

**GENETIC VARIABILITY, CORRELATION,
SELECTION INDICES AND PATH ANALYSIS
FOR FRUIT YIELD AND ITS CONTRIBUTING
CHARACTERS IN OKRA
[*Abelmoschus esculentus* (L.) Moench]**

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SEPTEMBER - 2021

Dedicated to
My
Beloved
Parents & Family
For their Dreams, Hopes & endless
Prayers...
and
My Respected Guide
for his faith & confidence in me...

Komal....

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Date: 01/09/2021

This is to certify that the thesis entitled “**GENETIC VARIABILITY, CORRELATION, SELECTION INDICES AND PATH ANALYSIS FOR FRUIT YIELD AND ITS CONTRIBUTING CHARACTERS IN OKRA [*Abelmoschus esculentus* (L.) Moench]**” submitted by **Miss. JADAV KOMAL JEEVANBHAI (Reg. No. 2010119038)** to the Junagadh Agricultural University, Junagadh in partial fulfillment of the requirements for award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in the subject of **GENETICS AND PLANT BREEDING** after recommendation by the external examiners were defended by the candidate before the following members of the examination committee. The performance of the candidate in the oral examination was satisfactory. We, therefore, forward with recommendation.

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Place: Junagadh

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(Jadav Komal J.)

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CHAPTER I

INTRODUCTION



Okra (*Abelmoschus esculentus* L.) is one of the most widely known and utilized species of the *malvaceae* family. An economically important vegetable crop grown in tropical and sub-tropical parts of the world. Okra originated in Ethiopia. Okra is known by many local names in different parts of the world. It is called lady's finger in England, gumbo in United States of America, guino-gombo in Spanish, guibeiro in Portuguese and bhindi in India. Okra plants are grown commercially in many countries such as an India, Japan, Turkey, Iran, Western Africa, Yugoslavia, Bangladesh, Afghanistan, Pakistan, Myanmar, Malaysia and Thailand. Okra is a multipurpose crop due to its various uses of the fresh leaves, buds, flowers, pods, stems and seeds. Okra immature fruits, which are consumed as vegetables, can be used in salads, soups and stews, fresh or dried, fried or boiled. It offers mucilaginous consistency after cooking. Okra mucilage has medicinal applications when used as a plasma replacement or blood volume expander. The mucilage of okra binds cholesterol and bile acid carrying toxins dumped into it by the liver. The immature pods are also used in making pickle. The entire plant is edible and is used to have several foods. Okra seeds from Greece are a potential source of oil, with concentrations varying from 20% to 40%, depending on the extraction method. The oil mainly consists of linoleic acid (up to 47.4%). Okra seed oil is a rich source of linoleic acid, a polyunsaturated fatty acid essential for human nutrition. Proteins play a particularly important role in human nutrition. The amino acid contents, proportions, and their digestibility by humans characterize a protein's biological value.

Immature okra fruit contain 3100 calorie energy, 90 mg calcium, 1.8 g protein and 1.0 mg iron (Aykroyd, 1941). The composition of okra pods per 100 g edible portion (81% of the product as purchased, ends trimmed) is: water 88.6 g, energy 144.00 kJ (36 kcal), protein 2.10 g, carbohydrate 8.20 g, fat 0.20 g, fibre 1.70 g, Ca 84.00 mg, P 90.00 mg, Fe 1.20 mg, β -carotene 185.00 μ g, riboflavin 0.08 mg, thiamin 0.04 mg, niacin 0.60 mg and ascorbic acid 47.00 mg. The composition of okra leaves per 100 g edible portion is: water 81.50 g, energy 235.00 kJ (56.00 kcal), protein 4.40 g, fat 0.60 g, carbohydrate 11.30 g, fiber 2.10 g, Ca 532.00 mg, P 70.00 mg, Fe 0.70

mg, ascorbic acid 59.00 mg, β -carotene 385.00 μ g, thiamin 0.25 mg, riboflavin 2.80 mg, niacin 0.20 mg (Gopalan *et al.*, 2007, Varmudy, 2011). Fresh okra pods are the most important vegetable source of viscous fiber, an important dietary component to lower cholesterol. Seven-days-old fresh okra pods have the highest concentration of nutrients. Okra contains high fiber, which “helps to stabilize blood sugar by regulating the rate at which sugar is absorbed from the intestinal tract”. The frequent usage of okra might help avoid kidney disease.

In India, the okra crop has been grown in 5.09 lakh hectares area having production of 60.95 lakh tonnes with productivity of 11.84 tonnes/ha (Anon., 2018). The okra growing states are Andhra Pradesh, Gujarat, Uttar Pradesh, Maharashtra, Haryana, Punjab, Tamil Nadu and Karnataka. In Gujarat, main okra growing districts are Surat, Tapi, Navsari, Vadodara, Bharuch, Banaskantha, Anand, Kheda and Mahesana. In Gujarat, it is grown an about 0.75 lakh hectares with production of 9.24 lakh tonnes and productivity 12.19 tonnes/ ha (Anon., 2019).

Okra is mainly propagated by seeds. It is an upright annual, herbaceous 3 to 8 feet tall plant with a hibiscus-like flower. It is a tropical direct sown vegetable with duration of 90-100 days. Its stem is semi woody and sometimes pigmented with a green or reddish tinges color. It is erect, variable in branching, with many short branches that are attached to thick semi woody stem. Leaves are cordate (heart-shaped), simple, usually palmately 3-7 lobed, hirsute, serrate and veined. Leaves are subtended by a pair of narrow stipules. The okra leaf is dark green in color and resembles a maple leaf. The flower is axillary and solitary having epicalyx upto 10, 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. The flowers are hermaphrodite and actinomorphic. Calyx generally non-lobed, tubular; corolla with 5 large yellow petals, purplish red pigmentation on one or both sides of claw; tubular staminal column united to the base of petals with numerous stamens, attached to the corolla base; ovary superior, stigma 5-10 lobed, velvety red/purplish; fruit 5-10 chambered, beaked capsule, with or without sutures/ridges; seed dark green, grey or dark brown, rounded.

A logical way to start any breeding programme is to assess the variation existing in the available materials. It is said that genetic variability is the “sine quanon” of any such programme. Selection is said to be effective in a population

having large heritable variability. The genetic variability and its components are the genetic fractions of observed variability that provides measures of transmissibility of the variation and response to selection. The knowledge of pattern of inheritance of various characters are important consideration while, determining the most approximate breeding procedures applicable to any particular crop. The breeder's choice of the material for any improvement work consequently depends on the amount of genetic variability present. The phenotype is often not true indicator of its genotype. The phenotypic variability is the result of the effect of environment and genotype interaction. Attempts have been made to determine the magnitude of heritable and non-heritable components and genetic parameters such as phenotypic and genotypic coefficient of variation, heritability and genetic advance as percentage of mean in some of the quantitative characters of okra.

These studies along with the association analysis will be more useful in the estimation of inter-relationship among the yield contributing components. It is essential to have detail information on the association among different yield components and their relative contribution to yield. Association analysis of quantitative attributes would help in choosing component characters that are positively correlated. In addition, an understanding of association between the component characters is essential to judge their rational importance. Path coefficient analysis is also very useful in formulating breeding strategy to develop elite genotypes through selection in advanced generations. Thus, the nature and magnitude of variability present in the gene pool for different characters and relationship with each other determine the success of genetic improvement of a character. Since the pattern of inheritance of quantitative characters is highly complex, therefore, the present investigation was undertaken to study the association among different components and their direct and indirect contribution to fruit yield in okra.

Availability of sufficient genetic variability is very important in a crop improvement programme. For successful breeding programme, amount of genetic variability present in the experiment material is a basic requirement. Therefore, it is essential for breeder to measure the variability with help of parameters like; genotypic coefficient of variation, phenotypic coefficient of variation and path coefficient analysis, which provide the information regarding the availability of genetic variability for different character in okra germplasm.

A wide range of variation in quantitative characters provides the basis for selection in plant breeding programme. The knowledge of association among the characters is useful to the breeder for improving the efficiency of selection. Correlation coefficient analysis measures the mutual relationship between plant characters and determines the component character on which selection can be made for genetic improvement of yield. A positive correlation between desirable characters is favourable to plant breeder because it helps in simultaneous improvement of both the character. A negative correlation, on the other hand, will hinder the simultaneous expression of both the character with high values. In such situations, some economic compromise has to be made.

Path analysis helps in partitioning the correlation into direct and indirect effects of various yield components on yield. Yield being a complex character, is the result of action and interaction of more than one yield contributing character which effect directly or indirectly on yield.

Breeder can practice selection using this information for the isolation of superior accession from available material. The selection indices provide selection criteria for efficient selection strategies among okra genotypes. Quantitative estimate of genetic divergence among biological populations helps in selection of diverse parents in further breeding programme. Keeping in view of above facts, the present study on “Genetic variability, correlation, selection indices and path analysis for fruit yield and its contributing characters in okra [*Abelmoschus esculentus* (L.) Moench]” with 75 genotypes is proposed with following objectives:

1. To study the genetic variability for fruit yield and its contributing characters
2. To know the genotypic and phenotypic correlations between fruit yield and its contributing characters
3. To find out the direct and indirect effects of different characters on fruit yield using path coefficient analysis
4. To determine the selection indices for fruit yield and its contributing characters

CHAPTER II

REVIEW OF LITERATURE

In the present investigation an attempt has been made to study “**Genetic variability, correlation, selection indices and path analysis for fruit yield and its contributing characters in okra [*Abelmoschus esculentus* (L.) Moench]**”. The available literature pertaining to the various aspects of the present investigation has been reviewed under the following heads:

2.1 Genetic variability

2.2 Correlation coefficient

2.3 Path analysis

2.4 Selection indices

2.1 Genetic variability

Knowledge on the nature and magnitude of genotypic and phenotypic variability present in any crop species plays a vital role in formulating successful breeding programme for evolving superior cultivars. Genetic variability analysis is helpful to know about the nature and extent of variability that can be attributed to different causes, sensitive nature of the crop to environmental influences, heritability of the characters and genetic advance that can be realized in practical breeding in evolving varieties to various environmental conditions. Genetic variability is essential in order to realize response to selection pressure. The success of a breeding programme for the genetic improvement of quantitative characters depends on the magnitude of genetic variability existing in the germplasm and the extent to which the desirable characters are heritable. The determination of genetic variability and partitioning it into heritable and non-heritable components using the genetic parameters viz., phenotypic and genotypic coefficients of variation (GCV and PCV), heritability and genetic advance is necessary to have an insight into genetic nature of yield and its components on which selection can be effectively carried out. Character like yield is complex in inheritance and is improved through its component traits. High yield can be achieved by selection of those yield contributing characters that have high heritability coupled with high genetic advance.

AdeOluwa and Kehinde (2011) evaluated the 35 okra accessions and reported that phenotypic variances were generally higher than their respective genotypic variances, thus revealing the role of environmental factors. High PCV and high GCV were observed for pod yield per plant and peduncle length, respectively. Very low heritability estimate was observed for number of ridges per fruit. Moderately high heritability estimate (78.99%) was observed for peduncle length; moderately high PCV and GCV 35.71% and 31.74%, respectively, but low genetic advance of 1.99%.

Adiger *et al.* (2011) studied the genetic variability among 163 okra genotypes observed that the values of PCV were higher than that of GCV values for all the ten characters indicating influence of environmental effects in the expression of these characters. 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.

Chaukhande *et al.* (2011a) studied the genetic variability among 75 genotypes indicated the presence of high variation for all the 17 characters studied. The highest GCV as well as PCV was observed for incidence of yellow vein mosaic virus. The maximum difference between GCV and PVC was noted for inter nodal length. Character plant height exhibited high heritability (broad sense) percentage. The highest genetic advance was recorded for yellow vein mosaic virus, while the lowest for fruit diameter.

Prashant kumar *et al.* (2011) reported that the based on GCV and PCV indicated considerable genetic variability among the genotypes for height at first fruiting node, number of nodes at first pod appearance, plant height, number of nodes per plant, number of fruit per plant and fruit yield per plant.

Senapati *et al.* (2011) reported that analysis of variance showed significant amount of genetic variability among the studied characters in okra. The largest variability was recorded in fruit yield followed by plant height. In general, phenotypic coefficients of variation (PCV) were greater than genotypic coefficients of variation (GCV) in all the quantitative traits due to environmental influence. High heritability coupled with high genetic advance was obtained in fruit yield and days to 50% flowering indicating that these characters might be heritable and less influenced by the environment.

Das *et al.* (2012) studied genetic variability parameters and recorded phenotypic co-efficient of variation (PCV) agreed closely with the genotypic co-efficient of variation (GCV) but the magnitude of PCV was higher than GCV for almost all the characters. High phenotypic and genotypic coefficient of variation for fruit yield per plant, numbers of fruits per plant and plant height at flowering and moderate GCV & PCV for fruit length while, low for days to first flowering, node at first flowering and numbers of ridges per fruit. High heritability along with high genetic advance was recorded for fruit yield per plant, number of fruits per plant, plant height and fruit weight while, high heritability along with low genetic advance was recorded for number of ridges per fruit, node at first flowering, days to first flowering and fruit diameter.

Goswami *et al.* (2012) found that high magnitude of PCV and GCV for the plant height and number of branches per plant while, moderate GCV and PCV for internodal length, number of fruits per plant and fruit length. High heritability coupled with high genetic advance was observed for the plant height, number of branches per plant, number of nodes per plant, internodal length. High heritability with moderate genetic advance was observed for fruit weight.

Nwangburuka *et al.* (2012) evaluated the 29 okra accessions and observed high genotypic coefficient of variability, such as plant height (26.2), fresh pod length (23.9), fresh pod width (23.9), mature pod length (28.6), branching per plant (29.3) and pod weight per plant (33.9) suggesting the effect of additive genes and reliability of selection based on phenotype of these traits for crop improvement.

Reddy *et al.* (2012) evaluated 100 genotypes of okra and observed high magnitude of genetic variability and high degree of transmission of majority of the growth, earliness and yield associated traits under study. High magnitude of genotypic coefficient of variation (>20.00%) for number of branches per plant, total number of fruits per plant, number of marketable fruits per plant, total yield per plant (g), marketable yield per plant (g) and yellow vein mosaic virus infestation (%) on plants indicated high degree of genetic variability offering great scope for selection of these characters.

Duggi *et al.* (2013a) studied the genetic variability among 31 okra genotypes for yield and yield attributing traits. The magnitude of PCV was higher than that of

GCV for all the traits. The PCV and GCV were very close for most of the characters, which indicated less environmental influence on the expression of the characters under study. High values of PCV with correspondingly high values of GCV were observed for the characters viz., number of primary branches and number of fruits per plant, which indicated the presence of substantial variability for these characters thus suggesting good scope for improvement through selection.

Verma (2014) estimated genetic variability in okra involving 30 genotypes. The estimates of mean sum of squares due to genotypes were highly significant for all the characters indicating the presence of genetic diversity in the existing material. The variation was highest for fruit yield per plant followed by fruit yield per hectare, plant height at 120 DAS, plant height at 90 DAS, plant height 60 DAS and fruiting span. High heritability coupled with high genetic advance as percentage of mean for traits like unit yield per plant and fruit yield per plot suggested that the preponderance of additive genes. It also indicated higher response for selection of high yielding genotypes as these characters are governed by additive gene actions.

Yonas *et al.* (2014) reported that analysis of variance showed significant differences ($p < 0.01$) among the accessions for all the quantitative characters measured. Estimates of PCV and GCV also indicated the presence of variability among the accessions for the majority of the characters. High heritability (96.76 and 96.50%) coupled with high genetic advance as percent of mean (106.32 and 97.25%) were recorded for internodes length and plant height, respectively.

Kandasamy (2015) estimated variability, heritability and genetic advance in 25 genotypes of okra. The 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 internodal 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 revealed the predominance of additive gene action on these characters.

Phani *et al.* (2015) estimated genetic variability in okra involving 30 genotypes and found the high heritability coupled with high genetic advance as per cent mean were observed for plant height, internodal length, number of nodes, first

fruiting node, number of pickings, fruit and shoot borer infestation on plants, yellow vein mosaic virus infestation on plants and fruit yield per plant. High heritability coupled with moderate genetic advance per cent mean values were observed for days to first flowering, fruit girth and average fruit weight.

Rajkumar and Sundaram (2015) computed 33 diverse genotypes of okra revealed the presence of high variability for primary branches at flowering, internodal length, leaf area index, mucilage content, seed number and 100-seed weight. The traits viz., days to flowering, plant height, primary branches at flowering, internodal length, relative water content, mucilage content, crude fibre content, pedicel length, fruit length, fruit girth, fruit weight, seed number and 100-seed weight were found to be highly heritable and hence, could be considered while selection. High heritability with high genetic gain observed for plant height, primary branches at flowering and internodal length indicated the predominance of additive genes, while high heritability with low genetic gain observed for days to flowering indicated the role of non-additive gene action.

Chandramouli *et al.* (2016) studied genetic variability, heritability and genetic advance in 30 okra genotypes for yield and yield attributing traits. Wide variability was recorded for fruit yield per plant (g), fruit yield per plot (kg) and YVMV infestation (%) indicating the existence of more variability for these traits among the genotypes under study as they have high PCV and high GCV. High heritability coupled with high GAM indicated the operation of additive gene action as in case of number of primary branches per plant, nodes on main stem, intermodal length, leaf area, number of fruits per plant, fruit girth, fruit yield per plant, fruit yield per plot and YVMV infestation (%). Hence, direct selection based on these traits in genetically diverse material could be effective for desired improvement. Moderate GAM with high or moderate heritability indicated the action of both additive and non-additive genes as in case of petiole length, fruit length and fruit weight. Hence, direct selection has limited scope for further improvement of these traits.

Khajuria *et al.* (2016) studied the genetic variability among 60 genotypes indicated the phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters indicating the less environment influences. The results showed variation in all genotypes and characters. Seed yield per plant and number of fruits per plant showed high GCV, heritability and genetic advance, which indicates that selection of these characters.

Kumar *et al.* (2016) studied the genetic variability, heritability and genetic advance in okra and reported that high magnitude of genotypic and phenotypic coefficient of variation was recorded for fruit yield per plant, number of fruits per branch, number of leaves per plant, while fruit diameter showed lowest genotypic and phenotypic coefficient of variation. The highest heritability (%) was noted in number of flower per plant followed by fruit yield per plant, number of leaves per plant, number of fruits per plant, fruit weight, number of fruit per branch and plant height where as the lowest heritability was observed in number of branches per plant, stem diameter and number of days taken to flower. The highest genetic advance was observed for number of fruits per plant followed by number of leaves per plant, number of flower per plant, plant height and number of days taken to flower, while lower genetic advance were recorded for fruit length, number of fruits per branch, fruit diameter, number of branches per plant and fruit yield per plant.

Sharma *et al.* (2016) computed genetic variability in 30 okra genotypes for yield and its attributing traits. The magnitude phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits. Both PCV and GCV were high for plant height (11.10% and 10.60%, respectively). Fruit weight exhibited low value of GCV (2.31%) and PCV (4.74%) and likely to show less response under selection.

Deepanshu and Abdul Shamad (2017) studied genetic variability, heritability in 30 okra genotypes and observed that 12/OKHYB-5 was found superior in term of pod yield per plant (g). The genotypic and phenotypic variances were found highest for pod yield per plant (g) 4056.04 and 4130.58 followed by number of seeds per fruit 30.69 and 31.17. High GCV and PCV were found for yield per plant 4130.58 and 25.74, respectively. Heritability in broad sense was noticed high for all the traits. Higher genetic advance was observed for pod yield per plant (g), number of seeds per fruit. High genetic advance (as percent of mean) was found in days to 50% germination of seed (38.20), number of branches per plant (35.49), fruit length (29.68), fresh weight of fruit (29.75), number of seeds per fruit (21.47), number of fruits per plant (21.14) and yield per plant (52.55), High heritability (bs) coupled with high genetic advance (% of mean) were observed for characters like; pod yield per plant (98 & 52.55), number of branches per plant (98.00 & 35.489), days to 50% germination of seed (96.00 & 38.203), fresh weight of fruit (98.00 & 29.53), fruit

length (99.00 & 29.680), number of seed per fruit (98.00 & 21.474), number of fruits per plant (94.00 & 21.137), respectively.

Hallur *et al.* (2017) estimated genetic variability in okra and observed that the analysis of variance was significant for all the studied characters. The GCV, heritability and genetic advance were higher for fruit weight, number of branches per plant, fruit yield per plant, number of fruits per plant and days to 50% flowering.

Kerure *et al.* (2017) reported that high GCV and PCV were observed for yield per plant, number of fruits per plant and number of seeds per fruit, whereas moderate GCV and PCV was observed for average fruit weight. High heritability coupled with high GAM were observed for almost all the characters studied, except days to 50% flowering and days to 80% maturity showed low heritability with low GAM. The yield per plant, plant height and number of seeds per fruit showed high genetic advance that helped in effective and reliable selection through these characters for crop improvement.

Sravanthi (2017) evaluated 21 accessions of okra for variability for 12 characters. Highly significant differences were observed among the accessions. High phenotypic and genotypic coefficient of variation were observed for per cent incidence of YVMV, yield per plant, fruit weight, and number of fruits per plant indicating the existence of wider genetic variability for these traits in the germplasm. High heritability accompanied with high genetic advance was noticed for yield per plant, fruit weight and number of fruits per plant suggesting that they can be improved through direct selection due to predominant additive variation.

Priyanka *et al.* (2018) studied the genetic variability analysis on 29 genotypes of okra observed high magnitude of genetic variability and high degree of transmission of majority of the growth, earliness and yield associated traits under study. High magnitude of genotypic coefficient of variation (>20%) for number of marketable fruits per plant, marketable yield per plant and yellow vein mosaic virus infestation indicated high degree of genetic variability offering great scope for selection of these characters. High heritability (>60%) coupled with high expected genetic advance (>20%) for number of marketable fruits per plant, marketable yield per plant and yellow vein mosaic virus infestation indicated the involvement of additive gene action and more chances of fixing by selection to improve such traits.

Amba Kumari *et al.* (2019) noticed high values of phenotypic and genotypic coefficients of variation were recorded for important traits including yield per plant, number of fruits per plant and primary branches per plant, respectively. High heritability were recorded yield per plant (96.00%) followed by ascorbic acid (75.00%), fruit width (73.00%) and number of nodes per plant (61.00%). Genetic advance as percent of mean ranged from 33.03 for yield per plant to 0.70 for days to 50% flowering. High genetic advance was recorded for yield per plant (91.70%).

Kumar *et al.* (2019) studied genetic variability analysis on 68 genotypes of okra (pooled data analysis) showed high magnitude of genetic variability for the traits viz., pod yield and plant height under study. High magnitude of genotypic coefficient of variation (>20%) for number of pods per plant and plant height indicated high degree of genetic variability offering great scope for selection of these characters. The genotypes under study showed moderate heritability (30-60%) showed the environmental influence. High heritability coupled with high genetic advance for the traits like plant height and pod yield per plant indicated the involvement of additive gene action and more chances of fixing by selection to improve such traits.

Rathva *et al.* (2019) reported on ten characters showing considerable variability. The phenotypic coefficient of variations (PCV) was found slightly higher than the genotypic coefficient of variations (GCV) for all characters studied, indicating that the apparent variation is not only genetic but also influenced by the growing environment in the expression of the traits. The moderate magnitude of PCV and GCV was observed for internodal length and number of fruit per plant. High heritability coupled with high genetic advance as per cent of mean was observed for internodal length and number of fruits per plant revealing the importance of additive gene action in the inheritance of these characters and suggested reliable okra improvement through selection of the traits.

Alam *et al.* (2020) computed genetic variability in 40 genotypes of okra in RCBD with three replications. High PCV and GCV were observed for number of primary branches and moderate PCV and GCV were observed for length of internode, number of nodes per plant, plant height, number of fruits per plant, fruit yield per plant and fruit yield. High GCV along with high heritability and GAM was observed for number of primary branches, plant height, number of fruits per plant, fruit yield per plant, number of nodes per plant, fruit yield, length of internode, days to first flower initiation, days to 50% flowering and days to first fruit set.

Lateef *et al.* (2020) studied genetic variability, heritability and genetic advance with respect to various quantitative traits. The experimental material consisted of ten diverse genotypes of okra and 45 F₁ crosses generated through 10 x 10 diallel mating design. Analysis of variance revealed significant differences among genotypes for all the traits studied. The maximum range and the highest phenotypic and genotypic coefficients of variability were observed for fruit yield per plot. In general, the phenotypic coefficients of variation were slight higher than genotypic coefficients of variation, which indicated the minor role of environment in the expression of traits under observation. The estimates of heritability in broad sense were high for all the characters. The present investigation indicated a great scope in the improvement of these traits as these characters in general possessed high estimates of heritability coupled with high genetic advancement except for days to first flower, days to first fruit set and days to first fruit harvest, number (high heritability but moderate genetic gain) indicating the preponderance of additive gene action for control of these traits.

Rana *et al.* (2020) assessed the genetic variability for yield and yield contributing characters in 17 genotypes of okra. For all the characters, PCV value was higher than the GCV value with narrow difference indicating little influence of environment on the expression of characters. Among all the traits studied, moderate PCV and GCV were exhibited by internodal length (18.51% -17.27%), leaf area (11.83% - 11.82%), plant height at 45 and 90 DAS (12.03% -11.25% and 10.36% -10.26%, respectively). High magnitude of heritability coupled with high genetic advance was exhibited in characters viz., internodal length (87.07% - 33.06%), average fruit weight (91.56%- 34.28%) and fruit yield per plant (99.91%- 30.09%) indicating influence of additive gene action and suggesting that selection will be more effective.

Walling *et al.* (2020) evaluated 28 genotypes of okra and revealed that the highest phenotypic and genotypic coefficient of variation was observed in cumulative leaf area, yield per plant and protein content indicating the existence of wide range of genetic variability in the germplasm for these traits. High heritability coupled with high genetic advance as percentage of mean was observed for traits like plant height, size of leaf, number of leaves per plant and yield per plant which suggested that they can be improved through direct selection.

2.2 Correlation coefficient analysis

The knowledge of association among the characters is useful to the breeder for improving the efficiency of selection. Correlation coefficient analysis measures the mutual relationship between plant characters and determines the component character on which selection can be made for genetic improvement of yield. Investigation regarding the presence of component and nature of association among themselves is essential and pre-requisite for improvement in yield. Coefficient of correlation provides a clear picture of the extent of association between a pair of traits and indicates whether simultaneous improvement of the correlated traits may be possible or not. The knowledge of genetic association between yield and its component characters help in improving the efficiency of selection for yield by making proper choice and balancing one component with another. The magnitude of genotypic correlation was higher than the phenotypic correlation for all the traits that indicated inherent association between various characters. The review relating to this aspect has reviewed as under.

Balakrishnan and Sreenivasan (2010) studied correlation analysis in 15 diverse genotypes of okra for fruit yield, shoot and fruit borer infestation and its component traits. The study noticed that fruit yield was positively associated with number of fruits, number of internodes, fruit weight and fruit length. Shoot and fruit borer infestation recorded negative association with plant height, flowering period, fruit number, fruit yield and internodal length. Hence, selection of genotypes with short growth habit, short flowering period and short fruit length will help to minimize the shoot and fruit borer infestation.

Gangashetty *et al.* (2010) reported that positive and significant phenotypic association of plant height, number of branches per plant, fruit weight, fruit length and fruit yield per plant in okra. However, phenotypic correlation between fruit yield per plant and days to first flowering, internodal length and fruit diameter was significant negative indicating that this character shall have least significance for improving fruit yield in okra.

Adiger *et al.* (2011) found that the fruit yield had significantly positive correlation 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 levels, indicating mutual association of these traits.

Chaukhande *et al.* (2011b) carried out correlation analysis in 75 diverse okra genotypes and revealed that yield per plant exhibited positive and significant correlation with plant height, number of flowering nodes on main stem, number of fruits per plant and average weight of fruit.

Senapati *et al.* (2011) studied correlation analysis and observed that the genotypic estimates were higher than the phenotypic ones for the most of the characters indicating strong inherited association between the characters. Fruit yield showed positive and significant association with number of nodes per plant, number of fruits per plant and fruit length in okra.

Duggi *et al.* (2013b) showed strong genotypic correlation with number of fruits per plant, fruit weight and fruit girth. Significant negative correlation of yield with days to 50% flowering was noticed. Plant height and crop duration showed positive significant genotypic correlation among themselves. It is noteworthy that the present study suggested highly significant negative correlations between number of fruits per plant and fruit weight both at genotypic and phenotypic levels, whereas number of fruits per plant had positive genotypic correlation with fruit girth. The number of fruits per plant and fruit girth besides being positively associated with yield, showed positive genotypic correlation between them. These two characters had high heritability too. Hence, it would be worthwhile to give due consideration to these characters in selection programs aimed at yield improvement in okra. Highly significant positive correlation between per cent fruit infestation and larval count of shoot and fruit borer in 25 fruits suggested that fruit damage criteria may be employed for the evaluation of shoot and fruit borer resistance in okra.

Koundinya and Dhankhar (2013) reported that seed yield per plant had significant positive association with plant height, fruits per plant, fruit yield per plant and seeds per fruit, whereas it exhibited significant negative association with days to 50% flowering. Fruit yield per plant was having significant positive association with plant height, fruits per plant and fruit weight while it was having significant negative association with days to 50% flowering.

Balai *et al.* (2014) evaluated 27 genotypes of okra for fruit yield and its component traits. Yield per plant had highly significant positive genotypic and phenotypic correlations with plant height (0.49**, 0.47**), length of pod (0.78**, 0.78**), number of fruits per plant (0.78**, 0.78**), fruit weight (0.78**, 0.78**), fruit length (0.78**, 0.78**), fruit girth (0.78**, 0.78**), fruit yield (0.78**, 0.78**), and days to 50% flowering (0.78**, 0.78**).

0.75**), average weight of edible pod (0.93**, 0.91**) and number of seeds per pod (0.59**, 0.57**), respectively. Non-significant correlation was observed for yield component traits like; number of pods per plant and weight of 100-seeds with yield per plant. Correlation studies indicated that close relationship between genotypic and phenotypic correlation coefficients and magnitude of genotypic correlation were higher than their corresponding phenotypic correlation for most of the characters.

Ahamed *et al.* (2015) found that fruit yield had significantly positive correlations for plant height, number of fruits per plant, number of leaves per plant and yield per plant. Significant negative correlations were observed with number of branches per plant and days to 50% flowering.

Saryam *et al.* (2015) carried out correlation analysis in 60 okra genotypes and revealed that yield per plant had highly significant positive phenotypic correlation with viz., number of fruits per plant (0.803), fruit diameter (0.376), fruit length (0.349), number of seeds per fruit (0.316), days to maturity (0.301), fruit weight (0.274) leaf blade width (0.219), 100-seed weight (0.219), flower diameter (0.154), fruiting span (0.152), petiole length (0.151) and stem diameter (0.150). Highly negative non-significant association was observed with incidence of YVMV (-0.389), days to 50 per cent flowering (-0.319) and node at first flower appears (-0.307), this correlation study indicated that close interrelationship between genotypic and phenotypic correlation co-efficient and magnitude of genotypic correlation were higher than their corresponding phenotypic correlation for most of the traits.

Aminu *et al.* (2016) studied that the phenotypic correlation coefficients of the okra traits and showed a highly significant and positive correlations of the number of pods per plant with plant height ($r = 0.61$), days to 50% flowering ($r = 0.72$), fresh weight per pod ($r = 0.44$) and pod length (0.43).

Kumar and Reddy (2016) studied correlation coefficient analysis revealed that total number of fruits per plant and total yield per plant had positively significant association with marketable pod yield per plant. The genotypic correlation coefficient of plant height, number of branches per plant, intermodal length, fruit length, fruit weight and number of marketable fruits per plant with marketable yield per plant was significantly positive. Total number of fruits per plant and total yield per plant had strong influence on marketable pod yield per plant and are the main determiners of marketable pod yield per plant.

Pachiyappan and Saravannan (2016) studied correlation analysis among various characters in okra. They observed that fruit yield per plant was positive and significantly correlated with fruit girth, fruit length, number of fruiting nodes, number of branches per plant and plant height.

Deepanshu and Abdul Shamad (2017) studied correlation in 30 okra genotypes and observed that number of branches per plant, number of leaves per plant, fruit length, fruit girth, fresh weight of fruit, number of seeds per fruit, number of fruits per plant and T.S.S. of fruit showed positive correlation at both genotypic and phenotypic levels proved their genetic worth for selection and improvement of okra.

Dwivedi and Sharma (2017) revealed significant and positive correlations of plant height, fruiting span, number of branches per plant, length of internode, yield per plant, number of leaves per plant, number of fruits per plant. However, significant and negative association was observed with days to first picking, days to 50% flowering and number of seeds per fruit.

Kerure *et al.* (2017) reported that fruit yield per plant showed positive association with stem girth, number of branches per plant, plant height, first fruit producing node, fruit length, fruit diameter, average fruit weight, number of fruits per plant, number of seeds per fruit and 100-seed weight, while negative association with days to 50% flowering, number of locules per fruit and days to 80% maturity.

Pithiya *et al.* (2017) studied correlation analysis in 28 germplasm lines of okra and reported that number of fruits per plant had positive and significant correlation with yield and plant height. Fruit length exhibited significant and positive correlation at both genotypic and phenotypic levels with plant height and seed yield per plant. Fruit diameter exhibited significant and negative correlation with number of fruits per plant, days to 50% flowering and number of branches per plant at genotypic level. Days to 50% flowering exhibited significant and negative correlation both at genotypic and phenotypic levels with fruit length, number of fruits per plant and seed yield per plant.

Thulasiram *et al.* (2017) studied the correlation analysis in 30 okra genotypes. The genotypic and phenotypic correlations indicated that yield per plant was significantly associated with plant height, number of leaves per plant, number of lobes per leaves, number of primary branches per plant, number of nodes per plant and number of fruits per plant.

Yadav *et al.* (2017) observed that number of flowers per plant and number of fruits per plant showed the highest positive and very high significant correlation with yield per hectare followed by nodes on the main stem and plant height. Plant height and nodes on the main stem showed positive and significant correlation with yield per hectare. Stem diameter showed negative and significant correlation with first branching node and plant height with number of branches per plant and days taken to first flowering.

Shuirkar *et al.* (2018) studied the correlation coefficient analysis in okra and revealed that plant height was positive and significant correlation with length of internode (0.2871), days to 50% flowering (0.1882) and fresh fruit weight (0.3387). A high significant and negative association of this trait was observed with length of internode (-0.1673), first fruiting node (-0.3138) and days to first fruit length (-0.1665).

Binepal *et al.* (2019) computed correlation in 18 genotypes of okra in RCBD with three replications. The highest positive and significant correlation coefficient 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 had been noted with number of fruits per plant indicating that these characters are the primary yield determinant in okra.

Rambabu *et al.* (2019) carried out correlation analysis in 20 okra genotypes and revealed that plant height, number of branches per plant, number of fruits per plant, inter nodal length, last harvest, fruit length, fruit girth, fruit weight, number of fruits per plant, number of seeds per fruit, 100-seed weight, number of pickings and iodine content were found to possess significant and positive correlation with fruit yield per plant. It was observed that with increase in plant height and less intermodal length, there was corresponding increases of fruit yield per hectare.

Raval *et al.* (2019) studied correlation coefficient analysis using parents (female VRO - 6 and male AOL - 09 - 02), their F₁ and F₂ generations. Observations were recorded on 13 yield and its contributing characters. Fruit yield per plant exhibited positive and highly significant correlations with number of fruits per plants, plant height at final harvest, fruit weight, number of branches per plants, fruit girth, number of seeds per fruits, internodal length and 100-seed weight.

Alam *et al.* (2020) computed correlation in 40 genotypes of okra in RCBD with three replications. Fruit yield showed positive and significant correlations with fruit yield per plant, number of fruits per plant, plant height, length of internode, fruit length, number of primary branches and duration of crop at both phenotypic and genotypic correlation coefficients.

Ashraf *et al.* (2020) reported that fruits per plant and fruit weight of different genotypes had a high degree of significant positive association with fruit yield and a high positive direct effect indicated that these characters had a major contribution towards the fruit yield of the genotypes. The characters days to first flowering and days to first fruit harvest showed a significant positive correlation with picking duration both genotypic and phenotypic levels. The Picking duration showed a highly significant positive genotypic correlation with fruit diameter and fruit length. At final harvest plant height showed a highly significant positive genotypic correlation with fruit length and fruit weight at the genotypic level. The fruit length showed a highly significant positive genotypic correlation with fruit weight and fruit diameter and genotypic level. The fruits per plant showed a highly significant positive genotypic and phenotypic correlation with fruit yield. A significant positive genotypic correlation with fruit yield was shown by fruit weight.

Lateef *et al.* (2020) studied correlation with respect to various quantitative traits. The experimental material consisted of ten diverse genotypes of okra and forty five F₁ crosses generated through 10 x 10 diallel mating design. Number of fruits per plant, number of nodes per plant, average fruit weight and average fruit length showed positive correlations both at genotypic and phenotypic levels.

Rana *et al.* (2020) studied the correlation analysis for yield and yield contributing characters in 17 genotypes of okra. Correlation studies observed that fruit yield per plant had significant and positive correlation with average fruit weight followed by plant height at 45 DAS, number of leaves at 45 DAS, number of fruits per plant and number of primary branches at 45 DAS.

Ranganayaki *et al.* (2020) computed correlation analysis of 10 genotypes okra for yield and yield attributing traits. Observations were recorded on eleven yield and yield attributing characters. Fruit yield per plant had positive and significant correlations with fruit weight and number of fruits per plants.

Walling *et al.* (2020) evaluated 28 genotypes of okra under foothill conditions of Nagaland under School of Agricultural Sciences and Rural Development, Nagaland University in Randomized Block Design with three replications. The correlation studies indicated that yield per plant showed highly significant positive genotypic correlation coefficients with leaf area index, size of leaf, number of leaves, number of fruits per plant, weight of fruit, fruit length, number of ridges per fruit, number of seeds per fruit and fruit diameter signifying the importance of these traits in selection for yield and are identified as yield attributing characters on which selection can be relied upon for the genetic improvement of yield.

2.3 Path Coefficient analysis

Path coefficient analysis is helpful in partitioning the observed correlation coefficient into direct and indirect effects and their effective use in selection programme. The method of path coefficient analysis was originally developed by Wright (1921) and the technique was first used by Dewey and Lu (1959). The brief review pertaining to path coefficient analysis in okra is presented as under:

Adiger *et al.* (2011) studied path coefficient analysis and reported that fruit weight had the maximum direct contribution (0.884) towards fruit yield followed by number of fruits per plant (0.852), plant height (0.024) and number of branches per plant (0.020). Days to 50% flowering exhibited highest negative direct effect (- 0.013) followed by test weight (-0.009) and fruit diameter (-0.003).

Chaukhande *et al.* (2011b) computed path analysis of 75 diverse okra genotypes. The results indicated that number of fruits per plant exhibited maximum direct effect on yield per plant followed by average weight of fruit and internodal length. Thus, all the characters must be taken into consideration while selecting the genotypes for future breeding programme.

Senapati *et al.* (2011) studied path coefficient analysis and revealed that the number of fruits per plant, fruit girth and fruit length exhibited maximum direct effects on fruit yield at phenotypic level. On the basis of above findings, it was concluded that the number of fruits per plant, fruit girth and fruit length would be considered for improvement of fruit yield of okra hybrid.

Gangashetti *et al.* (2013) found in path analysis depicted high direct effect on number of fruits per plant, fruit weight, plant height and number of branches per plant with fruit yield per plant. However, days to 50 per cent flowering exhibited highest negative direct effect followed by fruit diameter. To release importance of fruit yield, direct selection can be practiced for these characters.

Balai *et al.* (2014) studied path coefficient analysis and revealed that average weight of edible pod had highest positive direct effect followed by number of pods per plant and number of leaves per plant on yield per plant.

Nirosha *et al.* (2014) studied path analysis in 49 genotypes of okra. Path coefficient analysis reported that number of fruits per plant had the maximum direct contribution towards total yield followed by fruit weight, days to 50 per cent flowering, plant height and number of branches per plant. However, days to first flowering exhibited the highest negative direct effect followed by internodal length and fruit length.

Ahamed *et al.* (2015) revealed that path coefficient analysis was done to determine direct and indirect effects of traits on fruit yield. Direct significant positive and negative effect of number of fruits per plant (-0.091), 100-seed weight (0.174), number of seeds per plant (-0.213) and average fruit yield (-0.310) towards yield.

Saryam *et al.* (2015) carried out path analysis in 60 okra genotypes. Phenotypic path coefficient analysis revealed that traits viz., number of fruits per plant (0.733) followed by number of seeds per fruit (0.165), number of branches per plant (0.147), fruit diameter (0.133), fruit weight (0.097), days to maturity (0.058), fruiting span (0.056), 100-seed weight (0.055), stem diameter (0.027) and plant height (0.023) have positive and high direct effects with fruit yield per plant.

Sharma and Prasad (2015) studied path co-efficient for growth and fruit characteristics in 57 okra genotypes. Number of fruits per plant and fruit weight contributed the maximum direct positive effect to fruit yield per plot, whereas number of branches per plant and days to first harvest showed highest negative direct effect on yield components. Plant height, however, showed highest positive indirect effect via number of fruits per plant and negative indirect effect via fruit weight. Number of branches showed positive indirect effect via number of fruits per plant and plant height and negative indirect effect via fruit weight.

Aminu *et al.* (2016) estimated path coefficient analysis in okra and they showed that the number of pods per plant exhibited positive and direct influence on the pod yield across the studied years. Indirect influence of other yield components through this character also contributed mainly towards pod yield. Therefore, days to 50% flowering, plant height, pod length, number of pods per plant, pod diameter, number of primary branches per plant, and fresh weight per pod could be taken into consideration for the selection and development of high pod yielding varieties in okra.

Kumar and Reddy (2016) studied that path coefficient analyses revealed that total number of fruits per plant and total yield per plant had positively high direct effect on marketable pod yield per plant and are regarded as the main determinants of marketable pod yield per plant and direct selection through these traits will be effective.

Sood *et al.* (2016) revealed that fruits per plant had the maximum positive direct contribution towards fruit yield per plant followed by average fruit weight and nodes per plant.

Dwivedi and Sharma (2017) found in path coefficient analysis of fruit yield per plant observed that plant height, diameter of fruit, number of branches per plant at 90 DAS, number of seeds per fruit, days taken to 50% flowering, length of internode and number of flowering nodes on main stem played an important role in determining the fruit yield per plant.

Hallur *et al.* (2017) found in path analysis that fruit weight had the maximum direct contribution towards fruit yield followed by number of fruits per plant. The top priority should be given to selection based on number of fruits per plant and fruit weight for yield improvement.

Pithiya *et al.* (2017) studied path coefficient analysis in 28 germplasm lines of okra. The path coefficient analysis indicated that the number of fruits per plant, plant height, fruit length and number of branches showed direct positive effect towards yield indicating their importance as reliable selection criteria for improvement of yield in okra.

Thulasiram *et al.* (2017) found in the path analysis that based on positive direct effects of different yield components on yield, it would be rewarding to give emphases on the number of primary branches per plant, number of nodes per plant,

number of leaves per plant, leaf area, diameter of fruit and node at which fruit appears, number of lobes per leaves, plant height, internodal length, number of fruits per plant and weight of fruit, however for positive indirect effect number of nodes per plant, plant height, node at which first fruit appears, length of fruit, weight of fruit, number of fruits per plant.

Yadav *et al.* (2017) performed path coefficient analysis on various yield contributing characters and revealed that fruits per plant, fruit length, number of seeds per fruit, number of branches per plant, plant height, fruit weight and number of flowers per plant showed direct positive effect towards yield.

Soni *et al.* (2018) performed path coefficient analysis in okra involving 24 genotypes and reported 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 are the most important characters contributing towards fruit yield. Direct selection of fruit yield per plant, days to 50% flowering, days to first flowering, fruit length and days to first picking should be avoided instead of direct selection.

Binepal *et al.* (2019) computed path analysis in 18 genotypes of okra in RCBD with three replications. Path coefficient analysis revealed that number of fruits per plant had highest positive direct effect followed by fruit weight, number of nodes to first flowering, number of branches per plant at 90 DAS (days after sowing), length of internodes, number of leaves per plant at 90 DAS, plant height at 90 DAS and fruiting span are the most important character contributing towards fruit yield and hence purposeful and balance selection based on these character would be rewarding improvement in okra. Direct selection of fruit yield per plant, days to 50% flowering, days to first flowering, fruit length and days to first picking should be avoided instead of direct selection.

Kumar *et al.* (2019) reported that 68 okra accessions were used for the evaluation of direct and indirect effects of pod yield and yield-related traits in okra. The maximum direct positive correlation on pod yield per plant showed by number of fruits per plant (0.108), plant height (0.084), fruit width (0.084), number of branches per plant (0.059) and number of nodes per plant (0.029) at phenotypic level. The

characters like; plant height, number of fruits per plant and number of branches per plant showed that they are the most important pod yield determinants, because of their high direct and indirect effects via many other yield improving characters. The study indicated that these characters can be used as key traits for improving the pod yield of okra.

Rambabu *et al.* (2019) reported that 20 okra genotypes were studied for evaluation of path coefficient analysis of fruits yield and yield attributes in okra. Path coefficient analysis of different yield and yield contributing traits on fruit yield per plant revealed with plant height, number of branches per plant inter nodal length, days to first flowering, days to 50% flowering, days to first harvest, days to last harvest, fruit length, fruit weight, number of fruits per plant, number of seeds per fruit, 100-seed weight, crude fiber content and iron content showed positive direct effect on fruit yield, these characters played a major role in recombination breeding and suggested that direct selection based on these traits will be rewarded for crop improvement of okra.

Raval *et al.* (2019) studied path analysis using parents (female VRO - 6 and male AOL - 09 - 02), their F₁ and F₂ generations. They revealed that number of fruits per plants, fruit weight, days to first picking, internodal length, 100-seed weight and fruit length recorded positive direct effect on fruit yield per plant.

Alam *et al.* (2020) reported that path coefficient analysis indicated high positive direct effect for fruit yield per plant, plant height, days to first flower initiation, number of primary branches and days to first fruit picking and high but negative direct effect exhibited by length of internode, number of nodes per plant, number of fruits per plant, fruit length, days to 50% flowering, days to second fruit picking, duration of crop and days to first fruit set on fruit yield.

Ashraf *et al.* (2020) reported that fruits per plant and fruit weight of different genotypes had a high positive direct effect indicated that these characters had a major contribution towards the fruit yield of the genotypes. The fruits per plant (0.979) and fruit weight (0.554) also showed a high positive direct effect on fruit yield.

Lateef *et al.* (2020) reported that path coefficient analysis made it apparent that the highest direct positive effect on fruit yield was recorded by number of fruits per plant followed by number of nodes per plant and average fruit weight, therefore being the most important characters contributing towards fruit yield.

Rana *et al.* (2020) studied path analysis for yield and yield contributing characters in 17 genotypes of okra. Phenotypic path coefficient analysis showed positive and direct effect of average fruit weight, number of fruits per plant, number of leaves per plant at 45 and 90 DAS, fruit length, plant height at 45 DAS and 90 DAS, internodal length, days to 50% flowering, leaf area on fruit yield per plant and therefore, selection of these traits would be beneficial for improvement in okra.

Ranganayaki *et al.* (2020) computed path coefficient analysis of 10 genotypes okra for yield and yield attributing traits. Observations were recorded on eleven yield and yield attributing characters. Path coefficient analysis revealed that the traits days to first flowering, number of fruits per plants, fruit length, number of ridges per pod, fruit weight have positive direct effect on fruit yield per plant.

2.4 Selection indices

Yield is a complex character influenced by number of factors. Direct selection on the basis of yield may not be effective because many component traits affect it. To make an effective selection for higher yield, it is necessary to determine the relative efficiency of selection through discriminant function technique over straight selection. This discriminant function technique over suitable selection indices was developed by Fisher (1936). The literature related to the selection indices in different crops has been reviewed below:

Singh and Singh (1978) studied 30 strains of okra and constructed the selection indices and reported that out of nine quantitative characters studied, fruit yield per plant + fruits per plant + plant height was the best selection index, resulted in 10% increase over selection based on yield alone.

Al-Rawi *et al.* (1984) studied relative efficiencies of several selection indices for predicting yield performance in ten F₂ populations of five parental diallel cross in upland cotton. Reports of this study had favoured the yield, bolls per plant and seeds per boll as the best selection index in combination.

Lal (1986) reported selection indices by applying discriminant function technique in forty one okra genotypes. The maximum genetic advance for yield was obtained through selection considering the combination of three characters viz., primary branches, 100-seed weight and nodes on main stem. The estimate of genetic advance for seed yield obtained through index construction was 58.72% more than that obtained through straight selection.

Monpara and Chhatrola (2010) studied 68 advanced breeding lines of okra along with their 7 parents and check varieties were evaluated for 12 characters. Genetic differences were significant for all the traits. Discriminant function analysis based on six characters namely; fruit yield per plant, nodes per plant, plant height, internodal length, primary branches and ten fruit weight indicated that selection efficiency of the function was improved by increasing number of characters in the index. The index involving all the six traits recorded the highest genetic gain and selection efficiency. However, the index with three parameters, *i.e.* fruit yield per plant + plant height + ten fruit weight was comparable and practically possible to use for selecting suitable plant types.

Kachhadia *et al.* (2014) studied 63 selection indices involving seed yield and five yield components *viz.*, number of primary branches per plant, 100-seed weight, biological yield per plant, harvest index and days to maturity were constructed using the discriminant function technique. Among the single character index, biological yield per plant exhibited higher genetic advance and relative efficiency over straight selection for seed yield. The index based on five characters *viz.*, seed yield per plant, 100-seed weight, biological yield per plant, harvest index and days to maturity recorded the highest genetic advance as well as relative efficiency and selection efficiency. These characters could be advantageously exploited in the soybean breeding programmes.

Gupta *et al.* (2015) evaluated 60 diverse genotypes of Virginia groundnut in a randomized block design with three replications to study of selection indices under rainfed conditions during *kharif* 2013. The 63 selection indices involving pod yield per plant (X1) and five yield components *viz.*, 100-kernel weight (X2) shelling out-turn (X3), biological yield per plant (X4), harvest index (X5) and kernel yield per plant (X6) were constructed using the discriminant function technique. Discriminant function analysis indicated that selection efficiency of the function was improved by increasing number of characters in the index. Among the single character index, 100-kernel weight exhibited higher genetic advance and relative efficiency over straight selection for pod yield per plant. The index based on four characters *viz.*, pod yield per plant, 100-kernel weight, shelling out-turn and kernel yield per plant recorded the highest genetic advance as well as relative efficiency and selection efficiency. These characters could be advantageously exploited in the groundnut breeding programmes.

Sana *et al.* (2017) used the discriminant function technique to construct selection indices in F_2 populations of mungbean. The 31 selection indices involving seed yield per plant and its four components were constructed using discriminant function technique. In general, the more the number of characters included in a selection index, the better was its performance. The index based on four characters viz., seed yield per plant, number of pods per plant, number of seeds per pod and plant height had highest genetic advance and relative efficiency 61.701g and 701.134%, respectively followed by an index based on three characters viz., seed yield per plant, number of pods per plant and plant height, which possessed genetic gain and relative efficiency of 16.59g and 696.474%, respectively. The use of both these indices is advocated for selecting high yielding genotypes of mungbean.

Leite *et al.* (2018) studied the selection of superior genotypes of soybean is a complex process, thus exploratory multivariate techniques can be applied to select genotypes analyzing the agronomic traits altogether, increasing the chance of success of a breeding program. The experiment was conducted in an increased block experimental being evaluated 227 genotypes of F_5 generation, which 85 of those were detected to be glyphosate-resistant by PCR. The following traits were evaluated; number of days to maturity, plant height at maturity, lodging, number of branches per plant, number of pods per plant, hundred seeds weight and seed yield. The principal components analysis resulted in the selection of 16 genotypes with higher seed yield.

Sisodia and Ramgiry (2018) computed selection indices on the basis of linear combination of 40 soybean germplasm based on nodulation, yield and quality traits during 2007-08 and 2008-09 under rainfed condition. The range for selection indices was from 6.34 to 19.43, 3.15 to 15.18 and 3.08 to 17.68 during first, second year and in pooled analysis respectively. The results revealed that gene stock TG $\times$ 1025-2F, BR35, AGS 153B, BP1159, BR-15-126-3-13 and TG $\times$ 802-IIIE exhibited high index value for nodulation, yield and quality traits. An overall observation of selection criteria (both varietal indices and *per se* performance basis) TG $\times$ 1025F recorded the highest estimate value followed by AGS 153B, TG $\times$ 802-IIIE and BP1159. Thus, this gene stock is valuable source for new variety released as well as selecting diverse parents for use in hybridization programme.

Reddy and Babaryia (2020) used discriminate-function technique to construct selection indices in 48 genotypes of bread wheat. The 63 selection indices involving

grain yield per plant and its five components were constructed using the discriminant function technique. The efficiency of selection increased with the inclusion of more characters in the selection index. The index based on four characters viz., grain yield per plant, the number of grains per main spike, grain weight per main spike and biological yield per plant recorded the highest genetic gain and relative efficiency. The use of these indices is advocated for selecting high yielding genotypes of bread wheat.

CHAPTER III

MATERIALS AND METHODS

The present investigation was conducted to assess the genetic variability, correlation, selection indices and path analysis and selection indices in okra [*Abelmoschus esculentus* (L) Moench. The study was carried out during *kharif* 2020 at the Vegetable Research Station, Junagadh Agricultural University, Junagadh. Geographically Junagadh is situated at 21.5°N latitude and 70.5°E longitude with an elevation of 82.92 meters above the mean sea level. The soil of experimental site is medium black with pH 7.8. The climate of the area represents semi-arid and tropical. The weather during the growing season was favourable for normal growth and development of crop. The details of weather parameters recorded for the year of 2020 during which the experiment was conducted is presented in Appendix-I. The details of materials used and methods adopted in present investigation are described under following heads.

3.1 EXPERIMENTAL MATERIALS

The experimental material consisted of 75 diverse genotypes of okra representing different geographic origin (Table 3.1). The Experimental materials of these genotypes were obtained from the Vegetable Research Station, Junagadh Agricultural University, Junagadh. The list of genotypes used in the present investigation and their source are mentioned in Table 3.1.

3.2 EXPERIMENTAL DETAILS

Seventy five genotypes of okra were sown in a Randomized Block Design with two replications during *kharif* 2020 at Vegetable Research Station, Junagadh Agricultural University, Junagadh. Plot size was 1.20 m × 2.40 m length with spacing of 60 cm × 30 cm. The genotypes were randomly allotted to the plots in each replication. The recommended agronomical practices along with necessary plant protection measures were followed for the successful raising of the crop. The observations were recorded on five randomly selected plants from sixteen plants in each genotype from each replication.

Table 3.1 List of genotypes and its sources

Sr. No.	Genotypes	Source
1	2	3
1	GO-6	VRS, J. A. U., Junagadh
2	JOL-09-05	VRS, J. A. U., Junagadh
3	HRB-55	HAU, Hariyana
4	GO-2	VRS, J. A. U., Junagadh
5	AOL-09-02	MVRS, , Anand
6	AOL-08-05	MVRS, , Anand
7	JOL-14-10	VRS, J. A. U., Junagadh
8	JDNOL-11-12	S. D. A. U, Jagudan
9	JOL-13-05	VRS, J. A. U., Junagadh
10	PUSA SAWANI	IARI, Pusa, New Delhi
11	AOL-15-19	MVRS, Anand
12	AOL-18-06	MVRS, A. A. U, Anand
13	AOL-13-144	MVRS, A. A. U, Anand
14	NOL-17-05	N. A. U, Navsari
15	AOL-16-01	MVRS, A. A. U, Anand
16	2019/OKYVRES-11	IIVR, Varanasi
17	2019/OKYVRES-2	IIVR, Varanasi
18	2018/OKYVRES-1	IIVR, Varanasi
19	2019/OKYVRES-10	IIVR, Varanasi
20	2017/OKYVRES-10	IIVR, Varanasi
21	2019/OKYVRES-3	IIVR, Varanasi
22	2017/OKYVRES-2	IIVR, Varanasi
23	2019/OKYVRES-12	IIVR, Varanasi
24	2019/OKYVRES-8	IIVR, Varanasi
25	2018/OKYVRES-6	IIVR, Varanasi
26	2019/OKYVRES-6	IIVR, Varanasi
27	2017/OKYVRES-4	IIVR, Varanasi
28	2019/OKYVRES-1	IIVR, Varanasi
29	2018/OKYVRES-7	IIVR, Varanasi
30	2018/OKYVRES-5	IIVR, Varanasi
31	2018/OKYVRES-8	IIVR, Varanasi
32	NBPGR-1	NBPGR, New Delhi
33	NBPGR-2	NBPGR, New Delhi
34	NBPGR-3	NBPGR, New Delhi
35	NBPGR-4	NBPGR, New Delhi
36	NBPGR-5	NBPGR, New Delhi
37	NBPGR-6	NBPGR, New Delhi

(Contd.)

Table 3.1 (Contd.)

1	2	3
38	NBPGR-7	NBPGR, New Delhi
39	NBPGR-8	NBPGR, New Delhi
40	NBPGR-9	NBPGR, New Delhi
41	NBPGR-10	NBPGR, New Delhi
42	NBPGR-11	NBPGR, New Delhi
43	NBPGR-12	NBPGR, New Delhi
44	NBPGR-13	NBPGR, New Delhi
45	NBPGR-14	NBPGR, New Delhi
46	NBPGR-15	NBPGR, New Delhi
47	NBPGR-16	NBPGR, New Delhi
48	NBPGR-17	NBPGR, New Delhi
49	NBPGR-18	NBPGR, New Delhi
50	AOL-12-59	MVRS, A. A. U, Anand
51	NOL-17-09	N. A. U, Navsari
52	AOL-03-01	MVRS, A. A. U., Anand
53	JOL-7-K-14	VRS, J. A. U., Junagadh
54	AOL-13-73	MVRS, A. A. U., Anand
55	AOL-15-59	MVRS, A. A. U., Anand
56	KS-404	CSAUAT, Kalyanpur
57	GP-130	VRS, J. A. U., Junagadh
58	GP-129	VRS, J. A. U., Junagadh
59	GP-128	VRS, J. A. U., Junagadh
60	GP-127	VRS, J. A. U., Junagadh
61	GP-126	VRS, J. A. U., Junagadh
62	GP-125	VRS, J. A. U., Junagadh
63	GP-124	VRS, J. A. U., Junagadh
64	GP-123	VRS, J. A. U., Junagadh
65	GP-122	VRS, J. A. U., Junagadh
66	GP-121	VRS, J. A. U., Junagadh
67	GP-120	VRS, J. A. U., Junagadh
68	GP-119	VRS, J. A. U., Junagadh
69	GP-118	VRS, J. A. U., Junagadh
70	GP-117	VRS, J. A. U., Junagadh
71	GP-116	VRS, J. A. U., Junagadh
72	GP-115	VRS, J. A. U., Junagadh
73	GP-114	VRS, J. A. U., Junagadh
74	GP-113	VRS, J. A. U., Junagadh
75	GP-112	VRS, J. A. U., Junagadh

3.3 CHARACTERS STUDIED

3.3.1 Observation recorded

Five competitive plants per genotype were selected randomly for the purpose of recording observation on different characters except days to 50% flowering and days to first picking. The following observation to be recorded:

1. Days to 50% flowering

Number of days from the date of sowing to the date of first flower opening in 50% plants was recorded.

2. Days to first picking

The number of days was recorded from the date of sowing to date of first picking harvested as marketable green fruit.

3. Plant height (cm)

The height of the plant was measured in centimeters from ground level to tip of main shoot on basis of randomly selected plants at the time of last picking.

4. Number of branches per plant

The total number of branches arising on the main stem of the plant was recorded at the time of last picking.

5. Number of nodes on main stem per plant

The total number of the nodes from the base of the plant to tip at the last picking was recorded as number of nodes per plant.

6. Internodal length (cm)

The length of middle internode was measured and recorded in centimetres at the time of last picking.

7. Number of fruits per plant

The total number of marketable fruits harvested from selected from a plant was recorded as fruits per plant.

8. Fruit length (cm)

The fruit length was measured in centimeters from base of calyx to the tip of the fruit during peak picking of 2nd/3rd picking.

9. Fruit girth (cm)

The middle portion of the fruit was measured in centimeters and recorded as fruit girth during peak picking of 2nd/3rd picking.

10. Fruits weight (g)

Five fruits were randomly selected during peak picking period and weighed in gram.

11. Total number of pickings

Number of pickings of fruit harvesting was counted from first picking to last picking and was summed up and recorded as total number of pickings.

12. Fruit yield per plant (g)

Yield of marketable fruits of five plants at each picking were summed for total number of picking and average was calculated in grams and taken as fruit yield per plant.

3.4. STATISTICAL ANALYSIS

The replication-wise mean values of five randomly selected plants in each entry were used for the statistical analysis for different 12 characters under study. The data recorded for various characters were statistically analyzed at the Computer Cell, Department of Genetics and Plant Breeding, College of Agriculture, J.A.U., Junagadh for the various parameters viz., genetic variability, genotypic and phenotypic correlations, path coefficient analysis and selection indices.

3.4.1. Analysis of variance

The analysis of variance for randomized block design (RBD) was done for each character as per Panse and Sukhatme (1985). The statistical model used for analysis of variance was based on the following linear model;

$$Y_{ij} = \mu + r_i + g_j + \varepsilon_{ij}$$

$i = 1, 2, 3, \dots, r$

$j = 1, 2, 3, \dots, g$

Where,

Y_{ij} = Value of i^{th} genotype in j^{th} replication

μ = General mean

g_i = Effect of i^{th} genotype ($j = 1, 2, \dots, g$)

r_j = Effect of j^{th} replication ($i = 1, 2, \dots, r$)

ϵ_{ij} = Uncontrolled random error associated with i^{th} genotype and j^{th} replication

The format of analysis of variance is given as under:

Table 3.2 Analysis of variance for experimental design

Source	d. f.	Mean sum of squares	Expected mean squares
Replications	(r-1)	M_r	$\sigma_e^2 + g \sigma_r^2$
Genotypes	(g-1)	M_g	$\sigma_e^2 + r \sigma_g^2$
Error	(r-1) (g-1)	M_e	σ_e^2

Significance of replications mean sum of square (M_r) and genotypes mean sum of square (M_g) was tested against error mean sum of square (M_e).

3.4.2. Estimation of components of variance

The phenotypic, genotypic and error variances were worked out as follows:

$$\sigma_e^2 = M_e$$

$$\sigma_g^2 = (M_g - M_e)/r$$

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Where,

R = Number of replications

G = Number of genotypes

M_g = Mean sum of square due to genotypes

M_r = Mean sum of square due to replications

M_e	=	Mean sum of square due to error
σ_e^2	=	Error variance
σ_g^2	=	Genotypic variance
σ_p^2	=	Phenotypic variance

The standard error of mean (S. Em.±) was calculated using following formula:

$$\text{S. Em. } \pm = \sqrt{\frac{M_e}{r}}$$

The critical difference (C.D.) for comparing mean of any two genotypes was calculated using following formula:

$$\text{C. D.} = \text{S. Em.} \pm \times \sqrt{2} \times t_{0.05}$$

Where,

‘t’= Table value of ‘t’ at 5% level of significance and error degree of freedom.

The coefficient of variation (C.V.) was determined according to the following formula;

$$\text{CV}(\%) = \frac{\sqrt{M_e}}{\bar{X}} \times 100$$

Where,

$\bar{X}$ = Mean of the character.

3.4.3. Measures of genetic variability

1. Phenotypic Range

It is the difference between maximum value and minimum value in a particular trait.

Range = Maximum value – Minimum value

While comparing the range of different traits, it is necessary to make it unit less. Hence, coefficient of range was calculated as per the following formula:

$$\text{Coefficient of range (\%)} = \frac{\text{Range}}{\text{Maximum value} + \text{Minimum value}} \times 100$$

2. Genotypic coefficient of variation (GCV)

The genotypic coefficient of variation, which measures the magnitude of genotypic variation present in a particular character, was estimated as per the formula suggested by Burton and De Vane (1953).

$$\text{GCV (\%)} = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

Where,

GCV (%) = Genotypic coefficient of variation

σ_g^2 = Genotypic variance

$\bar{X}$ = Mean of the character

3. Phenotypic coefficient of variation (PCV)

The phenotypic coefficient of variation, which measures the magnitude of phenotypic variation present in a particular character, was estimated as per the formula suggested by Burton and De Vane (1953).

$$\text{PCV (\%)} = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

Where,

PCV (%) = Phenotypic coefficient of variation

σ_p^2 = Phenotypic variance

$\bar{X}$ = Mean of the character

The GCV and PCV values were classified as follows as suggested by Sivasubramaniam and Madhva Menon (1973).

GCV and PCV Values (%)	Classification
0 – 10	Low
10 – 20	Medium
>20	High

4. Heritability in broad sense (h^2_{bs})

It is the ratio of genotypic variance (σ_g^2) to the phenotypic variance (σ_p^2), was calculated according to formula suggested by Allard (1960).

$$h^2(\%) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

h^2 = Heritability in broad sense

σ_p^2 = Phenotypic variance

σ_g^2 = Genotypic variance

The heritability was classified as a low, medium and high according to Hanson *et al.* (1956) as given below;

Classification	Heritability (%)
Low	0 – 30
Medium	30 – 60
High	> 60

5. Genetic advance (Gs)

The expected genetic advance at 5% selection intensity was estimated as per the formula described by Allard (1960).

$$GA = k \times \sigma_p \times h^2$$

Where,

Gs = Genetic advance under selection

k = Selection differential (value of k at 5% selection intensity is 2.06)

σ_p = Phenotypic standard deviation

h^2 = Heritability value of the character

6. Genetic advance as per cent of mean (GAM %)

The genetic advance expressed as per cent of mean was computed as under:

$$\text{Genetic advance as per cent of mean} = \frac{\text{Genetic advance (Gs)}}{\text{Mean of character } (\bar{X})} \times 100$$

Genetic advance as per cent of mean was categorized as low, moderate and high as given by Johnson *et al.* (1955) as follow:

Classification	GAM (%)
Low	0 – 10
Medium	10 – 20
High	>20

3.4.4 CORRELATION COEFFICIENT

Correlation coefficient is the measurement of relationship between two or more series of variables. The genotypic correlation coefficient provides a measure of genotypic association between different characters, while phenotypic correlation includes both genotypic as well as environmental influences.

The phenotypic and genotypic correlation coefficients of all the pair of characters were worked out as per Al-Jibouri *et al.* (1958). The data were subjected to covariance analysis from which different components of mean sum of products were estimated.

Table 3.3 Analysis of covariance between two characters

Source	d. f.	Mean sum of products	Expectation of mean sum of products
Replications	(r-1)	MP_r	-
Genotypes	(g-1)	MP_g	$Cov_{e1.2} + r Cov_{g1.2}$
Error	(r-1) (g-1)	MP_e	$Cov_{e1.2}$

Where,

r = Number of replications

g = Number of genotypes

$Cov_{e1.2}$ = Environment covariance between first and second characters

$Cov_{g1.2}$ = Genotypic covariance between first and second characters

1. Genotypic covariance ($Cov_{g1.2}$)

$$\text{Genotypic covariance } (Cov_{g1.2}) = (MP_g - MP_e)/r$$

Where,

MP_g = Mean sum of product due to genotypes between first and second characters

MP_e = Mean sum of product due to error between first and second characters

r = Number of replications

2. Phenotypic covariance ($Cov_{p1.2}$)

$$\text{Phenotypic covariance } (Cov_{p1.2}) = (Cov_{g1.2} + Me)/r$$

Where,

M_e = Mean sum of products due to error between character first and second

r = Number of replications

3. Error covariance ($Cov_{e1.2}$)

Error covariance ($Cov_{e1.2}$) = MP_e

Where,

MP_e = Mean sum of product due to error between first and second characters

The genotypic, phenotypic variances and error variance and covariances were used for calculating the genotypic and phenotypic correlation coefficients, respectively (Al-Jibouri *et al.*, 1958).

a) Genotypic correlation coefficient ($r_{g1.2}$)

$$\text{Genotypic correlation coefficient } r_{g1.2} = \frac{Cov_{g1.2}}{\sqrt{\sigma_{g1}^2 \cdot \sigma_{g2}^2}}$$

Where,

$Cov_{g1.2}$ = Genotypic covariance between first and second characters

σ_{g1}^2 = Genotypic variance for first character

σ_{g2}^2 = Genotypic variance for second character

b) Phenotypic correlation coefficient ($r_{p1.2}$)

$$\text{Phenotypic correlation coefficient } r_{p1.2} = \frac{Cov_{p1.2}}{\sqrt{\sigma_{p1}^2 \cdot \sigma_{p2}^2}}$$

Where,

$Cov_{p1.2}$ = Phenotypic covariance between first and second characters

σ_{p1}^2 = Phenotypic variance for first character

σ_{p2}^2 = Phenotypic variance for second character

The significance of the correlation values at (n-2) degrees of freedom was tested by adopting the formula suggested by Panse and Sukhatme (1985).

The Political Science Department at Quinnipiac University, Quinnipiac University, 275 Mt Carmel Ave, Hamden, CT 06518, Connecticut, suggested to use following Pearson's correlation coefficients for interpreting strengths of correlations

were used in the present investigation.

'r' value	Classification
+ 0.70 or higher	Very strong positive relationship
+ 0.40 to + 0.69	Strong positive relationship
+ 0.30 to + 0.39	Moderate positive relationship
+ 0.20 to + 0.29	Weak positive relationship
+ 0.01 to + 0.19	No or negligible relationship
0	No relationship (zero order correlation)
- 0.01 to - 0.19	No or negligible relationship
- 0.20 to - 0.29	Weak negative relationship
- 0.30 to - 0.39	Moderate negative relationship
- 0.40 to - 0.69	Strong negative relationship
- 0.70 or higher	Very strong negative relationship

3.4.5 PATH COEFFICIENT ANALYSIS

Path coefficient is a standardized partial regression coefficient and measures the direct and indirect influence of one variable upon another thereby permitting the separation of the correlation coefficient into the component of direct and indirect effects.

The path coefficient analysis was carried-out as per the method suggested by Dewey and Lu (1959). Genotypic correlation coefficients of 12 variables with bulb yield were used to estimate the path coefficient for the direct effects of various independent characters on yield. The direct effects designated as 'p' were calculated by increasing the underlying correlation matrix as per Doolittle method described by Steel and Torrie (1960).

$$r_{1y} = P_{1y} + P_{2y}r_{1.2} + \dots + P_{12y}r_{1.12}$$

$$r_{2y} = P_{1y}r_{1.2} + P_{2y} + \dots + P_{12y}r_{2.12}$$

, , , , ,

$$r_{11y} = P_{1y} r_{1.11} + P_{2y} r_{2.11} + \dots + P_{11y}$$

Where,

$r_{1y}, r_{2y}, r_{3y}, \dots, r_{11y}$ are the genotypic correlations of days to 50% flowering, days to first picking, plant height (cm), number of branches per plant, number of nodes on main stem per plant, internodal length (cm), number of fruits per plant, fruit length (cm), fruit girth (cm), fruits weight (g), total number of pickings, fruit yield per plant (g).

$P_{1y}, P_{2y}, P_{3y}, \dots, P_{11y}$ are the direct effects of characters viz., days to 50% flowering, days to first picking, plant height (cm), number of branches per plant, number of nodes on main stem per plant, internodal length (cm), number of fruits per plant, fruit length (cm), fruit girth (cm), fruits weight (g), total number of pickings, fruit yield per plant (g).

The coefficient of determination was calculated by using the following relationship:

$$1 = P_{1y}^2 + 2P_{1y} r_{1.2}P_{2y} + 2P_{1y} r_{1.3}P_{3y} + 2P_{1y} r_{1.4}P_{4y} + 2P_{1y} r_{1.5}P_{5y} + 2P_{1y} r_{1.6}P_{6y} + 2P_{1y} r_{1.7}P_{7y} + 2P_{1y} r_{1.8}P_{8y} + 2P_{1y} r_{1.9}P_{9y} + 2P_{1y} r_{1.10}P_{10y} + 2P_{1y} r_{1.11}P_{11y} + P_{2y}^2 + \dots + P_{10y}^2 + 2P_{10y} r_{10.11}P_{11y} + R$$

The residual variation (R) *i.e.* variation in dependent character yield due to uncontrolled causes was estimated by subtracting this value from unity.

Path coefficients were rated as suggested by Lenka and Mishra (1973).

Classification	Scales
Negligible	0.00 – 0.09
Low	0.10 – 0.19
Moderate	0.20 – 0.29
High	0.30 – 1.00
Very high	>1.00

3.4.6 SELECTION INDICES

Application of discriminant function as a basis for making selection on several characters simultaneously is aimed at discriminating the desirable genotypes from undesirable ones on the basis of their phenotypic performance. The concept of

selection index was first proposed by Smith (1936) on the basis of discriminant function of Fisher (1936). The model suggested by Robinson *et al.* (1951) was used for the construction of selection indices and development of a required discriminant function. Smith (1936) defined the genetic worth (H) of an individual as,

$$H = a_1G_1 + a_2G_2 + \dots + a_nG_n$$

Where, $G_1, G_2, \dots, G_n$ are the genotypic values of individual characters and $a_1, a_2, \dots, a_n$ signify their relative economic importance

Another function (I), based on phenotypic performance of various characters was defined as:

$$I = b_1p_1 + b_2p_2 + \dots + b_np_n$$

Where, $b_1, b_2, \dots, b_n$ are to be estimated such that the correlation between H and I *i.e.* $r(H, I)$ becomes maximum. Once such function is obtained, discrimination of good genotypes/characters from the undesirable ones could be possible on the basis of phenotypic performance *i.e.* $p_1, p_2, \dots, p_n$ directly.

The maximization of $r(H, I)$ leads to a set of simultaneous equations which upon solving give the desired estimate of “ b_i ” values. Considering three characters as an example, the simultaneous equations look like as follows.

$$b_1X_{11} + b_2X_{12} + b_3X_{13} = a_1G_{11} + a_2G_{12} + a_3G_{13}$$

$$b_1X_{21} + b_2X_{22} + b_3X_{23} = a_1G_{21} + a_2G_{22} + a_3G_{23}$$

$$b_1X_{31} + b_2X_{32} + b_3X_{33} = a_1G_{31} + a_2G_{32} + a_3G_{33}$$

The matrix form of above simultaneous equations is as under

$$\begin{bmatrix} X_{11} & X_{12} & X_{13} \\ X_{21} & X_{22} & X_{23} \\ X_{31} & X_{32} & X_{33} \end{bmatrix} \begin{bmatrix} b_1 \\ b_2 \\ b_3 \end{bmatrix} = \begin{bmatrix} G_{11} & G_{12} & G_{13} \\ G_{21} & G_{22} & G_{23} \\ G_{31} & G_{32} & G_{33} \end{bmatrix} \begin{bmatrix} a_1 \\ a_2 \\ a_3 \end{bmatrix}$$

Where,

X = Phenotypic variance-covariance

b = Discriminant function coefficient

G = Genotypic variance-covariance

a = Economic weightage

The solution of these equations gives the estimate of 'b_i' values in the following manner.

$$b_i = X^{-1}.G.a.$$

Where,

X^{-1} = Inverse matrix of X

G = Genotypic variance-covariance matrix

a = Economic weightage matrix

The mathematical description of the function (I) is known as selection index.

$$I = b_1p_1 + b_2p_2 + \dots + b_np_n$$

Using this function, it is possible to discriminate among the superior and inferior plants or combination of characters. Selection index or score is calculated for all the plants or combination of characters and those with the highest values are considered.

1) Expected genetic advance

The expected genetic advance through selection was calculated as per the formula suggested by Robinson *et al.* (1951).

$$G = \frac{Z}{P} \frac{\sum \sum a_i b_j G_{ij}}{\sqrt{\sum \sum b_i b_j P_{ij}}}$$

Where,

Z/P = Standardized selection differential (s) indicating the intensity of selection

(i) at 5% (k = 2.06)

a_i = Economic weightage

b_i = Regression coefficient in row form

b_j = Regression coefficient in column form

G_{ij} = Genotypic variance-covariance

P_{ij} = Phenotypic variance-covariance

2) Relative efficiency

The relative efficiency of different discriminant functions was calculated according to Robinson *et al.* (1951), assuming the efficiency of selection for grain yield per plant as 100%.

$$RI \% = \left[\frac{GA(D)}{GA(S)} \right] \times 100$$

Where,

RI = Relative efficiency

GA (D) = Genetic advance through discriminant function

GA (S) = Genetic advance through straight selection

CHAPTER-IV

EXPERIMENTAL RESULTS



The present investigation entitled “Genetic variability, correlation coefficient, selection indices and path analysis for fruit yield and its contributing characters in okra [*Abelmoschus esculentus* (L) Moench]” using 75 genotypes of okra were evaluated in Randomized Block Design (RBD) during *kharif* -2020 with an objective to estimate the genetic variability and determination of association among different attributes with each other and with fruit yield. The results obtained in the present investigation are presented with following heads:

4.1 Analysis of variance

4.2 Genetic variability

4.2.1 Mean performance and range

4.2.2 Phenotypic coefficient of variation (PCV)

4.2.3 Genotypic coefficient of variation (GCV)

4.2.4 Heritability (h^2bs)

4.2.5 Genetic advance (Gs)

4.2.6 Genetic advance expressed as percentage of mean (GAM %)

4.3 Correlation coefficient

4.4 Path coefficient analysis

4.5 Selection indices

4.1 ANALYSIS OF VARIANCE

The analysis of variance for experimental design indicated highly significant differences among all the genotypes for all the twelve traits viz., days to 50% flowering, days to first picking, plant height (cm), number of branches per plant, number of nodes on main stem per plant, internodal length (cm), number of fruits per plant, fruit length (cm), fruit girth (cm), fruit weight (g), total number of pickings and fruit yield per plant(g) (Table 4.1). The mean square due to genotypes indicated the presence of considerable amount of variability in the experimental material, which can be exploited for improvement of fruit yield and yield attributes in okra.

Table 4.1 Analysis of variance showing mean squares of 12 characters in 75 genotypes of okra

Source	d. f.	Days to 50% flowering	Days to first picking	Plant height (cm)	Number of branches per plant	Number of nodes per plant	Internodal length (cm)
Replications	1	14.11	19.44	227.33	0.14	4.64	0.40
Genotypes	74	14.78**	12.56**	592.12**	0.70**	19.84**	2.69**
Error	74	5.59	6.76	67.02	0.04	1.59	0.18

Source	d. f.	Number of fruits per plant	Fruit length (cm)	Fruit girth (cm)	Fruit weight (g)	Total number of pickings	Fruit yield per plant (g)
Replications	1	1.12	0.61	0.26	7.39	1.31	282.71
Genotypes	74	11.28**	4.17**	1.14**	154.95**	2.82**	2326.73**
Error	74	0.51	0.36	0.08	10.39	0.43	138.79

*, ** Significant at 5% and 1% levels, respectively

4.2 GENETIC VARIABILITY

The results obtained on various parameters of genetic variability have been presented here under:

4.2.1 Mean performance and range of variation

The mean performance and range of 75 genotypes for all the 12 characters along with standard error of mean (S. Em.±), critical difference (C. D.) and coefficient of variation (C. V.) are presented in Appendix – II. The summary is also presented in Table 4.2.

4.2.1.1 Days to 50% flowering

The mean values for days to 50% flowering ranged from 41.50 days (GP-123) to 54.50 days (2018/OKYVRES-6 and GP-129). The genotype GP-123 was earliest to days to 50% flowering (41.50 days) followed by AOL- 16- 01 (44.50 days), JDNOL- 11-12 (45.00 days), Pusa Sawani (45.00 days) and GP-125 (45.50 days), while genotypes 2018/OKYVRES-6 and GP-129 registered late for days to 50% flowering (54.50 days) followed by 2018/OKYVRES-7 (53.50 days), NBPGR-1 (53.00 days), NOL-17-09 (53.00 days), AOL-03-01 (53.00 days) and GP-122 (53.00 days). The overall mean for days 50% flowering was 49.20 days and the coefficient of range was found to be 13.54% for this character.

4.2.1.2 Days to first picking

The mean values for days to first picking ranged from 51.00 days (GP-123) to 61.50 days (2017/OKYVRES-4). Days to first picking was recorded minimum in genotype GP-123 (51.00 days) followed by Pusa Sawani and GP-113 (51.50 days), while the genotype 2017/OKYVRES-4 takes maximum days (61.50) followed by GP-129 (61.00 days), 2019/OKYVRES-12 (59.00 days), NOL-17-09 (59.00 days) and GP-119 (59.00 days) for days to first picking. The average days for first picking were 55.47 days and the coefficient of range was found to be 9.33% for this character.

4.2.1.3 Plant height (cm)

The mean values for plant height ranged from 64.17 cm (NOL-17-09) to 145.00 cm (2019/OKYVRES-12). The genotype 2019/OKYVRES-12 exhibited maximum plant height (145.00 cm) followed by the AOL-16-01 (133.33 cm), NBPGR-5 (131.67 cm) and 2019/OKYVRES-12 (131.50 cm). Genotype NOL-17-09 had lowest plant height (64.17 cm) followed by JDNOL-11-12 (64.33 cm),

GP-116 (72.50 cm) and AOL-15-59 (75.34 cm). The overall mean for plant height was 105.01 cm and the coefficient of range was found to be 38.62% for this character.

4.2.1.4 Number of branches per plant

In case of number of branches per plant ranged varied from 0.90 to 3.30. Genotype AOL-15-59, GP-129 and GP-122 produced the lowest number of branches (0.90) followed by 2017/OKYVRES-10 (1.10), 2017/OKYVRES-2 (1.10), NBPGR-7 (1.10), NBPGR-10 (1.10) and GP-113 (1.10), while JOL-14-10 showed the highest number of branches per plant (3.30) followed by GO-6 (3.20) and NOL-17-09 (3.20). The overall mean for number of branches per plant was 1.79 and the coefficient of range was found to be 57.14% for this character.

4.2.1.5 Number of nodes on main stem per plant

In respect of number of nodes on main stem per plant ranged from 8.33 to 20.50. The genotype GP-115 showed the highest number nodes per plant (20.50) followed by NBPGR-3 and JOL-7-K-14 (19.67) and 2019/OKYVRES-11 (19.33), while genotype GP-129 produced the lowest number of nodes on main stem per plant (8.33) followed by 2018/OKYVRES-7 (8.50), AOL-08-05 (8.83) and GO-6 (8.84). The overall mean for number of nodes on main stem per plant was 14.72 and the coefficient range was found to be 42.36% for this character.

4.2.1.6 Internodal length (cm)

In case of internodal length varied from 3.58 to 8.92 cm with a mean performance of 6.23 cm. Genotype NOL-17-09 had the lowest internodal length (3.58 cm) followed by 2019/OKYVRES-12 (3.67 cm), GP-119 (3.83 cm), GP-128 (3.92 cm) and KS-404 (4.17 cm), while GP-114 had the maximum internodal length (8.92 cm) followed by NBPGR-18 and GP-126 (8.17 cm) and GP-125 (8.08 cm). The coefficient of ranged was found to be 41.26% for this character.

4.2.1.7 Number of fruits per plant

The mean values for number of fruits per plant ranged from 5.00 to 14.83. The maximum number of fruits per plant was produced by genotype NBPGR-8 (14.83) followed by 2019/OKYVRES-12 (14.17), 2019/OKYVRES-6 and NBPGR-4 (14.00), while it was minimum in genotype GP-116 (5.0) followed by AOL-08-05 (5.67) and AOL-15-59 (5.83), while it was maximum in the average number of fruits per plant was 9.20 and the coefficient range was found to be 49.49% for this character.

Table 4.2 Range, Coefficient of range (%), Mean, GCV (%), PCV (%), Heritability, GA and GA expressed as % of mean for various characters in okra

Sr. No.	Characters	Range	Coefficient of range (%)	Mean	Genotypic coefficients of variance (GCV %)	Phenotypic coefficients of variance (PCV %)	Heritability in broad sense h^2_{bs} (%)	Genetic advance (Gs)	Genetic advance as % of mean (GAM %)
1.	Days to 50% flowering	41.50 – 54.50	13.54	49.20	4.36	5.53	62.17	3.48	7.08
2.	Days to first picking	51.00 – 61.50	9.33	55.47	3.07	4.52	46.14	2.38	4.29
3.	Plant height (cm)	64.17 – 145.00	38.62	105.01	15.43	16.39	88.68	31.43	29.93
4.	No. of branches per plant	0.90 – 3.30	57.14	1.79	32.21	33.08	94.84	1.16	64.63
5.	No. of nodes on main stem per plant	8.33 – 20.50	42.36	14.72	20.52	21.39	91.98	5.97	40.53
6.	Internodal length (cm)	3.58– 8.92	41.26	6.23	17.97	18.59	93.47	2.23	35.80
7.	No. of fruits per plant	5.00 – 14. 83	49.49	9.20	25.21	25.80	95.47	4.67	50.75
8.	Fruit length (cm)	7.15 – 13.55	30.76	9.92	13.90	14.55	91.24	2.71	27.35
9.	Fruit girth (cm)	4.45 – 7.95	28.00	5.89	12.39	12.82	93.40	1.45	24.66
10.	Fruit weight (g)	48.50 – 82.20	25.78	62.47	13.61	14.09	93.30	16.92	27.08
11.	Total number of pickings	7.50 – 12.50	25.00	9.82	11.12	12.08	84.80	2.07	21.10
12.	Fruit yield per plant (g)	67.90 – 234.55	55.10	116.76	28.33	29.21	94.03	66.07	56.58

4.2.1.8 Fruit length (cm)

The fruit length varied from 7.15 to 13.55 cm with the average was calculated to be 9.92 cm. Fruit length was found to be highest in genotype 2019/OKYVRES-12 (13.55 cm) followed by AOL-15-59 (12.70 cm), 2019/ OKYVRES-3 (12.65 cm) and GP-125 (12.55 cm), while it was recorded to be least in genotype AOL-09-02 (7.15 cm) followed by AOL-13-144, NBPGR-10 (both 7.60 cm), 2019/OKYVRES-11 and 2018/OKYVRES-5 (both 7.65 cm). The coefficient of range was found to be 30.76% for this character.

4.2.1.9 Fruit girth (cm)

The fruit girth ranged from 4.45 to 7.95 cm with a mean value of 5.89 cm. Fruit girth was found to be highest in genotype 2018/OKYVRES-6 (7.95 cm) followed by GP-118 (7.85 cm), 2019/OKYVRES-8 (7.55 cm), 2019/OKYVRES-6 (7.50 cm) and NBPGR-7 (7.40 cm), while it was recorded to be least in genotype NBPGR-4 (4.45 cm) followed by GO-6 (4.65 cm), HRB-55 (4.70 cm) and 2019/OKYVRES-11 (4.75 cm). The coefficient of range was found to be 28.0% for this character.

4.2.1.10 Fruit weight (g)

In respect of fruit weight, the range was observed from 48.50 to 82.20 g with a mean value of 62.47 g. The maximum weight of fruit was showed by 2019/OKYVRES-6 (82.20 g) followed by NBPGR-18 (80.85 g), 2019/OKYVRES-12 (80.00 g) and JDNOL-11-12 (79.50 g), while the minimum weight of fruit was recorded in 2019/OKYVRES-11 (48.50 g) followed by NBPGR-10 (49.00 g), NBPGR-4 (51.00 g) and 2018/OKYVRES-5 (51.50 g). The coefficient of range was found to be 25.78% for this character.

4.2.1.11 Total number of pickings

The total number of pickings among 75 genotypes ranged from 7.50 to 12.50 with the average 9.82. The highest number of pickings was recorded in genotype 2019/OKYVRES-12 (12.50) and 2019/OKYVRES-6 (12.50) followed by NBPGR-1 (12.00), while lowest number of pickings 7.50 was recorded in HRB-55, AOL-08-05, GP-128 and GP-123, GP-116 followed by GO-2 (8.00), AOL-09-02 (8.00), GP-130 (8.00) and GP-122 (8.00). The coefficient of range was found to be 25.00% for this character.

4.2.1.12 Fruit yield per plant (g)

In respect of fruit yield per plant ranged from 46.09 to 133.13 g among 75 genotypes with average 86.42 g. The maximum fruit yield per plant was produced by genotype 2019/OKYVRES-12 (234.55) followed by 2019/OKYVRES-6 (228.30), NBPGR-2 (208.85) and JOL-13-05 (184.73), while the minimum fruit yield per plant was produced by genotype HRB-55 (67.90) followed by GP-128 (70.90), AOL-08-05 (72.70) and GP-123 (73.70). The coefficient of range was found to be 55.10% for this character.

4.2.2 Variability parameters

Estimation of component of genetic parameters of variation for fruit yield and its attributes exhibited a wide range of variation for the characters studied (Table 4.2) and the result indicated that the values of phenotypic variance and phenotypic coefficient of variations were of higher in magnitude than that of genotypic variance and genotypic coefficient of variations for all the characters showing, that the environment had an important role in influencing the expressions of the characters.

4.2.2.1 Genotypic coefficient of variation (GCV)

It is revealed from the Table 4.2 that genotypic coefficient of variation varied from 3.07% for days to first picking to 32.21% for number of branches per plant. The genotypic coefficient of variation was highest for characters like; number of branches per plant (32.21%) followed by fruit yield per plant (28.33%), number of fruits per plant (25.21%) and number of nodes on main stem per plant (20.52%). However, it was exhibited moderate for characters viz., internodal length (17.97%), plant height (15.43%), fruit length (13.90%), fruit weight (13.61%), fruit girth (12.39%) and total number of picking (11.12%), while rest of the characters such as days to first picking (3.07%) and days to 50% flowering (4.36%) exhibited low genotypic coefficient of variation.

4.2.2.2 Phenotypic coefficient of variation (PCV)

It is revealed from the Table 4.2 that phenotypic coefficient of variation varied from 4.52% for days to first picking to 33.08% for number of branches per plant. The phenotypic coefficient of variation was highest for number of branches per plant (33.08%) followed by fruit yield per plant (29.21%), number of fruits per plant (25.80%) and number of nodes on main stem per plant (21.39%). However, it

exhibited moderate for characters viz., internodal length (18.59%), plant height (16.39%), fruit length (14.55%), fruit weight (14.09%) and fruit girth (12.82%) and total number of picking (12.08), while rest of the characters such as days to first picking (4.52%) and days to 50% flowering (5.53%) exhibited low phenotypic coefficient of variation.

4.2.2.3 Heritability (h^2_{bs})

The heritability (bs) was computed for each of the characters by the variance components for estimating their relative magnitudes of genotypic and phenotypic variability contributed through environmental factors. The estimates of heritability (bs) for all the characters have been discussed as follows (Table 4.2).

The results indicated that the heritability estimates were high for all the characters viz., number of fruits per plant (95.47%), number of branches per plant (94.84%), fruit yield per plant (94.03%), internodal length (93.47%), fruit girth (93.40%), fruit weight (93.30%), number of nodes on main stem per plant (91.98%), fruit length (91.24%), plant height (88.68%), total number of pickings (84.80%) and days to 50% flowering (62.17%) except days to first picking (46.14%), which was found to be moderate.

4.2.2.4 Genetic advance (Gs)

Based on the estimate of heritability (bs) expected genetic advance was computed on the hypothetical selection at 5 per cent best individual ($K= 2.06$). Due to masking influence of environment upon characters concerned, values of genetic advance exhibited high fluctuations. Therefore, to attain relative comparison of the characters in relation to environment, genetic advance as percentage of mean was calculated to predict the genetic gain (Table 4.2).

The highest Genetic advance (Gs) was observed for fruit yield per plant (66.07) followed by plant height (31.43). Moderate Gs was observed for fruit weight (16.92). Low genetic advance was observed for number of nodes on main stem per plant (5.97), number of fruits per plant (4.67), days to 50% flowering (3.48), fruit length (2.71), days to first picking (2.38), internodal length (2.23), total number of picking (2.07), fruit girth (1.45) and number of branches per plant (1.16).

Genetic advance as percentage of mean ranged between 4.29% for days to first picking to 64.63% for number of branches per plant. The highest estimate of genetic advance as percentage of mean was recorded for number of branches per plant

(64.63%) followed by fruit yield per plant (56.58), number of fruits per plant (50.75), number of nodes on main stem per plant (40.53%), internodal length (35.80%), plant height (29.93%), fruit length (27.35) fruit weight (27.08), fruit girth (24.66) and total number of pickings (21.10%). Whereas, low estimates were observed for days to 50% flowering (7.08%) and days to first picking (4.29%).

4.3 CORRELATION COEFFICIENT ANALYSIS

Correlation coefficient was worked out at phenotypic, genotypic and environmental levels for all possible combination of yield and its attributing characters (Table 4.3). The results indicated that in general genotypic correlation coefficients were of higher magnitude than the corresponding phenotypic correlation coefficients for all the characters taken under study. The results of phenotypic correlation coefficients have been discussed only as the genotypic and environmental correlations were mainly influenced by the environmental conditions, thus phenotypic correlation will give the correct idea about the association between two variables.

4.3.1 Fruit yield per plant with component attributes

Fruit yield per plant exhibited highly significant and positive correlation with plant height ($r_g = 0.5031$, $r_p = 0.4664$), number of nodes on main stem per plant ($r_g = 0.5042$, $r_p = 0.4700$), number of fruits per plant ($r_g = 0.8782$, $r_p = 0.8404$), fruit length ($r_g = 0.4645$, $r_p = 0.4166$), fruit weight ($r_g = 0.4411$, $r_p = 0.4145$) and total number of pickings ($r_g = 0.9748$, $r_p = 0.8672$) at both genotypic and phenotypic levels.

4.3.2 Days to 50% flowering

Days to 50% flowering exhibited highly significant and positive correlation with days to first picking ($r_g = 0.7399$, $r_p = 0.8028$) at both genotypic and phenotypic levels. It had positive and non-significant correlation with fruit length ($r_g = 0.0210$, $r_p = 0.0093$) at both genotypic and phenotypic levels. The plant height ($r_g = -0.1805$, $r_p = -0.1744$), number of branches per plant ($r_g = -0.1297$, $r_p = -0.1260$), number of nodes on main stem per plant ($r_g = -0.0625$, $r_p = -0.0592$), internodal length ($r_g = -0.1675$, $r_p = -0.1373$), number of fruits per plant ($r_g = -0.0323$, $r_p = -0.0310$), fruit girth ($r_g = -0.0902$, $r_p = -0.0972$), fruit weight ($r_g = -0.0247$, $r_p = -0.0147$), total number of pickings ($r_g = -0.0245$, $r_p = -0.0446$) and fruit yield per plant ($r_g = -0.0850$, $r_p = -0.0498$) had negative and non-significant correlation with days to 50% flowering at both genotypic and phenotypic levels.

4.3.3 Days to first picking

Days to first picking exhibited significant and positive correlation with total number of picking ($r_g = 0.2694$, $r_p = 0.1412$) at genotypic level, but non-significant and positive at phenotypic level. It had positive and non significant correlation with plant height ($r_g = 0.1315$, $r_p = 0.0427$), number of branches per plant ($r_g = 0.0454$, $r_p = 0.0048$), number of nodes on main stem per plant ($r_g = 0.1877$, $r_p = 0.1003$), number of fruits per plant ($r_g = 0.1958$, $r_p = 0.1249$), fruit length ($r_g = 0.0322$, $r_p = 0.273$), fruit weight ($r_g = 0.0162$, $r_p = 0.0127$) and fruit yield per plant ($r_g = 0.1494$, $r_p = 0.1081$) at both genotypic and phenotypic levels. Internodal length ($r_g = -0.0352$, $r_p = -0.0233$) and fruit girth ($r_g = -0.0962$, $r_p = -0.0884$) had negative and non-significant correlation with days to first picking at both genotypic and phenotypic levels.

4.3.4 Plant height (cm)

The plant height had highly significant and positive correlation with number of nodes on main stem per plant ($r_g = 0.6550$, $r_p = 0.6006$), number of fruits per plant ($r_g = 0.5972$, $r_p = 0.5544$), total number of pickings ($r_g = 0.5452$, $r_p = 0.4425$) and fruit yield per plant ($r_g = 0.5031$, $r_p = 0.4664$) at both genotypic and phenotypic levels. It had positive and non significant correlation with number of branches per plant ($r_g = 0.1047$, $r_p = 0.0878$) and internodal length ($r_g = 0.2053$, $r_p = 0.1910$) at both genotypic and phenotypic levels. Fruit length ($r_g = -0.0542$, $r_p = -0.0484$), fruit girth ($r_g = -0.1166$, $r_p = -0.0876$) and fruit weight ($r_g = -0.0922$, $r_p = -0.0792$) had negative and non-significant correlation with plant height at both genotypic and phenotypic levels.

4.3.5 Number of branches per plant

The number of branches per plant had positive and non-significant correlation with number of nodes on main stem per plant ($r_g = 0.0031$, $r_p = 0.0065$) and number of fruits per plant ($r_g = 0.0294$, $r_p = 0.0260$) at both genotypic and phenotypic levels. Internodal length ($r_g = -0.0668$, $r_p = -0.0744$), fruit length ($r_g = -0.1443$, $r_p = -0.1317$), fruit girth ($r_g = -0.0775$, $r_p = -0.0732$), fruit weight ($r_g = -0.1564$, $r_p = -0.1425$) total number of pickings ($r_g = -0.0865$, $r_p = -0.0590$) and fruit yield per plant ($r_g = -0.0380$, $r_p = -0.0367$) had negative and non-significant correlation with number of branches per plant at both genotypic and phenotypic levels.

Table 4.3 Genotypic (r_g) and phenotypic (r_p) correlation coefficients among 12 characters in okra

Characters	Cor.	Days to 50% flowering	Days to first picking	Plant height (cm)	No. of branches per plant	No. of nodes on main stem per plant	Intermodal length (cm)	No. of fruits per plant	Fruit length (cm)	Fruit girth (cm)	Fruit weight (cm)	Total number of pickings	Fruit yield per plant (g)
Days to 50% flowering	r_g	1.0000	0.7399**	-0.1805	-0.1297	-0.0625	-0.1675	-0.0323	0.0210	-0.0902	-0.0247	-0.0245	-0.0850
	r_p	1.0000	0.8028**	-0.1744	-0.1260	-0.0592	-0.1373	-0.0310	0.0093	-0.0972	-0.0147	-0.0446	-0.0498
Days to first picking	r_g		1.0000	0.1315	0.0454	0.1877	-0.0352	0.1958	0.0322	-0.0962	0.0162	0.2694*	0.1494
	r_p		1.0000	0.0427	0.0048	0.1003	-0.0233	0.1249	0.0273	-0.0884	0.0127	0.1412	0.1081
Plant height (cm)	r_g			1.0000	0.1047	0.6550**	0.2053	0.5972**	-0.0542	-0.1166	-0.0922	0.5452**	0.5031**
	r_p			1.0000	0.0878	0.6006**	0.1910	0.5544**	-0.0484	-0.0876	-0.0792	0.4425**	0.4664**
No. of branches per plant	r_g				1.0000	0.0031	-0.0668	0.0294	-0.1443	-0.0775	-0.1564	-0.0865	-0.0380
	r_p				1.0000	0.0065	-0.0744	0.0260	-0.1317	-0.0732	-0.1425	-0.0590	-0.0367
No. of nodes on main stem per plant	r_g					1.0000	0.0996	0.6070**	-0.0407	-0.1230	-0.0803	0.5444**	0.5042**
	r_p					1.0000	0.0887	0.5760**	-0.0413	-0.1028	-0.0736	0.4714**	0.4700**
Intermodal length (cm)	r_g						1.0000	0.0694	0.0536	-0.0804	0.0023	0.0769	0.0225
	r_p						1.0000	0.0597	0.0471	-0.0740	0.0056	0.0586	0.0145
No. of fruits per plant	r_g							1.0000	-0.0804	-0.1562	-0.0939	0.8643**	0.8782**
	r_p							1.0000	-0.0719	-0.1335	-0.0937	0.7762**	0.8404**
Fruit length (cm)	r_g								1.0000	0.3298**	0.9617**	0.3703**	0.4645**
	r_p								1.0000	0.3059**	0.8767**	0.3386**	0.4166**
Fruit girth (cm)	r_g									1.0000	0.5160**	0.1173	0.1634
	r_p									1.0000	0.4643**	0.0861	0.1439
Fruit weight (g)	r_g										1.0000	0.3885**	0.4411**
	r_p										1.0000	0.3432**	0.4145**
Total no. of pickings	r_g											1.0000	0.9748**
	r_p											1.0000	0.8672**

*, ** significant at 5% and 1% levels, respectively

4.3.6 Number of nodes on main stem per plant

The number of nodes on main stem per plant had positive and highly significant correlation with number of fruits per plant ($r_g = 0.6070$, $r_p = 0.5760$), total number of pickings ($r_g = 0.5444$, $r_p = 0.4714$) and fruit yield per plant ($r_g = 0.5042$, $r_p = 0.4700$) at both genotypic and phenotypic levels. Internodal length ($r_g = 0.0996$, $r_p = 0.0887$) had positive and non significant correlation with number of nodes on main stem per plant, while fruit length ($r_g = -0.0407$, $r_p = -0.0413$), fruit girth ($r_g = -0.1230$, $r_p = -0.1028$) and fruit weight ($r_g = -0.0803$, $r_p = -0.0736$) had negative and non significant correlation with number of nodes on main stem per plant at both phenotypic and genotypic level.

4.3.7 Internodal length (cm)

The internodal length had positive and non-significant correlation with number of fruits per plant ($r_g = 0.0694$, $r_p = 0.0597$), fruit length ($r_g = 0.0536$, $r_p = 0.0471$), fruit weight ($r_g = 0.0023$, $r_p = 0.0056$), total number of pickings ($r_g = 0.0769$, $r_p = 0.0586$) and fruit yield per plant ($r_g = 0.0225$, $r_p = 0.0145$) at both genotypic and phenotypic levels. Fruit girth ($r_g = -0.0804$, $r_p = -0.0740$) had negative and non significant correlation with internodal length at both genotypic and phenotypic levels.

4.3.8 Number of fruits per plant

The number of fruits per plant had positive and highly significant correlation with total number of pickings ($r_g = 0.8643$, $r_p = 0.7762$) and fruit yield per plant ($r_g = 0.8782$, $r_p = 0.8404$) at both genotypic and phenotypic levels. Fruit length ($r_g = -0.0804$, $r_p = -0.0719$), fruit girth ($r_g = -0.1562$, $r_p = -0.1335$) and fruit weight ($r_g = -0.0939$, $r_p = -0.0937$) had negative and non significant correlation with number of fruits per plant at both genotypic and phenotypic levels.

4.3.9 Fruit length (cm)

The fruit length had positive and highly significant correlation with fruit girth ($r_g = 0.3298$, $r_p = 0.3059$), fruit weight ($r_g = 0.9617$, $r_p = 0.8767$), total number of pickings ($r_g = 0.3703$, $r_p = 0.3386$) and fruit yield per plant ($r_g = 0.4645$, $r_p = 0.4166$) at both genotypic and phenotypic levels.

4.3.10 Fruit girth (cm)

The fruit girth had positive and highly significant correlation with fruit weight ($r_g = 0.5160$, $r_p = 0.4643$) at both genotypic and phenotypic levels. It had positive and non significant correlation with total number of pickings ($r_g = 0.1173$, $r_p = 0.0861$) and fruit yield per plant ($r_g = 0.1634$, $r_p = 0.1439$) at both genotypic and phenotypic levels.

4.3.11 Fruit weight (g)

The fruit weight had positive and highly significant correlation with total number of pickings ($r_g = 0.3885$, $r_p = 0.3432$) and fruit yield per plant ($r_g = 0.4411$, $r_p = 0.4145$) at both genotypic and phenotypic levels.

4.3.12 Total number of pickings

The total number of pickings had positive and highly significant correlation with fruit yield per plant ($r_g = 0.9748$, $r_p = 0.8672$) at both genotypic and phenotypic levels.

4.4 PATH COEFFICIENT ANALYSIS

The phenotypic correlation coefficients calculated for different pairs of characters were subjected to path coefficient analysis for partitioning these values into the direct and indirect effects. The results obtained for direct and indirect effects of different characters on fruit yield per plant are presented in Table 4.4.

4.4.1 Days to 50% flowering vs fruit yield per plant

The phenotypic correlation between days to 50% flowering and fruit yield per plant was non-significant and negative ($r_p = -0.0498$). Days to 50% flowering had negative and very low direct effect (-0.0290) on fruit yield per plant. It had positive and very low indirect effect through days to first picking (0.0132), number of nodes on main stem per plant (0.0013), internodal length (0.0070) and fruit length (0.0017) on fruit yield per plant. It had negative and very low indirect effect *via* plant height (-0.0051), number of branches per plant (-0.0002), number of fruits per plant (-0.0265), fruit girth (-0.0065), fruit weight (-0.0040) and total number of pickings (-0.0017) on fruit yield per plant.

4.4.2 Days to first picking vs fruit yield per plant

The phenotypic correlation between days to first picking and fruit yield per plant was non-significant and positive ($r_p = 0.1081$). Days to first picking had positive

Table 4.4 Phenotypic path coefficient analysis showing direct (diagonal) and indirect effects of different characters on fruit yield per plant in okra

Characters	Days to 50 % flowering	Days to first picking	Plant height (cm)	No. of branches per plant	No. of nodes on main stem per plant	Internodal length (cm)	No. of fruits per plant	Fruit length (cm)	Fruit girth (cm)	Fruit weight (g)	Total number of pickings	Phenotypic correlation with fruit yield per plant (g)
Days to 50% flowering	-0.0290	0.0132	-0.0051	-0.0002	0.0013	0.0070	-0.0265	0.0017	-0.0065	-0.0040	-0.0017	-0.0498
Days to first picking	-0.0233	0.0164	0.0012	0.0001	-0.0023	0.0012	0.1068	0.0050	-0.0059	0.0035	0.0054	0.1081
Plant height (cm)	0.0051	0.0007	0.0290	0.0001	-0.0135	-0.0098	0.4743	-0.0089	-0.0058	-0.0217	0.0169	0.4664**
No. of branches per plant	0.0037	0.0001	0.0025	0.0016	-0.0001	0.0038	0.0223	-0.0243	-0.0049	-0.0390	-0.0023	-0.0367
No. of nodes on main stem per plant	0.0017	0.0016	0.0174	0.0001	-0.0225	-0.0045	0.4928	-0.0076	-0.0068	-0.0201	0.0180	0.4700**
Internodal length (cm)	0.0040	-0.0004	0.0055	-0.0001	-0.0020	-0.0511	0.0511	0.0087	-0.0049	0.0015	0.0022	0.0145
No. of fruits per plant	0.0009	0.0020	0.0161	0.0001	-0.0129	-0.0031	0.8555	-0.0133	-0.0089	-0.0257	0.0297	0.8404**
Fruit length (cm)	-0.0003	0.0004	-0.0014	-0.0002	0.0009	-0.0024	-0.0615	0.1844	0.0203	0.2633	0.0130	0.4166**
Fruit girth (cm)	0.0028	-0.0014	-0.0025	-0.0001	0.0023	0.0038	-0.1142	0.0564	0.0665	0.1271	0.0033	0.1439
Fruit weight (g)	0.0004	0.0002	-0.0023	-0.0002	0.0017	-0.0003	-0.0802	0.1774	0.0309	0.2738	0.0131	0.4145**
Total number of pickings	0.0013	0.0023	0.0128	-0.0001	-0.0106	-0.0030	0.6640	0.0625	0.0057	0.0940	0.0382	0.8672**

*, ** significant at 5% and 1% levels, respectively; Residual effect, R = 0.2065

and very low direct effect (0.0164) on fruit yield per plant. It had positive and low indirect effect through number of fruits per plant (0.1068) on fruit yield per plant. It had positive and very low indirect effect via plant height (0.0012), number branches per plant (0.0001), internodal length (0.0012), fruit length (0.0050), fruit weight (0.0035) and total number of pickings (0.0054) on fruit yield per plant. It had negative and very low indirect effect *via* days to 50% flowering (-0.0233), number of nodes on main stem per plant (-0.0023) and fruit girth (-0.0059) on fruit yield per plant.

4.4.3 Plant height vs fruit yield per plant

The phenotypic correlation between plant height and fruit yield per plant was highly significant and positive ($r_p = 0.4664$). Plant height had positive and very low direct effect (0.0290) on fruit yield per plant. It had positive and high indirect effect through number of fruits per plant (0.4743), while positive and very low indirect effect through days to 50% flowering (0.0051), days to first picking (0.0007), number of branches per plant (0.0001) and total number of pickings (0.0169) on fruit yield per plant. It had negative and very low indirect effect *via* number of nodes on main stem per plant (-0.0135), internodal length (-0.0098), fruit length (-0.0089), fruit girth (-0.0058) and fruit weight (-0.0217) on fruit yield per plant.

4.4.4 Number of branches per plant vs fruit yield per plant

The phenotypic correlation between number of branches per plant and fruit yield per plant was non-significant and negative ($r_p = -0.0367$). Number of branches per plant had positive and very low indirect effect (0.0016) on fruit yield per plant. It had positive and very low indirect effect *via* days to 50% flowering (0.0037), days to first picking (0.0001), plant height (0.0025), internodal length (0.0038) and number of fruits per plant (0.0223) on fruit yield per plant. It had negative and very low indirect effect through number of nodes on main stem per plant (-0.0001), fruit length (-0.0243) and fruit girth (-0.0049), fruit weight (-0.0390) and total number of pickings (-0.0023) on fruit yield per plant.

4.4.5 Number of nodes on main stem per plant vs fruit yield per plant

The phenotypic correlation between number of nodes on main stem per plant and fruit yield per plant was highly significant and positive ($r_p = 0.4700$). Number of nodes on main stem per plant had negative and very low direct effect (-0.0225) on fruit yield per plant. It had positive and high indirect effect through number of fruits per plant (0.4928), while positive and very low indirect effect *via* days to 50%

flowering (0.0017), days to first picking (0.0016), plant height (0.0174), number of branches per plant (0.0001) and total number of pickings (0.0180) on fruit yield per plant. It had negative and very low indirect effect through internodal length (-0.0045), fruit length (-0.0076), fruit girth (-0.0068) and fruit weight (-0.0201) on fruit yield per plant.

4.4.6 Internodal length (cm) vs fruit yield per plant

The phenotypic correlation between internodal length and fruit yield per plant was non-significant and positive ($r_p = 0.0145$). Internodal length had negative and very low direct effect (-0.0511) on fruit yield per plant. It had positive and very low indirect effect *via* days to 50% flowering (0.0040), plant height (0.0055), number of fruits per plant (0.0511), fruit length (0.0087), fruit weight (0.0015) and total number of pickings (0.0022) on fruit yield per plant. It had negative and very low indirect effect *via* days to first picking (-0.0004), number of branches per plant (-0.0001), number of nodes on main stem per plant (-0.0020) and fruit girth (-0.0049) on fruit yield per plant.

4.4.7 Number of fruits per plant vs fruit yield per plant

The phenotypic correlation between number of fruits per plant and fruit yield per plant was highly significant and positive ($r_p = 0.8404$). Number of fruits per plant had positive and high direct effect (0.8555) on fruit yield per plant. It had positive and very low indirect effect *via* days to 50% flowering (0.0009), days to first picking (0.0020), plant height (0.0161), number of branches per plant (0.0001) and total number of pickings (0.0297) on fruit yield per plant. It had negative and very low indirect effect *via* number of nodes on main stem per plant (-0.0129), internodal length (-0.0031), fruit length (-0.0133), fruit girth (-0.0089) and fruit weight (-0.0257) on fruit yield per plant.

4.4.8 Fruit length vs fruit yield per plant

The phenotypic correlation between fruit length and fruit yield per plant was highly significant and positive ($r_p = 0.4166$). Fruit length had positive and low direct effect (0.1844) on fruit yield per plant. It had positive and moderate indirect effect through fruit weight (0.2633), while positive and very low indirect effect *via* days to first picking (0.0004), number of nodes on main stem per plant (0.0009), fruit girth (0.0203) and total number of pickings (0.0130) on fruit yield per plant. It had negative and very low indirect effect *via* days 50% flowering (-0.0003), plant height (-0.0014),

number of branches per plant (-0.0002), internodal length (-0.0024) and number of fruits per plant (-0.0615) on fruit yield per plant.

4.4.9 Fruit girth vs fruit yield per plant

The phenotypic correlation between fruit girth and fruit yield per plant was non-significant and positive ($r_p = 0.1439$). Fruit girth had positive and very low direct effect (0.0665) on fruit yield per plant. It had positive and low indirect effect through fruit weight (0.1271), while positive and very low indirect effect through days to 50% flowering (0.0028), number of nodes on main stem per plant (0.0023), internodal length (0.0038), fruit length (0.0564) and total number of pickings (0.0033) on fruit yield per plant. It had negative and very low indirect effect through days to first picking (-0.0014), plant height (-0.0025) and number of branches per plant (-0.0001), while negative and low indirect effect through number of fruits per plant (-0.1142) on fruit yield per plant.

4.4.10 Fruit weight vs fruit yield per plant

The phenotypic correlation between fruit weight and fruit yield per plant was highly significant and positive ($r_p = 0.4145$). Fruit weight had positive and moderate direct effect (0.2738) on fruit yield per plant. It had positive and low indirect through fruit length (0.1774), while positive and very low indirect effect *via* days to 50% flowering (0.0004), days to first picking (0.0002), number of nodes on main stem per plant (0.0017), fruit girth (0.0309) and total number of pickings (0.0131) on fruit yield per plant. It had negative and very low indirect effect through plant height (-0.0023), number of branches per plant (-0.0002), internodal length (-0.0003) and number of fruits per plant (-0.0802) on fruit yield per plant.

4.4.11 Total number of pickings vs fruit yield per plant

The phenotypic correlation between total number of pickings and fruit yield per plant was highly significant and positive ($r_p = 0.8672$). Total number of pickings had positive and very low direct effect (0.0382) on fruit yield per plant. It had positive and high indirect effect through number of fruits per plant (0.6640), while positive and very low indirect effect *via* days to 50% flowering (0.0013), days to first picking (0.0023), plant height (0.0128), fruit length (0.0625), fruit girth (0.0057) and fruit weight (0.0940) on fruit yield per plant. It had negative and very low indirect effect through number of branches per plant (-0.0001), number of nodes on main stem per plant (-0.0106) and internodal length (-0.0030) on fruit yield per plant.

4.5 SELECTION INDICES

For the construction of selection indices, the characters, which had desirable correlation as well as moderate to high direct effect on fruit yield per plant and high genetic advance were considered. In this context, fruit yield per plant (X_1) along with its four components viz., plant height (X_2), fruit weight (X_3), number of nodes on main stem per plant (X_4) and number of fruits per plant (X_5) were identified and considered for the construction of selection indices.

Thirty-one selection indices were constructed in all possible combinations of the four yield contributing characters and fruit yield per plant. Their respective genetic advances were calculated and relative efficiency of different discriminant functions in relation to the straight selection for fruit yield per plant was compared. The data on selection indices, discriminant functions, genetic gain and relative efficiency are given in Table 4.5, assuming the efficiency of straight selection for fruit yield per plant as 100%.

The results suggested that the selection efficiency was slightly higher, in general, over straight selection when the selection was based on component character, which further slightly increased with the inclusion of two or more characters. The highest efficiency was noted when four or five characters were considered together.

When the relative efficiency of single character index was measured, it was noted that the maximum efficiency of 100% was exhibited by fruit yield per plant followed by plant height (47.58%), fruit weight (25.60%), number of nodes on main stem per plant (9.03%) and number of fruits per plant (7.06%)

Among the combinations involving two component characters, fruit yield per plant and plant height (X_1+X_2) exhibited the maximum relative efficiency of 131.95% followed by fruit yield per plant and fruit weight [(X_1+X_3) , 114.27%], fruit yield per plant and number of fruits per plant [(X_1+X_5) , 106.80%], fruit yield per plant and number of nodes on main stem per plant [(X_1+X_4) , 105.18%], plant height and fruit weight [(X_2+X_3) , 54.01%], plant height and number of nodes on main stem per plant [(X_2+X_4) , 48.56%], plant height and number of fruits per plant [(X_2+X_5) , 48.22%], fruit weight and number of fruits per plant [(X_3+X_5) , 27.81%], fruit weight and number of nodes on main stem per plant [(X_3+X_4) , 26.54%] and number of nodes on main stem per plant and number of fruits per plant [(X_4+X_5) , 11.99%].

Table 4.5 Selection index, discriminant function, expected genetic advance in yield and relative efficiency from the use of different selection indices in okra

Sr. No.	Selection Index	Discriminant function	Expected genetic advance (Gs)	Relative efficiency (RE) (%)	Relative efficiency per character
1	X ₁	0.9403 X ₁ (Fruit yield per plant)	66.07	100.00	100.00
2	X ₂	0.8868 X ₂ (plant height)	31.43	47.58	47.57
3	X ₃	0.9330 X ₃ (fruit weight)	16.91	25.60	25.60
4	X ₄	0.9198 X ₄ (number of nodes on main stem per plant)	5.96	9.03	9.03
5	X ₅	0.9547 X ₅ (number of fruits per plant)	4.67	7.06	7.06
6	X ₁ .X ₂	0.9547 X ₁ + 0.9123 X ₂	87.18	131.95	65.97
7	X ₁ .X ₃	0.9368 X ₁ + 1.0292 X ₃	75.49	114.27	57.13
8	X ₁ .X ₄	0.9284 X ₁ + 1.2724 X ₄	69.49	105.18	52.59
9	X ₁ .X ₅	0.8277 X ₁ + 2.9139 X ₅	70.56	106.80	53.40
10	X ₂ .X ₃	0.8867 X ₂ + 0.9326 X ₃	35.68	54.01	27.00
11	X ₂ .X ₄	0.8871 X ₂ + 0.9321 X ₄	32.08	48.56	24.28
12	X ₂ .X ₅	0.8870 X ₂ + 0.9734 X ₅	31.86	48.22	24.11
13	X ₃ .X ₄	0.9333 X ₃ + 0.9249 X ₄	17.53	26.54	13.27
14	X ₃ .X ₅	0.9762 X ₃ + 1.4015 X ₅	18.37	27.81	13.90
15	X ₄ .X ₅	0.9248 X ₄ + 0.9679 X ₅	7.92	11.99	5.10
16	X ₁ .X ₂ .X ₃	0.9576 X ₁ + 0.9120 X ₂ + 0.9956 X ₃	94.52	143.05	47.68
17	X ₁ .X ₂ .X ₄	0.9469 X ₁ + 0.9217 X ₂ + 1.1884 X ₄	89.83	135.96	45.31
18	X ₁ .X ₂ .X ₅	0.7058 X ₁ + 1.1387 X ₂ + 4.3799 X ₅	90.69	137.26	45.75
19	X ₁ .X ₃ .X ₄	0.9179 X ₁ + 1.0681 X ₃ + 1.3372 X ₄	78.40	118.67	39.55
20	X ₁ .X ₃ .X ₅	0.1204 X ₁ + 2.6208 X ₃ + 12.034 X ₅	80.26	121.47	40.49
21	X ₁ .X ₄ .X ₅	0.6264 X ₁ + 2.5693 X ₄ + 5.1898 X ₅	74.11	112.17	37.39
22	X ₂ .X ₃ .X ₄	0.8871 X ₂ + 0.9301 X ₃ + 0.9154 X ₄	36.02	54.51	18.17
23	X ₂ .X ₃ .X ₅	0.8869 X ₂ + 0.9332 X ₃ + 0.9690 X ₅	35.86	54.27	18.09
24	X ₂ .X ₄ .X ₅	0.8873 X ₂ + 0.9361 X ₄ + 0.9854 X ₅	32.59	49.32	16.44
25	X ₃ .X ₄ .X ₅	0.9307 X ₃ + 0.9084 X ₄ + 0.9643 X ₅	17.79	26.93	8.97
26	X ₁ .X ₂ .X ₃ .X ₄	0.9407 X ₁ + 0.9274 X ₂ + 1.0283 X ₃ + 1.2231 X ₄	96.88	146.62	36.65
27	X ₁ .X ₂ .X ₃ .X ₅	1.1096 X ₁ + 0.7744 X ₂ + 0.7137 X ₃ + -0.5400 X ₅	97.46	147.50	36.87
28	X ₁ .X ₂ .X ₄ .X ₅	1.3130 X ₁ + 0.5937 X ₂ + -0.4347 X ₄ + -2.7449 X ₅	92.87	140.56	35.14
29	X ₁ .X ₃ .X ₄ .X ₅	1.2667 X ₁ + 0.3772 X ₃ + -0.3774 X ₄ + -2.4370 X ₅	81.58	123.48	30.86
30	X ₂ .X ₃ .X ₄ .X ₅	0.8872 X ₁ + 0.9311 X ₃ + 0.9197 X ₄ + 0.9820 X ₅	36.26	54.88	13.72
31	X ₁ .X ₂ .X ₃ .X ₄ .X ₅	1.0412 X ₁ + 0.8367 X ₂ + 0.8386 X ₃ + 0.7183 X ₄ + 0.3573 X ₅	99.80	151.05	30.21

The selection index based on three characters combinations indicated that a discriminant function with fruit yield per plant, plant height and fruit weight exerted highest relative efficiency $[(X_1+X_2+X_3), 143.05\%]$ followed by fruit yield per plant, plant height and number of fruits per plant $[(X_1+X_2+X_5), 137.26\%]$, fruit yield per plant, plant height and number of nodes on main stem per plant $[(X_1+X_2+X_4), 135.96\%]$, fruit yield per plant, fruit weight and number of fruits per plants $[(X_1+X_3+X_5), 121.47\%]$, fruit yield per plant, fruit weight and number of nodes on main stem per plant $[(X_1+X_3+X_4), 118.67\%]$, fruit yield per plant, number of nodes on main stem per plant and number of fruits per plant $[(X_1+X_4+X_5), 112.17\%]$, plant height, fruit weight and number of nodes on main stem per plant $[(X_2+X_3+X_4), 54.51\%]$, plant height, fruit weight and number of fruits per plant $[(X_2+X_3+X_5), 54.27\%]$, plant height, number of nodes on main stem per plant and number of fruits per plant $[(X_2+X_4+X_5), 49.32\%]$ and fruit weight, number of nodes on main stem per plant and number of fruits per plant $[(X_3+X_4+X_5), 26.93\%]$.

The selection index based on four characters combinations indicated that a discriminant function with fruit yield per plant, plant height, fruit weight and number of fruits per plant $(X_1+X_2+X_3+X_5)$ exerted 147.50% relative efficiency followed by fruit yield per plant, plant height, fruit weight and number of nodes on main stem per plant $[(X_1+X_2+X_3+X_4), 146.62\%]$, fruit yield per plant, plant height, number of nodes on main stem per plant and number of fruits per plant $[(X_1+X_2+X_4+X_5), 140.56\%]$, fruit yield per plant, fruit weight, number of nodes on main stem per plant and number of fruits per plant $[(X_1+X_3+X_4+X_5), 123.48\%]$ and plant height, fruit weight, number of nodes on main stem per plant and number of fruits per plant $[(X_2+X_3+X_4+X_5), 54.88\%]$.

The selection index based on five characters combinations indicated that a discriminant function with fruit yield per plant, plant height, fruit weight, number of nodes on main stem per plant and number of fruits per plant $(X_1+X_2+X_3+X_4+X_5)$ exerted 151.05% relative efficiency.

Among all the 31 selection indices (Table 4.5), the index based on five characters viz., fruit yield per plant, plant height, fruit weight, number of nodes on main stem per plant and number of fruits per plant $(X_1+X_2+X_3+X_4+X_5)$ possessed the highest genetic gain and relative efficiency (99.80g, 151.05%) respectively, as compared to straight selection for fruit yield per plant. Other two important indices

based on four characters viz., fruit yield per plant, plant height, fruit weight and number of fruits per plant ($X_1+X_2+X_3+X_5$) possessed the genetic gain and relative efficiency (97.46g, 147.50%), while the other possessing, fruit yield per plant, plant height, fruit weight and number of nodes on main stem per plant ($X_1+X_2+X_3+X_4$) exerted genetic gain of 96.88g and relative efficiency of 146.62% as compared to straight selection for fruit yield per plant.

CHAPTER-V

DISCUSSION

The belief aim of the present investigation was to identify appropriate accessions from the germplasm to be utilized in the future breeding program. Prior to commence the breeding programme for higher yield, it necessary to generate the information regarding the interrelationship between the different plant characters with the yield and among themselves for quicker assessment of high yield in the selection programme. Success of plant breeding programme depends on the choice of proper parents.

The magnitude of genetic variability can find out the pace and quantum of genetic improvement through selection or hybridization followed by selection. Phenotypic variance measures the magnitude of variation arising out of differences in phenotypic values, whereas the genotypic variance measures the magnitude of variation due to difference within the genotypic values. Thus, study of genetic variability along with heritability is the first stage to succeed in selection and utilization of genotypes in breeding programme. Hence, it is important to study the cause and effect relationship between fruit yield and its component characters.

To plan an efficient plant breeding programme, adequate knowledge of the magnitude and direction of interrelationship of quantitative traits of economic importance with fruit yield and among themselves is necessary. For this reason, correlation studies are helpful to some extent to the breeders, but they do not take into consideration the cause and effect relationship, which restricts the practical utility of correlations in selection programme. The path coefficient analysis disintegrating the total correlation between two variables into direct and indirect effects. This technique could be used to understand the cause of association between two variables and provides basis for selection of superior genotypes from the diverse breeding populations.

In view of obtaining information on variability, heritability, genetic advance, correlation coefficient, path coefficient analysis and selection indices for 12 different characters, a study was undertaken on “Genetic variability, correlation, selection indices and path analysis for fruit yield and its contributing characters in okra

[*Abelmoschus esculentus* (L.) Moench]” during *kharif*- 2020 involving 75 genotypes of okra. The results obtained in the present investigation are given in the preceding chapter; the salient features are discussed as under:

5.1 Analysis of variance

5.2 Genetic variability

5.3 Correlation coefficient

5.4 Path coefficient analysis

5.5 Selection indices

5.1 ANALYSIS OF VARIANCE

The estimates of mean sum of squares due to genotypes were highly significant for all the traits indicating the presence of sufficient amount of genetic variability among the germplasm. Similar results were found by Prashant Kumar *et al.* (2011), Senapathi *et al.* (2011), Reddy *et al.* (2012), Verma *et al.* (2014), Yonas *et al.* (2014), Chandramouli *et al.* (2016), Sharma *et al.* (2016), Hallur *et al.* (2017) and Kumar *et al.* (2019). Thus, considerable amount of genetic variability was present in the experimental material, which can be exploited for improvement of fruit yield and yield attributes in okra.

5.2 GENETIC VARIABILITY

Variability refers to the presence of differences among the individuals of plant population. Variability results due to difference either in the genetic constitution of the individuals of a population or in the environment in which they are grown. The existence of variability is necessary for resistance to biotic and abiotic factors as well as for wide adaptability. The reality of variability is vital for any crop improvement programme. Selection is effective only when there is presence of sufficient genetic variability among the individuals in a population. Thus, perception into the magnitude of variability present in a population is of paramount significance to a plant breeder for starting a judicious breeding programme.

The amount of genetic variability present in any base population is most important for the success of breeding programme. There is more genetic potentiality in the genetically variable populations increased the chances for selecting promising

and desired types. The genetic variability calculated from phenotypic observations, which are the results of interaction of genotypes and environment. Since environment has a great influence on many quantitative characters, the observed variability may be split under heritable and non heritable components with the help of appropriate parameters like; GCV, heritability and genetic advance to choose the criteria of selection in a breeding programme.

The better index for measuring the genetic variability is genetic coefficient of variation as described by Burton and De Vane (1952) to compare the genetic variability present in different traits. The total variability in each of these characters could be partitioned into three components viz., phenotypic, genotypic and environmental variances. This helps to determine the heritable and non heritable portion of variation in respect to the characters under study. The least genotypic and phenotypic variances were noticed for days to first picking, while the number of branches per plant had maximum genotypic and phenotypic variances.

5.2.1 Genotypic and phenotypic coefficients of variation (GCV and PCV)

By prospect to compare different quantitative characters in respect of phenotypic and genotypic variability, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated. The genotypic coefficient of variation measures the range of inherent variation present in a character and helps to compare the variability present in different characters.

The PCV and GCV measure the amount of variation present in the population in the particular character. In the present examination, PCV was slightly higher than the respective GCV for all the characters studied, indicated that the environment had less influence on the expression of these characters, which is in accordance with findings of Adiger *et al.* (2011), Senapati *et al.* (2011), Reddy *et al.* (2012), Duggi *et al.* (2013a), Sharma *et al.* (2016) and Rana *et al.* (2020).

The high magnitude of GCV and PCV were observed for number of branches per plant, fruit yield per plant, number of fruits per plant and number of nodes on main stem per plant. This is in relation with the earlier reports of Reddy *et al.* (2012), Duggi *et al.* (2013a) for number of branches per plant, number of fruits per plant and fruit yield per plant; Adiger *et al.* (2011) and Yonas *et al.* (2014) for number of branches per plant; Duggi *et al.* (2013) and Khajuria *et al.* (2016) for number of fruits

per plant; Chandramouli *et al.* (2016) for fruit yield per plant and Das *et al.* (2012) for number of nodes on main stem per plant.

The moderate magnitude of GCV and PCV were observed internodal length, plant height, fruit length, fruit weight, fruit girth and total number of pickings. This is in relation with earlier reports of Reddy *et al.* (2012) for internodal length, plant height and fruit length; Chandramouli *et al.* (2016) for internodal length, fruit length and fruit girth; Das *et al.* (2012), Nwangburka *et al.* (2012) and Koundinya *et al.* (2013) for plant height; Das *et al.* (2012), Goswami *et al.* (2012) and Duggi *et al.* (2013a) for fruit length and Goswami *et al.* (2012) for internodal length; Reddy *et al.* (2012) and Ahamed *et al.* (2015) for fruit weight.

However, low magnitudes of GCV and PCV were recorded for days to 50% flowering and days to first picking. The most probable reason could be the phenotypic plasticity occurring in these characters is the main source of variation than the genetic variance. Such results also indicated that selection is not effective for these characters because of the narrow genetic base. Lower magnitudes of GCV and PCV were also reported by Chandramouli *et al.* (2016) for days to 50% flowering and days to first picking and Reddy *et al.* (2012) and Duggi *et al.* (2013a) for days to 50% flowering.

5.2.2 Heritability (h^2_{bs})

Though, the genotypic coefficient of variation measures the relative amount of variation present in a particular character. However, it is not possible to determine the proportion of heritable variation present in the total variation. Consequently, heritability which represents the heritable variation existing in the character was calculated. High values of heritability in broad sense are useful in identifying the appropriate character for selection and in enabling the breeders to select superior genotypes on the basis of phenotypic expression of quantitative characters (Johnson *et al.*, 1955).

In the present investigation, high heritability estimates were observed for days to 50% flowering, plant height, number of branches per plant, number of nodes on main stem per plant, internodal length, number of fruits per plant, fruit length, fruit girth, fruit weight, total number of pickings and fruit yield per plant. High heritability estimates indicated that the characters were least influenced by the environmental effects. This also recommended that the phenotypes were the true representative of

their genotypes for these traits and selection based on phenotypic value could be more reliable.

Similar results of high heritability were reported by Adiger *et al.* (2011), Das *et al.* (2012), Nwangburuka *et al.* (2012), Reddy *et al.* (2012), Duggi *et al.* (2013a), Yonas *et al.* (2014), Ahamed *et al.* (2015) and Kerure *et al.* (2017) for fruit weight; Das *et al.* (2012), Reddy *et al.* (2012), Duggi *et al.* (2013a), Ahamed *et al.* (2015), Chandramouli *et al.* (2016) and Kerure *et al.* (2017) for number of fruits per plant; Nwangburuka *et al.* (2012), Reddy *et al.* (2012), Duggi *et al.* (2013a) and Chandramouli *et al.* (2016) for number of branches per plant; Adiger *et al.* (2011), Oluwa and Kehinde (2011), Das *et al.* (2012), Goswami *et al.* (2012), Reddy *et al.* (2012), Yonas *et al.* (2014), Chandramouli *et al.* (2016) and Rambabu *et al.* (2019) for intermodal length; Nwangburuka *et al.* (2012), Reddy *et al.* (2012), Duggi *et al.* (2013a), Chandramouli *et al.* (2016) and Amba Kumari *et al.* (2019) for fruit girth; Amba Kumari *et al.* (2019) for number of nodes per plant; Nwangburuka *et al.* (2012), Reddy *et al.* (2012), Duggi *et al.* (2013a) and Kerure *et al.* (2017) for fruit length; Adiger *et al.* (2011), Oluwa and Kehinde (2011), Senapati *et al.* (2011), Das *et al.* (2012), Goswami *et al.* (2012), Reddy *et al.* (2012), Duggi *et al.* (2013a), Verma *et al.* (2014), Ahamed *et al.* (2015), Chandramouli *et al.* (2016), Kerure *et al.* (2017), Amba Kumari *et al.* (2019) and Rambabu *et al.* (2019) for fruit yield per plant; Adiger *et al.* (2011), Chaukhande *et al.* (2011a), Das *et al.* (2012), Goswami *et al.* (2012), Nwangburuka *et al.* (2012), Reddy *et al.* (2012), Duggi *et al.* (2013a), Yonas *et al.* (2014), Sharma *et al.* (2016), Kerure *et al.* (2017) and Rambabu *et al.* (2019) for plant height; Phani Krishna *et al.* (2015) for total number of picking; Adiger *et al.* (2011), Reddy *et al.* (2012) and Duggi *et al.* (2013a) for days to 50% flowering.

The estimates of heritability were moderate for days to first picking. None of the scientist reported moderate heritability for days to first picking.

5.2.3 Genetic advance (G_s)

The expected genetic advance value was high for characters; plant height and fruit yield per plant. Similar results were also observed by Das *et al.* (2012), Nwangburuka *et al.* (2012), Reddy *et al.* (2012), Yonas *et al.* (2014), Ahamed *et al.* (2015), Kerure *et al.* (2017) and Rambabu *et al.* (2019) for plant height and Reddy *et al.* (2012), Ahamed *et al.* (2015), Chandramouli *et al.* (2016), Kerure *et al.* (2017), Amba Kumari *et al.* (2019) and Rambabu *et al.* (2019) for fruit yield per plant.

The expected genetic advance value was moderate for fruit weight. Similar results were also observed by Rambabu *et al.* (2019) for fruit weight.

In the present investigation, low genetic advance was observed for number of nodes on main stem per plant, number of fruits per plant, days to 50% flowering, total number of pickings, fruit length, days to first picking, internodal length, fruit girth and number of branches per plant. The results are in agreement with the findings of Chandramouli *et al.* (2016) and Amba Kumari *et al.* (2019) for number of nodes on main stem per plant; Reddy *et al.* (2012), Chandramouli *et al.* (2016), Amba Kumari *et al.* (2019) and Rambabu *et al.* (2019) for number of fruits per plant; Reddy *et al.* (2012), Yonas *et al.* (2014), Chandramouli *et al.* (2016), Kerure *et al.* (2017) and Amba Kumari *et al.* (2019) for days to 50% flowering; Chandramouli *et al.* (2016) and Rambabu *et al.* (2019) for total number of pickings; Reddy *et al.* (2012), Chandramouli *et al.* (2016), Kerure *et al.* (2017), Amba Kumari *et al.* (2019) and Rambabu *et al.* (2019) for fruit length; Chandramouli *et al.* (2016) for days to first picking; Reddy *et al.* (2012), Yonas *et al.* (2014), Chandramouli *et al.* (2016), Amba Kumari *et al.* (2019) and Rambabu *et al.* (2019) for internodal length; Chandramouli *et al.* (2016) and Rambabu *et al.* (2019) for fruit girth and Reddy *et al.* (2012), Chandramouli *et al.* (2016), Kerure *et al.* (2017), Amba Kumari *et al.* (2019) and Rambabu *et al.* (2019) for number of branches per plant.

5.2.4 Genetic advance expressed as percentage of mean (GAM %)

The highest genetic advance expressed as percentage of mean was exhibited by number of branches per plant followed by fruit yield per plant, number of fruits per plant, number of nodes on main stem per plant, internodal length, plant height, fruit length, fruit weight, fruit girth and total number of pickings. The results are in agreement with the findings of Nwangburuka *et al.* (2012), Reddy *et al.* (2012), Duggi *et al.* (2013a), Yonas *et al.* (2014), Chandramouli *et al.* (2016) and Hallur *et al.* (2017) for number of branches per plant; Adiger *et al.* (2011), Das *et al.* (2012), Goswami *et al.* (2012), Reddy *et al.* (2012), Duggi *et al.* (2013a), Verma *et al.* (2014), Yonas *et al.* (2014), Chandramouli *et al.* (2016) and Hallur *et al.* (2017) and Rambabu *et al.* (2019) for fruit yield per plant; Reddy *et al.* (2012), Duggi *et al.* (2013a), Yonas *et al.* (2014), Chandramouli *et al.* (2016) and Hallur *et al.* (2017) for number of fruits per plant; Adiger *et al.* (2011), Das *et al.* (2012), Goswami *et al.* (2012), Reddy *et al.* (2012), Yonas *et al.* (2014), Chandramouli *et al.* (2016) and Rambabu *et al.* (2019)

for internodal length; Nwangburuka *et al.* (2012), Reddy *et al.* (2012), Duggi *et al.* (2013a) and Yonas *et al.* (2014) for fruit length; Reddy *et al.* (2012), Duggi *et al.* (2013a) and Yonas *et al.* (2014) for fruit weight; Rambabu *et al.* (2019) for total number of pickings; Adiger *et al.* (2011), Das *et al.* (2012), Goswami *et al.* (2012), Nwangburuka *et al.* (2012), Reddy *et al.* (2012), Duggi *et al.* (2013a), Yonas *et al.* (2014), Sharma *et al.* (2016) and Rambabu *et al.* (2019) for plant height and Chandramouli *et al.* (2016) for fruit girth.

Low genetic advance expressed as percent of mean was observed for days to 50% flowering and days to first picking. The results are in agreement with the findings of Chandramouli *et al.* (2016), Sharma *et al.* (2016), Kerure *et al.* (2017) and Rathava *et al.* (2019) for days to 50% flowering and Goswami *et al.* (2012) and Chandramouli *et al.* (2016) for days to first picking.

Johnson *et al.* (1955) recommended that the heritability and genetic advance when considered together would be more reliable and helpful in predicting the resultant effects of selection. Rapid progress in selection can be achieved when high heritability is accompanied with high genetic advance, which forms the most reliable index of selection (Burton, 1952). In the present investigation, high estimates of heritability coupled with high genetic advance expressed as percentage of mean were observed for all the characters except days to 50% flowering and days to first picking. The results are in agreement with Das *et al.* (2012), Reddy *et al.* (2012), Duggi *et al.* (2013a), Yonas *et al.* (2014), Ahamed *et al.* (2015), Sharma *et al.* (2016), Kerure *et al.* (2017) and Rambabu *et al.* (2019) for plant height; Reddy *et al.* (2012), Duggi *et al.* (2013a), Yonas *et al.* (2014), Chandramouli *et al.* (2016), Kerure *et al.* (2017) and Rambabu *et al.* (2019) for number of branches per plant; Yonas *et al.* (2014) and Chandramouli *et al.* (2016) for number of nodes on main stem per plant; Reddy *et al.* (2012), Yonas *et al.* (2014) and Chandramouli *et al.* (2016) for internodal length; Das *et al.* (2012), Reddy *et al.* (2012), Duggi *et al.* (2013a), Yonas *et al.* (2014), Ahamed *et al.* (2015), Chandramouli *et al.* (2016), Kerure *et al.* (2017) and Rambabu *et al.* (2019) for number of fruits per plant; Das *et al.* (2012), Reddy *et al.* (2012), Duggi *et al.* (2013a), Yonas *et al.* (2014), Ahamed *et al.* (2015), Chandramouli *et al.* (2016) and Kerure *et al.* (2017) for fruit length; Chandramouli *et al.* (2016) for fruit girth; Das *et al.* (2012), Reddy *et al.* (2012), Duggi *et al.* (2013a), Yonas *et al.* (2014), Ahamed *et al.* (2015), Kerure *et al.* (2017) and Rambabu *et al.* (2019) for fruit weight

and Reddy *et al.* (2012), Duggi *et al.* (2013), Yonas *et al.* (2014), Ahamed *et al.* (2015), Chandramouli *et al.* (2016), Kerure *et al.* (2017), Amba Kumari *et al.* (2019) and Rambabu *et al.* (2019) for fruit yield per plant, which may be attributed to the preponderance of additive gene action and possess high selective value and thus, selection pressure could profitably be applied on these traits for their rational improvement in okra. High or moderate estimates of heritability with low genetic advance as percent of mean were observed for days to 50% flowering and days to first picking. The results were in agreement with the findings of Chandramouli *et al.* (2016) for days 50% flowering and days to first picking, which revealed the presence of non-additive gene action and influence of environment in the expression of this character and thus, the selection would be less effective.

5.3 CORRELATION COEFFICIENT

The knowledge of association among the characters is helpful to the breeder for improving the efficiency of selection. Correlation coefficient analysis measures the mutual relationship between plant characters and determines the component character on which selection can be made for genetic improvement of yield. Study regarding the presence of component and nature of association among themselves is necessary and pre-requisite for improvement in yield. Correlation coefficient provides a clear image of the amount of association between a pair of traits and indicates whether simultaneous improvement of the correlated traits may be possible or not. The knowledge of genetic association between yield and its component attributes help in improving the efficiency of selection for yield by making appropriate choice and balancing one component with another.

Correlation among characters may result from pleiotrophy, physiological associations or linkage among characters. The linkage is a cause of transfer correlations particularly in a population resultant from crosses between divergent strains. The correlation is the overall or net effect of the segregating genes; some of the genes may increase both the characters causing the positive correlation, whereas the others may increase the one and decrease the other causing the negative correlation (Falconer, 1981) Thus, to accumulate optimal combination of yield contributing characters in a single genotype, it is necessary to know the inference of the interrelationship of various characters.

In the present investigation, the values of genotypic correlations were higher than their corresponding phenotypic correlations except in few cases. This indicated that though there was high degree of association between two variables at genotypic level, its phenotypic expression was deflated by the influence of environment. It also indicated that there was an inherent relationship between the characters studied, which is in agreement with the conclusions of Senapathi *et al.* (2011), Saryam *et al.* (2015) and Shuirkar *et al.* (2018).

Correlation between yield and its components

In the present investigation fruit yield per plant showed highly significant and positive correlations with plant height, number of nodes on main stem per plant, number of fruits per plant, fruit length, fruit weight and total number of pickings at both genotypic and phenotypic levels. Similar results were also reported by Balakrishnan and Sreenivasan (2010), Chaukhande *et al.* (2011b), Koundinya and Dhankhar (2013), Balai *et al.* (2014), Nirosha *et al.* (2014) and Thulasiram *et al.* (2017) for plant height; Thulasiram *et al.* (2017) for number of nodes on main stem per plant; Balakrishnan and Sreenivasan (2010), Senapati *et al.* (2011) and Amba Kumari *et al.* (2017), Hallur *et al.* (2017), Pithiya *et al.* (2017) and Thulasiram *et al.* (2017) for number of fruits per plant; Balakrishnan and Sreenivasan (2010), Adiger *et al.* (2011), Senapati *et al.* (2011), Saryam *et al.* (2015), Amba Kumari *et al.* (2017) and Hallur *et al.* (2017) for fruit length; Balakrishnan and Sreenivasan (2010), Adiger *et al.* (2011), Senapati *et al.* (2011) and Hallur *et al.* (2017) for fruit weight and Ahamed *et al.* (2015) for total number of pickings.

Plant height had highly significant and positive association with number of nodes on main stem per plant, number of fruits per plant, total number of pickings and fruit yield per plant. Similar results were reported by Das *et al.* (2012) for number of nodes on main stem per plant; Koundinya and Dhankhar (2013) and Ahamed *et al.* (2015) for number of fruits per plant; Balakrishnan and Sreenivasan (2010), Chaukhande *et al.* (2011b), Koundinya and Dhankhar (2013), Balai *et al.* (2014) and Nirosha *et al.* (2014) for fruit yield per plant. Number of nodes on main stem per plant had highly significant and positive correlation with number of fruits per plant and total number of pickings. Similar results were earlier reported by Das *et al.* (2012) for number of fruits per plant. Fruit length had positive and highly significant correlation with fruit girth, fruit weight and total number of pickings. Similar results were earlier

reported by Deepanshu and Shamad (2017) for fruit girth; Das *et al.* (2012), Balai *et al.* (2014), Yonas *et al.* (2014) and Ahamed *et al.* (2015) for fruit weight. Fruit girth had positive and highly significant correlation with fruit weight. Similar results were earlier reported by Deepanshu and Shamad (2017) for fruit weight. Fruit weight had positive and highly significant correlation with total number of pickings.

5.4 PATH ANALYSIS

The aim of the breeder is to discover remedies for specific defects to a complex aim of maximizing the yield potential. Yield is a complex character and is the multiplicative end product of several component traits. Some of them may be grouped as main component which directly contribute towards yield, where, other cannot contribute directly to the yield but indirectly may influence the yield by changing the performance and growth of different components, for that reason it would be better to know how the yield is directly and indirectly influenced by other characters.

The path analysis is partition the correlation coefficient into direct and indirect effects, so that, a relative merit of each trait is established and their number is reduced in selection programmes. In order to achieve a clear picture of inter-relationship of various component traits with yield, direct and indirect effects were calculated using path analysis at genotypic level.

In the present study, path coefficient analysis revealed that number of fruit per plant had highest positive direct effect on fruit yield per plant. This is reflected in their significant and positive association with fruit yield. These results are in close harmony with the findings of Gangashetti *et al.* (2013), Sharma and prasad (2015) and Pithiya *et al.* (2017) for the number of fruit per plant.

Fruit weight had positive and moderate direct effect on fruit yield per plant. None of the scientist reported moderate direct effect for fruit weight. Fruit length had positive and low direct effect on fruit yield per plant. Days to first picking, plant height, number of branches per plant, fruit girth and total number of pickings had positive and very low direct effect on fruit yield per plant. Similar results were reported by Alam *et al.* (2020) for fruit length and days to first picking; Adiger *et al.* (2011) for plant height; Adiger *et al.* (2011), Kumar and Reddy (2016), Kumar *et al.* (2019), Alam *et al.* (2020) and Ashraf *et al.* (2020) for number of branches per plant.

Days to 50% flowering, number of nodes on main stem per plant and internodal length had negative and very low direct effect on fruit yield per plant. Similar results were reported by Adiger *et al.* (2011) and Alam *et al.* (2020) for days to 50% flowering; Saryam *et al.* (2015), Kumar and Reddy (2016), Dwivedi and Sharma (2017) recorded same results for internodal length.

5.5 SELECTION INDICES

The plant breeder has certain desired plant characteristics in his mind, while selecting for particular genotypes and for this he applies various weights to different traits for arriving on decisions. The better way of exploiting genetic correlations with several characters having high heritability is to construct an index which combines information on all the characters associated with fruit yield. This suggests the use of selection index, which gives proper weight to each of the two or more characters to be considered.

Hazel and Lush (1943) reported that the selection based on such an index was more efficient than selecting individually for the various characters. The basis for the development of the selection indices has been provided by Smith (1936), Hazel and Lush (1943) and Robinson *et al.* (1951).

Hazel and Lush (1943) reported that the superiority of selection based on index increases with an increase in the number of characters under selection. In the present investigation also, the genetic advance and relative efficiency assessed for different indices slightly increased, when selection was based on two or more characters. The maximum genetic advance (Gs) and relative efficiency (RE) in single character discriminant function were 66.07g and 100%, respectively, which however, increased to 87.18g and 131.95% in two character combinations, respectively, 94.52g and 143.05% in three character combinations, respectively and 96.88g and 146.62%, in four characters combinations, respectively. Thus, there was an increase in the genetic gain as well as in relative efficiency with inclusion of an additional trait in the character combinations. In five characters combination, the highest genetic advance and relative efficiency were observed of 99.80g and 151.05%, respectively.

Singh and Singh (1978), Al-Rawi *et al.* (1984), Lal (1986) and Monpara *et al.* (2010) were also with the same observations that an increase in characters results in

an increase in genetic gain and that the selection indices improve the efficiency of selection than the straight selection for yield alone.

In the present study, it was also observed that the straight selection for yield was not that much rewarding ($G_s=66.07g$, $RE=100.00\%$) as it was through its components like; plant height ($G_s=31.43g$, $RE=47.58\%$), fruit weight ($G_s=16.91g$, $RE=25.60\%$), number of nodes on main stem per plant ($G_s=5.96g$, $RE=9.03\%$) and number of fruits per plant ($G_s=4.67g$, $RE=7.06\%$). The maximum efficiency in selection for fruit yield was exhibited by a discriminant function involving fruit yield per plant, plant height, fruit weight, number of nodes on main stem per plant and number of fruits per plant, which had a genetic advance and relative efficiency of 99.80g and 151.05%, respectively followed by an index of four characters viz., fruit yield per plant, plant height, fruit weight and number of fruits per plant, which had a genetic advance and relative efficiency of 97.46g and 147.50%, respectively.

Further, there was a consistent increase in the relative efficiency of the succeeding index with simultaneous inclusion of each character. However, in practice, the plant breeder might be interested in the maximum gain with the minimum number of characters. In such a case, selection index involving fruit yield per plant, plant height, fruit weight, number of nodes on main stem per plant and number of fruits per plant ($X_1.X_2.X_3.X_4.X_5$) followed by fruit yield per plant, plant height, fruit weight and number of fruits per plant ($X_1.X_2.X_3.X_5$) and fruit yield per plant, plant height, fruit weight and number of nodes on main stem per plant ($X_1.X_2.X_3.X_4$) could be advantageously exploited in the okra breeding programmes. The results of the present investigation also revealed that the discriminant function method of making selection in plants appeared to be the most useful than the straight selection for fruit yield alone and thus, due weightage should be given to the important selection indices while making selection for yield advancement in okra.

CHAPTER - VI

SUMMARY AND CONCLUSION

The present investigation on “Genetic variability, correlation, selection indices and path analysis for fruit yield and its contributing characters in okra [*Abelmoschus esculentus* (L.) Moench]” was carried out to study coefficient of variation, heritability, and genetic advance, correlations among different characters, selection indices and path coefficient analysis in 75 genotypes of okra. The study was conducted in Randomized Block Design with two replications at Vegetable Research Station, Junagadh Agricultural University, Junagadh during *kharif* -2020.

The observations were recorded on five randomly selected plants in each genotype and replication and their mean values were used for statistical analysis except days to 50% flowering and days to first picking which were recorded plot basis. The characters studied were days to 50% flowering, days to first picking, plant height, number of branches per plant, number of nodes on main stem per plant, internodal length, number of fruits per plant, fruit length (cm), fruit girth (cm), fruit weight (g), total number of pickings and fruit yield per plant. The salient findings of the present study are summarized as under:

1. The analysis of variance revealed that mean squares due to genotypes were found highly significant for all the characters indicating the existence of ample genetic variability in the experimental material.
2. Number of branches per plant recorded the maximum coefficient of range followed by fruit yield per plant, number of fruits per plant, number of nodes on main stem per plant and internodal length.
3. The values of phenotypic coefficient of variation were slightly higher than that of genotypic coefficient of variation for all the characters studied, representing less effect of environment on the expression of characters studied. This suggests that phenotypic variation can be used to judge genetic variation.
4. The high to moderate genotypic coefficient of variation and phenotypic coefficient of variation was observed for number of branches per plant followed by fruit yield per plant, number of fruits per plant, number of nodes on main stem per plant,

internodal length, plant height, fruit length, fruit weight, fruit girth and total number of pickings. The results indicated the presence of wide variation for the traits under study to allow further improvement by selection of the individual traits. This indicated that existence of genetic variation for these characters and selection of better segregated populations on the basis of phenotypic performance.

5. The high heritability (broad sense) values were observed for all the twelve characters except days to first picking. The high heritability values point out that heritability may be due to higher contribution of genotypic components in these characters.
6. The genetic advance expressed as percentage of mean was found high for number of branches per plant followed by fruit yield per plant, number of fruit per plant, number of nodes on main stem per plant, internodal length, plant height, fruit length, fruit weight, fruit girth and total number of pickings. It was found low for days to 50% flowering and days to first picking.
7. High heritability along with high genetic advance was reported for plant height, number of branches per plant, number of nodes on main stem per plant, internodal length, number of fruits per plant, fruit length, fruit girth, fruit weight, total number of pickings and fruit yield per plant, it indicate presence of additive gene action for these traits. So, direct selection is effective.
8. The value of genotypic correlation was higher as compared to the corresponding phenotypic correlation for most of the characters. This indicated that there was a high degree of association between two variables at genotypic level and phenotypic expression was deflated by the influence of the environment.
9. Highly significant and positive correlation of fruit yield per plant was found with plant height, number of nodes on main stem per plant, number of fruits per plant, fruit length, fruit weight and total number of pickings at genotypic and phenotypic levels.
10. The path coefficient analysis revealed high and positive direct effects of number of fruits per plant on fruit yield per plant, while, fruit weight had moderate and positive direct effect on fruit yield per plant. It revealed that for improvement of fruit yield per plant in okra through a selection programme, more emphasis should be given to number of fruits per plant and fruit weight for direct selection in okra.

11. The phenotypic residual effects was low which suggesting that the most of the yield attributes have been included in the study of path analysis.
12. The discriminant function selection had higher genetic gain and relative efficiency over straight selection for fruit yield per plant alone. There was an increase in genetic gain and relative efficiency with an increase of an additional trait in character combination.
13. The results of the present investigation also revealed that the discriminant function method of making selection in plants appeared to be the most helpful than the straight selection for fruit yield per plant alone and therefore, due weightage should be given to the important selection indices while making selection for yield advancement in okra.
14. The discriminant functions based on a single character index indicated the fruit yield per plant showed the highest relative efficiency followed by plant height, fruit weight, number of nodes on main stem per plant and number of fruits per plant. Among the combinations involving two component characters, fruit yield per plant and plant height had the maximum relative efficiency thus, there was an increase in the genetic gain as well as relative efficiency with inclusion of an additional trait in the character combinations.
15. Among all the 31 selection indices, the index based on five characters viz., fruit yield per plant, plant height, fruit weight, number of nodes on main stem per plant and number of fruits per plant possessed the highest genetic gain and relative efficiency as compared to straight selection for fruit yield per plant. The results therefore indicated that the maximum weightage should be given to these functions while making selection for isolating high yielding genotypes in okra.

CONCLUSION

It can be concluded from variability parameters that additive gene action was operating for number of fruits per plant, number of branches per plant, fruit yield per plant, internodal length, fruit girth, fruit weight, number of nodes on main stem per plant, fruit length, plant height and total number of pickings. Correlation study revealed that plant height, number of nodes on main stem per plant, number of fruits per plant, fruit length, fruit weight and total number of pickings were positively correlated with fruit yield per plant. Path coefficient analysis also reported that high to

Summary and Conclusions

moderate direct effect of number of fruits per plant and fruit weight on fruit yield per plant thus, due weightage should be given to these characters for selection in okra. Selection index involving fruit yield per plant, plant height, fruit weight, number of nodes on main stem per plant and number of fruits per plant could be advantageously exploited in okra breeding programmes.

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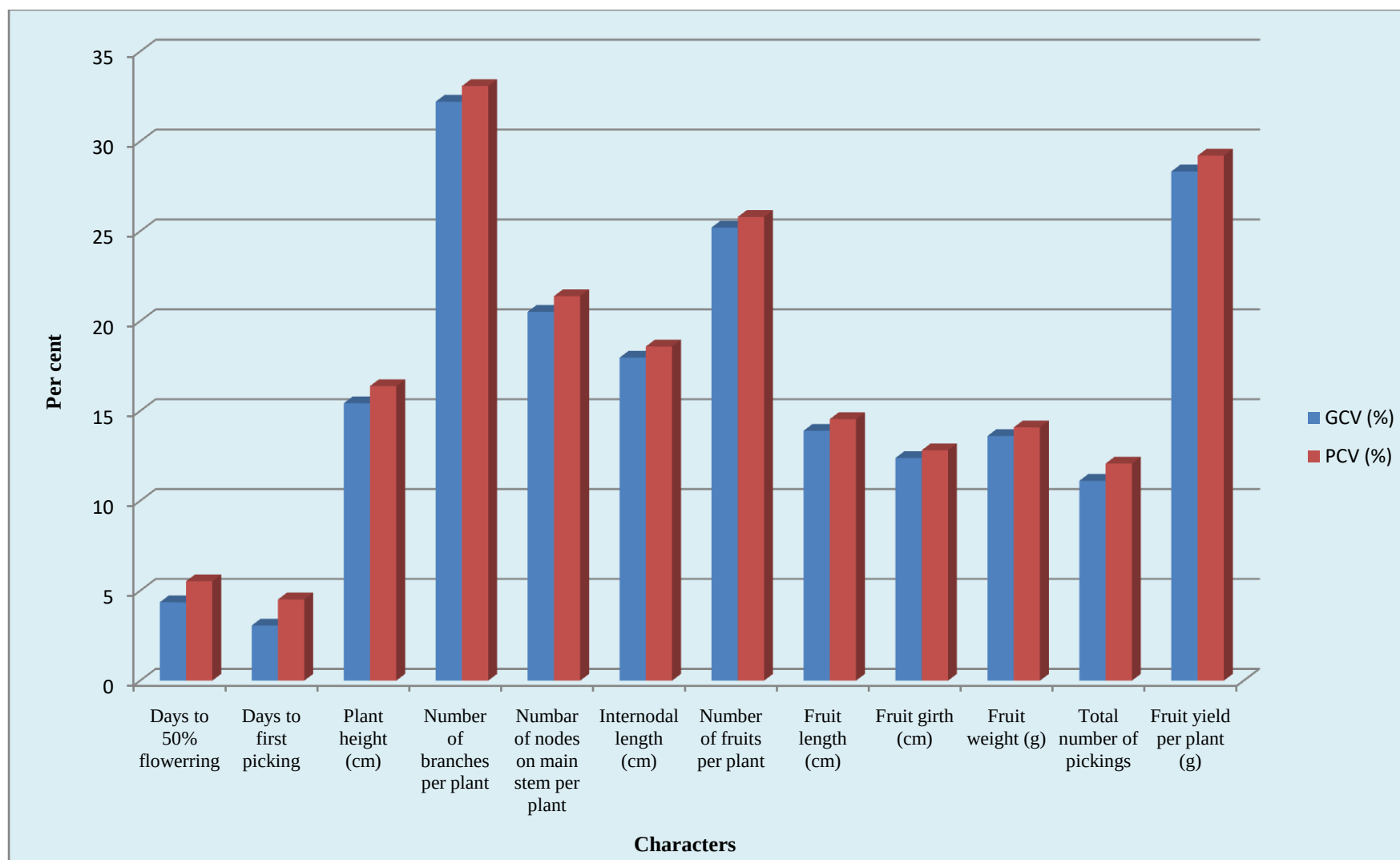


Figure 4.1 Genotypic coefficient of variation and phenotypic coefficient of variation of twelve characters in okra

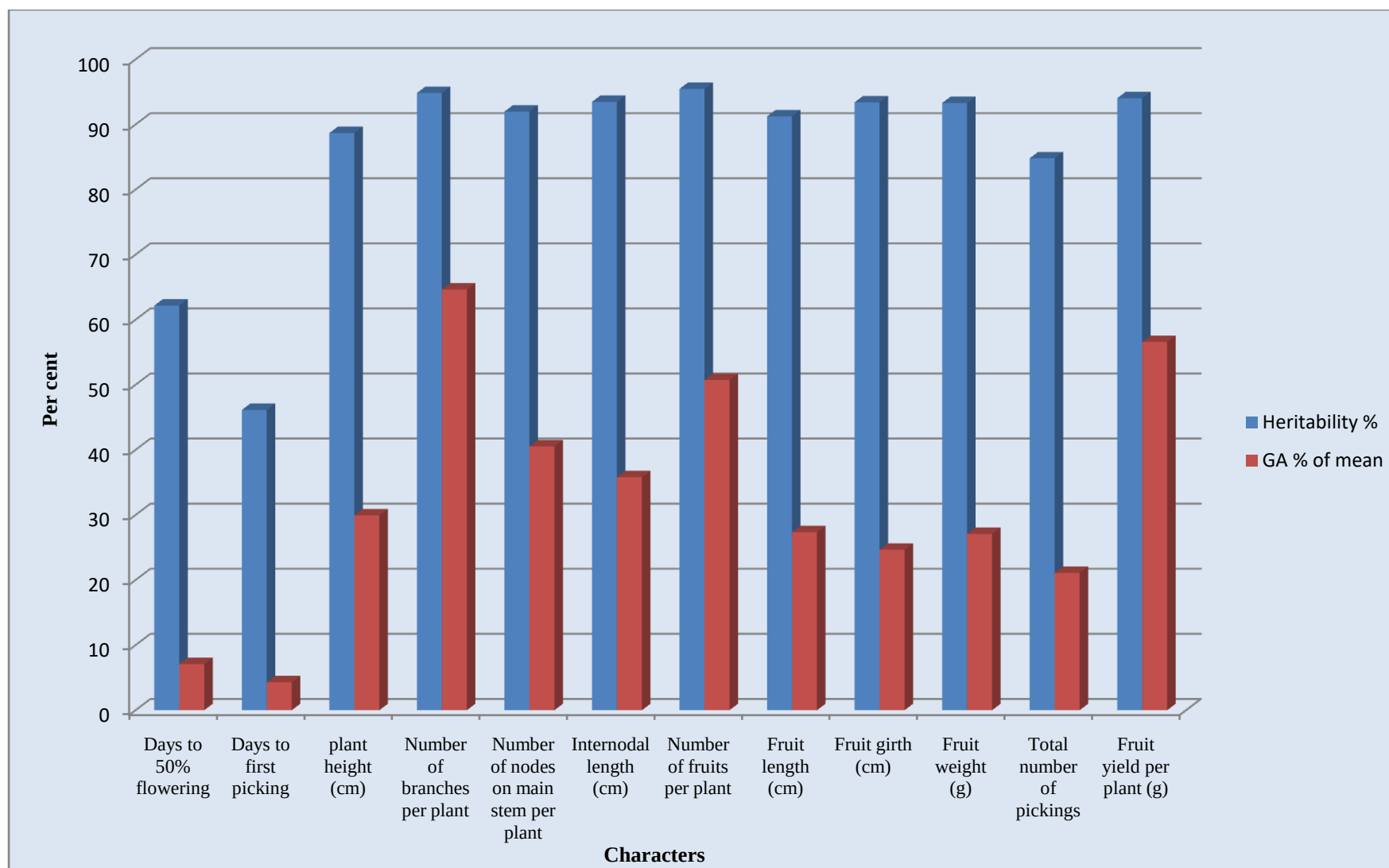


Figure 4.2 Heritability and Genetic advance expressed as per cent of mean for twelve characters in okra

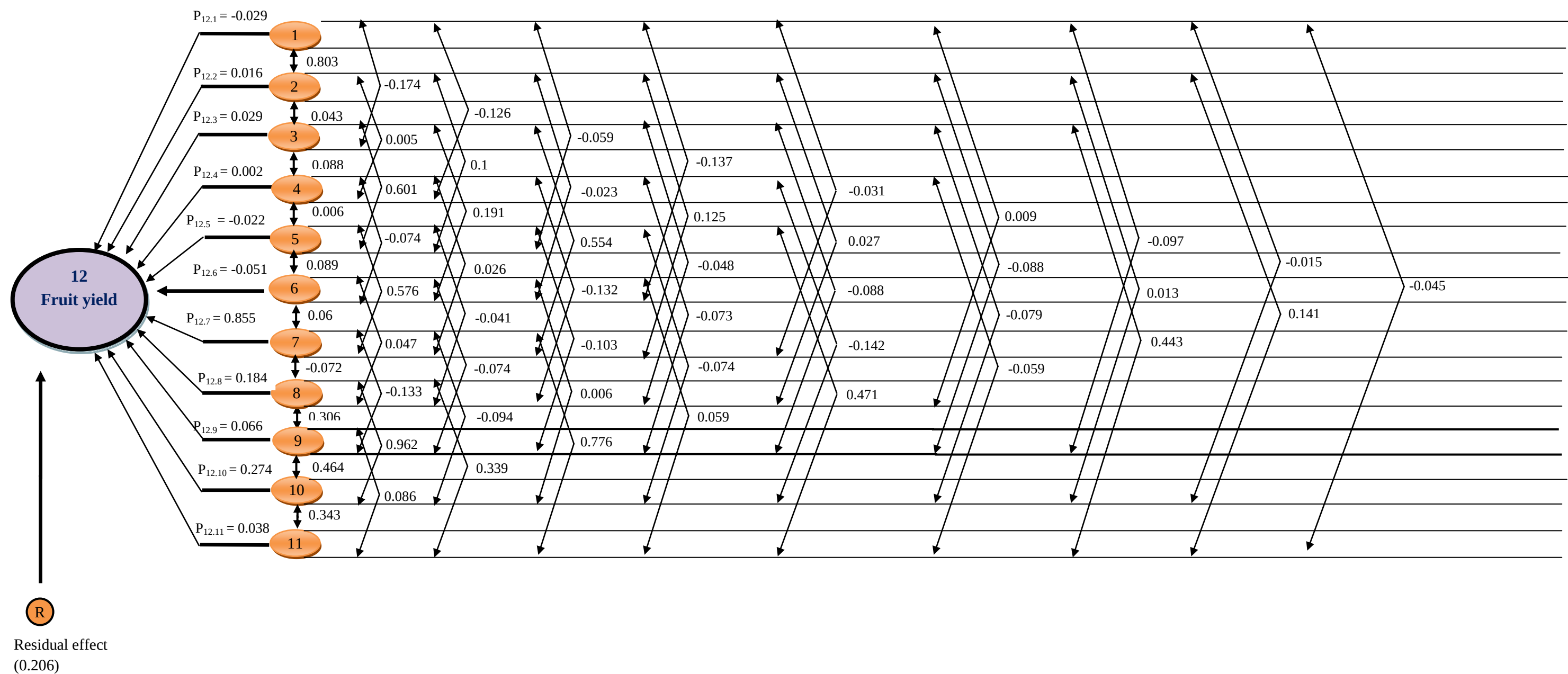


Fig 4.3:- Diagrammatic representation of phenotypic path analysis in okra

Where, double arrowed lines indicate genotypic correlation coefficient and single arrowed lines indicate direct effect

- 1) Days to 50% flowering
- 2) Days to first picking
- 3) Plant height (cm)
- 4) Number of branches per plant
- 5) Number of nodes on main stem per plant
- 6) Internodal length (cm)
- 7) Number of fruits per plant
- 8) Fruit length (cm)
- 9) Fruit girth (cm)
- 10) Fruit weight (g)
- 11) Total number of pickings
- 12) Fruit yield per plant (g)



Plate 3.1: General view of field experiment