CHARACTERIZATION OF OKRA [*Abelmoschus esculentus L* .Moench] GENOTYPES IN NORTH KERALA

by

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THESIS

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KERALA, INDIA
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DECLARATION

I, hereby declare that this thesis entitled **"Characterization of okra [*Abelmoschus esculentus L* .Moench] genotypes in North Kerala"** is a bonafide record of research work done by me during the course of research and the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title, of any other University or Society.

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LIST OF ABBREVIATIONS AND SYMBOLS USED

%	Per cent
AE	*Abelmoschus esculentus*
ANOVA	Analysis of Variance
C-1	Check-1
C-2	Check-2
CD	Critical difference
cm	Centimetre
C.V	Coefficient of Variation
DAS	Days after sowing
DUS	Distinctiveness, Uniformity and Stability
et al.	Co- workers/ Co-authors
Fig.	Figure
g	Gram
GA	Genetic advance
GCV	Genotypic coefficient of variation
i.e.	that is
IHD	Indian Horticulture Database
IIHR	Indian Institute of Horticultural Research
IPGRI	International Plant Genetic Resources Institute
KAU	Kerala Agricultural University
NHB	National Horticulture Board
PCV	Phenotypic coefficient of variation
POP	Package of Practices
PPVFRA	Protection of Plant Variety and Farmers Right Act
RARS	Regional Agricultural Research Station
SE	Standard error
UPGMA	Unweighted Pair Group Method with Arithmetic mean
viz.,	Namely

Introduction

1. INTRODUCTION

Okra (*Abelmoschus esculentus* L. Moench) is an important vegetable crop grown in the subtropical to tropical regions of Asia, Africa, America and temperate regions of the Mediterranean basin mainly because of its easy cultivation, dependable yield, adaptability to varying moisture levels and resistance to diseases and pests. In India, it is cultivated as an annual and day neutral plant in all seasons for its delicious tender pods. Its average nutritive value is higher than that of tomato, brinjal and most of the cucurbits.

Cooked okra fruits contain 3.9g carbohydrates, 2g dietary fibers, 0.2g fats, 1.5g proteins and various vitamins and minerals (NHB, 2013). Besides being rich in protein, vitamins, minerals (especially iron) and dietary fiber, the high iodine content makes it unique among vegetables and helps to play a vital role in controlling goiter disease and also helps in easy peristalsis of digested food particles (Sindhu *et.al.*,2013). India is the leading producer of okra in the world with production of 63.5 lakh tons and an average productivity of 11.9 t/ha (IHD, 2014) as compared to the world average productivity of 7.80 t/ ha. One of the major reasons for this increased productivity is the significant contribution of more than fifty improved varieties and hybrids developed through intensive research efforts.

In India, a number of ICAR Institutes, State Agricultural Universities and private seed companies are working on various aspects of genetic improvement of okra in order to develop high yielding and disease resistant varieties. However, still a vast gap exists in the research efforts and the expected outcome. The major challenges that need to be addressed are emerging biotypes of whitefly, new virus strains and breakdown of resistance in okra varieties/hybrids. The yield potential in okra crop has become almost static over the years mainly because of reduction in yield due to frequent attacks of pests and diseases, especially fruit and shoot borer and yellow vein mosaic virus (Reddy *et al.*, 2012).

According to Misra *et al.* (2008) spotted bollworm can cause 36-90 per cent loss in the fruit yield of okra. However, yield levels can be improved through heterosis breeding. Exploitation of heterosis mainly depends up on the screening and selection of available germplasm. Several research workers have reported considerable heterosis for fruit yield and its various components (Jindal *et al.*, 2009). High percentage of fruit setting indicates the possibilities for the exploitation of hybrid vigour in okra and thus producing hybrid varieties.

The present day high yielding varieties in okra have been developed by exploiting the available genetic diversity in widely cultivated species *Abelmoshes esculentus* also called Sudanien type and the other one Guanien type an intermediate of *A. esculentus* and *A.manihot*. The germplasm of okra is relatively narrow. There is also a potential danger of genetic erosion due to the growing popularity of early high yielding varieties (Sharma, 2013). Hence there is a need to augment the presently available germplasm for broadening the genetic base of okra not only for direct breeding but also for conservation.

Kerala Agricultural University has released five varieties viz; Kiran, Salkeerthi, Susthira, Anjitha and Manjima of okra till date and the last variety was released in 2006. These varieties have been developed by either selection or combination breeding method based on germplasm collections from South and Central Kerala. It is therefore necessary to undertake exploration and collection works and diversity analysis, especially in North Kerala. It was in this back ground, the present study taken to explore and assess the genetic variability in this crop in different areas of North Kerala which will form a basic document for further crop improvement works. The present study was undertaken with the following objectives:

- Exploration and collection of okra genotypes in North Kerala.
- Evaluation of collected accessions for morphological characterization, genetic variability and diversity in qualitative and quantitative traits.

Review of Literature

2. REVIEW OF LITERATURE

2.1 CLASSIFICATION, ORIGIN AND GEOGRAPHICAL DISTRIBUTION

The cultivated species, *Abelmoschus esculentus* (L.) Moench was earlier included in the genus *Hibiscus,* section *Abelmoschus* in the family Malvaceae under the order Malvales. Subsequently it was separated from the genus *Hibiscus* and raised to the rank of distinct genus as distinguished by the spathulate calyx, with five short teeth, connate to the corolla and caducous after flowering. The authentic number of species included in the genus *Abelmoschus* is still uncertain, as they have not been studied in detail with respect to their taxonomic delimitation. Over fifty species were described from the world that comprises many synonyms and misidentifications. The taxonomical revision undertaken by Waalkes (1966) and Bates (1968) which was cited by Tripathi *et al.* (2011) constitutes the most fully documented studies of the genus *Abelmoschus.*

In a systematic review of the genus *Abelmoschus,* Patil *et al.* (2015) reported that presently the genus *Abelmoschus* comprises of 11 species, 3 subspecies and 4 varieties with the discovery of two new species *viz., A. enbeepeegearense* from the Western Ghats (John *et al.* ,2012) and *A. palianus* from Chhattisgarh (Sutar *et al.*,2013) in India. Among these, three species are cultivated. *Abelmoschus esculentus* is having wide cultivation throughout the world and the cultivation of another economically important species *viz.*, *A. caillei* is limited to West and Central Africa. The species *A. moschatus* is cultivated for aromatic seeds as well as an ornamental plant. The rest of species namely, *A. manihot*, *A. tetraphyllus*, *A. tuberculatus*, *A. ficulneus*, *A. crinitus*, *A. enbeepeegearense*, *A. palianus* and *A. angulosus* are truly wild species (Sutar *et al.*,2013).

The chromosome number (2n) of *A. esculentus* L. (Moench) has been variably reported by different authors. The most frequently observed somatic chromosome number however, is 2n = 130, although Datta and Naug (1968) suggest that the numbers 2n=72, 108, 120, 132 and 144 are in regular series of polyploids with x=12 and the genus *Abelmoschus* is accepted to be of Asiatic origin. According to Bisht and Bhat (2006) there are two hypotheses concerning the geographical origin of *A. esculentus* as Asian origin with one putative ancestor (*A. tuberculatus*) being native to Uttar Pradesh in northern India and other as Ethiopian domestication on the basis of ancient cultivation in East Africa and area of domestication is north Egypt or Ethiopia.

The species of *Abelmoschus* are naturally distributed throughout the tropical and subtropical countries (Vredebregt, 1991). Majority of the species occur in South Asia and Southwest Pacific (Bisht and Bhat, 2006). Occurrence of some of the wild forms has also been reported in North Australia, South America and Africa (IBPGR, 1991). In India, species of *Abelmoschus* are widely distributed in different phyto geographical regions from Himalayan region (Velayudhan & Upadhay, 1994; Negi & Pant, 1998), to Southern peninsular parts of India (Sivarajan & Pradeep, 1996; Velayudhan *et al.*, 1996).

2.2 BOTANY

Okra is an upright annual, herbaceous plant with a hibiscus-like flower. It is a tropical direct sown vegetable with duration of 90-100 days. The plants have a deeply penetrating taproot with dense shallow feeder roots that reaches out in all direction in the upper 45cm of the soil. Stem is semi woody in nature with a green or reddish tinge. It is erect and variable in branching, with many short branches. The stem attains height of 3 feet in dwarf varieties to 7 or 8 feet in others. The woody stem bear alternate palmate broad leaves with a pair of narrow stipules. They are lobed and are generally hairy, some reaches up to 12 inches in length. The plant begins to flower about 35-60 days after emergence and the flower remains open for a day. The flowers are borne vertically only on the orthotropic axis every two or three days. The flower was axillary and solitary, borne on a peduncle 2.0 – 2.5 cm long. The flowers are large around 2 inches in diameter, with five white to yellow petals with a red or purple spot at the base of each petal. They are perfect flowers (male and female reproductive parts in the same flower) and self-pollinating. Although insects are unnecessary for pollination and fertilization in case of okra, the flowers are very attractive to bees and the plants are cross-pollinated. Cross pollination up to the extent of 4-19% with maximum of 42.2% has been reported by Sharma (2013).

The fruits are normally yellowish green to green, but sometimes purple or whitish green and on attaining maturity become dark brown dehiscent or indehiscent capsules. Immature fruits are ready to harvest 4-6 days after anthesis. Seeds are dicotyledonous in nature and they vary in shape; round kidney or spherical with epigeal germination (Hamon and Koechlin, 1991; Ariyo, 1993)

In okra substantial contribution has been made to the literature regarding genetics and breeding in the recent years. A comprehensive review on various aspects is presented under the following heads:

1. Exploration and collection of okra germplasm

2. Characterization and evaluation of genetic variability of okra genotypes.

2.3 EXPLORATION AND COLLECTION OF OKRA GERMPLASM

In any crop improvement programme, germplasm serve as a valuable source of base population, which offers much scope for further improvement. Explorations are the primary source of all germplasm present in various germplasms collections. These are planned not only for breeding purpose but also to conserve the variability remaining in the crop and its relatives. The cultivated okra has a narrow genetic base and there is a need to augment the presently available germplasm for broadening the genetic base of okra.

Exploration and collection of okra and its relatives were conducted under the joint sponsorship of IBPGR and NBPGR in southern region of India. A total of 236 accessions of the genus *Abelmoschus were* collected which included 205 samples of cultivated okra belonging to *Abelmoschus esculentus* and *A. callei* and 30 of five wild species and one of a semi wild hybrid form. Cultivated okra had wide spread distribution. Three wild species and one variety were found to occur in Western Ghat areas and two others in plains. Wide variability in the collections mainly in fruit and plant types have been noticed in *A. esculentus* and on the basis of fruit characters 12 distinct types could be identified. (Velayudhan *et al.*, 1996).

Within India germplasm collection in okra is being carried out mainly through NBPGR, New Delhi and Akola in Maharashtra. More than eight specific explorations in okra have been organized and collections made from Punjab, Haryana, Gujarat, central and western parts of Madhya Pradesh, Maharashtra, southern peninsular tract in Karanataka, Tamilnadu and Kerala and eastwards Andhra Pradesh, Orissa, Assam plains and adjoining hilly tracts of North-eastern region (Rai and Rai, 2006).

John *et al.* (2012) conducted an eco-geographic survey of *Abelmoschus* in the Western Ghats and came across a strikingly distinct form of *Abelmoschu*s named *Abelmoschus enbeepeegearense* growing in dry grassy slopes of the lower Western Ghats.

Extensive and intensive field surveys made by Sutar *et al.* (2013) in Chhattisgarh region of Madhya Pradesh in India led out the discovery of a new species *Abelmoschus palianus* like its close relative *A.angulosus.*

Special agro-biodiversity surveys were undertaken by (Pandravada *et al.* (2015) to collect, salvage and conserve the current spectrum of landrace diversity in different agri-horticultural crops including okra from Adilabad district, Telangana. A total of 22 typical landrace populations of okra (*Abelmoschus esculentus* L. Moench) conserved on-farm by the ethnic tribal groups in the district were collected, characterized and evaluated along with check varieties, Arka Anamika, P-8 and Pusa A-4 .

2.4 CHARACTERIZATION AND EVALUATION OF GENETIC VARIABILITY

2.4.1 Characterization

Characterization of crops is a very essential step in any crop improvement programme (De Vicente *et al.*, 2005). Morphological characterization helps to identify duplicates in the collection and to develop a core collection for conservation as well as for varietal improvement. Characterization based on phenotypic traits is not easily reproducible particularly, since these traits are influenced largely by environmental variations However, the tool has remained useful as a necessary first step prior to more in-depth biochemical or molecular studies in okra germplasm exploitation (Amoatey *et al.*, 2014).

2.4.1.1 Morphological characterization of okra genotypes based on qualitative traits

Forty five land varieties of okra collected in Turkey were evaluated for phenotypic traits. Considerable variation was observed in leaf shape and leaf colour and fruit shape. A distinct leaf-shape was observed, which does not exist in IBPGR descriptor (Bas and Koludar, 2001).

Omonhinmin and Osawaru (2005) carried out morphological characterization of two species of *Abelmoschus*: *Abelmoschus esculentus* and *Abelmoschus caillei* based on twelve qualitative and quantitative traits respectively. They reported indeterminate growth pattern; weak procumbent, green stem and short to moderate internodes length for *A. esculentus*. Sawadogo *et al.* (2006), characterized diversity in okra on the basis of colour of fruits and stems.

One hundred and twenty one okra genotypes collected from different parts of Bangladesh were characterized and evaluated for different quantitative and qualitative traits. Each character was classified into different categories. For growth habit, the okra genotypes fell into three categories *viz.*, erect, procumbent and medium. Likewise, the genotypes were grouped into different categories for branching habit, stem colour, leaf shape, leaf and petal colour, red colour of petal base, shape of epicalyx segments, fruit colour, fruit pubescence, seed colour, seed shape, seed hairiness, yellow vein mosaic virus reaction and fruit and shoot borer infestation. Considerable variability among the genotypes existed in respect of qualitative characters of okra as reported by (Saifulla and Rabbani, 2009).

Sekyere *et al.* (2011) evaluated twenty five accessions of okra collected in Ghana for phenotypic identity, diversity and quality based on morphological characters. The study also revealed that distinct morphotypes exist in the Ghanaian okra germplasm, depicted by variation in petal colour, pubescence of the leaf and stem, fruit shape, anthocyanin pigmentation and number of days to 50% flowering. In general, all the okra accessions showed relatively wide ranges of variations for all morphological characters observed. Most of the plants showed erect growth habits while leaf and stem colours were predominantly green. Petal or flower colour was mostly golden yellow among the okra, whereas fruit orientation was largely intermediate for all accession studied. Majority of the fruits produced green and smooth fruits.

Kumar (2013) characterized twenty genotypes of okra based on plant and seed characters. All the genotypes could be distinguished with the help of identification keys based on five different diagnostic characters *viz.*, serration of leaf blade margin, vein colour, intensity of colour between vein, depth of lobing and petal base colour.

Thirty six genetically diverse genotypes of okra were evaluated by Ali *et al.* (2014) to find out their similarities and differences based on their morphological traits. Great variation was observed in branching at main stem among okra accessions. Branching was either orthotropic, strong or medium type, plants with medium branching was predominant while orthotropic was least frequent.

Kumar and Reddy (2015) characterized fifteen YMV resistant single cross hybrids in okra on the basis of eighteen qualitative traits. All the hybrids showed erect growth habit, with no differences in mature leaf color (only green) and leaf rib colour .There was no difference in shape of epicalyx segments (only lanceolate) among the hybrids. The fruits of majority of the hybrids under study had erect position on main stem downy pubescence and green immature fruit colour), five ridges and angular shape.

Preliminary characterization of twenty two landraces from the tribal pockets of Telangana for 20 qualitative traits revealed distinct variability especially in leaf tip, petiole colour, stem colour, leaf shape overall variability and flowering habit (Pandravada *et al.*,2015).

Ouedraogo *et al.* (2016) conducted agro-morphological evaluation on of 16 accessions of okra (*Abelmoschus esculentus*). The study revealed variability among accessions for shape, color and pubescence of the stems and leaves. A high percentage of accessions were having purple stem (55.9%) from the observed three main colors of the stem (purple, green, purple).The majority of accessions had little hairy stems (81%). A diversity of colors of leaves was observed. The leaves are uniformly green (47%), dark green (46%) and green variegated purple (7%). An important proportion of accessions had pubescent leaves (90%) that are lobed shape (94%) or fingered. Among fruit characters for fruit colour, green colour was the most frequent (53%). As the form of fruits, 92% of the capsules were elongated against 8% short.

2.4.1.2 Mean performance of okra genotypes based on quantitative traits

Variation in quantitative character is continuous and mean performance is one of the simplest genetic parameter used to measure variability. A field experiment was conducted with twenty diverse genotypes of okra .The mean sum of square was highly significant for all traits, indicating the presence of wide variability in the genotypes of okra. Yield per plant (g) showed a wide range (307.41 – 702.67), the minimum and maximum yield per plant at edible stage was recorded in genotypes Bhindi Vaphy and Pusa Makhamali, respectively with a mean value 401.48. Pusa Makhamali recorded maximum plant height (114.71), maximum fruits diameter (10.53 mm), maximum fruits length and days to flower appearance ranged from 45.32 to 65.32 (Kumar *et al.,* 2012).

The analysis of variance of thirty one okra genotypes for yield and yield attributing traits revealed highly significant differences among the genotypes for all the characters. The mean values for days to 50% flowering ranged from 43.33 to 59.33; the range for number of primary branches was from 0.73 to 3.60. Wide variation in plant height was noticed among varieties ranging from 67.46 cm to 133.43 cm. Fruit characters *viz.,* fruit weight, fruit length and fruit girth differed significantly among the genotypes. Fruit weight ranged from 14.91 g to 30.35 g (Duggi *et al.*, 2013).

Jagan *et al.*(2013) reported significant differences among the genotypes of okra for days to 50% flowering, node at which first flower appears, number of branches per plant, number of fruit per plant, fruit yield per plant and fruit yield per hectare, indicated wide spectrum of variation among the genotypes.

Amoatey *et al.* (2014) reported significant variation in 13 quantitative traits among the 29 accessions of okra assembled from eight geographic regions of Ghana. An accession named Nkran Nkuruma recorded the highest maximum plant height (MPH), maximum number of internodes (MNI) and first fruit-producing node (FFPN). Another accession Yeji-Local recorded the highest total number of leaves per plant (TNLP) and number of seeds per fruit (NSPF) stem diameter at the base (STB), and total number of fruits per plant (TNFP).

One hundred and one accessions of okra [*Abelmoschus esculentus* (L.) Moench], collected from various parts of India were evaluated for yield and 11 yield attributes. ANOVA revealed remarkable variation for all the traits studied. Varsha Uphar, Parbhani Kranti and NBPGR/TCR-985 were the most promising genotypes identified during the investigation. Fruit number varied significantly among the genotypes and it ranged from 2.50 (NBPGR/TCR-1981) to 13.67. Average fruit weight showed wide range of variation among the genotypes from 12.18 (NBPGR/TCR-1533) to 34.47. Parbhani Kranti was the best yielder, with a fruit yield of 373.25 g per plant whereas the lowest fruit yielder was NBPGR/TCR-1981 with 34.52 g per plant). The longest (27.18cm) and the shortest (8.99 cm) fruits were produced by Anakkomban-II and NBPGR/TCR-1507 respectively. The fruits with maximum girth (10.08 cm) were produced by Kilikolloor Local and Kollam Local-1.

Fruit girth was minimum (4.20 cm) in NBPGR/TCR-1507. Ridges per fruit among the various genotypes ranged from 5.00 to 8.17(Sindhumole and Manju, 2014).

Thirty five diverse genotypes of okra were evaluated for yield and its contributing traits and analysis of variance showed significant differences among all the genotypes for all the characters under study. Five genotypes namely IC-58235, LC-13-9, VRO-3, LC-12-5 and Arka Anamika gave higher yield and also performed better for other horticultural traits *viz.,* days taken to marketable maturity, fruit breadth, average fruit weight, harvest duration, number of marketable pods per plant than the check variety P-8.(Chandra *et al.*, 2014).

Pandravada *et al.* (2015) reported significant differences among the 22 landraces studied for seven quantitative characters. The traits, fresh fruit weight (g), ridges per fruit (no) and fruit length (cm) were found to be more variable in the germplasm. They identified two superior germplasm lines NSJ-320, PSRJ-12952 and RJR-265 based on the mean performance for growth, earliness and acceptable pod which can be utilized for the development of open pollinated varieties or hybrids.

2.4.2 Components of genetic variability for quantitative traits of okra

Genetic variability in breeding populations can be assessed using simple measures of variability such as standard deviation, variance and coefficient of variation, the basic idea in the study of variation and it's partitioning into components attributable to different causes. The relative magnitude of this variability is measured using the genetic parameters like heritability and genetic advance. Heritability and genetic advance are the important selection parameters. Heritability along with genetic advance are normally more helpful in predicting the gain under selection.

2.4.2.1 GCV, PCV, Heritability and Genetic gain

Saifullah and Rabbani (2009) observed low difference between GCV (29.90) and PCV (30.50) for primary branches per plant and number of internodes per plant in okra which also had high heritability (97.32%) with high genetic advance (59.15). Low difference between GCV and PCV with high heritability with medium genetic advance was also observed for number of fruits per plant and fruit yield per plant. The results indicated low environmental influences upon the expression of these characters and effectiveness of selection for these traits.

Akotkar *et al.* (2010) evaluated the genetic variability of some yield contributing characters, and the genetic diversity in fifty genotypes of okra. The magnitude of PCV was higher than that of GCV for all the traits. The GCV and PCV were high for number of fruiting nodes, fruit yield per plant; moderate for plant height, inter nodal distance, number of nodes on main stem and seeds per fruit; and low for number of ridges per fruit, fruit diameter, fruit length and number of primary branches per plant indicating these characters might be controlled by additive genes. 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 characters except number of primary branches.

In a genetic variability study undertaken by Adiger *et al.* (2011) on 163 genotypes including 43 parents and 120 crosses of okra the values of PCV were higher than that of GCV values for all nine characters indicating influence of environmental effects in the expression of these characters. However, the GCV, heritability and genetic advance as percentage of mean were higher for plant height, fruit yield per plant, fruit weight and days to 50 per cent flowering which might be attributed to additive gene action of inheritance.

Kumar *et al.* (2012) noticed that the analysis of variance indicated significant differences among genotypes for all the characters under study. The result based on GCV and PCV showed a considerable genetic variability among the genotypes for height at first fruiting node, number of node at first pod appearance, plant height, number of nodes per plant, number of pods per plant and pod yield per plant.

Prakash and Pitchaimuthu (2011) in a study to evaluate the nature and magnitude of genetic variability of yield contributing characters in forty-four genotypes of okra collected from the IIHR, Bangalore, reported higher magnitude of PCV than that of GCV for all the traits. They observed high GCV and PCV for plant height, internode length, first flowering node and average fruit weight. High magnitude of broad sense heritability (above 90 %) was noticed for average fruit weight, number of seeds per fruit, days to 50% flowering, first fruit producing node, yield per plant, plant height and hundred seed weight. High heritability coupled with high GAM (Genetic Advance expressed as percentage of Mean) were observed for almost all the characters studied, except for days to 50% flowering and days to 80% maturity.

Assessment of genetic variability in twenty-nine okra accessions by Nwangburuka and Denton (2011) from different agro-ecological regions in Nigeria revealed high GCV, broad-sense heritability and genetic advance in traits such as plant height (26.2, 90.7, 51.5), fresh pod length (23.9,98.5, 48.8), fresh pod width (23.9, 98.5, 48.8), mature pod length (28.6, 98.5, 52.3), branching per plant (29.3, 82.3,54.8) and pod weight per plant (33.9, 90.0, 63.3) suggesting the effect of additive genes and reliability of selection based on phenotype of these traits for crop improvement.

Jagan *et al* (2013) reported high heritability coupled with high genetic advance for number of branches per plant and days to maturity in an experiment comprising of nineteen genotypes of okra containing four lines and fifteen testers along with sixty combinations indicating that they are governed by additive genes and could be effectively improved through selection.

Ramanjinappa *et al.*, (2011) reported high heritability in some characters such as days to 50 percent flowering, days to first flowering, plant height and number of seeds per fruit but low heritability for characters like fruit weight and number of fruits per plant shows low heritability.

Duggi *et al.* (2013) evaluated 31 okra genotypes and reported high magnitude of heritability coupled with high genetic advance for the characters *viz.*, leaf axil bearing first fruit, plant height , yield per plant, number of fruits per plant, number of primary branches, fruit weight and fruit length suggesting the scope for their improvement through selection.

Chandra *et al.* (2014) reported higher magnitude of PCV than GCV for all thirteen characters of okra indicating these traits to be less influenced by environmental factors. High heritability estimates coupled with high genetic gain were observed for fruit yield per plant and per hectare indicating that these characters are governed by additive gene effects and are more reliable for effective selection. High heritability coupled with moderate genetic gain was observed for number of primary branches per plant, number of marketable fruits per plant, fruit length and average fruit weight that indicates that these characters are under non-additive gene effects and selection for these characters will be less effective. Such traits are more under the influence of environment and do not respond to selection.

Twenty five genotypes of okra collected from different districts of Tamil Nadu were evaluated by Kandasamy (2016) to assess the variability, heritability, genetic advance. Maximum phenotypic and genotypic co-efficient of variation (PCV and GCV) was found for yield per plant followed by plant height and number of fruits per plant. High heritability was recorded for all the characters except intermodal length and fruit girth. Traits like plant height, number of branches per plant, node at first fruit, fruit length, number of fruits per plant, fruit weight and yield per plant had high heritability along with high genetic gain which reveals the predominance of additive gene action on these characters.

2.4.2.2 Correlation coefficient analysis

Correlation studies to determine the inter-relationship among various traits are useful in making selection. The estimation of genotypic and phenotypic correlation coefficient helps to determine the true association due to genetic causes. In okra, correlation and path coefficient analyses have been used by several researchers to measure the associations between yield and other traits and to clarify interrelationships between pod yield and other traits respectively.

The association analysis among nine quantitative characters of okra as reported by Adiger *et al.* (2011) showed highly significant and positive correlation of fruit yield per plant with plant height, number of branches per plant, inter nodal length, fruit length, fruit weight and number of fruits per plant at both genotypic and phenotypic level, indicating mutual association of these traits. It could be suggested from correlation estimates that yield could be improved through selection based on these characters.

The characters fruits length, average fruit weight, number of fruits per plant, number of branches per plant and plant height showed significant positive association with fruit yield per plant, and also showed significant positive association among themselves in segregating populations of okra (Somashekhar *et al.*,2011).

Correlation coefficient analysis was carried out by Reddy *et al.* (2013) to study the character association and contribution, respectively for thirteen quantitative characters in one hundred germplasm lines of okra for the identification of appropriate selection indices. The analysis revealed that plant height, fruit length, fruit width, fruit weight, total number of fruits per plant , number of marketable fruits per plant had significant positive correlation with total yield per plant while number of branches per plant, internodal length, days to 50% flowering, first flowering node and first fruiting node had significant negative correlation with marketable yield per plant.

Gogineni *et al.* (2015) reported significant positive association of all the fruit traits like length, width, weight and total number of fruits per plant with fruit yield per plant and also among themselves in the correlation analysis carried out in ten different okra hybrids for fruit yield and its component traits.

The magnitude of genotypic correlation was reported to be higher than the phenotypic correlation for all the traits studied in 24 okra genotypes by Soni (2016) indicating inherent association between various characters. Significant positive phenotypic correlation of fruit yield per plant was observed with number of fruits per plant and fruit length. The highest positive and significant correlation coefficient of fruit yield per plant has been noted with number of fruits per plant. However, fruit weight expressed significant and negative correlation with number of fruits per plant. Plant height at 90 DAS recorded highly significant positive association with number of leaves per plant at 90 DAS and length of internodes whereas it recorded highly significant negative association with number of branches per plant at 90 DAS. Number of branches per plant at 90 DAS recorded significant negative association with length of internodes and fruit width. Association of number of nodes to first flowering was recorded significant and positive with days to first flowering, days to 50% flowering and days to first picking while it was found significant and negative with fruiting span, fruit width and fruit yield per plant.

2.4.2.3 Path coefficient analysis

Usefulness of the information obtained from the correlation coefficients can be enhanced by partitioning into direct and indirect effects for a set of a pair-wise cause-effect inter relationships (Kang *et al.*, 1983). Path coefficient analysis permits the separation of correlation coefficient into direct and indirect effects.

Path coefficient analysis of nine quantitative traits of okra by Adiger *et al* (2011) revealed that fruit weight had maximum direct contribution towards fruit yield followed by number of fruits per plant, plant height and number of branches per plant. However, days to 50 per cent flowering exhibited highest negative direct effect followed by test weight and fruit diameter. High positive indirect effect was found in case of number of fruits per plant via number of branches per plant, plant height and fruit length. Therefore, one can rely upon fruit weight, number of branches per plant, plant height and number of fruits per plant while selecting high fruit yielding genotypes in okra.

Reddy *et al.* (2013) reported that fruit weight and number of fruits per plant had high positive direct effect on pod yield per plant. First fruiting node had the maximum positive direct effect on marketable yield per plant. Indirect effect of total yield per plant via number of branches per plant, internodal length, days to 50% flowering, first flowering node and first fruiting node was observed to be positive and moderate to high in magnitude resulting in a significant positive association with marketable yield per plant.

Gogineni *et al.* (2015) observed the characters fruit girth, fruit weight, number of fruits per plant, plant height and duration exhibited positive direct effects on yield revealing that these were the major yield contributing characters in okra .On the contrary negative direct effects were exhibited by days to first flowering and fruit length. The characters fruit length, fruit weight, number of fruits per plant, plant height and duration showed positive indirect effect through fruit girth on fruit yield. Plant height exhibited positive indirect effects via fruit length, fruit girth, number of fruits per plant and duration. However, it exhibited negative indirect effects via days to first flowering and fruit weight. Plant duration exhibited indirect positive effects through all characters.

Path coefficient analysis of different characters contributing towards fruit yield per plant showed that number of fruits per plant had the highest positive direct effect followed by fruit weight, number of nodes to first flowering, number of branches per plant at 90 DAS, length of internodes, number of leaves per plant at 90 DAS, plant height at 90 DAS and fruiting span. (Soni, 2016).

The number of pods per plant had the greatest direct influence on pod yield, followed by fresh weight per pod, which had positive genotypic association with pod yield. Pod length had highest negative direct effect followed by plant height and days to 50% flowering as reported by Aminu *et al.* (2016).

Path coefficient analysis in 180 genotypes of okra by Singh *et al.* (2017) revealed that fruit width had maximum direct contribution towards fruit yield followed by number of fruits per plant first fruit producing node and average fruit weight. However, 100 seed weight exhibited highest negative direct effect followed by first flower producing node, 50 per cent flowering and internodal length plant height at 45 days after sowing and days to first flowering.

2.4.3 Genetic diversity analysis

Genetic diversity arises either due to geographic separation or due to genetic barrier in crossability. Populations from widely separated geographic regions are the one usually included in the hybridization program. Among the several statistical method used to quantify genetic divergence multivariate analysis is a important tool (Rao, 1969). These multivariate techniques can be used for grouping of genotypes i.e. clustering and measuring the genetic distance between the genotypes.

Genetic diversity analysis in South Asian okra (*Abelmoschus esculentus*) germplasm collection by Bisht *et al.* (1995) resulted in grouping of accessions into eight clusters based on both qualitative and quantitative descriptors. The grouping pattern revealed pubescence, pigmentation, days to flowering, plant height and various parameters to be most important and effective criteria for distinguishing the accessions. Cluster analysis revealed that there was no association between geographic distribution and variability. The two check varieties Pusa sawani and Sel-2 were grouped into cluster I. Similar observations of clustering pattern of okra genotypes not following their geographic distribution were also reported by Akotkar *et al.* (2010), Reddy *et al.* (2012),and Balai *et al.* (2015) They also observed that geographical distance between the genotypes of okra had no relation with the genetic divergence and the genotypes from the same source had fallen into different clusters as well as the same clusters containing genotypes from different sources.

2.4.3.1 Cluster analysis

Cluster analysis, also called segmentation analysis or taxonomy analysis is a group of multivariate techniques used to group objects based on the characteristics they possess and allows one to visualize similarities among taxa by the levels at which they are grouped together.

Cluster analysis of 25 okra accessions by Sekyere *et al.* (2011) collected from various regions of Ghana produced four main sub-cluster groups. 23 out of the 25 okra accessions studied were distinct accessions. There was no unique relationship between the cluster groups and the regions of collection. Accessions with similar quantitative and qualitative morphological characters appeared well grouped in the same cluster. Okra accessions with common local names were also found in the same cluster.

Amoatey *et al* .(2015) however reported some degree of association between quantitative characters and geographic origin of collections based on the pattern of clustering of twenty-nine accessions of okra (*Abelmoschus spp* L.) assembled from eight geographic regions of Ghana.

2.4.3.2 Genetic Distance

The various approaches used for measuring genetic diversity are D^2, metroglyph analysis and principal component analysis. These techniques are generally used for replicated design. To measure distance among clusters, a number of methods are available and vary according to the way in which "closest" is defined at each stage of merging groups. Some common examples are Single link (nearest neighbour), Complete link (farthest neighbour) and Average link (UPGMA).Qualitative data generally take binary (taking only two values: present (or absent (absent) or categorical (taking a value among many possibilities); and are either Ordinal (categories that have an order) or Nominal (categories that are unrelated). In case of quantitative characters distances rather than similarities are considered and the common measure used is the Euclidian distance (Aldenderfer and Blashfield, 1984). Genetic distance or diversity of genotypes is considered as a good start in plant breeding to improve crops either by means of hybridization or direct selection of genotypes for their desirable traits. The high yielding varieties in okra has been developed by exploiting the genetic diversity available in the crop.

Amoetey (2012) grouped 29 accessions of okra were into two major clusters and subsequently into five sub-clusters based on both quantitative and qualitative characters studied. The results revealed that most of the genotypes of cultivated okra were highly variable considering individual character but considering constellation of characters, collectively they belong to the same group. Four accessions, were placed in cluster one while cluster two contained the rest of the accessions with six sub-clusters. These four accessions had in common the following characteristics; long pod length, medium type of branching, reniform seed shape, glabrous aspect of seed surface, green leaf colour, creamy petal colour, position of their fruits on main stem being pendulous, slight stem pubescence, number of ridges per pod ranges from 5 to 10, and green stem pubescence.

Genetic distance of 25 okra accessions consisting of 23 Ethiopian collections and two collections from India was measured using Euclidean distance based on 25 quantitative and 10 qualitative traits. The distance matrix from phenotype traits was used to construct dendrograms based on the Unweighted Pair-group Method with Arithmetic Means (UPGMA) and the okra accessions were grouped under ten major clusters with four solitary clusters and six clusters consisted of more than one, up to maximum of 10 accessions. Genotypes in solitary clusters being diverse from others may serve as potential parents for breeding programmes and it indicates their independent identity and importance due to various unique characters possessed by them. In general, the genotypes grouped together in one cluster are less divergent than those which are placed in a different cluster (Demelie *et al.* 2016).

Genotypes belonging to divergent clusters may used in hybridization programmes to obtain transgressive segregants with broad spectrum of genetic variability for yield and other component traits to isolate high yielding genotypes in okra.

Materials and Methods

3. MATERIALS AND METHODS

3.1 Experiment-1: Exploration and collection of okra genotypes in North Kerala.

3.1.1 MATERIALS

Forty four genotypes of okra were collected from various parts of North Kerala.

3.1.2 METHODOLOGY

A survey was conducted on various parts of North Kerala especially Kasaragod, Kannur and Malappuram district. Krishi Bhavans of various panchayaths of the three districts were contacted for farmer's information especially vegetable growers growing local varieties of okra. The seeds of okra were collected by visiting the fields of these farmers.Total forty four accessions were collected. All these accessions were raised in grow bags to eliminate the duplicates and to get self seeds. Pest infestation was noticed in some accessions mainly mealy bug attack. Three accessions showing similarity hence these were eliminated to avoid duplication and three accessions were showing very low germination capacity were also not included in the study. Total six accessions were eliminated from these forty four accessions and the remaining thirty-eight accessions were finally selected for the study. Passport data of the collected accessions are presented below in Table 1. The collected accessions were carried over for further evaluation in experiment 2.

3.2 Experiment-2: Evaluation of collected accessions for morphological characterization, genetic variability and diversity in qualitative and quantitative traits.

Table 1 Passport data of thirty eight okra accessions

	Collectors number	Dateof collection	Collection source	Village	Panchayath	District	Latitude (E)	Longitude (N)	Altitude (MSL)	Main characteristics
1	AE-1	10-2-2016	Farm land	Kattai	Sreekandapuram	Kannur	9.11	78.01	58 m	Light green coloured pods More pricky in nature High mucilage content
2	AE-2	10-2-2016	Farm land	Kuniyanpuzha	Azhikode	Kannur	9.970	76.32	10 m	Long pods Light green in colour downy in nature
3	AE-3	10-2-2016	Farm land	Areekkamala	Kuniyampuzha	Kannur	12.13	75.56	213 m	Long green pods pricky in nature with 6 ridges
4	AE-4	11-2-2016	Farm land	Alakkode	Alakkode	Kannur	12.19	75.46	79 m	Light green pods resembles like elephant tusk Tall plant Less vegetative growth

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	Genus	Dateof collection	Collection source	Village	Panchayath	District	Latitude (E)	Longitude (N)	Altitude (MSL)	Main characteristics
5	AE-5	11-2-2016	Farm land	Edakkad	Chelora	Kannur	11.80	75.44	7 m	Light green pods pricky in nature
6	AE-6	12-2-2016	Farm land	Malur	Aralam	Kannur	13.00	77.94	909 m	Yellowish-green pods with high mucilage content, downy in nature Large broad leaves
7	AE-7	12-2-2016	Farm land	Kottiyur	Kottiyur	Kannur	11.87	75.85	125 m	Long pods prickly in nature
8	AE-8	12-2-2016	Farm land	Kiliyanthara	Payam	Kannur	9.32	76.59	12 m	Yellowish-green pods with high mucilage content and 8 ridges
9	AE-9	15-2-2016	Farm land	Pazhur	Pazhur	Malappuram	10.87	76.01	55 m	Short green pods downy in nature with 7 ridges
10	AE-10	3-5-2016	Farm land	Taliparamba	Chapparapadavu	Kannur	12.03	75.36	49 m	Light green pods slightly prickly in nature

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	Genus	Dateof collection	Collection source	Village	Panchayath	District	Latitude (E)	Longitude (N)	Altitude (MSL)	Main characteristics
11	AE-11	5-5-2016	Farm land	Pazhur	Pazhur	Malappuram	10.87	76.01	55 m	Light green long pods prickly in nature
12	AE-12	9-5-2016	Farm land	Cheruvathur	Cheruvathur	Kasaragod	12.21	75.16	12 m	Yellowish green pods slightly prickly in nature Purple pigmentation in stem
13	AE-13	9-5-2016	Farm land	Edayalakkad	Edayalakkad	Kasaragod	10.78	76.65	68 m	Green pods prickly in nature with 7 ridges in fruit
14	AE-14	11-5-2016	Farm land	Kayyur	Cheemeni	Kasaragod	12.26	75.18	48 m	Light green pods downy in nature Tall plants with less vegetative growth
15	AE-15	11-5-2016	Farm land	Kayyur	Cheemeni	Kasaragod	12.26	75.18	48 m	Short green pods downy in nature
16	AE-16	11-5-2016	Farm land	Karinthalam	Kinanoor karinthalam	Kasaragod	31.65	78.47	3595 m	Yellowish-green pods prickly in nature
17	AE-17	11-5-2016	Farm land	Karinthalam	Kinanoor karinthalam	Kasaragod	31.65	78.47	3595 m	Light green short pods prickly in nature

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	Genus	Dateof collection	Collection source	Village	Panchayath	District	Latitude (E)	Longitude (N)	Altitude (MSL)	Main characteristics
18	AE-18	5-7-2016	Farm land	Ajanur	Ajanur	Kasaragod	12.32	75.07	10 m	Light green long pods prickly in nature with 7 ridges
19	AE-19	5-7-2016	Farm land	Ajanur	Ajanur	Kasaragod	12.32	75.07	10 m	Yellowish-green fruit slightly prickly in nature with 6 ridges
20	AE-20	12-7-2016	Farm land	Parappa	Kinanoor Karindalam	Kasaragod	12.37	75.24	156 m	Long pods with high mucilage content prickly in nature with 6 ridges
21	AE-21	12-7-2016	Farm land	Parappa	Kinanoor Karindalam	Kasaragod	12.37	75.24	156 m	Yellowish-green fruit downy in nature
22	AE-22	18-7-2016	Farm land	Udayapuram	Balal	Kasaragod	12.42	75.18	91 m	Light green long pods prickly in nature with high mucilage content
23	AE-23	18-7-2016	Farm land	Mandam	Kuzhalmandam	Kasaragod	22.04	86.03	408 m	Light green long pods downy in nature with 6 ridges
24	AE-24	18-7-201	Farm land	Madakkara	Kariyil	Kasaragod	12.22	75.13	7 m	Light green pods slightly prickly in nature

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		Dateof collection	Collection source	Village	Panchayath	District	Latitude (E)	Longitude (N)	Altitude (MSL)	Main characteristics
25	AE-25	23-7-2016	Farm land	Kottakadav	Kottakadav	Kasaragod	11.14	75.83	14 m	Short pods Downy in nature with 8 ridges
26	AE-26	23-7-2016	Farm land	Kumbalam	Kumbalam	Kasaragod	9.90	76.31	7 m	Light green pods prickly in nature with 7 ridges
27	AE-27	23-7-2016	Farm land	Alambadi	Alambadi	Kasaragod	28.73	77.13	870 m	Yellowish-green fruit downy in nature Purple pigmentation in stem
28	AE-28	23-7-2016	Farm land	Alambadi	Alambadi	Kasaragod	28.73	77.13	870 m	Yellowish-green fruit downy in nature
29	AE-29	23-7-2016	Farm land	Alambadi	Alambadi	Kasaragod	28.73	77.13	870 m	Light green pods downy in nature
30	AE-30	25-7-2016	Farm land	Ennappara	Balal	Kasaragod	12.36	75.18	226 m	Green pods downy in nature with 7 ridges
31	AE-31	16-9-2016	Farm land	Periya	Pullur periya	Kasaragod	11.83	75.85	731 m	Light green pods Purple pigmentation in stem
32	AE-32	16-9-2016	Farm land	Periya	Pullur periya	Kasaragod	11.83	75.85	731 m	Light green pods downy in nature
33	AE-33	16-9-2016	Farm land	Periya	Pullur periya	Kasaragod	11.83	75.85	731 m	Light green short pods prickly in nature

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	Genus	Dateof collection	Collection source	Village	Panchayath	District	Latitude (E)	Longitude (N)	Altitude (MSL)	Main characteristics
34	AE-34	16-9-2016	Farm land	Periya	Pullur periya	Kasaragod	11.83	75.85	731 m	Light green long pods downy in nature
35	AE-35	25-9-2016	Farm land	Periya	Pullur periya	Kasaragod	11.83	11.83	731 m	Long green pods downy in nature
36	AE-36	25-9-2016	Farm land	Periya	Pullur periya	Kasaragod	11.83	11.83	731 m	Yellowish-green pods prickly in nature
37	AE-37	28-9-2016	Farm land	Cherupuzha	Cherupuzha	Kannur	12.27	75.36	69 m	Light green short pods prickly in nature
38	AE-38	30-9-2016	Farm land	Kuniyanpuzha	Azhikode	Kannur	9.97	76.32	10 m	Yellowish-green pods Slightly prickly in nature

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3.2.1 MATERIALS

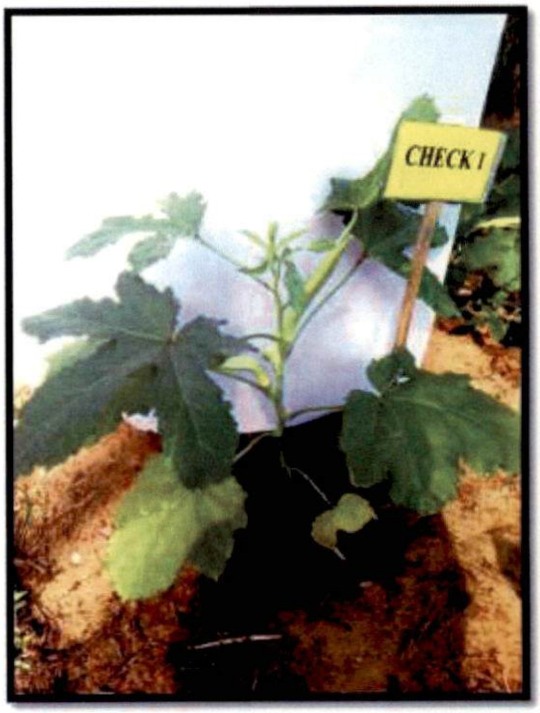
Thirty eight accessions of okra were raised in the field in augmented design for assessing various qualitative and quantitative characters. Augmented design is an unreplicated design mainly used for the evaluation of germplasm. Two varieties *viz;* Salkeerthi from Kerala Agricultural University (KAU) and Arka Anamika from Indian Institute of Horticultural Research (IIHR), Bangalore were used as checks.

3.2.2 METHODOLOGY

The experiment was conducted at Regional Agricultural Research Station (RARS) farm, Nileshwar during October and December 2016. The land was prepared after thorough ploughing and levelling. Seeds were sown in polybags. Two weeks old seedlings were transplanted to the main field in an area of 14m×18m. Observations on qualitative characters were recorded. However the experiment was abandoned due to severe attack of plant hoppers and jassids. The same experiment was repeated at College of Agriculture, Padannakkad in 5 cents of land during the period of January and April 2017. Seeds were sown directly in the field at the rate of two seeds with a spacing of 60 cm between rows and 45 cm between plants. The experiment was laid out in augmented design with ten blocks (four accessions in first eight blocks and three accessions in the remaining two blocks each) having a length of 315 cm and width of 30 cm and two checks were replicated in each block. Seedlings were thinned to one plant per stand two weeks after germination. There were a total of 58 experimental plots.

Fertilizers were applied to the plants in the ratio of 1:2:1 (1kg of Urea, 2 kg of Rajphos and 1 kg of Muriate of potash) respectively at 30 DAS (days after sowing). All other cultural practices were done as per POP (Package of Practices, 2011) recommendations. Acephate was sprayed against various insect pests mainly plant hoppers and jassids. Accessions were evaluated for various qualitative and quantitative traits and the following were the main items of observations made in the field.

Arka Anamika



Salkeerthi

Plate 1 Field overview of thirty eight okra accessions

3.3 Observations

Observations were recorded for fourteen qualitative and nineteen quantitative traits from five randomly selected plants of each accession including checks.

3.3.1 Qualitative characters

The observations on the following fourteen qualitative characters were taken based on the IPGRI (2000) descriptors and the details are shown below:

3.3.1.1 Branching pattern

The branching patterns were recorded and grouped into orthotropic stem only-3, medium-5 and strong-7.

3.3.1.2 Stem colour

The stem colour of okra was recorded and classified into three groups i.e., green-1, green with red patches-2 and purple-3.

3.3.1.3 Leaf colour and leaf rib colour

According to IPGRI leaf colour and leaf rib colour are same and these are grouped into green-1, green with red veins-2 and red-3.

3.3.1.4 Leaf shapes

Leaf shapes were recorded and classified into eleven groups as given in (Fig.1)

3.3.1.5 Colour of sepal

There is no classification in colour of sepal as per IPGRI descriptor.

3.3.1.6 Colour of petal

Petal colour was recorded and grouped into cream-1, yellow-2 and golden-3.

3.3.1.7 Colour of anthers and staminal column

There is no classification for colour of anthers and staminal column as per IPGRI descriptor.

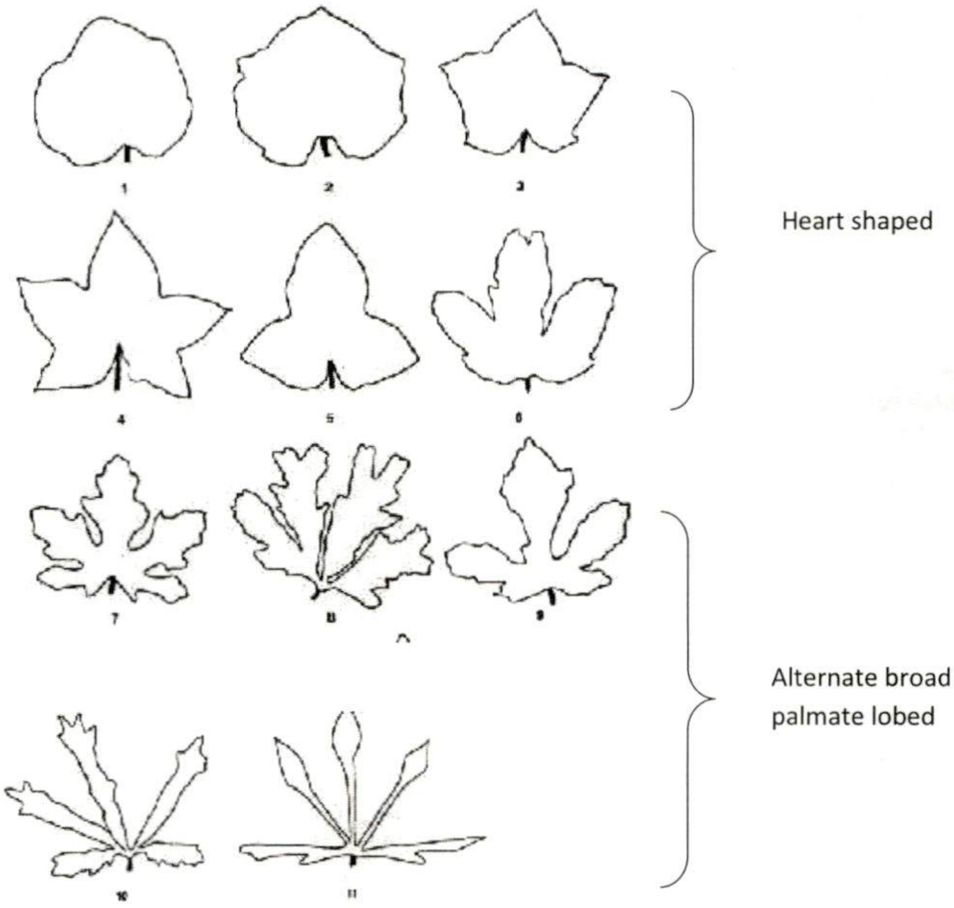


Figure 1. Leaf shape of okra as per IPGRI descriptor

3.3.1.8 Colour of fruit

Fruit colour was recorded and grouped into yellowish green-1, green-2, green with red patches-3 and red-4.

3.3.1.9 Colour of fruit ridges

There is no IPGRI descriptor for the colour of fruit ridges and no variation was noticed in this trait also.

3.3.1.10 Fruit shape

Shape of the fruit was recorded and classified into fifteen groups (Fig.2.)

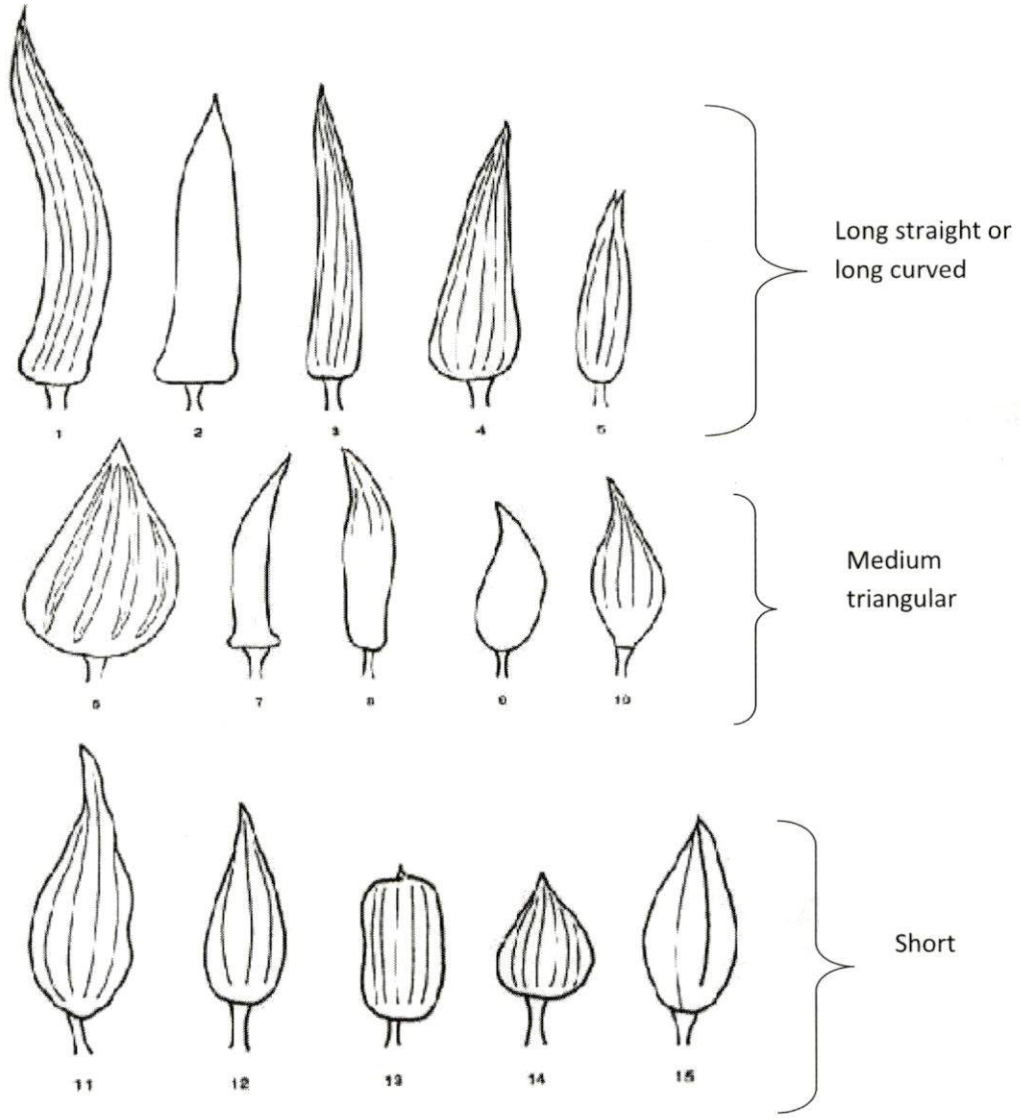


Figure 2. Fruit shape of okra as per IPGRI descriptor

3.3.1.11 Position of fruit

Fruit position was recorded and grouped into erect-3, horizontal-5 and pendulous-7.

3.3.1.12 Fruit pubescence

Fruit pubescence was recorded and grouped into downy-3, slightly rough-5 and prickly-7.

3.3.1.13 Ridges per fruit

Ridges per fruit were recorded and grouped into 1.none (smooth fruit)-1, from 5 to 7-2, from 8 to 10-3 and more than 10-4.

3.3.2 Quantitative Parameters

Observations on nineteen quantitative traits were recorded in five randomly selected plants of thirty eight okra accessions and the details are given below:

3.3.2.1 Plant height (cm)

Plant height was measured from the ground level to the growing tip of the plant at 60 DAS and 90 DAS and expressed in centimetres.

3.3.2.2 Primary branches per plant

The number of primary branches from the main stem in each plant was counted 90 DAS.

3.3.2.3 Internode length (cm)

The distance between the second and third node starting from the basal portion and between the remaining nodes on the main stem of the each plant were recorded 60 DAS and the average was worked out and expressed in centimeters.

3.3.2.4 First flowering node

The node number from the cotyledonous leaves at which first flower appears was counted in each plant.

3.3.2.5 Days to 50% flowering

The number of days taken from the date of sowing to the day on which 50 percent of the population in an accession flowered was recorded.

3.3.2.6 Number of fruiting node

Number of fruiting nodes in each plant was counted and mean worked out.

3.3.2.7 Number of units in epicalyx

Number of the units in the epicalyx of the flower from five randomly selected plants was counted.

3.3.2.8 Length of units in epicalyx (cm)

Average size of each unit in epicalyx was recorded from the base to the tip and expressed in centimetres.

3.3.2.9 Length of sepal (cm)

Average size of sepal was measured from the base to the tip and expressed in centimetres.

3.3.2.10 Length of petals (cm)

Size of petals was measured longitudinally from the point of attachment of base of the petal to the tip and was expressed in centimetres.

3.3.2.11 Length of stamen (cm)

Size of stamen was measured from the point of attachment of the staminal column to the tip of the stamen.

3.3.2.12 Fruit length (cm)

Fruit length of the tender fruit was measured from the base of the calyx to the tip of the fruit.

3.3.2.13 Length of fruit peduncle (cm)

Length of fruit peduncle was measured from the point of attachment on the main the stem to the calyx of the fruit.

3.3.2.14 Fruit diameter (cm)

The circumference of the immature pod was taken from the centre of the fruit and then the average was worked out using Vernier Calipers.

3.3.2.15 Number of locules in the fruit

The number of locules of the randomly selected five immature pods was counted.

3.3.2.16 Fruit weight (g)

Tender fruits of each harvest were weighed and recorded in grams.

3.3.2.17 Days to marketable maturity

Days taken from anthesis to marketable maturity of the fruit were recorded.

3.3.2.18 Marketable fruits per plant

The number of good quality edible and tender fruits excluding those infested by pest and diseases from the total number of fruits obtained from all pickings was recorded

3.3.2.19 Green fruit yield per plant (g)

Weight of total number of fruits including those infested by pest and diseases obtained from all pickings of each plant were recorded.

3.3.3 Pest and Disease

3.3.3.1 Fruit and shoot borer infestation

The number of plants affected by fruit and shoot borer infestation was counted 30 DAS and 60 DAS and percentage of incidence worked out in each accession.

3.3.3.2 Yellow vein mosaic infestation

The number of plants affected yellow vein mosaic infestation was counted 30 DAS and 60 DAS and percentage of incidence worked out in each accession.

3.3.3.3 Cercospora leaf spot infestation

The number of plants affected by cercospora leaf spot infestation was counted 30 DAS and 60 DAS and percentage of incidence worked out in each accession.

3.4 STATISTICAL ANALYSIS

The data on various observations studied during the course of experiment were subjected to statistical analysis. All qualitative data were converted to binary form based on IPGRI descriptors. For quantitative data analysis of variance (ANOVA) and covariance was performed using INDOSTAT. The components of variation such as coefficients of variation, heritability, genetic advance, correlation and path coefficient were estimated as per Nadarajan and Gunasekaran (2005). The significance of genotypic and phenotypic correlation coefficients among the characters observed were assessed at 5 % and 1 % levels from the table value at (n-2) degrees of freedom.

3.4.1 Components of variation

i) Coefficient of variation

a) Phenotypic coefficient of variation (PCV %) = $\frac{\sigma p}{\text{Mean}} \times 100$

b) Genotypic coefficient of variation (GCV %) = $\frac{\sigma g}{\text{Mean}} \times 100$

Where,

σp and σg are phenotypic and genotypic standard deviations respectively. The PCV and GCV were classified as follows:

Low : less than 10%

Moderate: 10-20%

High : More than 20%

ii) Heritability

Heritability in broad sense was estimated using the following formula

$$\text{Heritability } (h^2) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

$\sigma^2 g$ - genotypic variance
$\sigma^2 p$ - phenotypic variance

The heritability values were categorized as follows:

Low : less than 30%

Moderate: 30-60%

High : More than 60%

iii) Genetic advance

$GA = k \times h^2 \times \sigma p$

Where, k = standardized selection differential at particular level of selection intensity,

h^2 = heritability of the character under consideration

σp = phenotypic standard deviation of the original population.

iv) Genetic gain

It is the genetic advance expressed as percentage of mean.

$$GA\ (\%) = \frac{\text{Genetic Advance}}{\text{Mean}} \times 100$$

The range of GA as per cent of mean was classified as follows:

Low : less than 10%

Moderate: 10-20%

High : More than 20%

v) Phenotypic and genotypic correlations

The significance of correlation coefficients were ascertained from the table r value at (n-2) degrees of freedom where n is the number of pairs of observations used.

vi) Path coefficient analysis

The correlation between green fruit yield and other characters were split into direct and indirect effects using path analysis technique. The direct and indirect effects were classified as:

0.00-0.09 - Negligible

0.10-0.19 - Low

0.20-0.29 - Moderate

0.30-1.00 - High

>1.00 - Very high

3.5 Cluster analysis

Cluster analysis of qualitative characters was performed using UPGMA (Unweighted Pair Group Method with Arithmetic mean) method with the help of Minitab (software developed at the Pennsylvania State University). The cluster analysis for quantitative data was performed using Standardized Euclidean Square Distance and thirty eight genotypes of okra were grouped into clusters based on nineteen quantitative characters. Inter-intra cluster distance and cluster means were calculated for individual characters based on the performances of various genotypes in each cluster. Dendrogram showing the distance of accessions in each cluster was constructed in cluster analysis for both qualitative and quantitative data respectively.

Results

4. RESULTS

The results of the study, "Characterization of okra genotypes in North Kerala" are presented under the following heads.

1. Exploration and collection of different genotypes of okra
2. Morphological characterization based on qualitative traits
3. Evaluation of Genetic variability based on quantitative traits

4.1 Exploration and collection of different genotypes of okra

On the basis of eco-geographic survey conducted in various parts of North Kerala, thirty eight accessions of *Abelmoshes esculentus* L. were collected from three districts *viz.,* Kasargod, Kannur and Malappuram. Twenty five accessions were collected from Kasaragod, eleven from Kannur and two from Malappuram. The accessions and their districts of collection are presented in Table 2.

4.2 Morphological characterization based on qualitative traits

Thirty eight accessions of okra were evaluated for fourteen qualitative traits as per IPGRI descriptor. The frequency distribution of accessions for each descriptor state with respect to each trait is presented in Table 3.

4.2.1 Branching pattern

Majority of the accessions (33 Nos.) had orthotropic type of branching. Three accessions (AE-1, AE-9, and AE-10) had medium type of branching and two accessions (AE-4 and AE-8) had strong branching.

4.2.2 Stem colour

The results showed that stem colour displayed three distinct variations ranging from green, green with red patches to purple colour.

Table 2. Accessions collected from various districts

Accessions	District
AE-1	Kannur
AE-2	Kannur
AE-3	Kannur
AE-4	Kannur
AE-5	Kannur
AE-6	Kannur
AE-7	Kannur
AE-8	Kannur
AE-9	Malappuram
AE-10	Kannur
AE-11	Malappuram
AE-12	Kasargod
AE-13	Kasargod
AE-14	Kasargod
AE-15	Kasargod
AE-16	Kasargod
AE-17	Kasargod
AE-18	Kasargod
AE-19	Kasargod
AE-20	Kasargod
AE-21	Kasargod
AE-22	Kasargod
AE-23	Kasargod
AE-24	Kasargod
AE-25	Kasargod
AE-26	Kasargod
AE-27	Kasargod
AE-28	Kasargod
AE-29	Kasargod
AE-30	Kasargod
AE-31	Kasargod
AE-32	Kasargod
AE-33	Kasargod
AE-34	Kasargod
AE-35	Kasargod
AE-36	Kasargod
AE-37	Kannur
AE-38	Kannur

Out of thirty eight accessions, twenty four accessions had green colored stem and seven accessions had green with red patches and the remaining seven accessions had purple coloured stem.

4.2.3 Leaf colour and leaf rib colour

According to IPGRI leaf colour and leaf rib colour are same hence there was no separate descriptor for this observation. The intensity of the colour in leaf varied between dark green colour (30 accessions) to green with red veins (8 accessions) and no accessions had fully red coloured leaf rib.

4.2.4 Leaf shape

Out of thirty eight okra accessions, maximum number of eleven accessions belonged to fourth group of leaf shape followed by six accessions belonged to third group; four accessions each belonged to first group, second group, seventh group and ninth group respectively. Two accessions came under group eight and three accessions under group six of leaf shape.

4.2.5 Colour of sepal

As per IPGRI descriptor there is no classification in sepal colour and in the present study also there is no variation observed for this trait

4.2.6 Colour of petal

Three petal colours were observed *viz.*, cream, yellow and golden. Twenty five accessions had creamy petals. Seven accessions had yellow petals and the remaining six accessions had golden yellow petals.

4.2.7 Colour of anthers and staminal column

There is no classification for colour of anthers and staminal column as per IPGRI descriptor and no variation was noticed in these traits.

4.2.8 Colour of fruit

The descriptor for fruit colour were yellowish green, green, green with red patches and red. Out of thirty eight okra accessions twenty seven accessions produced yellowish green fruits, ten accessions produced green fruits and one accession (AE -10) alone produced green with red patches fruits and none of the accessions produced red coloured fruits.

4.2.9 Colour of fruit ridges

There was no variation in the colour of fruit ridges in these thirty eight okra accessions as per IPGRI descriptor.

4.2.10 Fruit shape

Out of thirty eight accessions, sixteen accessions had fruit shape score 1, nine accessions had fruit shape score 3, five accessions fruit shape score 2, four accessions had fruit shape score 7, three accessions had fruit shape score 8 and one accession had fruit shape score 4. There was no occurrence of the fruit shape scores 5, 6, 9, 10, 11, 12, 13, 14 and 15 among the thirty eight accessions.

4.2.11 Position of fruit

Position of the fruit on the main stem was classified into erect, horizontal and pendulous. Majority of the accessions (34 Nos.) had fruits in erect position, only 4 accessions had fruits in horizontal position and no accessions bore fruits in pendulous (drooping) position.

4.2.12 Fruit pubescence

Fruit pubescence was classified into downy, slightly rough and prickly. Seventeen accessions had fruits with downy surface, sixteen accessions had prickly fruits and the remaining five accessions produced fruits with slightly rough pubescence.

4.2.13 Ridges per fruit

Most of the accessions (36 Nos.) had 5-7 ridges per fruit. Only two accessions had 8-10 ridges per fruit. There was no accession having more than 10 ridges.

Table 3. Frequency distribution of thirty eighy okra accessions

SI. no	Descriptors	Descriptor state	Score code	No of Accessions	Accessions
1.	Stem colour	Green	1	24	AE -2 , AE- 3 , AE- 5 , AE- 6 , AE- 7 , AE- 13 , AE- 14 , AE- 15 , AE- 16 , AE- 17 , AE- 18 , AE- 19 , AE -22 , AE- 23 , AE- 26 , AE- 28 , AE- 29 , AE- 30 , AE- 32 , AE- 33 , AE- 35 , AE- 36, AE- 37 , AE- 38
		Green with red patches	2	7	AE- 4, AE-12 ,AE -21 , AE -27 , AE- 24 , AE- 31 , AE- 34
		Purple	3	7	AE- 1 , AE- 25 , AE- 8 , AE- 20 , AE- 9 , AE- 10 , AE-11
2.	Branching pattern	Orthotropic stem only	3	33	AE-2 , AE- 3, AE-5 , AE-6 , AE-7 , AE-11 , AE-12 , AE-13 , AE-14 , AE-15 , AE-16 , AE-17 , AE-18 , AE-19 , AE-20 , AE-21 , AE-22 , AE-23 , AE-24 , AE-25 , AE-26 , AE-27 , AE-28 , AE-29 , AE-30 , AE-31 , AE-32 , AE-33 , AE-34 , AE-35 , AE-36 , AE-37 , AE-38
		Medium	5	3	AE-1, AE-9 , AE-10
		Strong	7	2	AE-4 , AE-8
3.	Leaf colour and Leaf rib colour	Green	1	30	AE-2 , AE- 3, AE-4 , AE-5 , AE-11 , AE-12 , AE-13 , AE-14 , AE-15 , AE-17 , AE-18 , AE-19 , AE-21 , AE-22 , AE-23 , AE-24 , AE-25 , AE-26 , AE-27 , AE-28 , AE-29 , AE-30 , AE-31 , AE-32 , AE-33 , AE-34 , AE-35 , AE-36 , AE-37 , AE-38
		Green with red veins	2	8	AE1, AE6 , AE7 , AE8 , AE9 , AE10 , AE16 , AE20
		Red veins	3	Nil	
4.	Leaf shape	(as per IPGRI descriptors)	1	4	AE-33 , AE-23 , AE-1 , AE-35
			2	4	AE-16 , AE-19 , AE-24 , AE-25
			3	6	AE-4 , AE-7 , AE-9 , AE-10 , AE-13 , AE-22
			4	11	AE-2 , AE -3 , AE-5 , AE-6 , AE-8 , AE-11 , AE-18 , AE-20 , AE-26 , AE-27 , AE-29
			5	Nil	
			6	3	AE-32 , AE-34 , AE-37

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SI. no	Descriptors	Descriptor state	Score code	No of Accessions	Accessions
			7	4	AE-12 , AE-28 , AE-30 , AE-31
			8	2	AE-17 , AE-36
			9	4	AE-14 , AE-15 , AE-21 , AE-38
			10	Nil	
			11	Nil	
5.	Colour of petal	Cream	1	25	AE-2 , AE- 3, AE-6, AE-7, AE-8, AE-11, AE-12, AE-15, AE-16, AE-17, AE-18 , AE-19 , AE-20 , AE-22 , AE-23 , AE-24 , AE-27 , AE-29 , AE-31 , AE-32 , AE-34 , AE-35 , AE-36 , AE-37 , AE-38
		Yellow	2	7	AE-1 , AE-10 , AE-13 , AE-14 , AE-21 , AE-26 , AE-30
		Golden	3	6	AE-4 , AE-5 , AE-9 , AE-25 , AE-28 , AE-33
6.	Colour of fruit	Yellowish green	1	27	AE-1 , AE-6 , AE-7 , AE-8 , AE-9 , AE-25 , AE-11 , AE-12 , AE-13 , AE-16 , AE-17 , AE-18 , AE-19 , AE-20 , AE-21 , AE-22 ,AE-23 , AE-24 , AE-27 AE-28 , AE-29 , AE-30 AE-31 ,AE-32 , AE-36, AE-37 ,AE-38
		Green	2	10	AE-2 , AE- 3 , AE-4 , AE-5 , AE-14 , AE-15 , AE-26 , AE-33 , AE-34 , AE-35
		Green with red patches	3	1	AE-10
		Red	4	Nil	
7.	Fruit shape	(as per IPGRI descriptors)	1	16	AE-2 , AE-6 , AE-12 , AE-14 , AE-16 , AE-18 , AE-21 , AE-24 , AE-26 , AE-28 , AE-30 , AE-31 , AE-32 , AE-34 , AE-37 , AE-38
			2	5	AE-7 , AE-8 , AE-11 , AE-13 , AE-25
			3	9	AE- 3 , AE-15 , AE-17 , AE-19 , AE-20 , AE-23 , AE-27 , AE-35 , AE-36
			4	1	AE-10
			5	Nil	

Sl.no	Descriptors	Descriptor state	Score code	No of Accessions	Accessions
			6	Nil	
			7	4	AE-5 ,AE-22 , AE-29,AE-33
			8	3	AE-1 , AE-4 , AE-9
			9	Nil	
			10	Nil	
			11	Nil	
			12	Nil	
			13	Nil	
			14	Nil	
			15	Nil	
8.	Position of fruit	Erect	3	34	AE-1 , AE-2 , AE-3 , AE-5 , AE-7 , AE-8 , AE-9 , AE-10 , AE-11 , AE-12 ,AE-14 , AE-15 ,AE-16 , AE-17 , AE-18 , AE-19 , AE-20 , AE-21 , AE-23 ,AE-24 ,AE-25 , AE-26 ,AE-27 , AE-28 , AE-29 , AE-30 , AE-31 , AE-32 ,AE-33 , AE-34 , AE-35 , AE-36 , AE-37 ,AE-38
		Horizontal	5	4	AE-4, AE-6, AE-13, AE-22
		Pendulous	7	Nil	
9.	Fruit pubescence	Downy	3	17	AE-2 , AE-6 , AE-8 , AE-9 , AE-14 , AE-15 , AE-20 , AE-21 , AE-23 , AE-25 , AE-27 , AE-28 , AE-29 , AE-30 , AE-32 , AE-34 , AE-35
		Slightly rough	5	5	AE-10 , AE-12 , AE-19 , AE-24 , AE-38
		Prickly	7	16	AE-1, AE- 3, AE-4, AE-5, A-7, AE-11, AE-13, AE-16, AE-17, AE-18, AE-22, AE-26, AE-31, AE-33, AE-36 , AE-37
10.	Ridges per fruit	None	1	Nil	
		From 5 to 7	2	36	AE-1 , AE-8, AE-18, AE-2, AE- 3, AE-4, AE-5, AE-6, AE-7, AE-9, AE-10, AE-11, AE-12, AE-13, AE-14 , AE-15 ,AE-16 , AE-17, AE-19 ,AE-20 , AE-21 , AE-22, AE-23 ,AE-24 , AE-26, AE-27, AE-28, AE-29, AE-30, AE-31, AE-33,AE-34, AE-36, AE-37,AE-38 AE-35
		from 8 to 10	3	2	AE-25 , AE-32
		more than 10	4	Nil	

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4.3 Evaluation of genetic variability based on quantitative traits

The extent of genetic variability with respect to nineteen characters in thirty eight accessions of okra was estimated and the results are presented in Table 4. The analysis of variance revealed that there were significant differences among the accessions for all the characters except number of locules in the fruit and fruit length. There were no significant differences among the checks for characters such as days to 50% flowering, internode length, number of units in epicalyx, length of sepal, length of petals and fruit diameter. Characters like number of fruiting nodes, length of sepals and length of petals did not show any significant difference between checks and accessions.

4.3.1 Mean performance of thirty eight okra accessions

The mean performance of thirty eight accessions of okra for nineteen quantitative characters is given in Table 5. Maximum height was recorded in AE-23 (77.34 cm) followed by AE-26 (71.47 cm). The accession AE-9 had recorded lowest value of 33.12 cm for this trait. Among checks Salkeerthi had the lower plant height (53.81 cm) than Arka Anamika (86.73 cm) which was the tallest when compared to the collected accessions. Among the thirty eight accessions, AE-16 had the maximum number of primary branches (2.01) followed by AE-20 (1.81). The lowest value of (0.91) for this trait was recorded in three accessions (AE-5, AE-6 and AE-7) and there were no primary branches in the check Arka Anamika.

The maximum mean value for internode length was recorded in AE-23 (6.61 cm) whereas the accession AE-6 and AE-28 recorded minimum value (3.06 cm). In checks it ranged from 5.39 to 5.43 cm. The number of node to first flower ranged from 1.84 (AE-17) to 3.59 (AE-4). In the case of checks it was 2.68 in Salkeerthi and 2.09 in Arka Anamika. Accession AE-31 (62.16) took maximum days to 50% flowering and minimum was recorded in AE-10 (48.81) and Salkeerthi recorded 61.07 days and Arka Anamika 61.65 days.

Table 4. Analysis of variance for quantitative trait

Sl.no	Characters	Source of variation			Mean Sum of Squares					
		Checks	Accessions	Accessions vs/ Checks	Checks	Accessions	Accessions vs/ Checks	SE ± m	CD	CV (%)
1.	Plant height (cm)	1	37	1	5418**	179.2**	5782**	3.67	7.71	28.20
2.	Primary branches per plant	1	37	1	5.20**	0.07**	5.41**	1.07	2.25	28.93
3.	Internode length (cm)	1	37	1	0.00	1.11**	11.74**	0.47	0.99	23.56
4.	First flowering node	1	37	1	1.74**	0.20**	0.97**	0.28	0.60	17.56
5.	Days to 50% flowering	1	37	1	1.68	18.16**	511.76**	1.31	2.75	7.88
6.	Number of fruiting nodes	1	37	1	8.84**	0.52**	0.15	0.48	1.02	15.90
7.	Number of units in epicalyx	1	37	1	0.00	1.98**	2.62**	0.00	0.00	14.59
8.	Length of units in epicalyx(cm)	1	37	1	0.39*	0.12*	0.25*	0.33	0.69	21.57
9.	Length of sepals (cm)	1	37	1	0.04	1.48**	0.07	0.50	1.06	32.50
10.	Length of petals (cm)	1	37	1	0.08	1.23**	0.37	0.46	0.98	24.98
11.	Length of stamens (cm)	1	37	1	1.01*	0.40*	1.87**	0.42	0.89	33.97
12.	Fruit length (cm)	1	37	1	230.52**	13.54	177.7**	2.83	5.95	16.47
13.	Length of fruit peduncle (cm)	1	37	1	0.84**	0.21**	0.71**	0.21	0.45	22.03
14.	Fruit diameter (cm)	1	37	1	0.01	0.13*	6.95**	0.54	1.14	24.92
15.	Number of locules in the fruit	1	37	1	9.80	0.84	21.43	4.42	NS	45.48
16.	Fruit weight (g)	1	37	1	99.01**	37.92*	176.02**	3.82	8.04	21.51
17.	Days to marketable maturity	1	37	1	0.84**	0.91**	3.86**	0.18	0.38	13.85
18.	Marketable fruits per plant	1	37	1	4.80*	3.60*	380.38**	2.06	4.34	14.02
19.	Green fruit yield per plant (g)	1	37	1	144670*	6235**	24265**	16.53	34.74	16.27

* Significance at 5% level

** Significance at 1% level

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Maximum number of fruiting nodes was recorded in AE-16 (6.00) and the minimum number of fruiting nodes in AE-27 (2.80). The number of fruiting nodes was 5.56 in Salkeerthi and 4.23 in Arka Anamika. Number of units in epicalyx ranged from 11 in eight accessions to 7 in five accessions. In both checks number of units in epicalyx was 9. Length of units in epicalyx was maximum in AE-1 and AE-10 (2.50 cm) and minimum in AE-24 (1.10 cm). In Salkeerthi it was 1.55 cm and in Arka Anamika 1.83 cm. Length of sepals recorded maximum in AE-24 (5.30 cm) and minimum in AE-9 (1.60 cm) followed by AE-15 (1.82 cm). In Salkeerthi it was 3.51 cm and in Arka Anamika sepal length was 3.61 cm. Length of petals recorded maximum in AE-3 (6.00 cm) and AE-28 had recorded the lowest value (2.95 cm) for this trait. In checks it ranged from 4.43 cm to 4.56 cm. Length of stamen was maximum in AE-32 (2.95 cm) and minimum in AE-28 (1.34 cm) and in Salkeerthi 2.67 cm and 2.22 cm in Arka Anamika.

The fruit length varied from 11.37 to 27.78 cm with a mean value of 22.32 cm. Accession AE-25 produced longest fruit (27.78cm), while AE-10 produced smallest fruit (11.37 cm). Fruit length in the checks Salkeerthi and Arka Anamika were 29.24 cm and 22.45 cm respectively. The length of the fruit peduncle varied from 1.39 to 3.23 cm. The accession AE-9 (3.23 cm) had maximum peduncle length followed by AE-32 (3.16 cm) while AE-5 (1.39 cm) had recorded the lowest value for this trait. Salkeerthi had peduncle length of 2.20 cm and Arka Anamika had 1.79 cm. The accession AE-5 (3.68 cm) had the largest fruit diameter and the smallest fruit diameter was recorded in AE-17 (1.18 cm). In checks it was 2.81 cm in Arka Anamika and 2.76 cm in Salkeerthi. Only two accessions, AE- 25 and AE-32 had eight locules whereas rest of all accessions and two checks Salkeerthi and Arka Anamika had five locules in their fruits. Maximum fruit weight was recorded in AE-5 (61.65 g) and minimum fruit weight was recorded in AE-10 (22.84 g). Salkeerthi had 28.82 g and Arka Anamika 24.37 g fruit weight.

Table 5. Mean performance of thirty eight okra accessions

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
AE-1	42.17	1.01	3.51	2.59	59.16	4.80	7.00	**2.50**	4.74	4.26	2.85	26.44	2.48	2.09	5.30	30.71	**5.18**	18.13	500.93
AE-2	48.77	1.01	3.91	2.59	55.56	5.40	**11.00**	1.94	3.26	4.74	2.39	19.64	2.26	2.57	6.30	27.57	6.98	19.73	488.51
AE-3	54.79	1.21	4.51	2.39	49.16	3.20	10.00	2.26	3.76	**6.00**	2.45	20.88	2.32	2.53	6.30	33.69	6.98	19.13	579.91
AE-4	34.35	1.01	3.31	**3.59**	58.16	5.40	9.00	2.28	3.84	5.34	2.85	25.60	2.64	2.17	5.30	27.51	5.98	19.13	475.89
AE-5	46.51	0.91	4.06	2.99	55.46	5.75	10.00	1.50	2.88	4.36	1.70	23.09	**1.39**	**3.68**	7.30	**61.65**	5.93	16.03	487.93
AE-6	34.47	0.91	**3.06**	2.59	60.86	4.55	7.00	2.22	3.30	5.20	2.08	25.51	1.91	2.58	5.30	27.12	7.93	16.83	475.51
AE-7	50.21	0.91	5.46	2.79	56.06	5.55	8.00	1.94	3.30	5.22	1.80	19.15	1.83	2.20	5.30	29.48	6.93	18.43	566.91
AE-8	34.49	1.51	3.66	2.79	56.26	3.95	8.00	2.24	4.44	4.12	2.74	20.23	2.03	2.48	5.30	33.82	5.93	19.03	462.89
AE-9	**33.12**	1.01	3.71	2.84	50.01	5.40	8.00	2.22	**1.60**	5.55	2.16	25.53	**3.23**	2.43	5.30	23.22	5.88	15.13	410.39
AE-10	44.50	1.21	3.91	3.64	**48.81**	5.40	**7.00**	2.50	2.26	5.71	1.70	**11.37**	2.25	2.03	7.30	**22.84**	5.88	19.33	514.35
AE-11	36.54	1.01	5.31	3.24	54.01	5.40	7.00	2.08	3.42	4.69	1.78	17.87	2.71	1.73	5.30	26.68	6.88	14.73	452.73
AE-12	45.34	1.01	4.51	2.84	56.81	5.20	10.00	1.30	3.88	5.27	1.98	24.51	1.83	2.45	**5.30**	26.98	6.88	14.33	447.57
AE-13	46.42	1.21	3.11	3.14	54.81	5.40	10.00	1.85	3.88	5.43	2.09	26.26	2.18	1.59	5.30	25.46	6.98	**12.53**	423.85
AE-14	50.32	1.01	5.11	2.34	54.21	5.00	11.00	2.03	2.92	4.53	1.65	16.28	2.00	1.47	5.30	24.48	5.98	14.33	455.85
AE-15	70.38	1.01	6.31	3.34	60.41	5.80	10.00	1.67	1.82	3.59	1.55	16.98	1.48	1.65	5.30	24.06	7.98	13.53	430.59
AE-16	59.18	**2.01**	3.51	2.34	61.61	**6.00**	11.00	1.95	3.82	3.33	1.81	24.78	2.18	1.35	6.30	32.20	6.98	20.48	**682.79**
AE-17	39.87	1.01	3.71	**1.84**	52.76	4.80	10.00	2.48	3.08	3.65	1.45	20.47	2.08	**1.18**	5.30	29.65	7.38	16.63	471.99
AE-18	54.09	1.21	3.91	2.44	52.96	4.60	10.00	1.30	3.04	4.59	2.05	22.55	1.56	1.62	6.30	31.77	6.98	19.83	601.77
AE-19	67.15	1.01	5.11	3.44	60.16	5.00	10.00	1.22	2.22	4.51	1.39	23.81	1.54	1.30	7.30	31.95	6.98	15.83	479.75
AE-20	53.17	1.81	3.51	2.04	56.96	5.80	8.00	1.88	3.34	5.59	1.55	20.81	2.48	2.24	7.30	32.51	5.38	21.63	678.03
AE-21	45.10	1.01	5.01	3.04	54.26	4.75	11.00	1.22	3.26	4.29	2.15	24.05	1.81	2.54	5.30	30.90	6.93	15.73	454.85
AE-22	48.02	1.01	5.01	2.44	48.86	4.75	11.00	1.78	3.60	4.05	1.41	23.61	1.99	2.52	5.30	31.98	6.93	18.13	542.37
AE-23	77.34	1.21	**6.61**	2.84	60.86	6.15	8.00	1.34	3.72	5.09	1.95	24.07	1.85	2.50	5.30	30.86	8.93	17.33	498.81
AE-24	53.12	1.01	5.01	2.04	54.46	4.75	10.00	**1.10**	**5.30**	3.49	2.03	22.41	1.55	2.64	5.30	25.22	6.73	16.73	382.45
AE-25	36.87	1.21	4.46	2.49	49.56	3.45	8.00	1.68	4.12	5.95	2.80	27.78	2.97	1.70	**8.30**	30.56	6.13	20.18	541.27

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	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
AE-26	71.47	1.21	5.06	2.49	54.56	4.85	10.00	1.54	4.02	5.91	2.18	27.42	2.79	1.92	5.30	37.06	7.13	16.68	530.95
AE-27	47.87	1.01	5.86	2.69	49.76	**2.80**	7.00	1.40	3.74	3.59	2.48	24.96	1.89	1.90	5.30	25.40	7.53	14.08	**285.83**
AE-28	34.53	1.01	3.06	1.89	61.36	5.45	11.00	2.20	2.20	**2.95**	**1.34**	22.04	2.13	2.50	6.30	41.66	7.13	16.88	595.47
AE-29	48.41	1.21	3.31	2.84	53.96	5.35	10.00	1.75	3.49	3.94	2.13	19.58	1.84	1.86	5.30	29.43	7.18	16.48	518.37
AE-30	57.01	1.41	5.11	2.04	57.56	4.35	10.00	1.81	3.45	3.16	2.05	25.78	3.06	1.90	7.30	33.21	5.18	15.68	563.99
AE-31	54.11	1.41	4.71	2.44	**62.16**	5.55	10.00	1.23	2.57	4.18	2.29	25.68	2.16	1.84	5.30	29.77	8.18	18.88	596.23
AE-32	51.23	1.01	5.11	3.04	54.76	5.15	11.00	2.13	3.23	3.84	**2.95**	18.36	3.16	1.24	**8.30**	26.01	7.18	13.88	390.87
AE-33	44.46	1.01	3.96	2.69	48.96	5.50	10.00	2.08	4.43	5.16	2.02	19.37	2.28	2.21	6.30	23.76	7.03	17.43	421.79
AE-34	51.98	1.01	4.36	2.49	61.76	5.70	11.00	1.80	3.49	4.04	1.98	25.91	2.12	1.95	5.30	27.98	7.03	17.63	493.35
AE-35	49.04	1.01	4.96	2.29	49.36	5.90	10.00	2.06	2.31	4.24	1.88	20.19	2.82	1.95	5.30	28.34	6.03	17.23	493.17
AE-36	36.91	1.01	4.56	2.19	50.86	5.25	10.00	1.30	2.97	3.96	1.80	20.22	2.99	1.35	5.30	33.60	**9.03**	15.03	481.99
AE-37	47.85	1.01	5.36	2.99	56.46	5.85	10.00	2.06	3.03	3.56	1.36	19.20	2.81	2.05	5.30	29.16	7.63	13.83	382.09
AE-38	61.27	1.01	3.76	2.19	50.26	4.65	10.00	1.58	3.25	3.84	2.00	19.02	2.13	2.05	5.30	30.32	7.03	16.63	496.77
C-1	53.81	1.02	5.39	2.68	61.07	5.56	9.00	1.55	3.51	4.56	2.67	**29.24**	2.20	2.76	5.00	28.82	7.27	**22.72**	621.80
C-2	**86.73**	**0.00**	5.43	2.09	61.65	4.23	9.00	1.83	3.61	4.43	2.22	22.45	1.79	2.81	5.60	24.37	7.68	21.74	451.70

A = Plant height (cm) , B = Primary branches per plant, C = Internode length (cm), D = First flowering node, E = Days to 50% flowering , F = Number of fruiting nodes, G = Number of units in epicalyx , H = Length of units in epicalyx (cm), I = , Length of sepals (cm), J = Length of petals (cm), K = Length of stamens (cm), L = Fruit length (cm) , M = Length of fruit peduncle (cm), N= Fruit diameter, O = Number of locules in the fruit , P = Fruit weight (g), Q = Days to marketable maturity, R= Marketable fruits per plant, S = Green fruit yield per plant (g).

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Days to attain marketable maturity for pods ranged from 5.18 to 9.03 days. AE-36 had recorded the maximum days of 9.03 to attain marketable maturity and minimum days was recorded in AE-1 (5.18) followed by AE-20 (5.38). In checks it was 7.27 and 7.68 days for Salkeerthi and Arka Anamika respectively. Number of marketable fruits per plant was highest in AE-20 (21.63) followed by AE-16 (20.48) and lowest in AE-13 (12.53). In checks marketable fruits ranged from 21.74 to 22.72. Maximum green fruit yield was recorded in AE-16 (682.79 g) followed by AE-20 (678.03 g). In the case of checks Salkeerthi (621.80 g) recorded higher yield than Arka Anamika (451.70 g).

4.3.2 Pest and Diseases

4.3.2.1 Fruit and shoot borer infestation

The incidence of fruit and shoot borer on different accessions was recorded and the percentage calculated. The results are presented in Table 6. Maximum incidence of 35% was noticed in two accession (AE-12 and AE-13) followed by 33% in AE-5 and 30% in four accessions (AE-6, AE-11, AE-36 and AE-37). Minimum incidence was found in accession AE-17, AE-21, AE- 32 and AE-38 (10%) followed by AE-3 and AE- 4 (11%), AE-19 (13%) and AE-24 (15%), AE-2, AE-27 and AE-28 (20%). No infestation was noticed in majority of the accessions (20 Nos.) as well as in the check Salkeerthi. Minor infestation of (10%) was noticed in Arka Anamika.

4.3.2.2 Yellow vein mosaic infestation

There was no incidence of yellow vein mosaic.

4.3.2.3 Cercospora leaf spot infestation

There was no incidence of cercospora leaf spot.

Table.6. Effect of fruit and shoot borer incidence in different accessions

Accessions	Percentage of fruit and shoot borer infestation
AE-1	Nil
AE-2	20
AE-3	11
AE-4	11
AE-5	33
AE-6	30
AE-7	Nil
AE-8	Nil
AE-9	Nil
AE-10	Nil
AE-11	30
AE-12	35
AE-13	35
AE-14	Nil
AE-15	Nil
AE-16	Nil
AE-17	10
AE-18	Nil
AE-19	13
AE-20	Nil
AE-21	10
AE-22	Nil
AE-23	Nil
AE-24	15
AE-25	Nil
AE-26	Nil
AE-27	20
AE-28	20
AE-29	Nil
AE-30	Nil
AE-31	Nil
AE-32	10
AE-33	Nil
AE-34	Nil
AE-35	Nil
AE-36	30
AE-37	30
AE-38	10
check-1	Nil
check-2	10

4.3.3 Components of variability

The estimates of genetic parameters viz., phenotypic and genotypic coefficient of variation (PCV and GCV), heritability, genetic advance and genetic gain (genetic advance expressed as percent of mean) for nineteen quantitative traits are presented in Table-7.

4.3.3.1 Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) coefficient of variation, Heritability and Genetic Advance

The PCV values were higher than the GCV values for all the characters studied. Maximum PCV was recorded for the sepal length (31.19) followed by number of locules in the fruit (30.50). High phenotypic coefficient of variation was recorded for length of stamen (27.90), plant height (23.98), primary branches per plant (20.86), internode length (21.30) and length of petals (21.17).

Moderate PCV values were exhibited by number of units in epicalyx (13.08), length of units in epicalyx (17.83), first flowering node (15.40), number of fruiting nodes (13.11), fruit length (15.36), fruit diameter (16.44), length of fruit peduncle (18.49), fruit weight (18.46), days to marketable maturity (12.13), green fruit yield per plant (14.08) and marketable fruits per plant (10.26). Low PCV value was recorded for days to 50% flowering (6.86).

High GCV was recorded for primary branches per plant (20.50), plant height (23.43), length of sepals (29.18), length of petals (20.20), and length of stamens (23.26). Moderate GCV values were exhibited by first flowering node (14.10), internode length (18.90), number of fruiting nodes (11.33), number of units in epicalyx (13.08), length of units in epicalyx (13.74), fruit length (11.57), fruit diameter (12.90), length of fruit peduncle (17.21), fruit weight (15.69), days to marketable maturity (11.99) and green fruit yield per plant (13.88). Low GCV values were recorded for days to 50% flowering (6.55), marketable fruits per plant (8.52) and number of locules in the fruit (-47.09).

Table 7. Genetic parameters for quantitative traits

SL. no	Traits	Mean	Range		Coefficient of variability		Heritability (%)	Genetic Advance	GA as percent of mean
			Maximum	Minimum	PCV (%)	GCV (%)			
1	Plant height (cm)	50.32	86.73	33.12	23.98	23.43	95.46	23.23	47.16
2	Primary branches per plant	1.12	2.01	0.0	20.86	20.50	96.54	0.47	41.49
3	Internode length (cm)	4.50	6.61	3.06	21.30	18.90	78.72	1.54	34.55
4	First flowering node	2.64	3.59	1.84	15.40	14.10	83.80	0.70	26.60
5	Days to 50% flowering	55.40	62.16	48.81	6.86	6.55	91.16	7.09	12.88
6	Number of fruiting nodes	4.99	6.00	2.80	13.11	11.33	74.71	1.01	20.18
7	Number of units in epicalyx	9.42	11.00	7.00	13.08	13.08	100.00	2.54	26.96
8	Length of units in epicalyx	1.82	2.50	1.10	17.83	13.74	59.46	0.39	21.83
9	Length of sepals (cm)	3.47	5.30	1.60	31.19	29.18	87.52	1.96	56.23
10	Length of petals (cm)	4.66	6.00	2.95	21.17	20.20	91.10	1.85	39.73
11	Length of stamens (cm)	2.08	2.95	1.34	27.90	23.26	69.50	0.82	39.94
12	Fruit length (cm)	22.32	27.78	11.37	15.36	11.57	56.79	3.98	17.97
13	Length of fruit peduncle(cm)	2.21	3.23	1.39	18.49	17.21	86.63	0.73	33.00
14	Fruit diameter (cm)	2.08	3.68	1.18	16.44	12.90	61.58	0.42	20.86
15	Number of locules in fruit	5.55	8.00	5.00	30.50	-47.09	-23.82	-8.35	-149.74
16	Fruit weight (g)	30.03	61.65	22.84	18.46	15.69	72.27	8.31	27.48
17	Days to marketable maturity	6.95	9.03	5.18	12.13	11.99	97.73	1.69	24.43
18	Marketable fruits per plant	17.11	22.72	12.53	10.26	8.52	68.97	2.45	14.58
19	Green fruit yield per plant (g)	495.80	682.79	285.83	14.08	13.88	97.19	139.24	28.20

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The broad sense heritability estimates are presented in the Table 7. High broad sense heritability was recorded by number of units in epicalyx (100) followed by days to marketable maturity (97.73), green fruit yield per plant (97.19), primary branches per plant (96.54), plant height (95.46), days to 50% flowering (91.16), length of petals (91.10), length of sepals (87.52), length of fruit peduncle (86.63), first flowering node (83.80), internode length (78.72), number of fruiting nodes (74.71), fruit weight (72.27), length of stamens (69.50), marketable fruits per plant (68.97) and fruit diameter (61.58).

The characters such as length of units in epicalyx (59.46) and fruit length (56.79) exhibited moderate broad sense heritability values while number of locules in the fruit (-23.82) exhibited low and negative heritability values.

High genetic gain, was observed for length of sepals (56.23) followed by plant height (47.16) and length of stamens (39.94). Genetic gain was moderate for fruit diameter (20.86) followed by number of fruiting nodes (20.18) and fruit length (17.97). Negative genetic gain was observed in number of locules in fruit (-149.74).

High heritability accompanied by high genetic gain was observed for characters like primary branches per plant, plant height, internode length, first flowering node, number of units in epicalyx, length of sepals, length of petals, length of stamens, length of fruit peduncle, fruit weight, green fruit yield per plant and days to marketable maturity.

High heritability with moderate genetic gain was recorded in characters like days to 50% flowering, number of fruiting nodes, fruit diameter and marketable fruits per plant.

4.3.4 Correlation

Correlation between nineteen quantitative traits of thirty eight okra accessions was assessed. Genotypic and phenotypic correlation coefficients among the nineteen traits are presented in Table 8. Genotypic correlation is higher than the phenotypic correlation for most of the traits. The traits showing significant positive genotypic correlation are also showing significance at phenotypic level.

Green fruit yield per plant showed significant positive genotypic and phenotypic correlation with primary branches per plant (rg 0.440, rp 0.432), fruit weight (rg 0.444, rp 0.346), marketable fruits per plant (rg 0.819, rp 0.696) and negative genotypic correlation with first flowering node (rg -0.363).

Internode length showed significant positive genotypic and phenotypic correlation with plant height (rg 0.524, rp 0.486). First flowering node showed significant positive correlation at both genotypic and phenotypic levels with internode length (rg 0.326, rp 0.330).

Days to 50% flowering showed significant positive genotypic and phenotypic correlation with plant height (rg 0.377, rp 0.343). Number of fruiting nodes showed significant positive correlation with days to 50% flowering both at genotypic and phenotypic levels (rg 0.343, rp 0.339). Number of units in epicalyx had negligible correlation with all other traits except number of fruiting nodes (rg 0.353). Length of units in epicalyx showed significant negative phenotypic and genotypic correlation with plant height (rg-0.516, rp-0.370) and internode length (rg-0.603, rp-0.350). It showed significant negative genotypic correlation with number of units in epicalyx (rg-0.370). Length of sepals has negligible correlation with all the characters except with number of fruiting nodes it showed significant negative genotypic and phenotypic correlation (rg-0.603, rp -409).

Length of petals showed significant negative genotypic correlation with number of fruiting nodes (rg-0.364). It showed negative genotypic and positive phenotypic correlation with number of units in epicalyx (rg-0.532, rp 0.508). Length of stamens showed significant positive genotypic correlation with length of petals (rg 0.361).

Table 8 Genotypic and phenotypic correlation coefficients of okra accessions

		A	B	C	D	E	F	G	H	I
A	rg	1								
	rp	1								
B	rg	0.236	1							
	rp	0.218	1							
C	rg	0.524**	-0.051	1						
	rp	0.486**	-0.077	1						
D	rg	0.023	-0.117	0.326*	1					
	rp	0.006	-0.104	0.330*	1					
E	rg	0.377*	0.112	0.246	0.120	1				
	rp	0.343*	0.100	0.150	0.127	1				
F	rg	0.192	-0.258	0.177	0.253	0.343*	1			
	rp	0.109	-0.207	0.050	0.256	0.339*	1			
G	rg	0.314	-0.142	-0.009	-0.188	0.059	0.353*	1		
	rp	0.306	-0.139	-0.008	-0.1721	0.056	0.305	1		
H	rg	-0.516**	0.153	-0.603**	-0.035	-0.324	-0.130	-0.370*	1	
	rp	-0.370*	0.085	-0.350*	-0.090	-0.174	-0.075	-0.285	1	
I	rg	0.140	-0.093	0.209	-0.039	-0.171	-0.603**	-0.305	-0.323	1
	rp	0.088	-0.073	0.091	-0.070	-0.089	-0.409**	-0.285	-0.118	1
J	rg	-0.199	0.118	-0.216	0.283	-0.212	-0.364*	-0.532**	0.286	0.115
	rp	-0.214	0.114	-0.248	0.274	-0.148	-0.212	0.508**	0.239	0.166
K	rg	-0.146	0.043	-0.252	-0.087	-0.261	-0.286	-0.082	0.090	0.236
	rp	-0.099	0.039	-0.243	-0.035	-0.165	-0.099	-0.068	-0.021	0.185
L	rg	0.101	0.298	0.126	-0.220	0.416**	-0.224	-0.110	-0.119	0.382*
	rp	0.034	0.250	-0.024	-0.169	0.252	-0.073	-0.083	-0.328*	0.257
M	rg	-0.151	0.282	0.065	-0.284	-0.309	-0.325	-0.110	0.494**	-0.127
	rp	-0.195	0.268	-0.046	-0.228	-0.243	-0.120	-0.103	0.287	-0.059
N	rg	0.057	0.270	-0.193	-0.00	0.270	-0.251	0.054	-0.273	-0.019
	rp	0.052	0.202	-0.115	-0.083	0.138	-0.082	0.043	-0.114	0.016
O	rg	-0.036	-0.067	-0.077	0.030	-0.058	0.306	-0.013	-0.136	-0.012
	rp	-0.025	0.064	0.028	0.079	-0.085	-0.011	0.021	-0.006	-0.068
P	rg	0.045	0.124	-0.178	-0.163	0.188	0.164	0.169	-0.234	-0.173
	rp	0.067	0.064	-0.049	-0.056	0.167	0.071	0.144	-0.141	-0.162
Q	rg	0.400**	-0.123	0.310	-0.223	0.280	0.108	0.193	-0.450**	-0.023
	rp	0.388*	-0.125	0.315	-0.221	0.241	0.051	0.191	-0.322*	-0.027
R	rg	0.068	0.537**	-0.392*	-0.122	0.163	-0.103	-0.031	0.300	-0.082
	rp	0.089	0.412**	-0.194	-0.123	0.035	-0.087	-0.026	0.081	-0.185
S	rg	0.279	0.440**	-0.114	-0.363*	0.237	-0.107	0.106	0.127	-0.303
	rp	0.261	0.432**	-0.141	-0.317	0.237	-0.030	0.105	0.046	-0.275

		J	K	L	M	N	O	P	Q	R	S
J	rg	1									
	rp	1									
K	rg	0.361*	1								
	rp	0.273	1								
L	rg	0.046	0.187	1							
	rp	0.094	0.041	1							
M	rg	0.099	0.122	0.232	1						
	rp	0.126	0.173	0.227	1						
N	rg	0.000	-0.261	0.309	-0.517**	1					
	rp	-0.007	-0.004	0.159	-0.347*	1					
O	rg	0.123	0.000	0.096	0.046	0.233	1				
	rp	0.036	0.118	0.036	0.144	0.200	1				
P	rg	-0.107	-0.490*	0.419**	-0.188	0.695**	0.008	1			
	rp	-0.089	-0.206	0.102	-0.193	0.572**	0.156	1			
Q	rg	-0.500**	-0.197	0.041	-0.078	-0.085	-0.037	-0.081	1		
	rp	-0.501**	-0.187	0.010	-0.094	-0.041	-0.045	-0.062	1		
R	rg	0.360*	0.236	-0.314	-0.022	0.080	-0.116	0.064	-0.168	1	
	rp	0.194	0.154	-0.063	-0.032	0.110	0.128	-0.045	-0.110	1	
S	rg	-0.029	-0.176	0.110	-0.014	0.268	-0.065	0.444**	0.139	0.819**	1
	rp	-0.014	-0.095	0.140	0.030	0.215	0.144	0.346*	0.120	0.696**	1

A= Plant height (cm), B= Primary branches per plant, C = Internode length (cm), D = First flowering node, E = Days to 50% flowering, F=Number of fruiting nodes, G= Number of units in epicalyx, H= Length of units in epicalyx (cm), I = Length of sepals (cm), J = Length of petals (cm), K = Length of stamens (cm), L = Fruit length(cm), M = Length of fruit peduncle (cm), N = Fruit diameter, O= Number of locules in the fruit, P= Fruit weight (g), Q= Days to marketable maturity, R = Marketable fruits per plant, S = Green fruit yield per plant (g).

Fruit length showed significant positive genotypic correlation with days to 50% flowering (rg 0.416), length of sepals (rg 0.382) and significant negative phenotypic correlation with length of units in epicalyx (rp-0.328). Length of fruit peduncle showed significant positive genotypic correlation with length of units in epicalyx (rg 0.494). Fruit diameter showed significant negative genotypic and phenotypic correlation with length of fruit peduncle (rg-0.517, rp-0.347). The trait number of locules per fruit showed negligible correlation with all the characters. Fruit weight showed significant positive genotypic and phenotypic correlation with fruit diameter (rg 0.695, rp 0.572) and showed significant negative genotypic correlation with length of stamens (rg-0.490)and significant positive correlation with fruit length (rg 0.419).

Days to marketable maturity showed significant positive genotypic phenotypic correlation with plant height (rg 0.400, rp 0.388). It showed significant negative genotypic and phenotypic correlation with length of units in epicalyx (rg-0.450, rp-0.322) and length of petals (rg-0.500, rp-0.501). Marketable fruits per plant showed significant positive genotypic and phenotypic correlation with primary branches per plant (rg 0.537, rp 0.412). It showed significant negative genotypic correlation with internode length (rg-0.392) and positive genotypic correlation with length of petals (rg 0.360).

4 .3.5 Path analysis

Green fruit yield is the major characteristic in okra dependent on several mutually related component traits. Hence, these related traits have to be analyzed for their direct effect as well as indirect effect through other parameters on green fruit yield. The genotypic correlations of eighteen quantitative characters on green fruit yield were partitioned into direct and indirect effect using genotypic path coefficient method and are presented in Table.9

Direct effects are the diagonal values and the residual effect of path analysis of thirty eight accessions of okra for eighteen quantitative characters was found to be 0.475. An examination of genotypic path coefficient analysis showed

Table .9 Path coefficient analysis among the eighteen quantitative characters

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
A	**-0.356**	-0.084	-0.187	-0.008	-0.135	-0.069	-0.112	0.184	-0.050	0.071	0.052	-0.036	0.054	-0.020	0.013	-0.016	-0.143	-0.024
B	-0.088	**-0.372**	0.019	0.044	-0.042	0.096	0.053	-0.057	0.035	-0.044	-0.016	-0.111	-0.105	-0.101	0.025	-0.046	0.046	-0.200
C	0.966	-0.095	**1.843**	0.602	0.455	0.327	-0.017	-1.112	0.386	-0.398	-0.465	0.233	0.120	-0.357	-0.142	-0.328	0.572	-0.723
D	-0.017	0.089	-0.248	**-0.758**	-0.091	-0.192	0.142	0.026	0.030	-0.215	0.067	0.168	0.216	0.003	-0.023	0.124	0.169	0.093
E	-0.167	-0.050	-0.109	-0.053	**-0.442**	-0.152	-0.026	0.144	0.076	0.094	0.115	-0.184	0.137	-0.120	0.026	-0.084	-0.124	-0.072
F	0.179	-0.240	0.165	0.236	0.320	**0.930**	0.329	-0.122	-0.561	-0.339	-0.266	-0.208	-0.303	-0.234	0.285	0.153	0.101	-0.096
G	0.200	-0.091	-0.006	-0.120	0.038	0.225	**0.636**	-0.236	-0.194	-0.339	-0.052	-0.070	-0.071	0.035	-0.009	0.108	0.123	-0.020
H	-0.908	0.270	-1.061	-0.062	-0.571	-0.230	-0.652	**1.759**	-0.568	0.504	0.159	-0.210	0.869	-0.481	-0.239	-0.412	-0.793	0.529
I	0.071	-0.047	0.106	-0.020	-0.086	-0.304	-0.154	-0.163	**0.504**	0.058	0.119	0.193	-0.064	-0.010	-0.006	-0.087	-0.012	-0.042
J	-0.104	0.062	-0.113	0.148	-0.111	-0.190	-0.278	0.149	0.060	**0.521**	0.188	0.024	0.052	0.000	0.064	-0.056	-0.261	0.188
K	-0.028	0.008	-0.048	-0.017	-0.050	-0.055	-0.016	0.017	0.045	0.069	**0.191**	0.036	0.023	-0.050	0.000	-0.093	-0.038	0.045
L	0.019	0.055	0.023	-0.041	0.077	-0.041	-0.020	-0.022	0.070	0.009	0.034	**0.184**	0.043	0.057	0.018	0.077	0.008	-0.058
M	0.015	-0.028	-0.007	0.029	0.031	0.033	0.011	-0.050	0.013	-0.010	-0.012	-0.023	**-0.100**	0.052	-0.005	0.019	0.008	0.002
N	0.086	0.407	-0.291	-0.007	0.406	-0.378	0.082	-0.411	-0.030	0.001	-0.392	0.464	-0.777	**1.502**	0.351	1.044	-0.128	0.122
O	0.009	0.017	0.020	-0.008	0.015	-0.078	0.004	0.035	0.003	-0.031	0.000	-0.025	-0.012	-0.060	**-0.255**	-0.002	0.010	0.030
P	0.002	0.004	-0.006	-0.006	0.007	0.006	0.006	-0.008	-0.006	-0.004	-0.017	0.015	-0.007	0.024	0.000	**0.035**	-0.003	0.002
Q	0.321	-0.099	0.249	-0.179	0.225	0.087	0.155	-0.361	-0.019	-0.401	-0.158	0.033	-0.063	-0.068	-0.030	-0.066	**0.801**	-0.135
R	0.080	0.634	-0.463	-0.145	0.192	-0.122	-0.038	0.355	-0.097	0.425	0.279	-0.371	-0.027	0.095	-0.138	0.076	-0.198	**1.179**
r(G)	0.279	**0.440** **	-0.114	-0.363	0.237	-0.107	0.106	0.127	-0.303	-0.029	-0.176	0.110	-0.014	0.268	-0.065	**0.444** **	0.139	**0.819** **

A= Plant height (cm), B= Primary branches per plant, C = Internode length (cm), D = First flowering node, E = Days to 50% flowering, F=Number of fruiting nodes, G= Number of units in epicalyx, H= Length of units in epicalyx (cm), I = Length of sepals (cm), J = Length of petals (cm), K = Length of stamens (cm), L = Fruit length(cm), M = Length of fruit peduncle (cm), N = Fruit diameter, O= Number of locules in the fruit, P= Fruit weight (g), Q= Days to marketable maturity, R = Marketable fruits per plant, r(G) = Genotypic correlation with green fruit yield per plant.

that the highest direct positive effect on green fruit yield was exhibited by internode length (1.843) followed by length of units in epicalyx (1.759), fruit diameter (1.502), marketable fruits per plant (1.179), number of fruiting nodes (0.930) and days to marketable maturity (0.801). The positive direct contribution of marketable fruits per plant is also indicated by the significant positive genotypic correlation with green fruit yield. The highest negative direct effect on green fruit yield was exhibited by first flowering node (-0.758) followed by days to 50% flowering (-0.442), primary branches (-0.372) and plant height (-0.356). Negative contribution of first flowering node is also indicated by significant negative genotype correlation with green fruit yield.

Indirect effect of all eighteen characters on green fruit yield through other characters was examined. Plant height had highest positive indirect effect through internode length (0.960) followed by days to marketable maturity (0.321) and moderate positive indirect effect through number of units in epicalyx (0.200) which resulted in positive genotypic correlation with green fruit yield even though its direct effect on green fruit yield was negative. It had negative indirect effect through length of units in epicalyx (-0.908) and days to 50% flowering (-0.167).

Number of primary branches had high positive indirect effect through marketable fruits per plant (0.634) and fruit diameter (0.407) which resulted in positive genotypic correlation with green fruit yield. Even though it had negative direct effect on green fruit yield through all traits.

Internode length had moderate positive indirect effect through days to marketable maturity (0.249) and low positive indirect effect through number of fruiting nodes (0.165). Among the vegetative traits it had maximum negative indirect effect *via.,* length of units in epicalyx (-1.061) and marketable fruits per plant (-0.463). First flowering node had moderate positive indirect effect through number of fruiting nodes (0.236) and low positive indirect effect through length of petals (0.148) while it had low negative indirect effect *via.,* days to marketable maturity (-0.179) and marketable fruits per plant (-0.145).

Days to 50% flowering had high positive indirect effect through internode length (0.455) fruit diameter (0.406) and number of fruiting nodes (0.320). It had negative indirect *via.*, length of units in epicalyx (-0.571) and plant height (-0.135). Number of fruiting nodes had high positive indirect effect through internode length (0.327) and number of units in epicalyx (0.225). It had negative indirect effect *via.*, fruit diameter (-0.378), length of sepals (-0.304) and length of units in epicalyx(-0.230).

Number of units in epicalyx had high positive indirect effect through number of fruiting nodes (0.329) and low positive indirect effect through days to marketable maturity (0.155). It had very high negative indirect effect *via.,* length of units in epicalyx (-0.652) and length of petals (-0.278). Length of units in epicalyx had high positive indirect effect through marketable fruits per plant (0.355) and low positive indirect effect through plant height (0.184). Among all the traits highest negative indirect effect was exhibited by this trait *via.*, internode length (-1.112) and fruit diameter (-0.411).

Length of sepals had high positive indirect effect through internode length (0.386) and negligible positive indirect effect through days to 50% flowering. There was a high negative indirect effect of length of sepals *via.*, length of units in epicalyx (-0.568) and number of units in epicalyx (-0.194).

Length of petals had high positive indirect effect through length of units in epicalyx (0.504) followed by marketable fruits per plant (0.425). Negative indirect effect was observed for this trait *via.*, days to marketable maturity (-0.401), internode length (-0.398) and number of fruiting nodes (-0.339).

Length of stamens had moderate positive indirect effect through marketable fruits per plant (0.279) and low positive indirect effect through length of petals (0.188). It had negative indirect effect *via.*, internode length (-0.465) and fruit diameter (-0.392).

Fruit length had high positive indirect effect through fruit diameter (0.464) and moderate positive indirect effect through internode length (0.233) and length of sepals (0.193). It had negative indirect effect *via.*, length of units in epicalyx (-0.210) and number of fruiting nodes (-0.208). Length of fruit peduncle had high positive indirect effect through length of units in epicalyx (0.869) followed by first flowering node (0.216) and internode length (0.120). It had high negative indirect effect *via.,* number of fruiting nodes (-0.303) and fruit diameter (-0.777).

Fruit diameter had high direct effect (1.502) but it had insignificant genotypic correlation with green fruit yield which was the result of high negative indirect effect of this trait through length of units in epicalyx (-0.481) and internode length (-0.357). Number of locules in the fruit had high positive indirect effect through fruit diameter (0.351) and moderate indirect effect *via* number of fruiting nodes (0.285). It had negative indirect effect through length of units in epicalyx (-0.239) and internode length (-0.142). Fruit weight had exhibited significant positive genotypic correlation with green fruit yield in contrast to very negligible direct effect (0.035) on green fuirt yield. The significant genotypic correlation was due to its very high positive indirect effect of this trait through fruit diameter (1.044) and low positive indirect effect through number of fruiting nodes (0.153) and first flowering node (0.124). It exhibited negative indirect effect *via* length of units in epicalyx (-0.412) and internode length (-0.328).

Days to marketable maturity had high positive direct effect but insignificant genotypic correlation. It had high positive indirect effect through internode length (0.572) followed by first flowering node (0.169) and number of units in epicalyx (0.123) but these were negated by high negative indirect effect through length of units in epicalyx (-0.793) followed by length of petals (-0.261) resulting in insignificant genotypic correlation. Marketable fruits per plant had high positive indirect effect through length of units in epicalyx (0.529) followed by length of petals (0.188) and fruit diameter (0.122). It had negative indirect effect *via.,* internode length (-0.723), primary branches per plant (-0.200) and days to marketable maturity (-0.135).

4.3.6 Diversity analysis

The diversity of thirty eight okra accessions was accessed on the basis of nineteen quantitative characters and fourteen qualitative characters. The results are presented under the following heads :

4.3.6.1 Clustering pattern of qualitative characters

Clustering pattern of qualitative characters of thirty eight accessions of okra are presented in (Table.10) Cluster diagram obtained from the morphological descriptors shows three main clusters of okra accessions at a co-efficient of 0.63 were shown in Fig.15. The accessions were put into clusters based on their similar characteristics. Cluster II recorded the highest number of accessions (34) Five accessions *viz* AE-1, AE-8, AE-9, AE-10 and AE-25 belongs to cluster III while cluster I consisted of only one accession (AE-4). Similarity coefficient ranged from 0.29 to 1.00.

4.3.6.1 .1 Similarity per a Cluster Group

Cluster II comprised 34 accessions, differing from accession in the other clusters by green coloured stem, orthotropic stem type branching pattern and green leaf colour. Within cluster II there are two sub-cluster A and B (Fig.15). Sub cluster A consist of seven accessions which differ from other cluster mainly due to prickly type fruit pubescence. Sub cluster B consists of twenty seven accessions differing from other due to its green leaf colour and number of ridges per fruit (5-7). Sub cluster B again divided into three sub clusters B1, B2 and B3. Sub cluster B1 consist of ten accessions and one check Arka Anamika which differ from other clusters mainly due to green stem colour, orthotropic stem type branching pattern, green leaf colour, cream coloured petal, erect position of the fruit.

Table.10 Clustering pattern of fourteen qualitative characters of thirty eight accessions of okra (UPGMA method).

Cluster	Number of accessions included in each cluster	Accession numbers
ClusterI	1	AE-4
Cluster II	34	AE-2
		AE-3
		AE-5
		AE-6
		AE-7
		AE-11
		AE-12
		AE-13
		AE-14
		AE-15
		AE-16
		AE-17
		AE-18
		AE-19
		AE-20
		AE-21
		AE-22
		AE-23
		AE-24
		AE-26
		AE-27
		AE-28
		AE-29
		AE-30
		AE-31
		AE-32
		AE-33
		AE-34
		AE-35
		AE-36
		AE-37
		AE-38
		C-1
		C-2
Cluster III	5	AE-1
		AE-8
		AE-9
		AE-10
		AE-25

number of ridges (5to7). Sub cluster B2 consist of twelve accessions and one check Salkeerthi which differed from other clusters mainly due to green stem colour, yellowish green colour fruit and long or straight curved fruit shape. Sub cluster B3 consist of three accessions which differ from other clusters mainly due to golden colour petal, green colour fruit and prickly type fruit pubescence. Cluster I comprised only one okra accession ie, AE-4 and this differed from accessions in the other clusters mainly due to its strong branching pattern. Cluster III the second largest cluster with 5 okra accessions was different from the others due to its purple stem colour.

4.3.6.2 Clustering pattern of thirty eight okra accessions based on quantitative characters

The okra accessions were grouped into seven clusters based on nineteen quantitative characters using Standard Euclidean square distance method and they are presented in Table11.

The clustering pattern revealed that cluster V was the largest consisting of eighteen accessions and cluster III and cluster VI were the smallest with one accession each. The remaining clusters *viz.,* cluster IV and cluster VII had five accessions each and cluster I had six accessions and cluster II had four accessions. Of the eleven accessions of okra collected from Kannur district, five accessions *viz.*, AE-1, AE-2, AE-4, AE-8 and AE-10 were grouped into cluster I; four accessions AE-6, AE-7, AE-37 and AE-38 got grouped into cluster V and the remaining two accessions AE-3 and AE-5 were grouped into cluster II and cluster VI respectively.

Twenty five accessions from Kasaragod were grouped into five clusters. The accession AE-27 formed a seperate cluster (Cluster III) and three accessions were grouped in cluster II. Maximum number of accessions (13) was grouped in cluster- V. Five accessions were grouped in cluster IV and the remaining three were grouped along with the checks Salkeerthi and Arka anamika in cluster VII.

Table.11 Clustering pattern of quantitative characters of thirty eight accessions of okra.

Cluster	Number of accessions included in each cluster	Accession numbers
I	6	AE-1 (Kannur)
		AE-2 (Kannur)
		AE-4 (Kannur)
		AE-8 (Kannur)
		AE-9 (Malappuram)
		AE-10 (Kannur)
II	4	AE-3 (Kannur)
		AE-20(Kasaragod)
		AE-25 (Kasaragod)
		AE-26 (Kasaragod)
III	1	AE-27 (Kasaragod)
IV	5	AE-16(Kasaragod)
		AE-29 (Kasaragod)
		AE-30 (Kasaragod)
		AE-31 (Kasaragod)
		AE-32 (Kasaragod)
V	18	AE-6 (Kannur)
		AE-7 (Kannur)
		AE-11 (Malappuram)
		AE-12 (Kasaragod)
		AE-13 (Kasaragod)
		AE-14 (Kasaragod)
		AE-17 (Kasaragod)
		AE-18 (Kasaragod)
		AE-21 (Kasaragod)
		AE-22 (Kasaragod)
		AE-24 (Kasaragod)
		AE-28 (Kasaragod)
		AE-33 (Kasaragod)
		AE-34 (Kasaragod)
		AE-35 (Kasaragod)
		AE-36 (Kasaragod)
		AE-37 (Kannur)
		AE-38 (Kannur)
VI	1	AE-5 (Kannur)
VII	5	AE-15 (Kasaragod)
		AE-19 (Kasaragod)
		AE-23 (Kasaragod)
		C-1(Salkeerthi)
		C-2(Arka Anamika)

4.3.6.2.1 Similarity level of thirty eight okra accessions

Similarity coefficient is a matching coefficient for binary data generated. The thirty eight okra accessions were grouped into seven clusters. Ward's minimum coefficient was used to determine the similarity between the accessions in the each cluster. The similarity levels between accessions in seven clusters are shown in Table 12. In cluster I, similarity levels ranged from 12.06 to 61.13. The highest genetic similarity level (61.13) was observed between accessions AE-10 and AE-2, while the lowest level (12.06) was found to be between AE-8 and AE-1 and rest of the accessions in the same cluster.

While in cluster-II, the similarity level between the accessions ranged from 16.43 to 29.74. The highest genetic similarity level (29.74) was observed between accessions AE-20 and AE-25, while the lowest level (16.43) was found to be between AE-3and AE-25.

Cluster III consists of only one accession AE-27. Cluster IV, the similarity coefficient ranged between 15.31 to 60.76. The highest genetic similarity level (60.76) was observed between accessions AE-16 and AE-32, while the lowest level (15.31) was found to be between AE-29 and AE-31.

In cluster V, the similarity coefficient ranged between 3.47 to 42.82. The highest genetic similarity level (42.82) was observed between accessions AE-13 and AE-28, while the lowest level (3.47) was found to be between AE-12 and AE-21. In cluster VI, there was only one accession AE-5.

In Cluster VII, the similarity coefficient ranged between 12.20 to 49.63. The highest genetic similarity level (49.63) was observed between check Salkeerthi and AE-15, while the lowest level (12.20) was found to be AE-15 and AE-19.

Table 12. Similarity level of thirty eight okra accessions

	AE-1	AE-2	AE-3	AE-4	AE-5	AE-6	AE-7	AE-8	AE-9	AE-10	AE-11	AE-12	AE-13	AE-14	AE-15	AE-16	AE-17	AE-18	AE-19	AE-20
AE-1																				
AE-2	45.07																			
AE-3	30.71	34.96																		
AE-4	12.68	32.38	32.88																	
AE-5	69.98	71.48	54.85	60.99																
AE-6	18.94	40.33	27.75	23.97	54.92															
AE-7	26.16	39.44	20.33	24.67	44.69	17.00														
AE-8	12.06	38.07	18.57	15.32	54.57	24.52	24.63													
AE-9	35.77	58.41	43.58	27.25	81.33	41.34	43.31	30.49												
AE-10	45.19	61.13	42.98	31.29	83.48	43.12	26.54	32.74	38.91											
AE-11	29.11	50.87	32.96	24.33	64.66	22.40	11.88	30.02	29.69	19.56										
AE-12	33.48	37.65	27.94	24.90	40.50	17.45	13.96	28.48	38.40	48.66	19.8									
AE-13	28.82	43.24	34.13	20.10	62.53	21.70	25.39	29.87	29.93	45.85	20.3	9.99								
AE-14	44.28	45.21	27.36	36.23	63.96	33.80	16.21	34.60	40.57	37.23	17.2	17.07	21.1							
AE-15	73.51	64.50	56.38	58.16	69.49	43.65	22.53	66.62	68.56	54.80	26.10	23.79	34.1	19.						
AE-16	63.82	63.68	47.52	59.90	78.03	56.49	37.45	62.44	64.21	85.20	55.00	42.97	45.05	39.93	44.49					
AE-17	41.58	47.69	27.84	41.53	69.86	24.04	25.49	39.57	46.10	45.94	27.15	29.70	25.95	14.83	43.02	42.58				
AE-18	40.90	36.61	18.38	35.57	48.49	27.06	13.96	31.05	50.80	46.72	32.12	16.62	27.01	21.19	35.94	29.16	21.39			
AE-19	63.59	71.32	48.93	50.70	57.98	46.29	22.43	58.26	68.69	64.00	31.63	21.07	33.76	26.43	12.20	40.57	50.24	25.51		
AE-20	48.67	65.96	17.64	60.97	81.87	39.62	32.90	38.58	63.01	65.89	51.94	49.02	59.10	50.55	68.59	37.72	44.89	25.60	56.87	
AE-21	44.94	35.72	24.87	29.76	34.31	24.77	16.33	32.95	43.09	50.34	24.23	3.47	18.02	18.56	23.69	44.70	32.31	14.10	18.31	48.36
AE-22	43.01	42.13	13.28	34.53	38.41	26.67	13.12	32.84	42.88	45.82	26.25	13.13	26.60	16.77	35.19	37.63	20.45	10.78	29.89	34.06
AE-23	53.05	57.79	44.77	53.02	56.04	32.96	17.40	55.77	68.36	71.12	33.15	20.71	37.54	41.03	21.96	36.01	55.15	30.77	20.70	44.27
AE-24	50.12	44.45	33.68	47.72	52.41	31.22	24.25	39.91	58.90	69.29	35.53	10.82	31.93	23.38	36.17	51.32	34.32	21.69	35.07	52.31
AE-25	22.43	43.34	16.43	25.81	74.53	31.80	30.46	22.45	35.69	50.08	32.76	32.27	33.77	41.43	75.07	58.74	37.86	22.91	52.51	29.74
AE-26	31.15	42.57	18.45	31.08	48.71	30.69	20.12	32.91	41.67	65.17	29.10	15.91	19.85	27.33	40.64	26.67	33.24	17.71	26.71	29.22
AE-27	62.34	84.47	58.48	72.23	102.34	54.87	57.47	59.84	87.75	95.02	48.30	41.24	51.27	59.04	73.49	96.80	65.88	61.72	66.85	82.39
AE-28	52.05	49.81	35.74	46.69	35.80	27.12	27.65	47.40	57.74	64.00	42.56	31.29	42.82	30.75	49.42	37.88	19.52	26.09	51.64	46.61
AE-29	43.21	33.71	26.72	32.82	47.75	26.34	18.30	34.69	44.83	35.44	24.12	17.53	21.51	19.34	30.37	34.25	20.91	13.87	30.50	41.25

	AE-1	AE-2	AE-3	AE-4	AE-5	AE-6	AE-7	AE-8	AE-9	AE-10	AE-11	AE-12	AE-13	AE-14	AE-15	AE-16	AE-17	AE-18	AE-19	AE-20
AE-30	64.79	60.15	39.17	63.09	73.01	43.97	42.79	64.39	59.85	80.25	44.14	40.42	49.32	42.70	56.07	37.45	37.17	35.22	47.28	38.97
AE-31	54.78	44.40	39.73	47.64	60.61	34.06	26.18	53.64	59.92	68.61	42.29	25.44	37.23	38.59	37.53	25.03	40.49	17.18	26.83	33.99
AE-32	64.31	48.36	49.24	48.63	89.61	56.00	45.17	61.64	55.61	54.90	31.45	41.61	37.29	30.34	42.63	60.76	42.30	50.15	45.02	73.92
AE-33	28.81	31.92	18.22	21.32	59.02	22.96	14.45	22.53	32.13	26.86	15.76	14.07	14.06	14.80	37.47	52.36	20.10	22.20	42.38	47.04
AE-34	39.55	48.65	33.57	29.79	49.55	21.05	15.58	40.56	46.45	56.57	26.63	11.54	19.78	17.40	24.94	25.15	19.68	17.07	22.32	43.19
AE-35	36.89	37.55	23.11	27.93	55.27	32.08	14.14	34.46	25.62	32.93	15.30	20.84	25.25	10.39	33.26	39.07	17.24	21.04	36.08	46.14
AE-36	65.68	53.42	39.23	57.89	68.48	38.52	30.22	62.56	55.08	61.74	24.78	26.60	32.75	25.31	36.87	48.54	21.15	25.25	39.89	51.82
AE-37	48.78	51.14	38.35	35.27	55.46	28.59	18.71	46.11	37.32	40.46	9.94	16.82	20.89	13.83	16.44	44.77	24.15	34.81	26.99	59.29
AE-38	41.63	31.83	17.77	37.35	48.42	24.73	18.13	33.09	42.69	44.76	25.73	15.77	22.46	14.18	34.24	36.88	12.32	10.36	38.36	34.35
C-1	35.51	36.47	31.82	30.28	54.14	25.96	18.10	40.55	57.77	65.30	41.52	24.49	42.96	47.19	49.63	37.16	50.09	21.13	36.42	35.70
C-2	55.66	53.86	42.10	60.03	76.23	36.94	30.11	62.61	99.11	86.91	55.42	38.58	62.78	46.38	47.16	71.30	53.29	41.65	47.60	54.50

	AE-21	AE-22	AE-23	AE-24	AE-25	AE-26	AE-27	AE-28	AE-29	AE-30	AE-31	AE-32	AE-33	AE-34	AE-35	AE-36	AE-37	AE-38	C-1	C-2
AE-21																				
AE-22	8.85																			
AE-23	24.01	30.55																		
AE-24	11.66	15.68	28.89																	
AE-25	32.27	26.44	54.43	40.54																
AE-26	17.14	15.75	21.11	27.06	20.05															
AE-27	45.38	52.25	59.86	28.30	51.24	52.60														

	AE-21	AE-22	AE-23	AE-24	AE-25	AE-26	AE-27	AE-28	AE-29	AE-30	AE-31	AE-32	AE-33	AE-34	AE-35	AE-36	AE-37	AE-38	C-1	C-2
AE-28	30.19	21.63	49.64	40.80	52.85	35.69	98.48													
AE-29	17.96	18.59	35.83	26.47	32.49	27.17	60.51	26.07												
AE-30	37.85	32.62	47.85	43.94	36.00	31.37	70.68	32.35	22.45											
AE-31	25.64	29.13	24.14	35.90	36.49	23.86	81.53	30.45	15.31	16.70										
AE-32	41.14	46.60	60.53	54.19	47.10	42.93	72.65	58.19	20.66	25.96	36.72									
AE-33	18.16	14.04	36.47	22.33	26.88	22.47	46.87	39.08	16.85	47.22	39.38	33.54								
AE-34	14.40	13.47	23.63	20.58	39.52	17.61	63.76	16.84	19.96	32.25	19.58	43.95	21.88							
AE-34	20.33	11.70	38.17	28.87	28.82	19.78	68.91	26.03	21.12	35.86	34.37	32.10	12.34	17.95						
AE-36	24.35	22.36	39.27	32.13	39.74	26.06	58.86	31.37	26.26	26.53	31.25	36.38	28.63	25.84	19.67					
AE-37	17.98	20.89	28.09	28.91	48.25	25.72	56.34	30.23	23.09	34.99	36.51	25.89	18.06	15.42	13.13	17.14				
AE-38	15.17	10.62	36.97	17.02	30.20	19.11	53.67	23.03	13.52	35.20	30.52	40.61	14.17	18.63	13.31	17.70	22.31			
C-1	23.95	23.10	20.41	32.47	30.10	21.38	74.45	35.40	33.94	40.65	18.38	64.64	36.24	20.10	32.66	46.56	42.06	35.53		
C-2	39.01	36.60	33.66	32.12	59.42	40.64	69.95	54.57	53.35	68.07	51.52	76.05	44.75	34.36	46.70	61.50	49.21	37.52	30.36	

4.3.6.2.2 Intra and inter cluster distance of thirty eight okra accessions

The intra and inter cluster values computed for thirty eight okra accessions are presented in Table.13. The diagonal values represent intra cluster distances. The maximum intra cluster distance was observed in cluster I followed by cluster VII (32.00) indicating high variability existing among the accessions of this cluster. The intra and inter cluster distance computed varied from 0 to 102.34. The inter-cluster distance was found to be more than intra-cluster distance. The maximum inter cluster distance was between cluster III and cluster VI (102.34) and the accessions in these cluster belong to Kasaragod and Kannur. They were not only showing genetic distance but also showing geographical distance. This was followed by cluster III and cluster IV (76.43) and the minimum inter cluster was observed between cluster V and cluster II (32.78).

Table.13 Intra and inter cluster distance computed for thirty eight okra accessions

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	ClusterVII
Cluster I	34.44	41.29	76.94	55.96	39.68	70.30	60.19
Cluster II		21.91	61.17	39.55	**32.78**	64.99	45.29
Cluster III			0	76.43	56.25	**102.34**	68.92
Cluster IV				29.52	35.04	69.80	44.82
Cluster V					21.32	52.59	35.33
Cluster VI						**0.000**	62.77
Cluster VII							32.00

4.3.6.2.3 Cluster means

The cluster mean values for the nineteen quantitative characters are presented in Table 14. For plant height and internode length cluster VII recorded the highest mean value of 71.08 and 6.17 respectively. This may be due to the presence of check Arka Anamika which has maximum plant height and also AE-23 which has maximum value for internode length in these clusters. Cluster I had recorded the lowest mean values for these traits. In the case of primary branches per plant cluster IV recorded the highest mean value of 1.41. This may be due to the presence of AE-16 in cluster IV which has maximum number of primary branches and lowest mean value for this trait was noticed in cluster VII (0.85).

From the table it is seen that, cluster I recorded highest mean values of 3.04 for first flowering node may be due to the presence of AE-4 in cluster I which has maximum value for first flowering node and cluster II recorded the lowest mean value for these trait. For days to 50% flowering Cluster VII recorded highest mean value of 60.83 and cluster III recorded the lowest mean value (49.76). In the case of number of fruiting nodes cluster VI recorded highest mean values of 5.75 and lowest was noticed in cluster III (3.25).

Cluster IV recorded highest mean values 10.40 in number of units in epicalyx and cluster I again recorded lowest mean value (8.17) for this character also. Cluster I recorded the highest mean value of 2.28 in length of units in epicalyx may be due to the presence of AE-1 in cluster I which has maximum value for this trait and the lowest value was observed in cluster III.

For length of sepals cluster III recorded the highest mean value of 8.64 and lowest in cluster VI (2.88). For length of petals cluster I recorded the highest mean value of 6.12 may be due to the presence of AE-10 in cluster I which has maximum value for this trait. The cluster IV recorded lowest mean value (3.49) for this character. For length of stamens cluster I recorded the highest mean value of 2.94 and cluster VI recorded lowest mean value (1.70) for this character.

Table 14. Cluster mean values for the nineteen quantitative characters of okra accessions.

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
Cluster I	36.23	1.29	3.50	**3.04**	54.66	5.05	8.17	**2.28**	3.36	**6.12**	**2.94**	21.46	2.48	2.29	5.80	27.61	5.47	18.41	475.49
Cluster II	58.08	1.36	4.64	2.35	52.56	3.57	9.00	1.84	3.81	5.86	2.24	24.22	**2.64**	2.09	5.80	33.45	7.05	**19.48**	**582.54**
Cluster III	47.87	1.01	5.86	2.69	49.76	3.25	7.00	1.40	**8.64**	3.59	2.48	**24.96**	1.89	1.90	5.30	25.40	7.53	14.08	285.83
Cluster IV	57.39	**1.41**	4.55	2.54	58.01	5.28	**10.40**	1.77	3.31	3.49	2.24	22.83	2.48	1.63	**8.10**	30.12	7.54	16.41	550.45
Cluster V	45.92	1.02	4.29	2.52	54.37	5.16	9.83	1.80	3.37	4.39	1.76	21.59	2.15	2.03	5.47	29.14	7.08	16.27	480.03
Cluster VI	46.51	0.91	4.06	2.99	55.46	**5.75**	10.00	1.50	2.88	4.36	1.70	23.09	1.39	**3.68**	6.30	**61.66**	5.93	16.03	487.93
Cluster VII	**71.08**	0.85	**6.17**	2.88	**60.83**	5.35	9.20	1.52	2.98	4.43	1.95	23.31	1.77	2.20	5.70	28.01	**7.77**	18.23	496.53
Mean	50.32	1.12	4.51	2.64	55.41	4.99	9.43	1.82	3.48	4.67	2.09	22.32	2.21	2.08	5.55	30.04	6.96	17.12	495.81

A = Plant height (cm) , B = Primary branches per plant, C = Internode length (cm), D = First flowering node, E = Days to 50% flowering , F = Number of fruiting nodes, G = Number of units in epicalyx , H = Length of units in epicalyx (cm), I = Length of sepals (cm), J = Length of petals (cm), K = Length of stamens (cm), L = Fruit length (cm) , M = Length of fruit peduncle (cm), N= Fruit diameter, O = Number of locules in the fruit , P = Fruit weight (g), Q = Days to marketable maturity, R= Marketable fruits per plant, S = Green fruit yield per plant (g)

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In the case of fruit length cluster III recorded the highest mean value of 24.96 and cluster I recorded lowest mean value (21.46). Cluster II recorded highest mean value of 2.64 in length of fruit peduncle and cluster VI recorded the lowest mean value (1.39) for this character. In the case of fruit diameter cluster VI recorded the highest mean value of 3.68 may be due to the presence of AE-5 in cluster VI which is the only accession that has maximum fruit diameter and cluster IV recorded lowest mean value (1.63) for this trait. Cluster IV recorded highest mean value of 8.10 in number of locules in the fruit may be due to the presence of AE-32 which has maximum number of locules and cluster III recorded the lowest mean value (5.30) for this character. Cluster VI recorded highest mean value of 61.66 g in fruit weight and may be due to the presence of AE-5 in cluster 6 which is the only accession that has maximum fruit weight and cluster III recorded the lowest mean value (25.40 g) for this character.

Cluster VII recorded highest mean value of 7.77 in days to marketable maturity and cluster I recorded the lowest mean value (5.47) for this character. Cluster II recorded highest mean values of 19.48 and 582.54 in marketable fruits per plant and green fruit yield per plant respectively. Cluster III recorded the lowest mean values 14.08 and 285.83 respectively for these characters. Among seven clusters, cluster I shows slightly higher mean values for majority of the traits.

4.3.6.2.4 Ranking of genotypes in clusters

The accessions in each cluster were ranked on the basis four characters *viz.*, fruit weight, marketable fruits per plant, green fruit yield per plant and days to marketable maturity (Table 15). These were sorted in the descending order for each of these characters and assigned ranks in that order. The mean rank obtained from each accession was calculated which helps to identify the overall best genotypes in each cluster. In cluster I, the accession AE-8 ranked superior. In cluster II, accession AE-3 and AE-20 ranked superior. In cluster IV, accession

AE-16 ranked superior. It was accession AE-18 in cluster V. In cluster VII Salkeerthi scored higher. Two accessions AE-20 and accession AE-16 from cluster II and cluster IV were identified as promising based on their superior ranking. AE-16 (prickly type pubescence) can be used as parents in future hybridization programs with Salkeerthi as the other parent is a popular variety released from KAU. The accessions AE-10 and AE-30 were also identified as promising from cluster I and cluster IV. The accession AE-5 in cluster VI had maximum fruit weight but it shows prickly type pubescence. Hence these accessions can be used in hybridization programmes.

The cluster III is the most divergent from all clusters but AE-27 in this cluster shows low mean values for yield and yield attributes. Hence the next divergent clusters IV and VI, clusters I and VI, clusters II and VI can also be considered as divergent as these are showing high inter cluster distance. So the accessions identified earlier AE-10 in cluster I, AE-20 in cluster II, AE-16 and AE-30 in cluster IV, AE-18 in cluster V and AE-5 in cluster VI were identified as promising because of maximum inter-cluster distance and one of the check Salkeerthi was also identified due to excellent pod characters.

Table. 15 Ranking of quantitative characters in clusters

Cluster I	Fruit weight (g)	Fruit weight (g) rank	Days to marketable maturity	Days to marketable maturity rank	Marketable fruits per plant	Marketable fruits per plant rank	Green fruit yield per plant (g)	Green fruit yield per plant(g) rank	Overall mean rank
AE-1	30.705	2	5.175	4	18.130	5	500.93	2	3.25
AE-2	27.565	3	6.975	6	19.730	1	488.51	3	3.25
AE-4	27.505	4	4.975	3	19.130	3	475.89	4	3.5
AE-8	33.815	1	4.925	2	19.030	4	462.89	5	3
AE-9	23.215	5	4.875	1	15.130	6	410.39	6	4.5
AE-10	22.835	6	5.875	5	19.330	2	514.35	1	3.5
Cluster II									
AE-3	33.685	2	6.975	2	19.130	3	579.91	2	2.25
AE-20	32.505	3	7.975	4	21.630	1	678.03	1	2.25
AE-25	30.555	4	6.125	1	20.480	2	541.27	3	2.5
AE-26	37.061	1	7.125	3	16.680	4	530.95	4	3
Cluster III									
AE-27	25.395	1	7.525	1	14.080	1	285.83	1	1
Cluster IV									
AE-16	32.195	2	6.975	1	17.130	2	682.79	1	1.5
AE-29	29.425	4	7.175	2	16.480	3	518.37	4	3.25
AE-30	33.205	1	8.175	4	15.680	4	563.99	3	3
AE-31	29.765	3	8.175	5	18.880	1	596.23	2	2.75
AE-32	26.005	5	7.175	3	13.880	5	390.87	5	4.5
Cluster V									
AE-6	27.115	12	7.925	17	16.830	8	475.51	9	11.5

	Fruit weight(g)	Fruit weight(g) rank	Days to marketable maturity	Days to marketable maturity rank	Marketable fruits/plant	Marketable fruits/plant rank	Green fruit yield/plant (g)	Green fruit yield/plant (g) rank	Overall mean rank
AE-7	29.475	8	6.925	6	18.430	2	566.91	3	4.75
AE-11	26.675	14	6.875	5	14.730	14	452.73	13	11.5
AE-12	26.975	13	6.875	4	14.330	16	447.57	14	11.75
AE-13	25.455	15	6.975	9	12.530	18	423.85	15	14.25
AE-14	24.475	17	5.975	1	14.330	14	455.85	11	10.75
AE-17	29.645	7	7.375	15	16.630	11	471.99	10	10.75
AE-18	31.765	4	6.975	10	19.830	1	601.77	1	4
AE-21	30.895	5	6.925	7	15.730	12	454.85	12	9
AE-22	31.975	3	6.925	8	18.130	3	542.37	4	4.5
AE-24	25.215	16	6.725	3	16.730	9	382.45	17	11.25
AE-28	41.655	1	7.125	14	16.880	7	595.47	2	6
AE-33	23.755	18	7.025	12	17.430	5	421.79	16	12.75
AE-34	27.975	11	7.025	13	17.630	4	493.350	6	8.5
AE-35	28.335	10	6.025	2	17.230	6	493.17	7	6.25
AE-36	33.595	2	9.025	18	15.030	13	481.99	8	10.25
AE-37	29.155	9	7.625	16	13.830	17	382.09	18	15
AE-38	30.315	6	7.025	11	16.630	10	496.77	5	8
Cluster VI									
AE-5	61.655	1	5.925	1	16.030	1	487.93	1	1
Cluster VII									
AE-15	24.055	5	7.975	4	13.530	5	430.59	5	4.75
AE-19	31.945	1	6.975	1	15.830	4	479.75	3	2.25
AE-23	30.855	2	8.925	5	17.330	3	498.81	2	3
C-1	28.820	3	7.270	2	22.720	1	621.80	1	1.75
C-2	24.370	4	7.680	3	21.740	2	451.70	4	3.25

Discussion

5. DISCUSSION

Valuable genetic resources of vegetable crop are rapidly vanishing. Among several factors, monoculture and changing crop pattern including use of hybrids or improved varieties are sources for loss of genetic diversity. Okra is one such crop where danger of genetic erosion is great, as a consequence of continuous cultivation of popular high yielding varieties. The germplasm base in okra is relatively narrow. The maximum variation is observed in the cultivated species of *Abelmoshus esculentus.*

To get a clear picture of the extent of variability occurring in okra *(Abelmoshus esculentus* L. Moench*)* genotypes of North Kerala an exploration and collection of landraces was carried out in the districts of Kannur, Malappuram and Kasaragod. Thirty eight accessions collected were raised in the field in augmented design for assessing various qualitative and quantitative characters. An attempt has been made here through studies of morphological characterization, genetic variability, character association and cluster analysis to identify the best genotypes for further crop improvement. The results obtained are discussed below.

5.1 Exploration and collection of okra genotypes

Detailed survey conducted in the regions of North Kerala showed a wide variation in the okra genotypes. Twenty five accessions were collected from Kasaragod district with maximum of six accessions from Periya. Majority of the collections in Kasaragod and Malappuram were made from vegetable growing farmers who were conserving landraces by on-farm cultivation along with popular varieties of okra. In Kannur district okra accessions were mainly collected from coconut farmers of high land areas cultivating okra for homestead purpose. During exploration, wide variability was noticed with respect to their morphological traits. Based on preliminary evaluation duplicates were eliminated and collector's number assigned to each genotype and passport data were prepared.

5.2 Morphological Characterization based on qualitative characters

Characterization plays an important role in the assessment of genetic diversity and assist in identification of a particular genotypes as distinctiveness is of key significance to complete the conditions of DUS (Novelty, distinctiveness, uniformity and stability) characters as laid out by PPVFRA (Protection of Plant Variety and Farmers Right Act, 2001)

The thirty eight accessions of okra were raised as field trial in augmented design and the data of qualitative traits were subjected to morphological characterization based on IPGRI descriptors. Wide variability was noticed in the characters such as stem colour, branching pattern, leaf shape, leaf rib colour, colour of petal, colour of fruit, fruit shape, position of the fruit, fruit pubescence and ridges per fruit. The results of characterization for each character are discussed below:

5.2.1 Stem characters

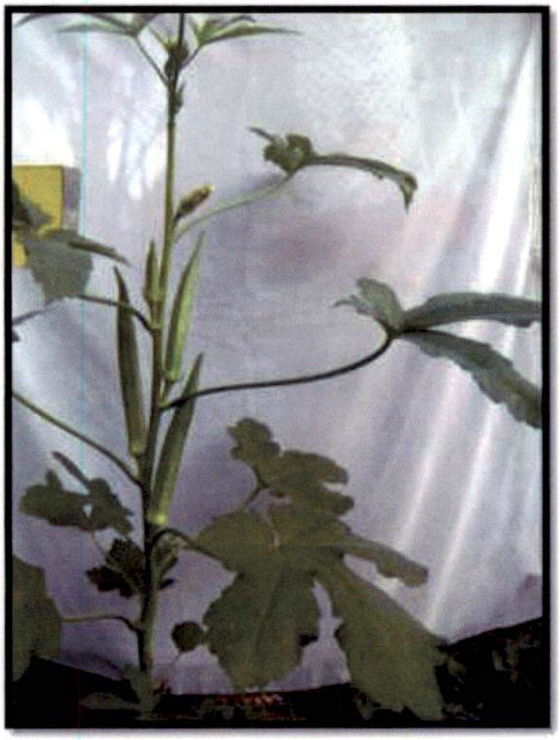
Based on stem colour okra genotypes were characterized as green coloured (63.1%), green with red patches (18%) and purple coloured (18%) as shown in Fig.3. Similar results were obtained by Demelie *et al.* (2016) and Sekyere *et al.* (2011). However contrary to this Osawaru and Dania (2007) observed that stem colour varies from green to red and red to purple. Nwangburuka and Denton (2011) observed wide variation in stem colour of twenty nine okra accessions of Nigeria. Orthotropic branching was observed in most of the accessions (86.8 %).Very few showed strong type branching (5.2 %) i.e., densely branched base and medium type branching (7.8 %) were shown in Fig.4. This was similar to the findings of Saifulla and Rabbani (2009), Sekyere *et al.* (2011). These results are against to that obtained by Ali *et al.* (2014) in which plants with medium branching are predominant while orthotropic was least frequent. This variation in branching may be due to the fact that accessions has

Green

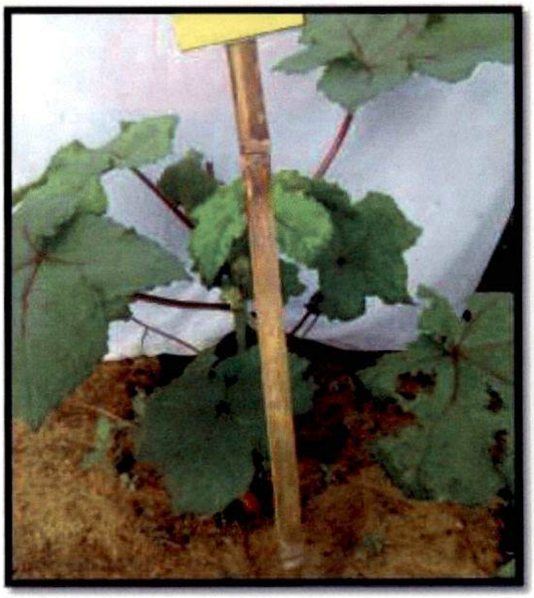
Green with red patches

Purple

Plate 2 Stem colour of okra accessions



Orthotropic stem only



Medium

Strong

Plate 3 Branching pattern of okra accessions

the ability to exhibit different growth habit which could be the result of selection or a natural adaptation mechanism. Erect plant growth is an important character for yield and the chance for the fruit to touch the ground is less. Thus reduces fruit rot and it allows for maximum exposure to the distribution of all leaves and other vegetative part for better interception of sunlight and also results in increase in dry matter production and subsequent increase in yield.

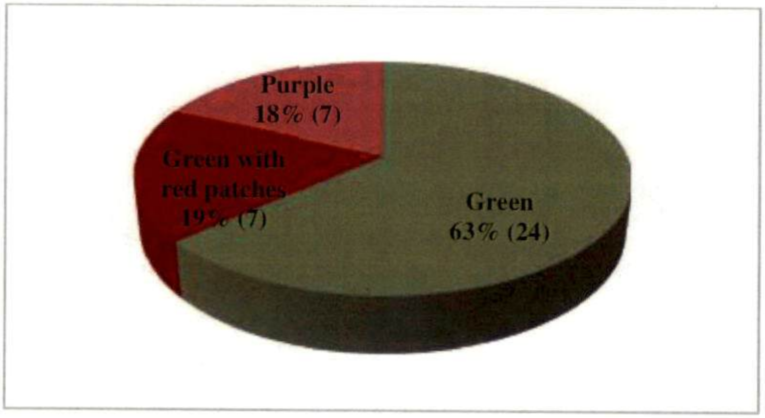


Fig 3. Stem colour of 38 okra accessions

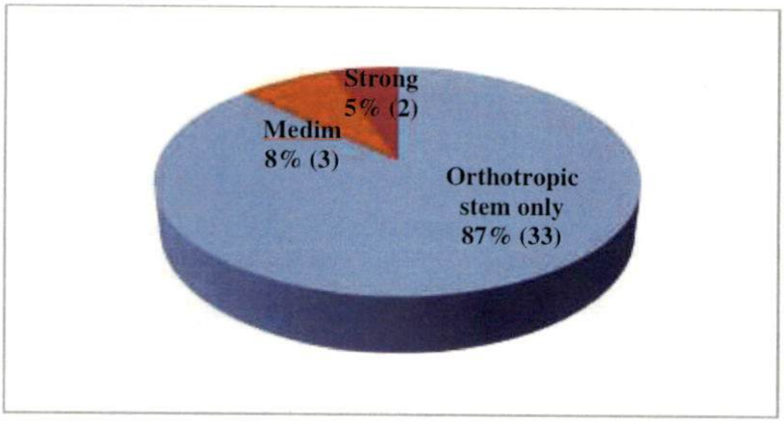
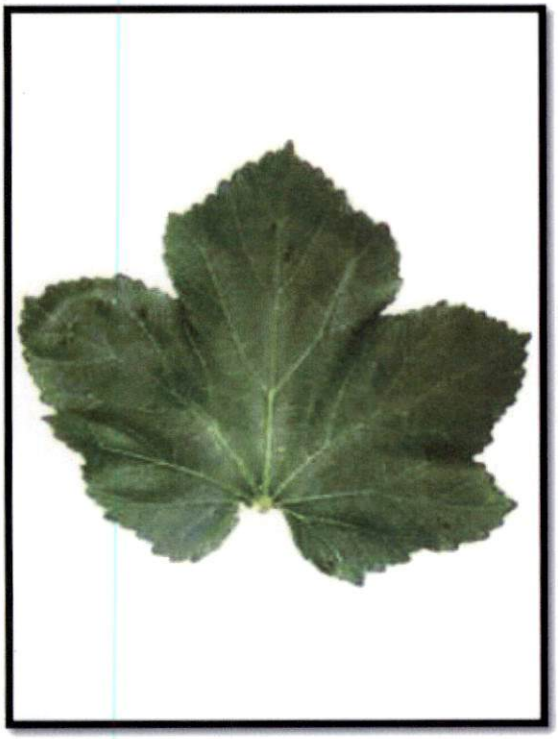
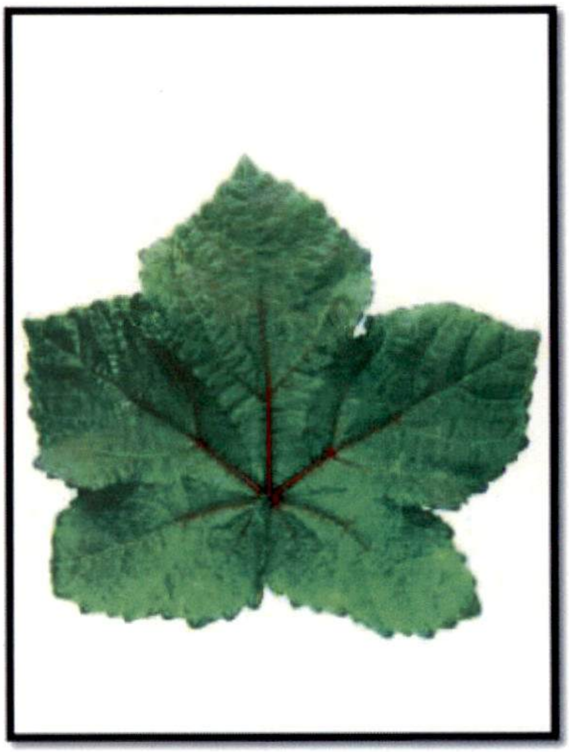


Fig 4. Branching pattern of 38 okra accessions

5.2.2 Leaf characters

Variation in leaf colour and leaf rib colour was observed among the genotypes and the most predominant was dark green colour (79%) and green with red veins were observed in 21% of the okra accessions in Fig.5. Similar





Green **Green with red veins**

Plate 4 Leaf colour of okra accessions

results were reported by Sekyere *et al*. (2011). Contrary to this Singh and Singh (2014) classified the genotypes into light green, green and dark green not based on IPGRI descriptor but based on the intensity of colour of leaf lamina between the veins. For leaf shape it is revealed that of all the accessions, 65.7% produced leaf with shallow lobing and 'heart' shape [1(10 %), 2 (10 %), 3 (16 %), 4 (29%)] 23.6% produced medium lobbing and alternate broad palmate lobed [6 (8%),7 (11%), 8 (5%)] and 10.52% produced leaf with deep lobbing 9 (11%) (Fig.6). In agreement to this Sekyere *et al.* (2011) and Demelie *et al.* (2016) reported leaf shape 2, 3, 4 and 7 in their studies on okra germplasm collections.

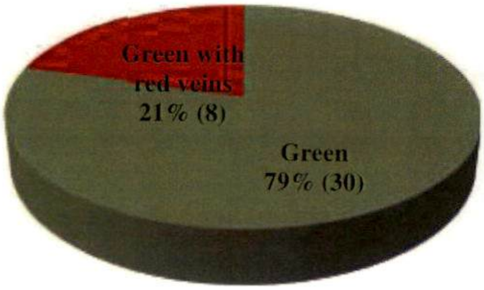


Fig 5. Leaf colour of 38 okra accessions

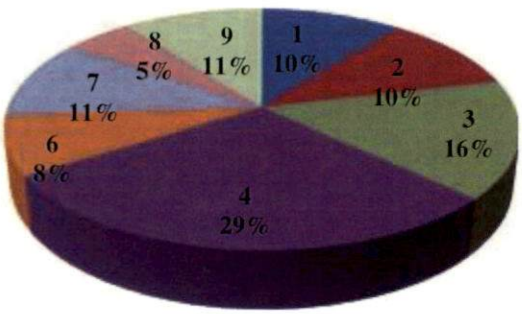


Fig 6. Leaf shape of 38 okra accessions (See plate-5)

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Plate 5 Leaf shape of okra accessions

5.2.3 Flowering characters

Colour of petal is one of the most important traits in the clear cut identification of Asian okra accessions. Petal colour varied from cream (65.7%), yellow (18%) and golden (16%) were shown in Fig.7. Similar results were reported by Sekyere *et al*. (2011) and Ahiakpa (2012).

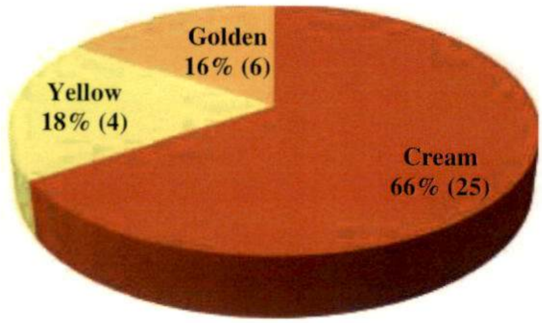
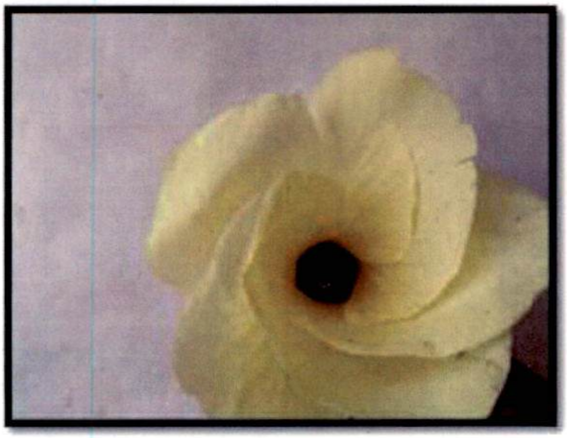


Fig 7. Petal colour of 38 okra accessions

5.2.4 Fruiting characters

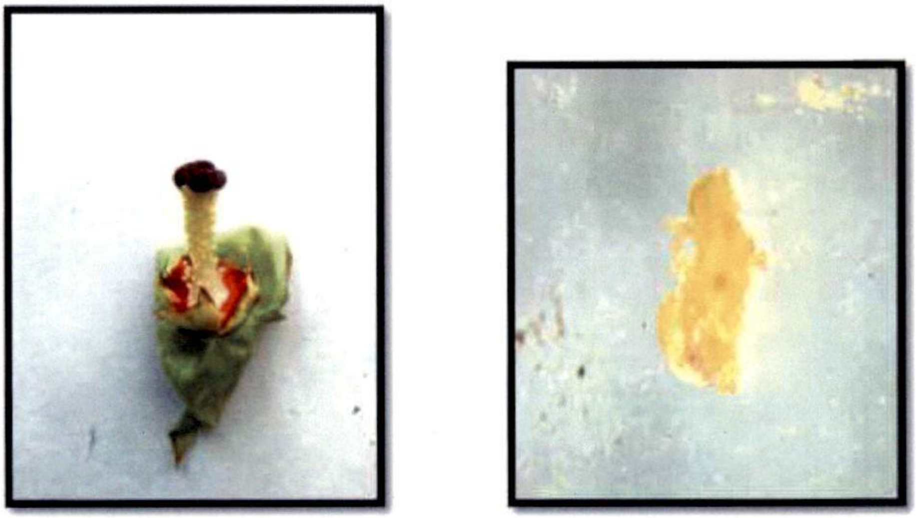
Fruits with attractive colour are preferred in market by consumers. So fruit colour at marketable stage is an important character in this study. Observation recorded for fruit colour in thirty eight accessions indicated that predominant fruit colour was yellowish green (71%) followed by green (26.3%) and green with red patches (3%) as shown in Fig.8. Similar observation was made by Ahiakpa (2012). The check Salkeerthi is a popular variety widely cultivated in Kasaragod is also light green in colour and is preferred by the vegetable growers and consumers. This preference is also seen in the landraces collected in the present study which might have been the result of selection for this trait. According to Sawadogo *et al.* (2006) okra is characterized by diversity on the basis of colour of fruits and stems.



Cream

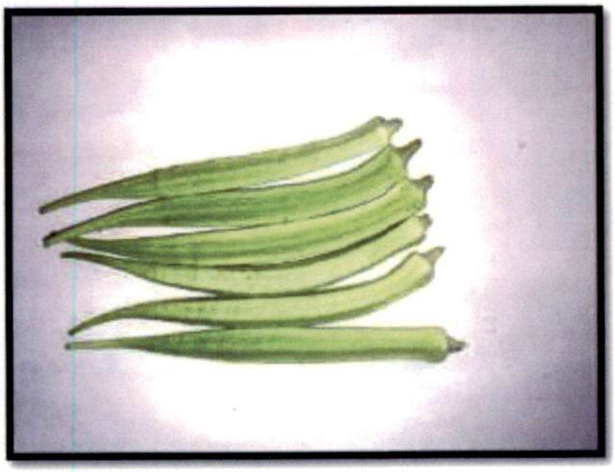
Golden yellow

Yellow

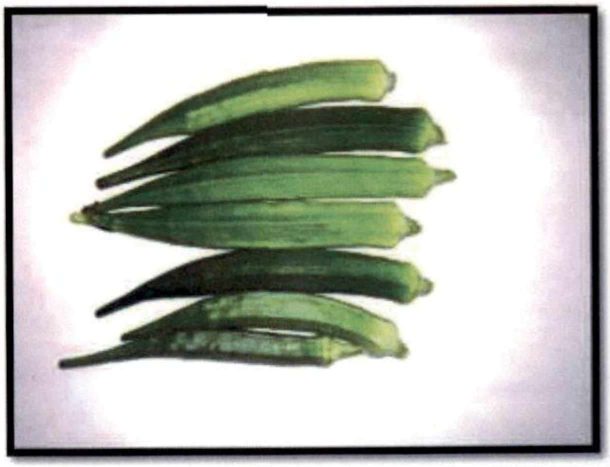


Colour of anther and stamina column

Plate 6 Floral characters of okra accessions



Yellowish green



Green

Green with red patches

Plate 7 Fruit colour of okra accessions

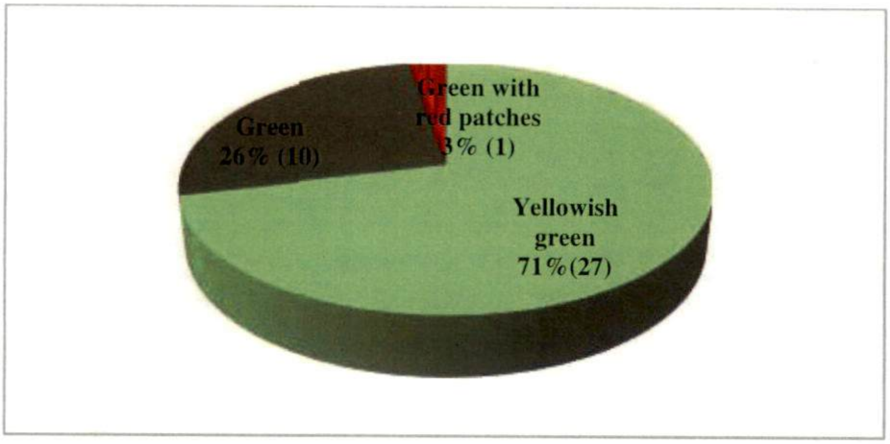


Fig 8. Fruit colour of 38 okra accessions

A wide variation in the fruit shape was noticed and fruit shapes classified into 6 groups as in Fig.9. Majority of the accessions in this study belongs to group 1 (42.1%) followed by group 3 (23.6%). Sekyere *et al.* (2011) reported that maximum occurrence of 32 % of the twenty five Ghanian okra accessions for fruit shape score 8. He also reported that maximum occurrence in fruit shapes ranging from short and triangular to long straight or long curved. In the present study fruit shape in the category 5, 6, 9, 10, 11, 12, 13, 14 and 15 were absent which was similar to the findings of Sekyere *et al.*(2011).

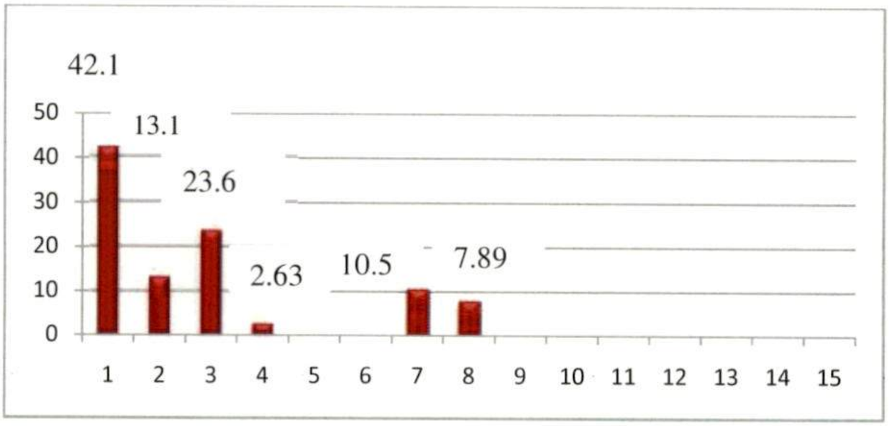


Fig 9. Fruit shape of 38 okra accessions

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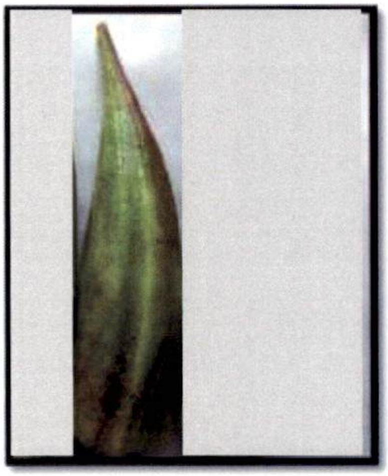

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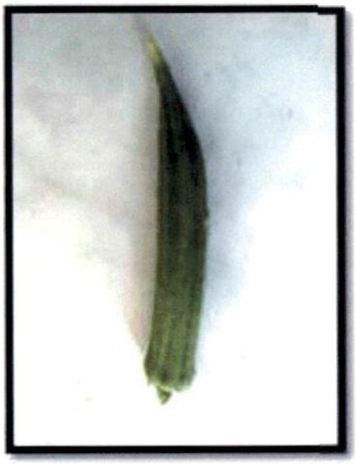

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Plate 8 Fruit shape of okra accessions

Position of the fruit on main stem showed two distinct variations: erect and horizontal. Fig.10 shows that 89.4% of the accessions are erect type and 10.5% of the accessions were horizontal type and there is no accession showing fruits with pendulous type or drooping position. Similar observations were made by Ahiakpa (2012) and Demelie *et al* (2016). *Abelmoshus esculentus* species is characterized by fruits that are erect on the main stem and low pigmentation in stem and leaves (Bisht *et al.,* 1995). However few accessions had shown fruits mounted with angle to the main stem (rather than parallel to the stem) as *Abelmoshus esculentus* which is similar to *Abelmoshus kale.* The occurrence of such genotypes may be ascribed to the probable out crossing between *Abelmoshus esculentus* and *Abelmoshus kale* as then later is naturalised in Western Ghats and Southern India (Bisht *et al.,* 1995).

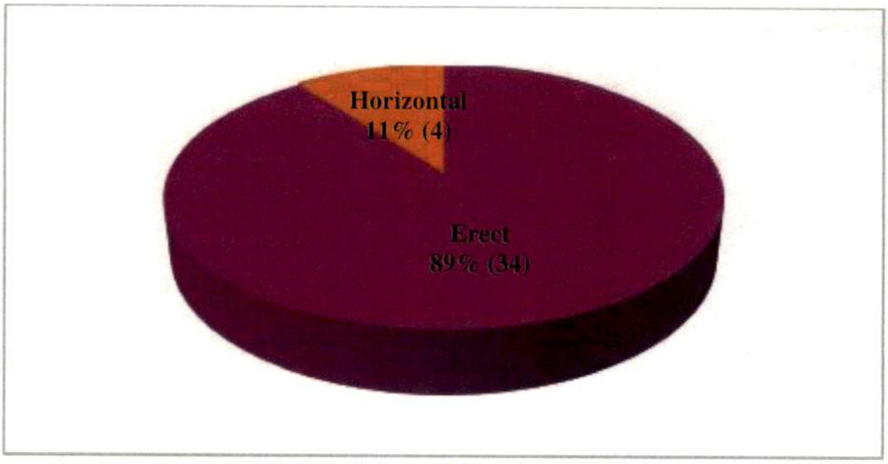

Fig 10.Position of the fruit of 38 okra accessions

The thirty eight okra accessions showed varying degrees of fruit pubescence namely downy type (45%), prickly type (42%), and slightly rough (13%) were shown in Fig.11. In this study there was predominance of prickly and downy types. However downy types were slightly higher than that of prickly types in frequency which indicates the preference for downy types. Similar observations were recorded by Bisht *et al.* (1995) and Nwangburuka and Denton

Erect

Horizontal

Plate 9 Position of the fruit on the main stem

(2011). Ahiakpa (2012) reported majority of the accessions having slightly rough fruits in the okra germplasm of Ghana. Martin *et al.* (1981) reported purple coloured stem, fruit colour, fruit pubescence and fruit shape were showing simple Mendelian inheritance suggesting that these characters are controlled by relatively few genes.

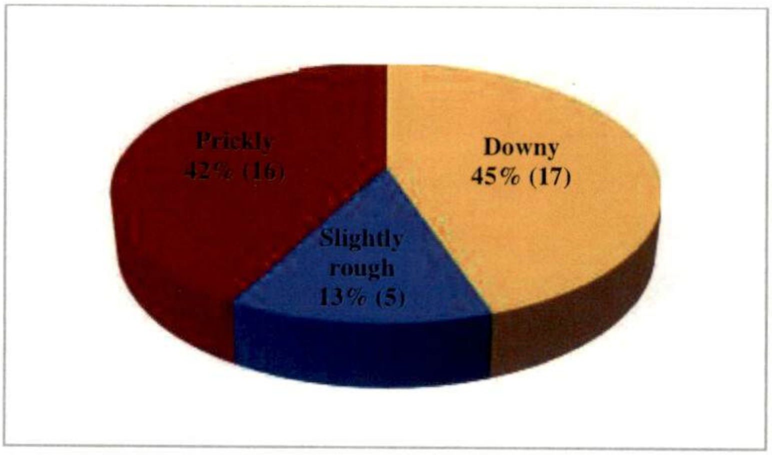

Fig 11.Fruit pubescence of 38 okra accessions

Number of ridges may directly relate to the seed yield. Hence more number of ridges higher will be the seed yield. Ninety five percent of the accessions showed ridges ranging from five to seven. Only 5% of the accessions showed ridges ranging from eight to ten in Fig.12. In commercial cultivation generally five edged medium fruits are preferred (Bisht *et al.,* 1995). Local landraces with multi edged and broad fruit types are preferred in tribal areas for diversified uses. So the result of the present study indicates the preference of 5 edged fruits for the farmers.

Frequency distribution shows that maximum number of variability in stem colour, fruit pubescence, leaf shape and fruit shape which were the important components of variability in the collected germplasm. Some of the qualitative traits such as leaf rib colour and leaf colour, position of the fruit on the main stem, mature fruit colour and number of ridges per fruit expressed limited variability. The collection under study represents there was intense variation in qualitative characters due to out crossing of characters.

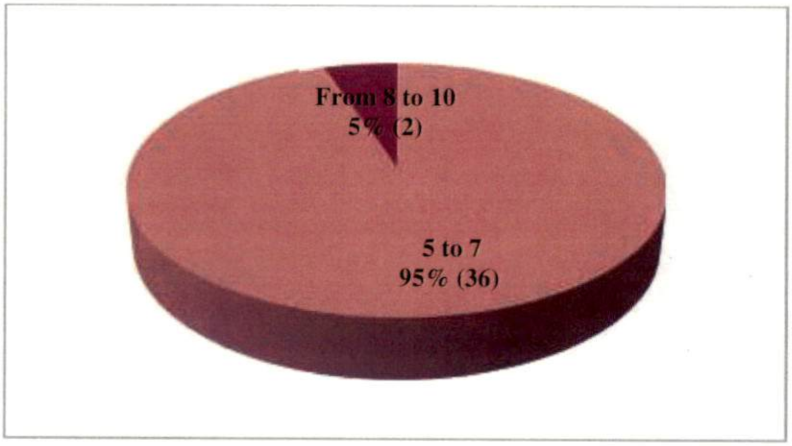

Fig 12. Ridges per fruit of 38 okra accessions

5.2.5 Development of identification keys for morphological characters

Identification keys were prepared by using ten different diagnostic characters such stem colour, branching pattern, leaf colour, leaf shape, colour of petal, colour of fruit, fruit shape, position of fruit, fruit pubescence and ridges per fruit were shown in Table 16.These traits were used to provide basis for identification of accessions to distinguish the cultivars. For example AE-10 having a path of ten characters i.e. stem colour (purple), branching pattern (medium), leaf colour (green with red veins), leaf shape (heart shaped), colour of petal (yellow), colour of fruit (green with red patches), fruit shape (long straight or curved), position of fruit (erect), fruit pubescence (slightly rough) and ridges per fruit (ranges 5-7). It is unique for this accession which means that no other accession can follow or repeat this path, so this unique path revealed the key diagnostic features of AE-10.

5.3 Variability analysis in quantitative characters

The thirty eight okra accessions were raised in augmented design in which controlled checks are replicated and the genotypes are not replicated. Analysis of variance, co-variance, coefficient of variation (PCV, GCV,

Table 16. Morphological Key Diagnostic Characters

	Stem colour	Branching pattern	Leaf colour	Leaf shape	Colour of petal	Colour of fruit	Fruit shape	Position of fruit	Fruit pubescence	Ridges per fruit
AE-1	Purple	Medium	Green with red veins	Heart shaped	Yellow	Yellowish green	Medium triangular	Erect	Prickly	Ranges 5-7
AE-2	Green	Orthotropic stem	Green	Heart shaped	Cream	Green	Long straight/curved	Erect	Downy	Ranges 5-7
AE-3	Green	Orthotropic stem	Green	Heart shaped	Cream	Green	Long straight/curved	Erect	Prickly	Ranges 5-7
AE-4	Green with red patches	Strong	Green	Heart shaped	Golden	Green	Medium triangular	Horizontal	Prickly	Ranges 5-7
AE-5	Green	Orthotropic stem	Green	Heart shaped	Golden	Green	Medium triangular	Erect	Prickly	Ranges 5-7
AE-6	Green	Orthotropic stem	Green with red veins	Heart shaped	Cream	Yellowish green	Long straight/curved	Horizontal	Downy	Ranges 5-7
AE-7	Green	Orthotropic stem	Green with red veins	Heart shaped	Cream	Yellowish green	Long straight/curved	Erect	Prickly	Ranges 5-7
AE-8	Purple	Strong	Green with red veins	Heart shaped	Cream	Yellowish green	Long straight/curved	Erect	Downy	Ranges 5-7
AE-9	Purple	Medium	Green with red veins	Heart shaped	Golden	Yellowish green	Medium triangular	Erect	Downy	Ranges 5-7
AE-10	Purple	Medium	Green with red veins	Heart shaped	Yellow	Green with red patches	Long straight/curved	Erect	Slightly rough	Ranges 5-7
AE-11	Purple	Orthotropic stem	Green	Heart shaped	Cream	Yellowish green	Long straight/curved	Erect	Prickly	Ranges 5-7
AE-12	Green with red patches	Orthotropic stem	Green	Alternate broad palmate	Cream	Yellowish green	Long straight/curved	Erect	Slightly rough	Ranges 5-7
AE-13	Green	Orthotropic stem	Green	Heart shaped	Yellow	Yellowish green	Long straight/curved	Horizontal	Prickly	Ranges 5-7

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	Stem colour	Branching pattern	Leaf colour	Leaf shape	Colour of petal	Colour of fruit	Fruit shape	Position of fruit	Fruit pubescence	Ridges per fruit
AE-14	Green	Orthotropic stem	Green	Alternate broad palmate	Yellow	Green	Long straight/curved	Erect	Downy	Ranges 5-7
AE-15	Green	Orthotropic stem	Green	Alternate broad palmate	Cream	Green	Long straight/curved	Erect	Downy	Ranges 5-7
AE-16	Green	Orthotropic stem	Green with red veins	Heart shaped	Cream	Yellowish green	Long straight/curved	Erect	Prickly	Ranges 5-7
AE-17	Green	Orthotropic stem	Green	Alternate broad palmate	Cream	Yellowish green	Long straight/curved	Erect	Prickly	Ranges 5-7
AE-18	Green	Orthotropic stem	Green	Heart shaped	Cream	Yellowish green	Long straight/curved	Erect	Prickly	Ranges 5-7
AE-19	Green	Orthotropic stem	Green	Heart shaped	Cream	Yellowish green	Long straight/curved	Erect	Slightly rough	Ranges 5-7
AE-20	Purple	Orthotropic stem	Green with red veins	Heart shaped	Cream	Yellowish green	Long straight/curved	Erect	Downy	Ranges 5-7
AE-21	Green with red patches	Orthotropic stem	Green	Alternate broad palmate	Yellow	Yellowish green	Long straight/curved	Erect	Downy	Ranges 5-7
AE-22	Green	Orthotropic stem	Green	Heart shaped	Cream	Yellowish green	Medium triangular	Horizontal	Prickly	Ranges 5-7
AE-23	Green	Orthotropic stem	Green	Heart shaped	Cream	Yellowish green	Long straight/curved	Erect	Downy	Ranges 5-7
AE-24	Green with red patches	Orthotropic stem	Green	Heart shaped	Cream	Yellowish green	Long straight/curved	Erect	Slightly rough	Ranges 5-7
AE-25	Purple	Orthotropic stem	Green	Heart shaped	Golden	Yellowish green	Long straight/curved	Erect	Downy	Ranges 8-10
AE-26	Green	Orthotropic stem	Green	Heart shaped	Yellow	Green	Long straight/curved	Erect	Prickly	Ranges 5-7
AE-27	Green with red patches	Orthotropic stem	Green	Heart shaped	Cream	Yellowish green	Long straight/curved	Erect	Downy	Ranges 5-7

Stem colour	Branching pattern	Leaf colour	Leaf shape	Colour of petal	Colour of fruit	Fruit shape	Position of fruit	Fruit pubescence	Ridges per fruit	Stem colour
AE-28	Green	Orthotropic stem	Green	Alternate broad palmate	Golden	Yellowish green	Long straight/curved	Erect	Downy	Ranges 5-7
AE-29	Green	Orthotropic stem	Green	Heart shaped	Cream	Yellowish green	Medium triangular	Erect	Downy	Ranges 5-7
AE-30	Green	Orthotropic stem	Green	Alternate broad palmate	Yellow	Yellowish green	Long straight/curved	Erect	Downy	Ranges 5-7
AE-31	Green with red patches	Orthotropic stem	Green	Alternate broad palmate	Cream	Yellowish green	Long straight/curved	Erect	Prickly	Ranges 5-7
AE-32	Green	Orthotropic stem	Green	Heart shaped	Cream	Yellowish green	Long straight/curved	Erect	Downy	Ranges 8-10
AE-33	Green	Orthotropic stem	Green	Heart shaped	Golden	Green	Medium triangular	Erect	Prickly	Ranges 5-7
AE-34	Green with red patches	Orthotropic stem	Green	Heart shaped	Cream	Green	Long straight/curved	Erect	Downy	Ranges 5-7
AE-35	Green	Orthotropic stem	Green	Heart shaped	Cream	Green	Long straight/curved	Erect	Downy	Ranges 5-7
AE-36	Green	Orthotropic stem	Green	Alternate broad palmate	Cream	Yellowish green	Long straight/curved	Erect	Prickly	Ranges 5-7
AE-37	Green	Orthotropic stem	Green	Heart shaped	Cream	Yellowish green	Long straight/curved	Erect	Prickly	Ranges 5-7
AE-38	Green	Orthotropic stem	Green	Alternate broad palmate	Cream	Yellowish green	Long straight/curved	Erect	Slightly rough	Ranges 5-7

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Heritability and Genetic advance), correlation and path coefficient analysis were estimated.

The analysis of variance divide the variations into variation between accessions, variation between checks and variation of accessions against checks. Thirty eight okra accessions showed high variability with respect to seventeen characters of the total nineteen characters studied. There was no variation observed in fruit length and number of locules in the fruit. The checks Salkeerthi and Arka Anamika did not show any variation in internode length, number of units in epicalyx, length of sepals, length of petals, days to 50% flowering, fruit diameter and number of locules in the fruit.

The accessions did not show any variation with checks in the characters such as length of sepals, length of petals, number of fruiting nodes and number of locules in the fruit. The results of the nineteen quantitative traits subjected to statistical analysis are discussed below

5.3.1 Mean performance

Mean performance of the accessions for the nineteen quantitative characters was studied. The thirty eight accessions of okra show significant difference in majority of the characters. Analysis of variance showed a wide range of variability with respect to in primary branches, plant height, internode length, first flowering node, number of units in epicalyx, length of units in epicalyx, length of sepals, length of petals, length of stamens, days to 50% flowering, number ,fruiting nodes, length of fruit peduncle fruit weight, fruit diameter, days to marketable maturity, green fruit yield per plant and marketable fruits per plant except fruit length and number of locules in the fruit.

The accession AE-16 followed by AE-20 was found as superior with high mean values of 2.01 and 1.81 respectively for number of primary branches. Among the checks Salkeerthi has maximum number of primary branches 1.02. No branches were observed in several accessions. This may due to the apical dominance and level of hormones. These results support the findings of Duggi *et al*. (2013).

Arka Anamika was found as superior for plant height (86.76 cm) and the lowest plant height (33.12 cm) was observed in accession AE-9. None of the accessions were taller than the check Arka Anamika. Tall plants are prone to lodging hence short plants are more favourable for maximum yield of fruits.

A wide variation was noticed in the internode length. This variation may be due to the genetic makeup of the accessions. Shortest internode length was detected in AE-28 and AE-6 (3.06 cm) and longest in AE-23 (6.61 cm). Shortest distance between internodes on stem with tall plant height is considered as a desirable trait in the point of view of okra breeding. Plant height, number of primary branches and internode length largely determine fruit bearing axils and considered as an important growth trait. Higher plant height and number of primary branches per plant can accommodate more number of fruits per plant. High mean values for plant height and number of primary branches and low mean values for internode length accounts more number of nodes and are desirable to get maximum fruit yield in okra. (Kumar and Reddy, 2015).

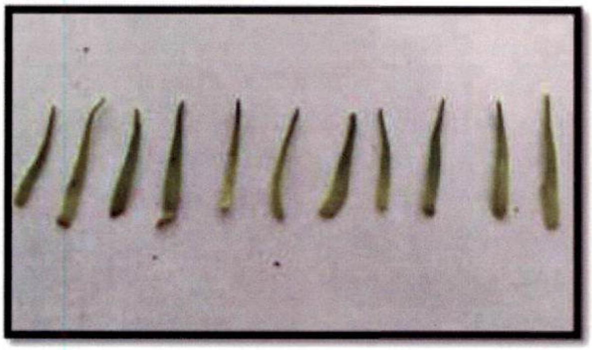
The node number bearing the first flower emergence ranged from 1.84 in AE-17 to 3.59 in AE-4. Flower and fruit at lower nodes are considered as advantage as they help in getting early and maximum number of fruits per plant (Reddy *et al.,* 2013). This variation in the first flowering node was reported by Bendale *et al.* (2003). Two accessions AE-1 and AE-10 recorded maximum (2.5 cm) for length of units in epicalyx and minimum(1.10 cm) was noticed in AE-24. Number of units in epicalyx ranged from 7 to 11 in AE-2 and AE-10 respectively (plate-11).

Regarding petal length longest petal (6.00 cm) was observed in AE-3 and the smallest petal (2.95 cm) was observed in AE-28. Similar results were made by Khajuria *et al*. (2015). Longest sepal (5.3 cm) was observed in AE-24 and the

Arka Anamika

AE-9

Plate 10 Variation in Plant height



AE-2 **AE-10**

Variation in Number of units in epicalyx

AE-24 **AE-9**

Variation in Size of sepals

AE-28

AE-3

Variation in Size of petals

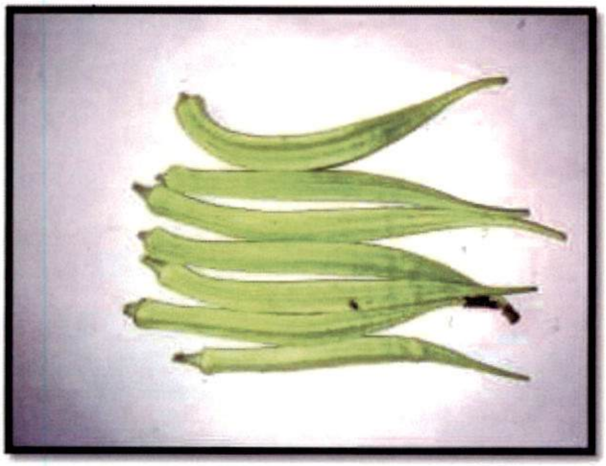
Plate 11 Variation in Floral characters

smallest sepal (1.60 cm) was observed in AE-9 in plate-11. Length of stamens ranged from 1.34 cm (AE-28) to 2.95 cm (AE-32).

Days to 50% flowering ranged from 48.81 (AE-10) to 62.16 (AE-31) Days to 50% flowering, first fruiting node and first flowering node are the indicators of earliness in okra. Early flowering not only gives early picking and better returns but also widens the fruiting period of the plant and ultimately reduces the loss of direct attack of insect and diseases. Flower and fruit at lower nodes are helpful in increasing the number of fruits per plant as well as yield (Reddy *et al.,* 2013).

Number of fruiting nodes ranged from 2.80 to 6.00. Maximum number of fruiting nodes was observed in AE-16 and minimum number of fruiting nodes was observed in AE-27.

Long fruits are generally preferred in market by the consumers. So fruit length at marketable stage is an important character. In this study there was no significant variation in accessions for fruit length. However, check Salkeerthi is popular in Kerala due to long pods of 29.24 cm than Arka anamika of 22.45 cm and exhibited significant difference between accessions. Among the thirty eight accessions of okra the average pod length was 22.16 cm. This variation in fruit length also been reported by Sindhumole and Manju (2014). Sarker *et al.* (2016) reported that the highest fruit length was recorded in Parbani Kranti (17.33 cm) and the lowest fruit length was recorded in Yuvraj (12.77 cm). Wide variation was noticed in fruit characters *viz.*, fruit weight, fruit length and fruit girth among the genotypes. Similar wide variation in fruit characters was observed by Chandra *et al.* (2014). In most of the accessions peduncle length ranged from 1.39 cm to 2.99 cm. Three accessions had peduncle length ranging above 3 cm *i.e.,* in AE-9 (3.23 cm), AE-32 (3.16 cm) and AE-30 (3.06 cm). There is no much variation in these characters. Similar results was made by Demelie *et al.* (2016) who noticed no significant difference among the Ethiopian okra collection for internode length, number of units in epicalyx and peduncle length. Bisht *et al.* (1995) had classified



Salkeerthi

AE-10

Salkeerthi

AE-10

Plate 12 Variation in Fruit length

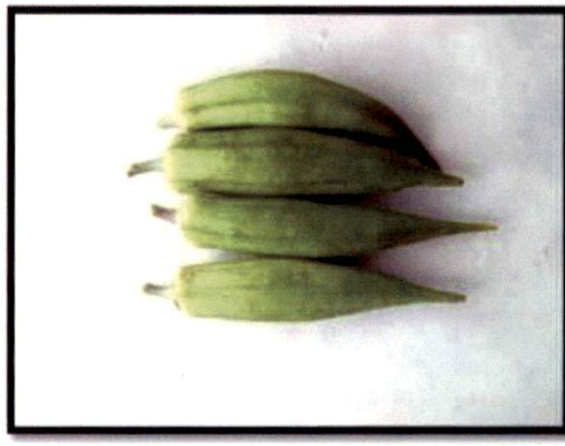
peduncle length under qualitative character as per NBPGR descriptors under two classes 1and 2 (class-1 ranges from 1-3cm and class-2 more than 3 cm).

Maximum fruit weight (61.65 g) and fruit diameter (3.68 cm) was noticed in accession AE-5 (plate-13). High fruit weight means larger will be the fruit length and more will be the seed content. Fruit weight, fruit length and number of fruits per plant has been consistently identified as very important components of yield (Adiger *et al.,* 2011). The variation in the number of locules ranges from 5 to 8. Majority of the accessions possessed 5 numbers of locules. Binelfew and Alenu (2016) observed more than 5 locules in 94% of the Ethiopian okra accessions. Similar observation was made by Kumar *et al*. (2012).

The accession AE-1 was found as the earliest among all the accessions with low mean values for days to marketable maturity (5.18 days) and high mean values for days to marketable maturity (9.03 days) was observed in AE-36. Number of marketable fruits per plant was obtained from the total number of green and tender fruits excluding those infested by fruit and shoot borer. Among the accessions marketable fruits per plant ranged from 12.53 (AE-13) to 21.63 (AE-20). In the case of checks maximum number of marketable fruits was noticed in Salkeerthi (22.72). Yield per plant showed impressive variation with values ranging from 285.83 g to 682.79 g. Highest green fruit yield was noticed in AE-16 (682.79 g) followed by AE-20 (678.03 g) which is more than the two checks and lowest green fruit yield was noticed in AE-27 (285.83 g). Existence of high variability of yield per plant in okra was reported by Pandravada *et al*. (2015), Amoatey *et al.* (2014), Chandra *et al.* (2014), Duggi *et al.* (2013), Jagan *et al.* (2013), Kumar *et al. (*2012) and Akotkar *et al*. (2010). Among the two parameters marketable fruits per plant and green fruit yield from the above results shows those accession with high green fruit yield also gave higher marketable fruits per plant i.e. these accessions are not only high yielding but also tolerant to fruit and shoot borer infestation.

5.3.2 Components of variation

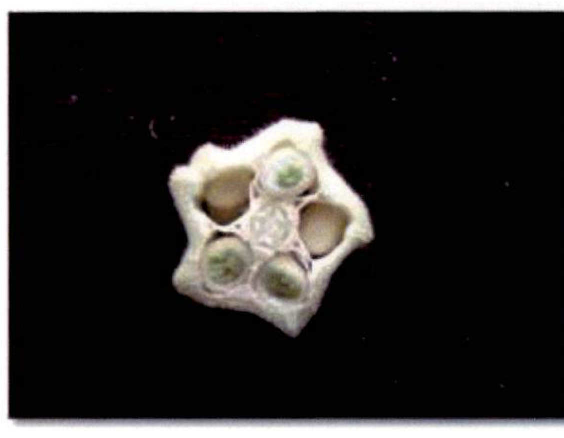
AE-5



AE-10

Variation in Fruit weight

AE-5



AE-17

Variation in Fruit diameter

Plate 13 Variation in Fruit weight and fruit diameter

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Plate 14 Variation in Number of locules

Knowledge of nature and magnitude of variability existing in available breeding material are requisite to choose characters for effective selection of desirable genotypes to undertake plant breeding programmes. The components of variability (such as coefficient of variation, heritability and genetic advance) and the magnitude of these components is a measure of type of gene action involved in the experiment of various traits. Information about gene action helps in deciding breeding procedures for the improvement of the trait. Component of variability were estimated and the results discussed below.

5.3.2.1 Genotypic coefficient of variation (GCV), Phenotypic Coefficient of variation (PCV), Heritability and Genetic Advance

Higher value of GCV (more than 20) indicates the character is low influenced by the environment. In the present study phenotypic coefficient of variation observed is higher than that of the genotypic coefficient of variation for all the nineteen characters studied in Fig.13. This indicates the apparent variation is not only due to genotypes but also due to the influence of environment. However the difference between GCV and PCV is low which implies that their relative resistance to environmental variation and also described that genetic factors were responsible for the expression of these attributes. In the present study low difference between PCV and GCV values were observed in characters like primary branches per plant and number of units in epicalyx indicating low influence of environment on these characters. Similar results were obtained by Chandra *et al.* (2014), Duggi *et al* (2013), Nwangburuka and Denton (2011), Prakash and Pitchaimuthu (2011), Saifullah and Rabbani (2009).

High GCV was observed for primary branches per plant, plant height, length of sepals, length of petals and length of stamens. This indicates the little influence of environment on the expression of character. Similar results were made by Reddy *et al.* (2013), Adiger *et al.* (2011), Prakash and Pitchaimuthu (2011) and Nwangburuka and Denton (2011). High PCV and moderate GCV values were noticed in internode length. Low GCV and PCV values were observed for yield components such as fruit length, fruit weight, fruit diameter, days to marketable maturity, marketable fruits per plant and green fruit yield which indicates the influence of environment on these characters. Hence selection based on these characters will not be rewording.

GCV and PCV indicates magnitude of variability but the extent of variability is transferable to progeny can be measured only from the parameter heritability and genetic advance. Genetic advance is a measure of genetic gain under selection and when it is expressed in percentage of mean, it is termed as genetic gain. So to have an effective selection along with GCV and PCV heritability and genetic gain should also be considered.

Heritability values for various quantitative characters ranged from 56.79 per cent to 100 per cent. Among the vegetative characters high heritability (more than 60%) was observed in primary branches per plant, plant height and internode length. Among the flowering characters high heritability was observed in first flowering node, days to 50% flowering, length of petals, length of sepals and length of stamens. Among the fruiting characters high heritability was observed in length of fruit peduncle, number of fruiting nodes, fruit weight, marketable fruits per plant, fruit diameter, days to marketable maturity and green fruit yield per plant. Characters such as length of units in epicalyx and fruit length exhibit moderate (30-60%) broad sense heritability values. Maximum genetic advance was expressed by length of sepals (56.23%) and minimum for days to 50% flowering (12.88%).

High heritability with high genetic advance indicates that the heritability is due to additive gene effects and selection will be very effective. In the present study, high heritability with high genetic advance was observed in characters like length of sepals, primary branches per plant, plant height, length of petals, length of stamens, internode length, length of fruit peduncle, green fruit yield per plant, fruit weight, first flowering node, number of units in epicalyx and days to marketable maturity were shown in Fig.13.

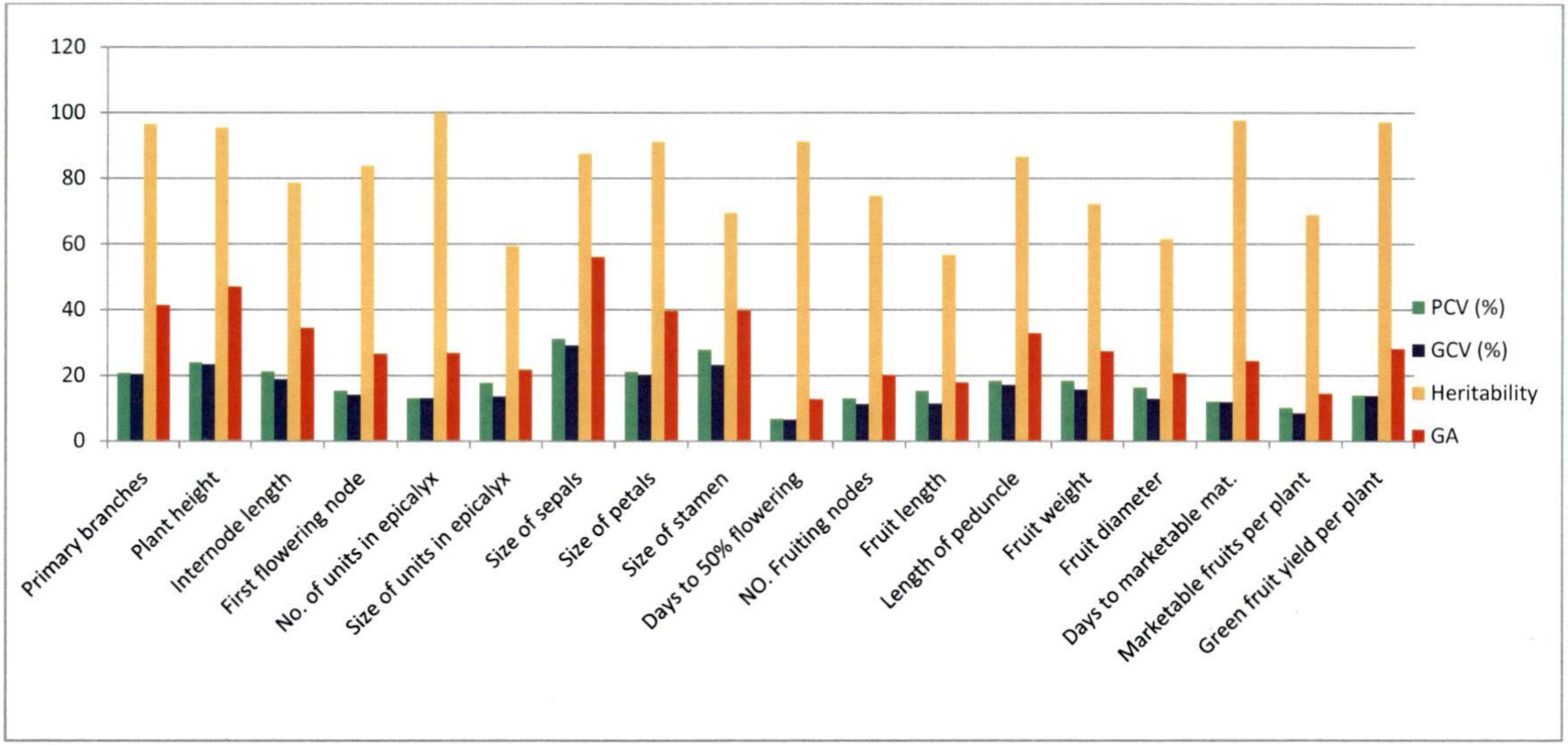

Figure.13 GCV, PCV and Heritability with genetic advance as percentage of mean of quantitative characters

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Similar results were reported by Kandasamy (2016), Chandra *et al.* (2014), Duggi *et al.* (2013) and Jagan *et al.* (2013). High heritability with moderate genetic advance was recorded in characters like days to 50% flowering, number of fruiting nodes, fruit diameter and marketable fruits per plant.

Primary branches and number of units in epicalyx and days to 50% flowering shows high heritability and very low difference between PCV and GCV values indicates that there is less influence of environment on these characters and are effective for selection. So variability analysis revealed that characters like primary branches, number of units in epicalyx and days to 50% flowering provide an ample scope for the improvement of yield in okra.

5.3.3 Correlation

Pod yield of okra is a complex quantitative trait, which is conditioned by the interaction of various growth and physiological processes throughout the life cycle (Adeniji and Peter, 2005). In general, plant breeders commonly select yield components which indirectly increase yield. Since direct selection for yield *per se* may not be the most efficient method for its improvement, indirect selection for other yield related characters, which are closely associated with yield, will be more effective and hence knowledge of inter-relationship between pairs of such characters and yield is essential to bring a rational improvement in the desirable traits and can significantly improve the efficiency of a breeding program.

In the present investigation, the correlation studies revealed that the genotypic correlation coefficients are higher than that of the phenotypic correlation coefficients which indicates the relationship among the various characters due to genetic effects. The present findings are in consonance with the earlier findings of Soni (2016), Reddy *et al.* (2012) and Adiger *et al.* (2011) indicating inherent association between various characters.

Among the correlation coefficients of nineteen characters green fruit yield showed significant positive genotypic and phenotypic correlation with fruit weight, primary branches per plant and marketable fruits per plant. Similar results were reported by Adiger *et al.* (2011) which indicates that yield could be improved through selection based on these characters. Negative genotypic correlation was shown by first flowering node with green fruit yield. Similar results was reported by Reddy *et al.* (2012), Somashekhar *et al.* (2011) and Adiger *et al.* (2011) indicating that lower nodes are helpful in increasing the number of fruits per plant as well as earliness.

Primary branches showed positive genotypic and phenotypic correlation with marketable fruits per plant. Plant height showed significant positive genotypic and phenotypic correlation with internode length. Similar results were made by Reddy *et al.* (2012).

Days to 50% flowering showed significant positive genotypic and phenotypic correlation with plant height. Number of fruiting nodes showed significant positive genotypic correlation with number of unit in epicalyx and days to 50% flowering which indicates that earliness in flowering increases the fruiting span and thus by increases the yield. Similar results were made by (Reddy *et al.*, 2013).

Length of fruit peduncle showed significant negative genotypic and phenotypic correlation with fruit diameter. Fruit length, fruit weight and fruit diameter are considerably important characters in improving the yield in okra. In the present study fruit weight showed significant positive genotypic and phenotypic correlation with fruit diameter and significant positive genotypic correlation with fruit length. Similar results were obtained by Gogineni *et al.* (2015), Reddy *et al.* (2013).

Marketable fruits per plant showed significant negative genotypic correlation with internode length and positive genotypic correlation with length of petals. Similar results were obtained by (Reddy *etal,* 2013).

Days to marketable maturity showed significant positive genotypic and phenotypic correlation with plant height which indicates tall plants will takes longer time to attain marketable maturity.

Majority of the characters showing high significant phenotypic associations are also showing significant genotypic correlation indicates that there was no environmental influence on these traits. Some of the characters which were showing high significant phenotypic associations but not showing significant genotypic correlation indicates that the effective influence of environment on these traits. High degree of genotypic correlation but non-significant phenotypic correlation indicates the reliability of the characters.

In general, in most crop plants negative correlation exist between two important yield components. For example boll number and boll weight in cotton; pod number and pod length in pulses; grain number/spike and grain length in cereal, pod number and pod length in okra. The undesirable linkages in such characters may occur due to gene reshuffling and breakage of such linkage could be achieved through biparental intermating in early segregating generation (Reddy *et al,* 2013).

Correlation analysis in the present study revealed that, the characters such as primary branches, fruit weight, and marketable fruits per plant are important yield component characteristics in okra. These are seen significantly correlated with green fruit yield per plant.

5.3.4 Path coefficient analysis

Correlation studies are very helpful in measuring the relation between yield and yield components but they do not provide the clear picture of the direct and indirect causes of such relations. It can be only obtained through path analysis. Path analysis is very useful to point out the important yield components which can be utilized for the selection of parameters.

In the present investigation path analysis revealed high and positive direct effects exhibited by internode length (1.843), length of units in epicalyx (1.759), fruit diameter (1.502), marketable fruits per plant (1.179), number of fruiting nodes (0.930), days to marketable maturity (0.801), number of units in epicalyx (0.636) on green fruit yield. Reddy *et al.* (2013) reported that fruit weight and number of fruits per plant had high positive direct effect on pod yield per plant. Gogineni *et al.* (2015) observed the characters fruit girth, fruit weight, number of fruits per plant, plant height and duration exhibited positive direct effects on yield revealing that these were the major yield contributing characters in okra

The positive association of the direct effect of marketable fruits per plant are due to the positive significant genotypic correlation of the same with green fruit yield. Thus correlation explains true relations of marketable fruit per plant on green fruit yield and direct selection of this trait is effective. This is in agreement with observation made by Reddy *et al.* (2013).

However the positive association of the direct effect of the characters such as internode length and days to marketable maturity show insignificant genotypic correlation with green fruit yield. This correlation may be the result of indirect negative influence of these characters through component character such as length of unit in epicalyx. Under this circumstance restricted simultaneous model should be followed.

Similarly, number of units in epicalyx, length of units in epicalyx and number of fruiting nodes had positive direct effect but insignificant genotypic correlation. These correlations may be the result of the indirect influence of these characters through the component characters such plant height, number of primary branches and internode length.

At the same time negative direct effects exhibited by first flowering node (-0.758) followed by days to 50% flowering (-0.442), primary branches (-0.372) and plant height. Similar results were made by Adiger *et al* (2011). Primary branches showed positive correlation with green fruit yield but its direct effect was negative which indicates the indirect effects of primary branches on green fruit yield was high through fruit diameter and marketable fruits per plant. In such situation indirect effect and positive correlation should be considered for the selection.

True relation between flowering node and green fruit yield also revealed by its negative genotypic correlation. However green fruit yield shows insignificant correlation with days to 50 % flowering due to the negative indirect influence through length of epicalyx *via* fruit diameter and number of fruiting nodes even though fruit diameter have high direct effect and insignificant correlation.

High indirect effects were also exhibited by many characters *viz* internode length *via,* marketable fruits per plant and length of petals. Length of units in epicalyx *via*, plant height; days to marketable maturity; number of units in epicalyx; days to 50% flowering; fruit weight; fruit diameter and length of sepals. number of fruiting nodes *via*, length of sepal; fruit diameter *via* length of fruit peduncle, length of units in epicalyx, length of stamens and number of fruiting nodes. Marketable fruits per plant *via* fruit length and internode length. This indicates that while selecting varieties reduced value of the above mentioned characteristics have to be given importance.

Path analysis revealed that number of marketable fruit, fruit diameter and internode length are the main determinant components of green fruit yield whereas correlation has revealed marketable fruits, fruit weight and primary branches are the highly positively associated characters in the yield. So improvement in yield will be efficient if selection done based on all these characters.

5.4 Genetic diversity analysis

The importance of genetic diversity has not only been appreciated by plant breeders but they also actually used this as a potential tool in many crop improvement programmes. Genetic distances of thirty eight okra accessions were measured by Standardized Euclidean Square Distance method. Nineteen quantitative traits has been used to classify the divergent genotypes. The concept of genetic distance is very important while differentiating a well defined population. It can be used to improve crops either by means of hybridization or direct selection of genotypes for desirable traits. The high yielding varieties in okra has been developed by exploiting the genetic diversity available in the crop.

5.4.1 Cluster analysis

Clustering is a multivariate technique that can conveniently show the pattern of genetic relationships or proximity among accessions (Afifi and Clark, 1990) such that each group is homogeneous with respect to certain characteristics and each group should be different from other groups with respect to the same characteristics. For qualitative data similarities are considered and for quantitative data distance rather than similarities are considered (Anderson, 1984).

5.4.1.1Clustering based on qualitative traits

Qualitative data are extremely varied in nature. It includes any information that is not numerical in nature. They refer to characters or qualities, and are either binary [i.e., only two values: present (1) or absent (0)] or categorical (i.e., a value among many possibilities) or either ordinal (categories that have an order) or nominal (categories that are unrelated). In the present study grouping of the okra accessions for qualitative characters was based on nominal values using UPGMA (Unweighted Pair Group Method with Arithmetic mean) method. In this cluster analysis similarity coefficients are calculated by Average linkage method.

Cluster diagram obtained from the morphological descriptors shows three main clusters of okra accessions (Fig.14). Based on qualitative characters AE-5, AE-16, AE-18, AE-20 and AE-30 were placed in the same cluster due to its green coloured stem, orthotropic branching pattern, and yellowish green coloured fruit. Accession AE-10 form a separate cluster may be due to purple coloured stem and medium type branching pattern.

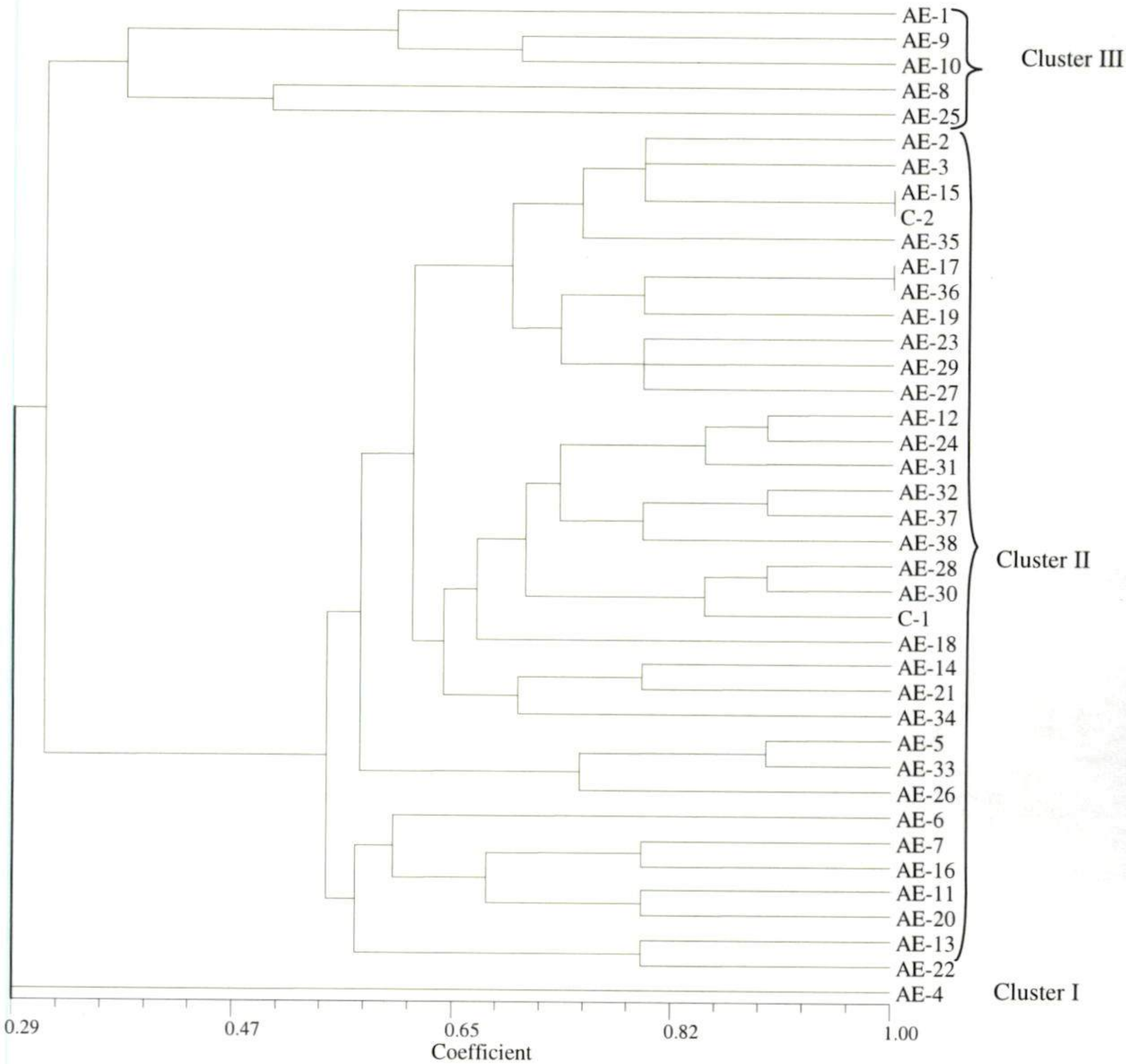

Figure: 14 Cluster diagram showing the relationship among 38 okra accessions by UPGMA cluster analysis based on qualitative characters.

Fruit pubescence is an important quality character of okra and consumers generally preferred downy type of fruits. Among the directly selected accessions based on ranking i.e. AE-20 and AE-30 falls on downy type pubescence. AE-10 had slightly rough fruits. The accessions AE-16 AE-18 and AE-5 belonging to the cluster II had prickly type pubescence. AE-16 which showed very good ranking based on green fruit yield and marketable fruits per plant can be improved for fruit pubescence by crossing with downy accession i.e., AE-20 or AE-30. Since the character fruit pubescence is a dominant strong simple Mendelian inheritance, the character can be incorporated with hybridization and selection.

Similarly for increasing the fruit weight AE-5 can be used in crossing but also have a prickly character, so it can be crossed with strong downy pubescent accessions. In the present investigation cluster analysis revealed that out of these six promising accessions four i.e. AE-16, AE-18, AE-20, AE-30 are from Kasaragod district and two i.e. AE-10 and AE-5 from Kannur district.

5.4.1.2Clustering based on quantitative traits

The distance matrix was used to construct the Ward's minimum dendrogram (Fig.15) which place the thirty eight okra accessions into seven clusters. Several measures of genetic distance has been proposed over the past decades to suit various objectives and Standardized Euclidean Square Distance can be considered as a powerful tool to assess the range of diversity among the accessions for quantitative characters. The present study indicated the presence of genetic divergence and grouping of the thirty eight okra germplasm into clusters based on quantitative traits and the results of the cluster analysis are discussed below:

5.4.1.3 Relationship between geographic diversity and genetic diversity

The grouping pattern of thirty eight accessions in seven clusters indicates that geographical distance between the genotypes of okra had no relation with the genetic divergence and the genotypes from the same source had fallen

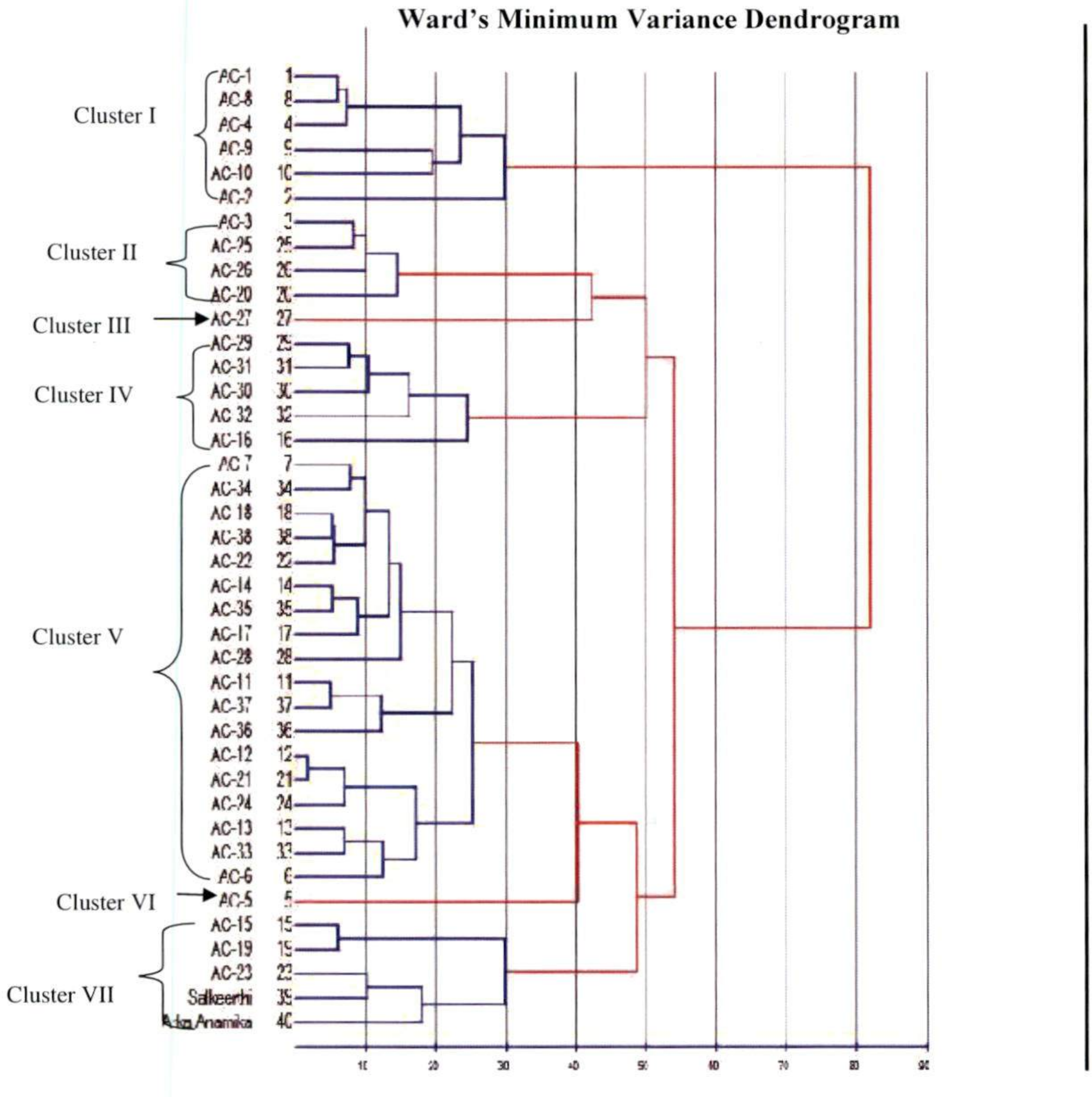

Figure 15: Cluster diagram showing the relationship among 38 okra accessions revealed by Standardized Euclidean Square Distance cluster analysis based on quantitative characters

into different clusters as well as the same clusters contains genotypes from different sources. Similar observation was made by Demelie *et al.* (2016), Balai *et al.* (2015), Reddy *et al.* (2012), Sekyere *et al.* (2011), Akotkar *et al.* (2010) and Bisht *et al.* (1995). This may be attributed to frequent exchange of breeding materials from one place to another and its future selection in different geographic regions which could result in genetic drift (Murty and Arunachalan, 1966 and Bhatt, 1970). Singh & Singh (1979) and Parbat & Mamtha (2012) reported that forces other than geographical distance are also responsible for divergence. Genetic drift and selection in different environments may cause greater diversity than geographical distance. Biotypes originating in particular habitat have different utility, only for certain traits for which selection has been practiced. Thus the constellations that might be assessed within a particular region in nature may lose their individuality under certain circumstances.

Of the seven clusters two are solitary while the remaining five clusters consist of more than one up to maximum eighteen accessions. Cluster III and cluster VI consist of only one accession i.e. AE-27 and AE-5 each represented by geographic areas of Kasaragod and Kannur respectively. This result in agreement with Demelie *et al.* (2016), Reddy *et al* (2013) and Akotkar *et al.* (2010) who reported that major clusters consist of solitary clusters.

5.4.1.4 Selection of parents for use in okra breeding programme

Genetic diversity analysis is carried out to identify suitable parents which may yield desirable recombinants in breeding programs (Akotkar *et al.*, 2010 and Ali *et al.*, 2014). Hybridization is an efficient approach for improving vegetable crops. It is one of the means of obtaining increased yield through transgressive segregation and exploitation of heterosis. Hence in any breeding program critical choice of parents is very important for yield improvement. According to Bhatt (1970) methods adopted for selection of parents fall in three broad categories

a) Method used to identify crosses which give rise to superior transgressive segregants: it involves study of F_4 and further generation lines in which estimation are made on means and variances.

b) Evaluation of parent using method of statistical genetics; It includes method in which selection of parents is based on combining ability.

c) Method used to study parents as homozygous lines; it involves yield component analysis and measure of genetic divergence. Bhatt (1970) used the following different method for selecting parents in wheat

i) By random method where there is no influence on parental types

ii) Conventional methods on the basis of *per se* performance

iii) On the basis of multivariate analysis and selection

iv) Selection on the basis of ecogeographical diversity

In the present study attempt is made to utilize the genetic diversity analysis for selection of parent for hybridization in okra breeding program. *Per se* performance of the genotypes in the clusters was also taken to consider for selection of parents. The practical significance of grouping genotypes into different clusters and computing statistical difference between them is discussed here. Crossing of genotypes not genetically diverse or with little genetic diversity might give lower heterotic value in F_1 and narrow range of variability in segregating populations. Therefore crosses between genotypes belonging to clusters having high inter cluster distance should be considered (Fig 14). Cross combinations of genotypes belonging to clusters with high inter cluster distance have been arranged in descending order of magnitude and promising cluster combination have been presented in Table 17.

The cluster consisting of only one genotypes *viz* cluster III and cluster VI are the most divergent cluster or appeared to be genetically diverse with highest inter cluster distance. The parents for crossing should be chosen from widely distant clusters. But, it is observed that the lone genotype AE-27 belonging to cluster III is not showing good performance and is ranking very low value for yield and other yield attributes as well as other quantitative traits. According to

Allard (1988) it is usually helpful in planning pedigree program to regard the variety to be produced as a replacement for some well established variety.

Table 17. Average inter cluster distance and cross combination by Standardized Euclidean Square Distance method

	Cluster combination	Average cluster distance	Cross combination
1	III × VI	102.34	AE-5 × AE-27
2	III × I	76.94	AE-10 × AE-27
3	III × IV	76.43	AE-16 × AE-27 AE-30 × AE-27
4	I × VI	70.30	AE-10 × AE-5
5	IV × VI	69.80	AE-16 × AE-5 AE-30 × AE-5
6	III × VII	68.90	C-1 × AE-27
7	II × VI	64.99	AE-20 × AE-5
8	VI × VII	62.77	C-1 × AE-5
9	I × VII	60.19	C-1 × AE-10
10	III × V	56.25	AE-18 × AE-27
11	I × IV	55.96	AE-10 × AE-16 AE-10 × AE-30
12	V × VI	52.59	AE-18 ×AE-5
13	II × VII	45.29	AE-20 × C-1
14	IV × VII	44.82	AE-16 × C-1 AE-30 × C-1
15	I × II	41.29	AE-10 × AE-20
16	I × V	39.68	AE-10 × AE-18
17	II × IV	39.55	AE-20 × AE-16 AE-20 × AE-30
18	V × VII	35.53	AE-18 × C-1
19	IV × V	35.04	AE-16 × AE-18 AE-30 × AE-18
20	II × V	32.78	AE-20 × AE-18

The new variety usually cannot be much poorer in yield, adaptation or dependable than the variety, it is intended to replace, irrespective of improvement of specific feature. Hence, it appear appropriate that other practical considerations like earliness, green fruit yield, marketable fruits per plant, fruit weight, days to marketable maturity etc should be taken into account in choosing okra genotypes as parents for breeding program.

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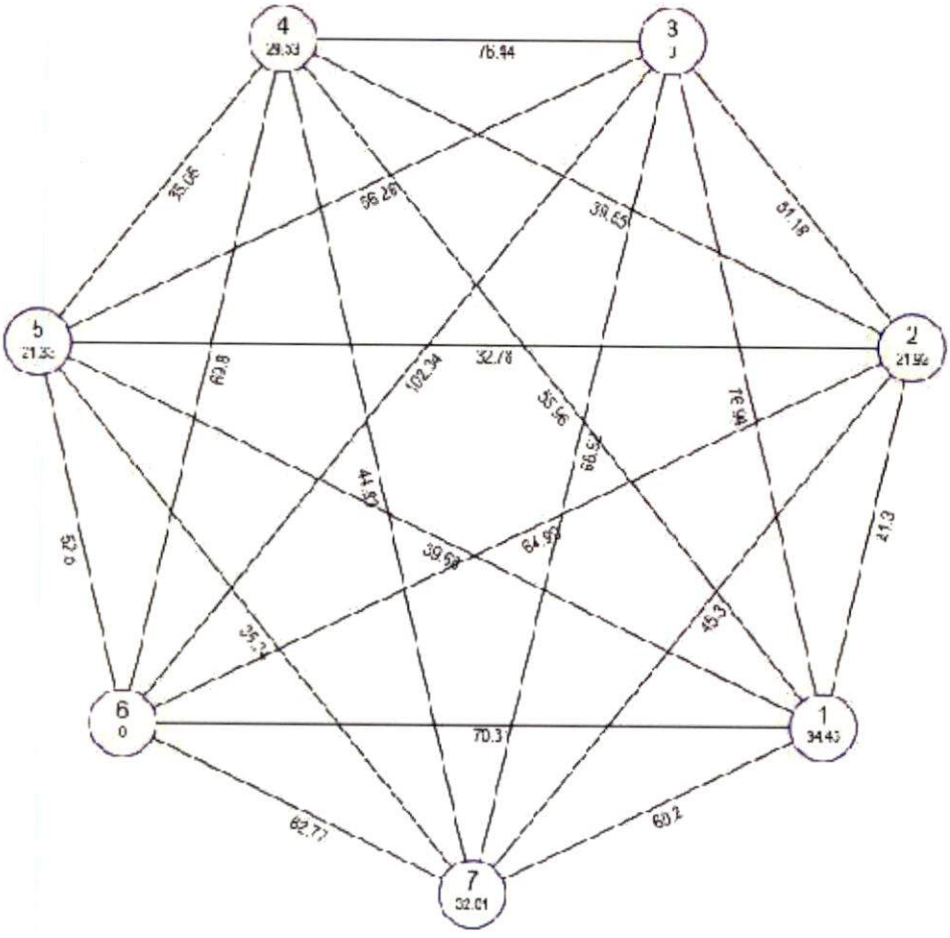
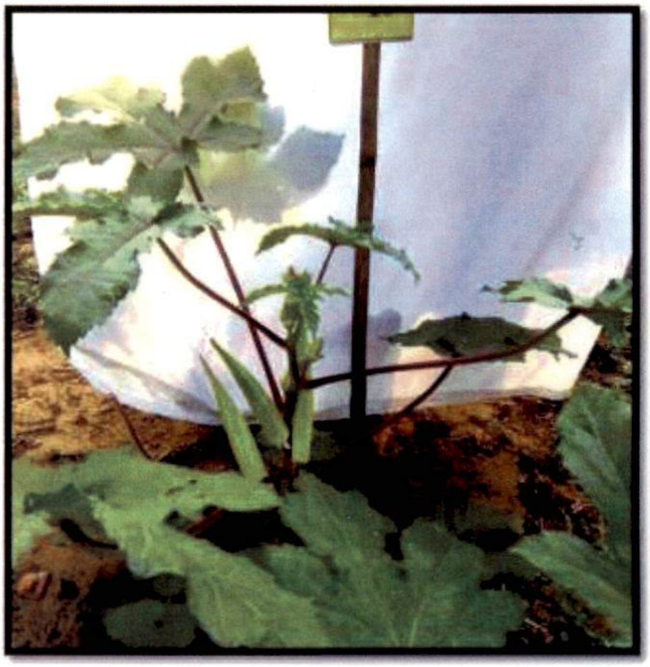


Figure.16 Euclidean Square Distance (Not to the Scale)

Based on the superior overall ranking in the clusters for four attributes i.e. fruit weight, green fruit yield, marketable fruit per plant and days to marketable maturity the accessions such as AE-10 (cluster I), AE-20 (cluster II), AE-16 and AE-30 (cluster IV), AE-18 (cluster V) and AE-5 (cluster VI) were identified as the promising accessions. The accessions AE-20, AE-30 and AE-10 were showing

AE-16



AE-20

AE-18

Plate 15 Promising accessions identified

AE-30

AE-10

AE-5

Plate 16 Promising accessions identified

downy type fruit pubescence which is mostly preferred by the consumers. Hence these accessions were included in the cross combination in table 17.

The present investigation projected the importance of AE-16 and AE-20 as one of the parents for higher heterosis in F_1 and potential transgrents in the subsequent generation. Both these accessions have considerably high green fruit yield per plant greater than the checks Salkeerthi and Arka Anamika. Similarly the accessions like AE-10, AE-18, AE-30 belonging to cluster I, V and IV as seen from the table were identified as superior in yield and AE-5 belonging to cluster VI as promising with highest fruit weight. If these genotypes are involved in crosses with Salkeerthi (C-1), as (seen in table 17) the popular variety of KAU with excellent fruit characters will give potentially high yielding hybrid or segregates with good market value.

Based on the information gathered from the present investigation the following future work has been made:

- Based on the passport data of the collected materials, these accessions can be registered at NBPGR, New Delhi and IC (indigenous collection) numbers obtained.

- The accessions have to be further evaluated for other yield components physiological parameters, nutritional quality and mucilage content by taking of trials in more seasons and locations.

- The study was entirely based on morphological characterization. It can be further validated with molecular markers.

Summary

6. SUMMARY

The present study entitled "Characterization of okra [*Abelmoschus esculentus* L. Moench] genotypes in North Kerala was carried out in the Department of Plant breeding and Genetics, College of Agriculture, Padannakkad during 2016-2017. The programme envisaged exploration and collection of okra genotypes in North Kerala and evaluation of these collected accessions for morphological characterization, genetic variability and diversity in qualitative and quantitative traits. The salient findings are presented below:

1. On the basis of eco-geographic survey conducted in North Kerala, forty four accessions of [(*Abelmoschus esculentus* L. Moench] okra were collected from Kannur, Malappuram and Kasaragod district. Out of this thirty eight accessions were taken for the final study.

2. Based on the information passport data of the collected material was prepared and catalogued and collectors number was assigned to these thirty eight okra accessions.

3. Identification keys for morphological characters were prepared by using ten different diagnostic characters such stem colour, branching pattern, leaf colour, leaf shape, colour of petal, colour of fruit, fruit shape, position of fruit, fruit pubescence and ridges per fruit.

4. The analysis of variance revealed that thirty eight okra accessions showed high variability with respect to seventeen characters of the total nineteen characters studied. There was no variation observed in fruit length and number of locules in the fruit.

5. Mean performance of the accessions for the nineteen quantitative characters revealed accession AE-16 to be superior with high mean values for number of primary branches, Arka Anamika was found superior for plant height as none of the accessions were taller than the check Arka Anamika. Maximum number of fruiting nodes were observed in AE-16. Maximum fruit weight and fruit diameter were noticed in AE-5. The accession AE-1 was found as the earliest among all the accessions with low mean values for days to marketable maturity and maximum number of marketable fruits was noticed in Salkeerthi, Highest green fruit yield was noticed in AE-16 followed by AE-20 which was greater than the checks as well.

6. High heritability with high genetic advance was observed in many characters like length of sepals, primary branches per plant, plant height, length of petals, length of stamens, internode length, length of fruit peduncle , green fruit yield per plant, fruit weight, first flowering node, number of units in epicalyx and days to marketable maturity.

7. Correlation analysis revealed that the characters such as fruit weight, primary branches and marketable fruits per plant showed significant positive genotypic correlation with green fruit yield per plant. Negative genotypic correlation exhibited by first flowering node on green fruit yield.

8. Path coefficient analysis revealed that maximum positive direct effect was exhibited by internode length which was followed by length of units in epicalyx, fruit diameter, marketable fruits per plant, number of fruiting nodes and days to marketable maturity.

9. Diversity analysis was carried out based on Standardized Euclidean Square Distance method and UPGMA (Unweighted Pair Group Method with Arithmetic mean) method for the nineteen quantitative and fourteen qualitative traits respectively. The thirty eight okra accessions were grouped into different clusters. Based on the superior ranking in the cluster and cluster distances twenty cross combinations were formed. Six promising accessions (AE-5, AE-10, AE-16, AE-18, AE-20, and AE-30,) including the check Salkeerthi were identified as promising that can be used as parents for the hybridization in future okra breeding programmes.

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Abstract

ABSTRACT

The study entitled "Characterization of okra [*Abelmoschus esculentus L.* Moench] genotypes in North Kerala" was carried out in the Department of Plant Breeding and Genetics, College of Agriculture, Padannakkad during 2015-2017. The main objective of the study was exploration and collection of okra genotypes in North Kerala and evaluation of collected accessions for morphological characterization, genetic variability and diversity in qualitative and quantitative traits. On the basis of eco-geographic survey conducted in North Kerala, 44 accessions of *Abelmoschus esculentus* were collected from Kannur, Malappuram and Kasaragod district and the passport data of these accessions were prepared. During the exploration in areas of okra collection, a wide variability was noticed with respect to its morphological traits.

Thirty eight accessions out of fourty five were evaluated for various qualitative and quantitative traits in augmented design using two checks *viz* Salkeerthi a variety released from Kerala Agricultural University and Arka Anamika from Indian Institute of Horticultural Research (ICAR-IIHR), Bangalore. They were subjected to morphological characterization for fourteen qualitative traits based on IPGRI descriptors and genetic variability analysis for nineteen quantitative traits.

The morphological characterization showed distinct morphotypes in the okra accessions as depicted by variation in branching habit, stem colour, leaf shape, leaf colour, flower colour, fruit shape, fruit pubescence and fruit position. The analysis of variance indicated significant differences among the accessions for all the quantitative characters except number of locules per fruit and fruit length. However among the checks there was no significant difference for characters such as days to 50 per cent flowering, internode length, number of units in epicalyx, size of sepal, size of petal and fruit diameter. When checks were compared with accessions, characters like number of fruiting nodes, size of sepals

and size of petals did not show any significant difference. Two accessions *viz*, AE-16 followed by AE-20 recorded higher green fruit yield than two checks with AE-16 recording maximum. The accession AE-20 was also superior for characters such as number of marketable fruits per plant, primary branches per plant and required lesser number of days to attain marketable maturity. The accession AE-5 had shown superiority for important fruit characters such as fruit weight and fruit diameter. All these accessions showed no incidence of fruit and shoot borer except AE-5.

Among the components of variability, high heritability coupled with high genetic advance as per cent of mean was observed for plant height, primary branches per plant, internode length, fruit weight, fruit diameter, days to marketable maturity and green fruit yield indicating effectiveness of selection based on phenotypic performance of these traits. Yield being a complex character, the association analysis of component characters of yield revealed high positive genotypic correlation for characters such as primary branches, fruit weight and number of marketable fruits. Significant negative genotypic correlation was exhibited by first flowering node with green fruit yield. Path coefficient analysis revealed that internode length, number of fruiting nodes, fruit diameter and number of marketable fruits per plant are the main determinants of green fruit yield in okra as indicated by their high positive direct effects and the characters first flowering node and days to 50 per cent flowering are major determinants of earliness as indicated by their high negative direct effect on green fruit yield. So improvement in yield will be efficient if selection is done based on all these characters.

Genetic diversity analysis based on Standardized Euclidean Square Distance for nineteen quantitative characters grouped thirty eight accessions into seven clusters. The clustering showed that there is no parallelism between the geographical distribution and clustering pattern. On the basis of qualitative characters cluster analysis with UPGMA (Unweighted Pair Group Method with

Arithmetic mean) method grouped the 38 okra accessions into three main clusters as distinguished by branching pattern, leaf and stem colour.

There was a total of twenty cross combinations of genotypes belonging to clusters with high inter cluster distance and superior mean performance based on the overall ranking in the clusters for the four attributes *viz.* fruit weight, marketable fruits per plant, days to marketable maturity and green fruit yield. AE-5, AE-10, AE-16, AE-18, AE-20 and AE-30 were identified as promising. The present investigation projected the importance of AE-16 and AE-20 as one of the parents for higher heterosis in F1 and potential transgrents in the subsequent generation. Both these accessions have considerably high green fruit yield per plant greater than the checks Salkeerthi and Arka Anamika. Similarly the accessions like AE-10, AE-18, AE-30 belonging to cluster I, V and IV were identified as superior in yield and AE-5 belonging to cluster VI as promising with highest fruit weight. If these genotypes are involved in crosses with Salkeerthi, the popular variety of KAU with excellent fruit characters will give potentially high yielding segregates with good market value.