cde}	91.33^{a-d}
Clemson spineless	8.33^{c-f}	61.55^{b-e}	71.89^{bcd}	100^{abc}
SOH701	17.33^{a}	60.48^{b-e}	72.15^{bc}	96.67^{a-d}
SOH714	11^{bcd}	60.82^{b-e}	70.49^{cde}	93^{a-d}
Mean	10.27	58.80	68.57	88.67
SD	2.73	2.23	2.97	7.62
CV (%)	26.59	3.79	4.33	8.59
Range	8 - 11.733	54.02 -61.55	64.18 -72.15	73.33 -100
LSD (5%)	3.424	5.172	6.496	16.17

Mean values with similar letter(s) had not significant differences in each row, SD = Standard deviation, CV (%) = coefficient of variation in percent and LSD (5%) = Least significant difference at P<0.05.

Appendix Table 2 .Mean values of 24 okra genotypes for growth traits evaluated at Dire Dawa in 2017

Genotypes	Plant height(cm)	Stem diameter(cm)	Number of branches per plant	Number of internodes per plant	Internodes length (cm)
92203	130.20^{c-f}	1.88^{b-f}	5.74^{cde}	21.44^{j-m}	8.92^{a}
240204	127.30^{d-g}	2.28^{ab}	4.47^{fgh}	30.48^{c}	7.46^{bc}
240207	139.50^{bcd}	1.88^{b-f}	6.45^{bc}	24.27^{g-j}	8.99^{a}
240586	152.60^{abc}	1.77^{c-h}	5.80^{cd}	29.77^{cd}	8.11^{ab}
240592	128.70^{c-g}	1.98^{b-e}	5.53^{cde}	26.90^{d-g}	7.18^{bc}
240600	104.90^{g-j}	2.11^{bc}	3.07^{i-l}	19.41^{lm}	6.44^{cde}
240609	130.90^{c-f}	1.81^{b-h}	5.13^{def}	29.42^{cde}	5.88^{d-g}
240784	155.80^{ab}	1.85^{b-g}	6.86^{b}	29.07^{c-f}	6.70^{cd}
242433	137.20^{bcd}	2.67^{a}	9.36^{a}	40.32^{b}	4.98^{ghi}
242444	111.70^{e-j}	2.05^{bcd}	5.15^{def}	19.91^{klm}	4.44^{i}
245157	138.80^{bcd}	2.06^{bc}	5.80^{cd}	41.33^{b}	6.40^{c-f}
245162	175.20^{a}	1.93^{b-f}	5.13^{def}	47.82^{a}	6.32^{c-f}
23793(Bamya-Humera)	106.70^{f-j}	1.79^{c-h}	2.93^{j-m}	7.77^{o}	6.80^{cd}
Humera 01	95.20^{j}	2.04^{bcd}	1.91^{n}	13.73^{n}	4.5^{hi}
Mean	131.05	2.01	5.24	27.26	6.66
SD	21.75	0.24	1.84	10.87	1.44
CV (%)	16.60	11.84	35.02	39.89	21.61
Range	95.2 -175.2	1.77 -2.67	1.91 -9.363	7.77 -47.82	4.44 - 8.99
Anoop	102.20^{hij}	1.52^{e-h}	2.13^{lmn}	20.65^{klm}	5.39^{e-i}
Arcanamica	126.80^{d-g}	1.36^{h}	3.713^{hij}	25.82^{f-i}	4.52^{hi}
ArkaAnamica	125.60^{d-h}	1.47^{fgh}	3.30^{ijk}	22.47^{i-l}	5.45^{e-i}
Dhenu	121.60^{d-i}	2.21^{abc}	4.80^{efg}	26.20^{e-h}	4.44^{i}
Kiran	98.30^{ij}	1.57^{d-h}	2.82^{j-n}	22.73^{h-l}	5.16^{f-i}
Mythri	89.20^{j}	1.39^{gh}	1.97^{mn}	20.10^{klm}	5.73^{d-h}
Namd Hari	98.50^{ij}	1.47^{fgh}	2.37^{k-n}	18.53^{m}	4.83^{ghi}
Clemson spineless	135.20^{b-e}	1.98^{b-e}	4.04^{ghi}	23.12^{h-k}	5.36^{e-i}
SOH701	123.60^{d-h}	1.55^{e-h}	4.02^{ghi}	20.11^{klm}	6.53^{cde}
SOH714	133.30^{b-e}	1.33^{h}	3.44^{ij}	18.82^{m}	6.75^{cd}
Mean	115.43	1.5897	3.2618	21.855	5.4208
SD	16.64	0.28	0.93	2.69	0.77
CV (%)	14.41	17.91	28.44	12.31	14.14
Range	89.2 -135.2	1.33 -2.21	1.95 - 4.8	18.53 -26.2	4.44 -6.751
L.S.D	24.299	0.483	0.987	3.474	1.249

Mean values with similar letter(s) had not significant differences in each row, SD =Standard deviation, CV (%) = Coefficient of variation in percent and LSD (5%) = Least significant difference at P<0.05.

Appendix Table 3. Mean values of for dry pod, seed yield and seed related traits of 24 okra genotypes evaluated at Dire Dawa in 2017

Genotypes	Number of dry pod per plant	Weight of dry pod per plant (g)	Number of ridge per pod	Average Dry Pod Weight (g)	Dry Pod Length (cm)	Dry Pod Width (cm)
92203	19.86^{a-e}	575^{d-h}	7.82^{abc}	26.68^{f-j}	10.11^{efg}	2.01^{cde}
240204	22.46^{abc}	800.3^{def}	8.06^{ab}	38.05^{de}	13.02^{bcd}	2.28^{bc}
240207	20.66^{a-d}	785.2^{def}	8.15^{a}	32.37^{e-h}	8^{g}	2.38^{ab}
240586	17.68^{cde}	771.6^{def}	8.30^{a}	35.74^{def}	8.11^{g}	2.65^{a}
240592	18.43^{cde}	531.7^{f-k}	6.95^{de}	29.91^{e-i}	12.41^{cde}	1.80^{e-h}
240600	24.14^{ab}	594.1^{d-g}	7.09^{de}	25.51^{g-j}	9.07^{fg}	2.10^{bcd}
240609	16.65^{def}	610^{d-g}	6.83^{de}	36.28^{def}	16.29^{a}	2.34^{b}
240784	19.28^{b-e}	513.3^{f-k}	7.81^{abc}	21.47^{i-l}	9.41^{fg}	1.78^{e-i}
242433	24.32^{ab}	877.1^{cde}	7.08^{de}	24.65^{g-k}	9.05^{fg}	2.00^{cde}
242444	14.52^{ef}	227.2^{jkl}	6.76^{de}	17.21^{jkl}	9.95^{fg}	1.50^{i-m}
245157	20.3^{a-d}	553.3^{e-i}	7.32^{cd}	22.95^{h-k}	10.89^{def}	1.85^{d-g}
245162	22.05^{a-d}	886^{cd}	8.46^{a}	33.83^{efg}	12.81^{bcd}	1.91^{def}
23793(Bamaya-Humera)	11.69^{fg}	257.4^{h-l}	5.86^{fgh}	24.91^{g-k}	9.69^{fg}	1.52^{h-m}
Humera 01	3.53^{h}	175.9^{l}	5.56^{ghi}	37.77^{de}	8.11^{g}	0.66 ^{o}
Mean	18.26	582.72	7.29	29.10	10.49	1.92
SD	5.50	233.63	0.88	6.67	2.37	0.49
CV (%)	30.15	40.09	12.02	22.92	22.60	25.33
Range	3.53 -24.32	175.9 -886	5.56 -8.46	17.21 -38.5	8 -16.29	0.66 -2.65
Anoop	18.48^{cde}	809.5^{def}	5.76^{ghi}	43.79^{cd}	14.38^{abc}	1.34^{k-n}
Arcanamica	7.82^{gh}	223.7^{kl}	5.37^{hi}	15.1^{kl}	5.24^{h}	1.09 ^{n}
ArkaAnamia	24.73^{a}	1518.9^{a}	6.45^{ef}	63.35 ^{b}	13.01^{bcd}	1.59^{g-l}
Dhenu	12.09^{fg}	1150.2^{bc}	7.37^{cd}	83.93^{a}	14.79^{ab}	1.76^{e-j}

Kiran	24.55^{ab}	1342.6^{ab}	5.66^{ghi}	53.46^{c}	13.4^{bc}	1.24^{mn}
Mythri	19.7^{a-e}	741.4^{d-g}	5.17^{i}	38.07^{de}	12.9^{bcd}	1.33^{lmn}
Namd Hari	19.52^{a-e}	617.8^{d-g}	5.52^{ghi}	29.81^{e-i}	12.77^{bcd}	1.23^{mn}
Clemson spineless	20.26^{a-d}	549.8^{f-j}	7.41^{bcd}	21.82^{i-l}	13.46^{bc}	2.35^{ab}
SOH701	21.37^{a-d}	428.5^{g-l}	6.07^{fg}	19.15^{jkl}	9.91^{fg}	1.63^{f-k}
SOH714	18.07^{cde}	233.2^{i-l}	5.84^{fgh}	12.55 ^{l}	8.6^{fg}	1.47^{j-m}
Mean	18.66	761.56	6.07	38.10	11.85	1.51
SD	5.21	448.43	0.78	23.29	3.01	0.36
CV (%)	27.92	58.88	12.92	61.12	25.38	24.04
Range	7.82 -24.73	223.7 -1518.9	5.17 -7.411	12.55 -83.93	5.24 - 14.79	1.09 -2.35
L.S.D	5.399	325.647	0.659	9.89	2.348	0.295

Mean values with similar letter(s) had not significant differences in each row, SD =Standard deviation, CV (%) = Coefficient of variation in percent and LSD (5%) = Least significant difference at P<0.05.

Appendix Table 3.Continued.

Genotypes	Number of Seeds Per Pod	Seed Weight Per Pod(g)	Hundred Seed Weight	Seed Yield Per Plant(g)	Seed Yield per Hectare (kg)
92203	95.7^{ab}	6.13^{abc}	6.21^{b-e}	122.33^{abc}	2549^{abc}
240204	96.36^{ab}	7.01^{a}	6.93^{ab}	153.89^{a}	3206^{a}
240207	105.47^{a}	7.09^{a}	6.56^{abc}	146.84^{ab}	3059^{ab}
240586	97.87^{ab}	7.05^{a}	7.01^{a}	124.85^{abc}	2601^{abc}
240592	97.61^{ab}	5.75^{abc}	5.93^{c-g}	105.94^{c-f}	2207^{c-f}
240600	80.44^{bcd}	4.64^{cde}	5.54^{e-j}	111.06^{bcd}	2314^{bcd}
240609	93.89^{abc}	6.41^{ab}	6.75^{ab}	108.08^{b-e}	2252^{b-e}
240784	110.11^{a}	5.49^{abc}	4.95^{ijk}	105.97^{c-f}	2208^{c-f}
242433	91.5^{abc}	5.30^{bcd}	5.54^{e-j}	129.35^{abc}	2695^{abc}
242444	104.21^{a}	5.46^{abc}	4.81^{jk}	78.96^{d-h}	1645^{d-h}
245157	97.78^{ab}	5.78^{abc}	5.92^{c-g}	117.29^{a-d}	2444^{a-d}
245162	110.17^{a}	7.00^{a}	6.18^{b-f}	153.55^{a}	3199^{a}
23793(Bamaya Humera)	42.79^{gh}	2.09^{ghi}	4.99^{ijk}	25.19^{ijk}	525^{ijk}
Humera 01	99.36^{ab}	1.342^{i}	1.42^{l}	5.86^{k}	122^{k}
Mean	94.52	5.47	5.63	106.37	2216.14
SD	16.74	1.76	1.41	43.71	910.58
CV (%)	17.72	32.27	25.04	41.09	41.09
Range	42.79 -110.17	1.34 - 7.09	1.423 -7.01	5.86 -153.89	122 – 3206
Anoop	56.67^{efg}	3.60^{efg}	6.21^{b-e}	66.46^{fgh}	1385^{fgh}
Arcanamica	33.96^{h}	1.58^{hi}	4.46^{k}	15.76^{jk}	328^{jk}
ArkaAnamica	74.14^{cde}	4.56^{cde}	5.84^{c-h}	115.26^{a-d}	2401^{a-d}
Dhenu	83.43^{bcd}	5.66^{abc}	6.46^{a-d}	67.97^{e-h}	1416^{e-h}
Kiran	68.94^{def}	3.73^{def}	5.44^{f-j}	93^{c-g}	1938^{c-g}
Mythri	60.16^{efg}	3.23^{efg}	5.13^{h-k}	64.05^{ghi}	1334^{ghi}
Namd Hari	44.14^{gh}	2.39^{f-i}	5.16^{h-k}	50.47^{hij}	1051^{hij}
Clemson spineless	90.75^{abc}	5.29^{bcd}	5.66^{e-i}	108.3^{b-e}	2256^{b-e}
SOH701	73.85^{cde}	4.64^{cde}	5.80^{d-h}	105.15^{c-f}	2191^{c-f}
SOH714	53.23^{fgh}	3.15^{e-h}	5.27^{g-j}	57.09^{ghi}	1189^{ghi}
Mean	63.93	3.79	5.55	74.35	1548.90
SD	17.63	1.28	0.58	30.97	645.37
CV (%)	27.58	33.70	10.45	41.65	41.67
Range	33.96 -90.75	1.58 -5.66	4.46 -6.46	15.76 -115.26	328 -2401
L.S.D	20.287	1.631	0.759	40.691	847.707

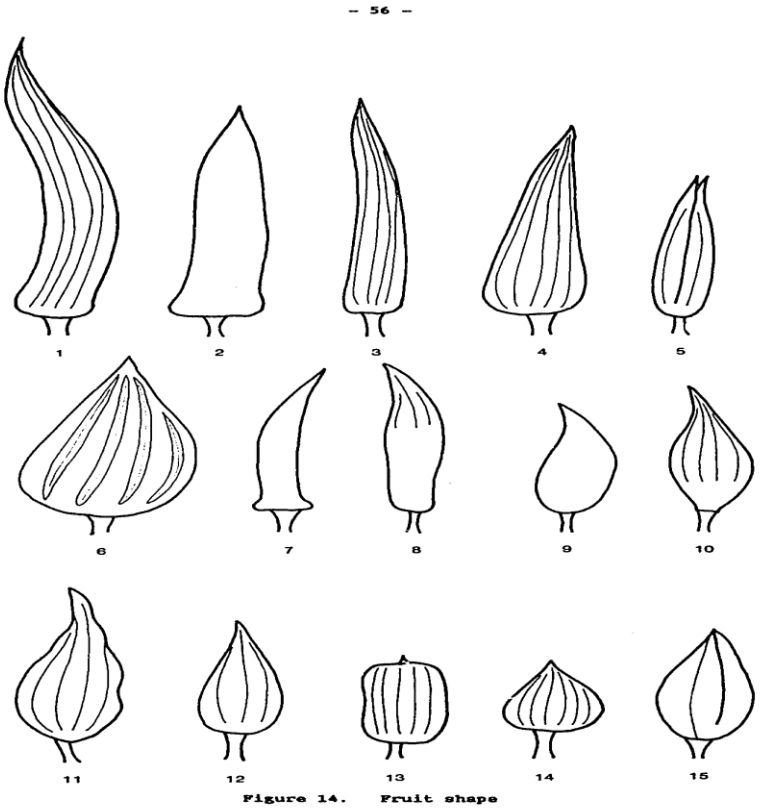
Mean values with similar letter(s) had not significant differences in each row, SD =Standard deviation, CV (%) = Coefficient of variation in percent and LSD (5%) =Least significant difference at P<0.05.

Appendix Table 4.Qualitative traits evaluated in 24 okra genotypes according to IPGR (1991) descriptors for okra

Parameters	Character codes
Pod color	1. Green 2. Red 3. Green yellow 4. Yellow
Pod Position	1. Erect 2. Intermediate 3. Horizontal 4. Slightly falling 5. Totally falling
Pod Pubescence	1.Smooth 2.Rough
Fruit shape	From types 1 to 15 in Appendix Figure 2.

Appendix Table 5.Qualitative traits evaluated in 24 okra genotypes according to IPGR (1991) descriptors for okra in 2017 at Dire Dawa

Genotype	Pod color	Pod position	Pod pubescence	Pod shape
23793 (Bamaya - Humera)	1	3	1	7
92203	3	2	1	14
240204	1	2	1	4
240207	2	1	1	12
240586	1	1	1	6
240592	3	2	2	1
240600	1	1	2	6
240609	2	2	1	1
240784	1	1	2	3
242433	1	2	1	12
242444	1	1	2	3
245157	1	1	2	4
245162	3	2	2	4
Humera 01	1	1	1	10
Anoop	1	1	1	3
Arcanamica	1	1	1	9
ArkaAnamica	3	3	1	3
Clemson spineless	1	3	1	4
Dhenu	3	4	2	3
Kiran	1	1	1	1
Mythri	1	1	1	1
Namd Hari	1	1	1	1
SOH701	1	1	2	3
SOH714	1	1	2	3



Appendix Figure 1.Different pod shapes as described by IBPGR, (1991)

Appendix Table 6. Euclidean distances of 24okra genotypes based on 20 quantitative traits evaluated at Dire Dawa in 2017

	Arcanamica	ArkaAnamica	Dhenu	Kiran	Mythri	NamdHari	23793	Humera 01	92203	240204	240207	240586
Anoop	6.08	4.58	5.06	3.45	1.96	3.46	10.01	8.44	6.02	7.37	8.00	7.46
Arcanamica		8.09	7.92	7.12	5.41	4.67	8.57	5.96	7.92	9.53	9.29	8.73
ArkaAnamica			3.93	2.20	4.65	4.99	9.45	9.21	5.32	5.08	6.03	5.82
Dhenu				4.51	5.57	5.74	9.78	8.73	6.15	5.94	6.88	6.12
Kiran					2.99	3.54	9.08	8.18	5.91	6.11	7.09	6.99
Mythri						2.39	9.05	7.25	6.01	7.22	7.81	7.57
NamdHari							7.47	6.33	6.45	7.19	7.95	7.70
23793								7.18	9.48	9.64	9.93	10.06
Humera 01									9.62	10.60	10.69	10.60
92203										3.94	2.86	2.82
240204											2.85	3.38
240207												2.07

Appendix Table 6.Continued.

	240592	240600	240609	240784	242433	242444	245157	245162	Clemson	SOH701	SOH714
Anoop	6.54	7.19	5.63	7.22	7.66	5.37	6.03	8.00	6.02	5.86	5.23
Arcanamica	7.50	8.12	8.04	7.36	8.21	5.43	7.23	9.68	7.39	6.50	4.05
ArkaAnamica	5.19	5.63	4.77	5.76	5.64	5.87	5.17	5.87	4.84	5.10	6.02
Dhenu	5.54	6.99	4.49	6.24	6.49	5.74	5.70	6.49	5.40	6.35	6.83
Kiran	5.53	5.80	5.30	6.36	6.27	5.42	5.60	7.08	5.29	5.00	5.44
Mythri	6.00	6.52	5.72	6.84	7.37	4.80	5.92	8.19	5.69	5.19	4.38
NamdHari	5.60	5.76	5.78	6.49	7.04	4.46	6.04	8.27	5.18	4.44	3.36
23793	8.14	6.71	9.28	8.70	9.71	8.12	9.78	11.36	8.35	7.07	6.76
Humera 01	8.39	8.24	9.46	8.46	9.94	6.37	9.30	11.28	8.54	7.62	6.54
92203	3.87	5.09	4.21	3.43	4.94	4.67	3.36	4.99	4.12	4.16	5.03
240204	2.91	5.43	3.23	4.17	4.58	5.84	3.61	3.65	3.25	5.13	6.55
240207	3.60	5.80	4.60	3.55	4.57	5.90	3.85	4.42	4.33	5.34	6.42
240586	4.09	5.68	4.26	3.54	4.59	5.74	3.51	4.00	4.20	5.17	6.17
240592		5.20	2.84	2.92	4.17	4.01	3.02	4.58	2.43	4.04	4.63
240600			6.01	5.07	5.81	5.31	5.77	7.11	4.74	2.61	5.01
240609				4.24	4.73	4.49	3.19	4.39	2.47	4.98	5.62
240784					3.30	3.86	2.71	4.04	3.33	4.01	4.77
242433						5.13	3.15	4.32	4.36	5.12	6.19
242444							4.03	6.49	3.71	4.00	3.82
245157								3.13	3.22	4.53	5.03
245162									4.58	6.37	7.41
Clemson										3.90	4.56
SOH701											3.16