COMPARATIVE ASSESSMENT OF BREEDING POTENTIAL IN THE DOUBLE CROSS F_2 POPULATIONS OF OKRA [*Abelmoschus esculentus* (L.) Moench]

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CERTIFICATE

This is to certify that the thesis entitled **'COMPARATIVE ASSESSMENT OF BREDING POTENTIAL IN THE DOUBLE CROSS F_2 POPULATIONS OF OKRA [*Abelmoschus esculentus* (L.) Moench]'** submitted in partial fulfillment of the requirements for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **GENETICS AND PLANT BREEDING** to the College of Agriculture, Shivamogga. Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga is a bonafide record of research work carried out by **Laavanya G. A., ID. No. MA1TBA0460** (laavanyaamar@gmail.com) during the period of study in this university under my guidance and supervision and no part of this thesis has previously formed the basis for the award of any other degree, diploma, associateship, fellowship or any other similar titles.

Shivamogga
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(Laavanya G. A.)

Comparative Assessment of Breeding Potential in Double Cross F_2 Population of Okra [*Abelmoschus esculentus* (L.) Moench]

(Laavanya G. A.)

ABSTRACT

Selection in populations derived from bi-parental crosses, usually results in the possible fixation of only two alleles governing traits in the populations. In contrast, selection in double cross derived segregating populations can result in fixation of more alleles governing complex traits. Thus, double cross derived F_2 populations generated by employing two single cross combinations are ideal for recovering superior recombinants and identifying suitable inbred lines. Okra is one of the important vegetable crops where heterosis has been exploited successfully. In this context, breeding potential of four double cross F_2 populations of okra designated as DC_1F_2 (NS864 × Arka Nikitha), DC_2F_2 (Mahyco10 × OH-102) , DC_3F_2 (Raadhika × Shakti) and DC_4F_2 (Samrat × SVOK5151) were evaluated in the field during *Rabi* 2022 at the experimental plots of College of Agriculture, Navile, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga for the traits plant height, number of internodes, internodal length, fruit length, average fruit weight, number of fruits per plant and fruit yield per plant. Breeding potential was assessed for the seven productivity traits in terms of means, standardized range, coefficient of variation and frequency of transgressive segregants recovered through rank-sum method. Double cross F_2 populations designated as DC_3F_2 (rank-sum 58) and DC_2F_2 (rank-sum 69) with lower rank-sum were considered to possess higher breeding potential. High frequency of transgressive segregants were recovered from the populations DC_3F_2 (19.33%), DC_1F_2 (13.00%) and DC_4F_2 (11.67%) which could be preferentially advanced to isolate inbred lines. Plant height, number of internodes and number of fruits per plant were identified as the field assayable proxy traits to select for fruit yield.

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ಬೆಂಡೆಯಲ್ಲಿ [*ಅಬೆಲ್ಮೋಸ್ಕಸ್ ಎಸ್ಕ್ಯುಲೆಂಟಸ್* (ಎಲ್.) ಮೊಎನ್ಚ್] ದ್ವಿಸಂಯೋಜಿತ ಗಿಡಗಳ ಸಂತಾನೋತ್ಪತ್ತಿ ಸಾಮರ್ಥ್ಯದ ತುಲನಾತ್ಮಕ ಅಧ್ಯಯನ

(ಲಾವಣ್ಯ ಜಿ.ಎ.)

ಸಾರಾಂಶ

ದ್ವಿ–ಪೋಷಕ ಸಂಯೋಜಿತಗಳಲ್ಲಿ ಪಡೆದ ಗಿಡಗಳ ಆಯ್ಕೆಯು ಸಾಮಾನ್ಯವಾಗಿ ಗಿಡಗಳಲ್ಲಿನ ಗುಣಲಕ್ಷಣಗಳನ್ನು ನಿಯಂತ್ರಿಸುವ ಎರಡು ಆಲೀಲ್‌ಗಳ ಸಂಭವನೀಯ ಸ್ಥಿರೀಕರಣಕ್ಕೆ ಕಾರಣವಾಗುತ್ತದೆ. ಇದಕ್ಕೆ ವ್ಯತಿರಿಕ್ತವಾಗಿ, ದ್ವಿಸಂಯೋಜಿತ ಗಿಡಗಳ ಆಯ್ಕೆಯು, ಸಂಕೀರ್ಣ ಲಕ್ಷಣಗಳನ್ನು ನಿಯಂತ್ರಿಸುವ ಹೆಚ್ಚಿನ ಆಲೀಲ್‌ಗಳ ಸ್ಥಿರೀಕರಣಕ್ಕೆ ಕಾರಣವಾಗಬಹುದು. ಹೀಗಾಗಿ, ಎರಡು ಏಕ ಸಂಯೋಜಿತ ಸಂಯೋಜನೆಗಳನ್ನು ಬಳಸಿಕೊಂಡು ಉತ್ಪತ್ತಿಯಾಗುವ ದ್ವಿಸಂಯೋಜಿತ ಗಿಡಗಳು ಉತ್ತಮವಾದ ಮರುಸಂಯೋಜಕಗಳನ್ನು ಚೇತರಿಸಿಕೊಳ್ಳಲು ಮತ್ತು ಸೂಕ್ತವಾದ ಜನ್ಮಜಾತ ಸಾಲುಗಳನ್ನು ಗುರುತಿಸಲು ಸೂಕ್ತವಾಗಿದೆ. ಹೆಟೆರೋಸಿಸ್ ಅನ್ನು ಯಶಸ್ವಿಯಾಗಿ ಬಳಸಿಕೊಳ್ಳುವ ಪ್ರಮುಖ ತರಕಾರಿ ಬೆಳೆಗಳಲ್ಲಿ ಬೆಂಡೆಕಾಯಿ ಒಂದಾಗಿದೆ. ಈ ಸನ್ನಿವೇಶದಡಿಯಲ್ಲಿ, ಡಿಸಿ$_1$ ಎಫ್$_2$ (ಎನ್‌ಎಸ್‌೮೬೪ x ಅರ್ಕ ನಿಕಿತ) ಡಿಸಿ$_2$ಎಫ್$_2$ (ಮಹಿಕೊ೧೦ x ಓಎಚ್–೧೦೨), ಡಿಸಿ$_3$ಎಫ್$_2$ (ರಾಧಿಕಾ x ಶಕ್ತಿ) ಮತ್ತು ಡಿಸಿ$_4$ಎಫ್$_2$ (ಸಾಮ್ರಾಟ್ x ಎಸ್‌ವಿಓಕೆ೫೧೫೧) ಎಂದು ಗೊತ್ತುಪಡಿಸಿದ ಬೆಂಡೆಯ ನಾಲ್ಕು ದ್ವಿಸಂಯೋಜಿತ ಎರಡನೇ ಪೀಳಿಗೆಯ ಗಿಡಗಳ ಸಂತಾನೋತ್ಪತ್ತಿ ಸಾಮರ್ಥ್ಯವನ್ನು ರಬಿ ೨೦೨೨ ರ ಅವಧಿಯಲ್ಲಿ ಕೃಷಿ ಮಹಾವಿದ್ಯಾಲಯ, ನವಿಲೆ, ಕೆಳದಿ ಶಿವಪ್ಪನಾಯಕ ಕೃಷಿ ಮತ್ತು ತೋಟಗಾರಿಕೆ ವಿಜ್ಞಾನ ವಿಶ್ವವಿದ್ಯಾಲಯ, ಶಿವಮೊಗ್ಗದ ಪ್ರಾಯೋಗಿಕ ಪ್ಲಾಟ್‌ಗಳಲ್ಲಿ ಗಿಡದ ಎತ್ತರ, ಗೆಣ್ಣುಗಳ ಸಂಖ್ಯೆ, ಗೆಣಣು ನಡುವಿನ ಅಂತರ, ಹಣ್ಣಿನ ಉದ್ದ, ಸರಾಸರಿ ಹಣ್ಣಿನ ತೂಕ, ಪ್ರತಿ ಗಿಡಕ್ಕೆ ಹಣ್ಣುಗಳ ಸಂಖ್ಯೆ ಮತ್ತು ಪ್ರತಿ ಗಿಡದ ಹಣ್ಣಿನ ಇಳುವರಿಯಂತೆ ವಿಶ್ಲೇಷಿಸಲಾಗಿದೆ. ತಳಿಯ ಸಾಮಥ್ಯವನ್ನು ಏಳು ಉತ್ಪಾದಕತೆಯ ಗುಣಲಕ್ಷಣಗಳಿಗೆ ವಿಧಾನಗಳು, ಪ್ರಮಾಣಿತ ಶ್ರೇಣಿ, ವ್ಯತ್ಯಾಸದ ಗುಣಾಂಕ ಮತ್ತು ಶ್ರೇಣಿ–ಮೊತ್ತ ವಿಧಾನದ ಮೂಲಕ ಮರುಪಡೆಯಲಾದ ಅತಿಕ್ರಮಣ ಪ್ರತ್ಯೇಕತೆಗಳ ಆವರ್ತನವನ್ನು ನಿರ್ಣಯಿಸಲಾಗಿದೆ. ಕಡಿಮೆ ಶ್ರೇಣಿಯ ಮೊತ್ತದೊಂದಿಗೆ ಡಿಸಿ$_3$ಎಫ್$_2$ (ಶ್ರೇಣಿ–ಮೊತ್ತ ೫೮) ಮತ್ತು ಡಿಸಿ$_2$ಎಫ್$_2$ (ಶ್ರೇಣಿ – ಮೊತ್ತ ೬೯) ಎಂದು ಗೊತ್ತುಪಡಿಸಿದ ದ್ವಿಸಂಯೋಜಿತ ಎರಡನೇ ಪೀಳಿಗೆಯ ಗಿಡಗಳು ಹೆಚ್ಚಿನ ಸಂತಾನೋತ್ಪತ್ತಿ ಸಾಮರ್ಥ್ಯವನ್ನು ಹೊಂದಿದೆ ಎಂದು ಪರಿಗಣಿಸಲಾಗಿದೆ. ಡಿಸಿ$_3$ಎಫ್$_2$ (೧೯.೩೩%), ಡಿಸಿ$_1$ಎಫ್$_2$ (೧೩.೦೦%) ಮತ್ತು ಡಿಸಿ$_4$ಎಫ್$_2$ (೧೧.೭೬%) ಜನಸಂಖ್ಯೆಯಿಂದ ಅತಿಕ್ರಮಣ ವಿಭಜಕಗಳ ಹೆಚ್ಚಿನ ಆವರ್ತನವನ್ನು ಮರುಪಡೆಯಲಾಗಿದೆ. ಇವುಗಳನ್ನು ಜನ್ಮಜಾತ ಸಾಲುಗಳನ್ನು ಪ್ರತ್ಯೇಕಿಸಲು ಆದ್ಯತೆಯಾಗಿ ಮುನ್ನಡೆಸಬಹುದು. ಗಿಡದ ಎತ್ತರ, ಗೆಣ್ಣುಗಳ ಸಂಖ್ಯೆ ಮತ್ತು ಪ್ರತಿ ಗಿಡಕ್ಕೆ ಹಣ್ಣುಗಳ ಸಂಖ್ಯೆಯನ್ನು ಹಣ್ಣಿನ ಇಳುವರಿಗಾಗಿ ಆಯ್ಕೆ ಮಾಡಲು ಸೂಕ್ತ ಪ್ರಾಕ್ಸಿ ಲಕ್ಷಣಗಳೆಂದು ಗುರುತಿಸಲಾಗಿದೆ.

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INTRODUCTION

I INTRODUCTION

Okra [*Abelmoschus esculentus* (L.) Moench.], is an economically important seed-propagated vegetable crop, grown in tropical and sub-tropical parts of the world, belonging to the Malvaceae family and has the chromosome number of 2n = 8x = 72 or 144. This crop is suitable for cultivation as a garden crop as well as on large commercial farms. It is a versatile crop with a broad range of adaptability due to ease of cultivation, short duration, high export potential and suitability to a wide range of environment and soil types (Priyanka *et al*., 2018).

It is grown commercially in India, Iran, Bangladesh, Afghanistan, Pakistan, Burma, Japan, Malaysia, Western Africa, Ghana, Ethiopia and the Southern United States. In India, okra has an annual production of 6.46 million tonnes, covering an area of 5.30 lakh hectares, with a productivity of 12.19 tonnes per hectare. In Karnataka, okra is cultivated over an area of 5.35 thousand hectares with an annual production of 64.01 thousand tonnes and productivity of 11.97 tonnes per hectare (Anonymous, 2020). India is the largest producer of okra with over 60% of the global production and ranks 12^{th} in terms of productivity.

Okra is cultivated for its green, non-fibrous fruits containing round seeds. Immature fruits are harvested prior to the differentiation of fibres and consumed as a vegetable. Vast culinary preparations are possible using okra fruits. Okra leaves are used as spinach by Africans. The roots and stems of okra are used for cleaning the cane juice from which jaggery or brown sugar is prepared (Chauhan, 1972). The greenish-yellow oil extracted from okra seeds is often seen as an alternative to edible oil and is found to be rich in oleic acid and linoleic acid. It has good nutritional value, particularly vitamin C (30 mg/100 g), vitamin A (20 mg/100 g), zinc (6 mg/100 g), β carotene (300 μg/100 g) and is a rich source of folic acid (300 μg/100 g) (Liu *et al*., 2021). A high level of dietary fibre, low caloric value and rich source of minerals like Ca, P, K and Mg have made okra a potential component which provides multiple nutritional benefits if incorporated into the human diet. It is a good source of iodine and is used as a diuretic agent to relieve gastric irritations owing to its high polysaccharide content, which causes mucilaginous texture.

Okra is categorized under often cross pollinated group of plants as natural outcrossing occurs in the range of 4 to 15 per cent (Kumar *et al*., 2010). It has large hermaphrodite flowers, five white to yellow petals with red or purple spots, monadelphous stamens and a prominent stigma. The floral morphology which aids for easy emasculation, self compatibility and a large number of seeds produced in a single pollination, make this crop highly ideal and amicable for geneticists and crop breeders to carry out multifaceted breeding.

Both public and private sector organizations have developed a large number of hybrids and varieties which have been widely adopted by Indian farmers. The availability of diverse cultivars of okra is crucial to meet the vital requirement of regional adaptation to varied agroclimatic conditions and to fulfil the farmers' requisites for divergent preferences of several phenotypic traits in okra. It is essential to develop improved varieties of okra that are perennial in growth habit. At the same time, they must combine higher yields and early maturity with longer harvest duration and resistance to diseases and pests (Oppong-Sekyere *et al.*, 2011). Such improved varieties must also meet the standards of fruit size, shape and colour as prescribed to meet the requirement for export.

Okra is one of the vegetable crops where heterosis has been exploited successfully. A rise in yield plateau is seen in heterotic hybrids. Owing to this, hybrid breeding is one of the most efficient and popular breeding programmes in India. The choice of diverse parents is essential to improve productivity, for which information on the nature and magnitude of genetic divergence becomes vital. Hybridization enables the breaking of yield barriers in the existing genotypes and also breeding for multiple market types.

There is a need to develop a truly potential inbred line which can produce novel hybrids with desirable maximum heterosis (Krushna *et al.*, 2007). Among the various approaches for developing inbred lines, the selection of potential segregating populations is an important one. Selection of segregating populations developed from double cross combinations involving parents with desired diversity may prove to be better than segregating populations derived from single cross combinations (Shanthakumar and Salimath, 2011). It is known that double cross combinations generated by employing two single cross combinations which are diverse may produce the desired double cross combinations. Such segregating populations help in identifying pure line varieties.

The breeder has to conduct selection for high yield indirectly, through yield associated and highly heritable characters, after obliterating environmental components of phenotypic variance. Selection of desired genotypes possessing amplified yield and other agronomic attributes requires a firm prerequisite of study of multiple variability parameters. In order to achieve genetic improvement in yield traits, it is imperative to generate information on variability, its heritable proportion and interrelationships existing in the breeding material. In order to decide on an appropriate breeding method, the breeders need to have a clear picture of the components of variances and their effects, heritability and genetic advance of the traits under consideration. The F_2 generation is critical for the success of the breeding programme, as there are remote chances of recovering superior recombinants in advanced generations.

Yield is regulated by polygenes and is greatly influenced by the environment. Therefore, selection based on yield alone is not adequate. A wide range of variation in quantitative characters provides the basis for selection in plant breeding programmes. In order to improve the efficiency of selection, knowledge of association among the characters is essential to the breeder. Correlation coefficient analysis measures the mutual relationship between plant characters and determines the component characters on which selection can be made for genetic improvement of yield. Correlation coefficient provides an understanding of the extent of association between a pair of traits and identifies whether simultaneous improvement of the correlated traits is feasible.

Usually, we observe a resource restraint while evaluating large numbers of bi or multiparent derived populations. As a consequence of this constraint, breeders resort to either limiting the number of crosses or reducing the population size to be evaluated. Therefore, the population with higher breeding potential must be chosen over the other populations under study to efficiently utilize the restricted resources at the breeder's disposal. Identification of the breeding potentiality of any population becomes the prerequisite in this context. Breeding potential of the cross can be assessed and is reflected in terms of variability and other statistical parameters *viz.,* quantitative trait means, standardized range, coefficient of variation (CV) and frequency of transgressive segregants recovered from multiple parent derived populations. These parameters can serve as valuable predictors of breeding potential of given double cross populations.

Considering all the above mentioned perspectives, the present study has been carried out with the following objectives:

1) To identify double cross derived F_2 population with high breeding potential based on transgressive segregation and useful index for fruit yield and its component traits.
2) To identify easily field assayable proxy traits, to select for fruit yield.
3) Identification of productive transgressive segregants.

REVIEW OF LITERATURE

II REVIEW OF LITERATURE

Genetic diversity is the base for crop improvement and diversity in plant genetic resources allows plant breeders to develop new and improved cultivars with desirable characteristics. Given that genetic variability is a prerequisite for selection, creating variability through hybridization accelerates crop improvement. A clear understanding of the nature of variability and character association helps develop sound breeding programs for crop improvement. Okra [*Abelmoschus esculentus* (L.) Moench] is a taxon with a large number of wild species and is highly polymorphic, showing a wide range of variability in morphological, physiological and biochemical properties. Without the knowledge of characterization and crossability relationships, utilization of genetic resources in breeding programs is impotent. The available literature pertaining to the present study is reviewed under the following headings:

2.1 Genetic variability, heritability and genetic advance

2.2 Correlation analysis to identify proxy traits to select for fruit yield

2.3 Transgressive segregants

2.1 Genetic variability, heritability and genetic advance

Variability is a prerequisite for improving yield and related characters for any breeding programme. Progress in any crop improvement programme depends mainly on the magnitude of genetic variability and heritability present in the source material. The extent of variability is measured by the genotypic coefficient of variation and phenotypic coefficient of variation, which provide information about the relative amount of variation that exists in different characters.

Yield and yield component traits are quantitative in nature and polygenic in inheritance, which is greatly influenced by the environment. The phenotype of a character is the result of interaction between genotype and environment. Since heritability estimates indicate the progress expected from the selection, they are most meaningful when accompanied by genetic advance estimates. The heritability estimates, along with the predicted genetic advance will be more reliable (Johnson *et al.*, 1955).

Solankey and Singh (2009) conducted a line × tester analysis in okra with 20 parents and their 51 F_1s (17 lines × 3 testers). High heritability was observed for all the traits with high genetic advance. Higher GCV was estimated for number of branches per plant, fruit yield per plant, internodal length and number of nodes per plant. High heritability was obtained for all traits, especially for number of ridges per fruit, number of branches per plant, ascorbic acid content, number of fruits per plant, number of seeds per fruit, number of nodes per plant, fruit yield per plant and single fruit weight.

Akotkar *et al*. (2010) investigated the genetic variability of some yield contributing characters and the genetic diversity in 50 genotypes of okra collected from NBPGR New Delhi, India. High values of GCV, PCV, heritability and genetic advance (% of mean) were observed for number of fruiting nodes, number of ridges per fruit, plant height and number of fruiting nodes, indicating that these characters might be controlled by additive genes. The value of GCV and PCV were found to be low for number of ridges per fruit, fruit diameter, fruit length and number of primary branches per plant. The magnitude of PCV was higher than that of GCV for all the traits.

Prakash and Pitchaimuthu (2010) performed an experiment evaluating the genetic variability of yield contributing characters and the genetic diversity in 44 genotypes of okra collected from the IIHR, Bangalore, India. High GCV and PCV were observed for plant height, inter-nodal length, first flowering node, first fruit producing node, height of first flowering node, average fruit weight and number of seeds per fruit. The magnitude of PCV was higher than that of GCV for all the traits. The estimate of heritability was highest for hundred seed weight, while it was least for stem girth.

Reddy *et al*. (2012a) conducted studies on genetic variability in 100 genotypes of okra, which revealed a high magnitude of genetic variability and a high degree of transmission of the majority of the yield associated traits under study. High magnitude of GCV and PCV for number of branches per plant, total number of fruits per plant, number of marketable fruits per plant, total yield per plant and marketable yield per plant on plants indicated a high degree of genetic variability offering tremendous scope for selection. The characters plant height, number of branches per plant, internodal length, first flowering node, fruit length, fruit weight, total number of fruits per plant, number of marketable fruits per plant, total yield per plant, marketable yield per plant, yellow vein mosaic virus infestation on fruits and plants showed high heritability coupled with high expected genetic advance.

Nwangburuka *et al.* (2012) assessed 29 okra accessions collected from different agroecological regions in Nigeria and grown during the rainy and dry seasons to determine their genetic variability, heritability and genetic advance from eight yield related characters. There was high GCV, % broad-sense heritability and genetic advance in traits such as plant height, fresh pod length, fresh pod width, mature pod length, branching per plant and pod weight per plant, suggesting the effect of additive genes.

Jagan *et al*. (2013) observed significant differences among the genotypes for all the characters studied except plant height, days to maturity, length of the fruit, diameter of the fruit, node at which mosaic disease appears and days at first mosaic symptoms appear. The GCV and PCV values for most of the characters were found to be very distant from each other. The heritability estimates in broad sense were high for number of branches per plant, days to maturity, length of the fruit, days to 50% flowering and node at which mosaic disease appears, while low heritability estimates were observed for number of fruits per plant and node at which first flower appears.

Sharma *et al*. (2016) observed a higher magnitude of PCV than GCV for all traits and they were distant from each other for most of the characters, suggesting the presence of a large amount of variability. Both PCV and GCV were high for plant height. Fruit weight exhibited low values of GCV and PCV and is likely to show less response under selection. High heritability with high genetic advance was recorded for plant height, whereas ridges per fruit had high heritability with moderate genetic advance.

Yadav *et al*. (2016) evaluated twenty genotypes and fifteen characters of okra. The PCV were generally higher than their respective GCV. High PCV was exhibited by plant height, number of branches per plant, number of seeds per fruit, first flowering node and yield per hectare. High GCV were observed for number of branches per plant, first branching node, number of seeds per fruit and plant height. High heritability coupled with high genetic advance was observed for plant height, fruit weight, number of branches per plant and first branching node.

Awadhesh *et al*. (2016) studied the variability, heritability, expected genetic advance, characters association and direct and indirect effect of components on fruit yield per plant in okra. A high magnitude of GCV and PCV was recorded for fruit yield per plant, number of fruits per branch, and number of leaves per plant, while fruit diameter showed the lowest GCV and PCV. The highest heritability was noted in number of flowers per plant, followed by fruit yield per plant, number of leaves per plant, number of fruits per plant, fruit weight, number of fruits per branch and plant height, whereas the lowest heritability was observed in number of branches per plant, stem diameter and number of days taken to flower.

Pachiyappan and Saravannan (2016) conducted an experiment to study the genetic variability and correlation in okra, involving 40 genotypes for eight important economic characters, namely days to first flowering, plant height, number of branches per plant, number of fruiting nodes, fruit length, fruit girth, fruit weight, fruit yield per plant. High PCV and GCV were observed for the traits fruit girth, fruit weight, and fruit yield per plant. Majority of the traits recorded high heritability. For fruit weight and fruit yield per plant, high heritability coupled with high genetic advance as per cent of mean were observed.

Thulasiram *et al*. (2017) studied 30 genotypes belonging to okra in the kharif season to work out variability and heritability. The GCV and PCV were highest for the character leaf area, diameter of fruit and number of primary branches per plant and lowest for the character crude fibre content of fruit and weight of fruit. Moderate GCV and PCV were recorded for the characters plant height and number of leaves per plant. High heritability as well as genetic advance was observed in the characters leaf area and yield per plant. Thus, there is ample scope for improving character through direct selection based on the phenotype characters.

Sravanthi (2017) assessed 21 accessions of okra for variability of 12 characters. The GCV and PCV were high for yield per plant, fruit weight, and number of fruits per plant; moderate for internodal length, number of ridges on fruit, fruit length, plant height, number of branches per plant, and per cent fibre content. High heritability accompanied by 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.

Badiger *et al*. (2017) analyzed the genetic variability, heritability, genetic advance and correlation among 15 quantitative traits in 12 okra genotypes. The lowest difference between PCV and GCV was recorded for plant height, followed by no. of fruits per plant, final stem girth, fruit girth and number of ridges per fruit as the indication of prevalence of genotypic effect on their expression. High heritability coupled with high genetic advance as per cent mean for number of fruits per plant, total yield per plant, plant height, internodal length and average fruit weight indicating the prevalence of additive gene action in their inheritance. This denotes that the selection based on these traits is quite effective.

Raval *et al*. (2018) carried out an investigation to create and assess the variability through hybridization using parameters like PCV, GCV, heritability and genetic advance in okra. The high magnitude of PCV and GCV was observed for number of branches/plant at final harvest, followed by fruit yield/plant, internodal length, number of fruits/plant and plant height at final harvest. This suggested greater phenotypic and genotypic variability among the F_2 segregating populations. High genetic advance coupled with high heritability was observed for most of the characters. It indicated that additive gene action was more important for these characters.

Verma *et al*. (2018) evaluated 50 genotypes of okra to study the variability, heritability and genetic advance for different morphological and agronomic traits. The characters like number of branches per plant, fruit yield per plant, width of fruit, number of first fruiting nodes and length of internode showed high GCV and PCV estimates. High heritability coupled with high genetic advance were observed for yield per plant, width of fruit, number of fruits per plant, length of internode and length of first fruiting node, indicating that additive genes govern them.

Kavya *et al*. (2019) assessed the genetic variability of yield and its contributing traits in F_2 segregating populations of three bi-parental crosses viz., IIHR-875 × IIHR-

478, IIHR-478 × IIHR-567 and IIHR-604 × IIHR-347 respectively. The magnitude of PCV and GCV values was high for number of fruits per plant in IIHR-875 × IIHR-478, plant height and total yield per plant in the bi-parental cross IIHR-478 × IIHR-567. The bi-parental cross IIHR-604 × IIHR-347 recorded high PCV and GCV values for number of fruits per plant and total yield per plant. High broad sense heritability values were recorded for the traits plant height and total yield per plant in the bi-parental crosses IIHR-478 × IIHR-567 and IIHR-604 × IIHR-347, whereas in the bi-parental cross IIHR-875 × IIHR-478 it was high for the trait plant height.

Chavan *et al*. (2019) evaluated segregating generations F_2, F_3, BC_1F_2 and BC_2F_2 to examine the genetic variability in the cross Arka Bahar x IC31032A. The estimated high genotypic and phenotypic coefficient of variation were observed for number of nodes per plant and fruit weight in F_2 generation, internodal length in F_3 generation, plant height, number of branches per plant, fruit diameter, number of fruits per plant and fruit yield per plant in BC_1F_2 generation, length of fruit in BC_2F_2 generation. The estimated heritability was appreciably moderate for fruit weight in BC_1F_2.

Rathod *et al*. (2019b) carried out an experiment to estimate genetic variability, heritability and genetic advance of 12 quantitative characters in 148 F_2 plants from cross AOL-09-02 x AOL-10-22 and 160 F_2 plants from cross AOL-09-02 x GAO-5 were studied. The characters viz., number of branches/plant at final harvest, internodal length, fruit yield/plant, number of fruits/ plant and plant height at final harvest showed high PCV and GCV in F□ populations of both crosses. High heritability was recorded for plant height at final harvest, fruit yield/plant, number of fruits/plant, days to first flowering and number of branches/plant at final harvest in F□ populations of both crosses.

Rambabu *et al*. (2019) conducted an experiment to estimate the genetic variability in 20 diverse okra germplasm accessions. The values PCV were higher than GCV for all the characters, indicating the influence of environmental factors. High estimates of heritability coupled with high genetic advance expressed as percentage of mean were observed for plant height, number of branches per plant, internodal length, days to 50% flowering, days to last harvest, fruit length, fruit girth, fruit weight, number of fruits per plant, number of seeds per fruit, fruit yield per plant, 100 seed weight, which may be attributed to the preponderance of additive gene action and possess high selective value. True agreement with the GCV and PCV values in the present investigation for most of the characters was noticed, indicating additive genetic variance.

Kumari *et al*. (2019) studied 31 hybrids of okra to estimate the extent of genetic variability for yield, its components and quality traits. High values of PCV and GCV were recorded for important traits, including yield per plant, number of fruits per plant and primary branches per plant, respectively. High heritability was recorded for yield per plant, followed by ascorbic acid, fruit width and number of nodes per plant. High heritability coupled with high genetic advance was recorded for yield per plant and number of fruits per plant, indicating that these characters are governed by additive gene effect.

Kumar *et al*. (2020) observed that the traits like number of fruits per plant fruit length showed comparatively higher values of PCV, GCV, heritability (in broad sense), genetic advance and expected genetic advance, revealing additive gene effect in 30 okra genotypes. High estimates of heritability coupled with genetic advance were obtained for total fruit yield and marketable fruit yield per plant, indicating the presence of additive gene effects, which indicated the effectiveness of selection for these traits.

2.2 Correlation analysis to identify proxy traits to select for fruit yield

Fruit yield is a complex quantitative character controlled by several genes that interact with the environment. Direct selection for yield alone is not adequate. Hence, selection based on contributing traits could be more efficient and reliable (Kumar *et al*., 2013). Correlation analysis is a prerequisite for improving any crop, including okra, for selecting superior genotypes and improving any trait. In plant breeding, correlation analysis provides information about yield components and thus helps in the selection of superior genotypes from diverse genetic populations. The correlation studies simply measure the associations between yield and other traits. The usefulness of the information obtained from the correlation coefficients can be enhanced by partitioning it into direct and indirect effects for a set of pair-wise cause and effect interrelationships (Mohammad and Marker, 2017).

Balai *et al*. (2014) performed correlation analysis in 27 genotypes of okra for fruit yield and its component traits. Yield per plant had highly significant positive genotypic and phenotypic correlation with plant height, length of pod, average weight of edible pod and number of seeds per pod. A 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 a close relationship between genotypic and phenotypic correlation coefficients. Path coefficient analysis revealed that the average weight of edible pods had the highest positive direct effect, followed by number of pods per plant and number of leaves per plant on yield per plant.

Gogineni *et al*. (2015) conducted correlation studies in ten different okra hybrids for fruit yield and its component traits. This indicated that fruit yield was significantly associated with fruit length, fruit girth, fruit weight, number of fruits per plant, plant height and duration at both genotypic and phenotypic levels, indicating mutual association of these traits. Path coefficient analysis revealed that number of fruits per plant had the maximum direct contribution towards total yield, followed by fruit weight, fruit girth, duration and plant height. However, days to first flowering and fruit length exhibited a negative direct effect.

Thulasiram *et al*. (2017) investigated 30 genotypes belonging to okra to work out the correlation and path coefficient. This indicated that yield per plant was significantly associated with plant height, number of primary branches per plant, number of nodes per plant and number of fruits per plant. Based on the positive direct effects of different yield components, it would be rewarding to give emphases on the number of primary branches per plant, number of nodes per plant, diameter of fruit, 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 and chlorophyll content of leaves.

Meena *et al*. (2017) evaluated six hybrids of okra for the association between characters, direct and indirect effects of component traits on yield and to identify desirable genotypes. Significant positive genotypic and phenotypic correlation was observed for number of fruits per plant and average fruit weight. Path coefficient studies revealed that the direct contribution of number of branches per plant, average fruit weight, and number of fruits per plant was of higher magnitude on fruit yield. Direct selection may be executed considering these traits as the main selection criteria during the development of high-yielding okra varieties/hybrids.

Mohammad and Marker (2017) evaluated 23 genotypes of okra for correlation and path coefficient analysis to study the character association and contribution, respectively. The correlation coefficient was revealed to be high and positively significant with fruit yield per plant, fruits per plant, marketable fruits per plant, seeds per fruit and fruit weight. Path coefficient analysis revealed that fruits per plant and marketable yield per plant had a direct effect and strong association with fruit yield per plant.

Pithiya *et al*. (2017) observed that the number of fruits per plant and number of seeds per fruit showed the highest positive and very high significant correlation with yield per hectare, followed by 100-seed weight and plant height in 28 germplasm lines of okra. Plant height and 100-seed weight showed a positive and significant correlation with yield per hectare. Stem diameter showed a negative and significant correlation with number of leaves per plant, fruit length and plant height with seed yield per plant. Path coefficient analysis on various yield contributing characters revealed that the number of fruits per plant, number of seeds per fruit, plant height, fruit length, 100-seed weight and number of branches showed a direct positive effect towards yield.

Oyetunde and Ariyo (2017) conducted a study on 16 hybrids to identify indirect selection criteria for yield in okra. Correlation and path coefficient analyses indicated that number of pods per plant, number of seeds per pod, and 100-seed weight are reliable candidate characters for indirect selection to enhance genotypic improvement of seed yield in okra. Results from path analysis indicated the importance of one or more of these characters in alternative paths of other characters, the selection of which might be ineffective in improving the seed yield of okra.

Rajat *et al*. (2018) studied the correlation between various morphological traits of okra genotypes. Various morphological parameters, viz. days to germination, plant height, number of branches per plant, number of pods per plant, days required for first flowering, days required for 50% flowering, fruit length, fruit weight and yield per plant, were recorded. Correlation studies at phenotypic and genotypic levels revealed that fruit yield per plant had a significant positive correlation with plant height, number of branches and fruit weight.

Karadi *et al.* (2018) conducted character association studies, which revealed that the fruit yield per plant had a significant and positive association with plant height at 45 DAS, 60 DAS, 90 DAS and number of fruits per plant. It was negatively and significantly associated with number of branches per plant, days to flowering, days to fifty per cent flowering and vitamin C content at both genotypic and phenotypic levels.

Kumar *et al*. (2019) evaluated character association and direct and indirect effects of pod yield and yield-related traits in 68 okra accessions. This revealed that pod yield per plant showed a positive correlation with plant height, number of fruits per plant, fruit width, number of branches per plant and number of nodes per plant at both genotypic and phenotype levels. The maximum direct positive correlation on pod yield per plant is shown by number of fruits per plant, plant height, fruit width, number of branches per plant and number of nodes per plant at phenotypic levels. 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.

Raval *et al*. (2019) studied the parents (female VRO - 6 and male AOL - 09 - 02) and their F_1 and F_2 generations and conducted correlation and path analysis. Observations were recorded on thirteen yield contributing characters. Among them, fruit yield/plant exhibited a positive and highly significant correlation with number of fruits/plants, plant height at final harvest, fruit weight, number of branches/ plants, fruit girth, number of seeds/fruits, internodal length, and 100 seed weight. Path coefficient analysis revealed that number of fruits/plants, fruit weight, days to first picking, internodal length, 100 seed weight and fruit length recorded a positive direct effect on fruit yield/plant.

Rathod *et al.* (2019a) conducted a correlation and path coefficient analysis of 12 quantitative characters in 148 F_2 plants from cross AOL-09-02 x AOL-10-22 and 160 F_2 plants from cross AOL-09- 02 x GAO-5. In the F_2 population of both crosses, fruit yield/plant exhibited positive and highly significant correlation with the number of fruits/plant, plant height at final harvest, internodal length, number of branches/plant and fruit length, indicating that these characters are the primary yield determinants in okra. Positive direct effect on fruit yield/plant was recorded by number of fruits/plant, fruit weight, 100 seed weight and fruit girth in F_2 populations of both crosses. However, internodal length had a negative and direct effect on fruit yield/plant.

Kelemoge *et al.* (2019) investigated the interrelationship between yield related characters and the extent of their contribution to fruit yield in okra. Correlation analysis revealed that the internodal length of the main stem, number of nodes per plant and average fruit weight registered a positive and significant correlation at both phenotypic and genotypic levels with fruit yield per plant, signifying the importance of these traits in selection for yield. Path coefficient analysis revealed that number of primary branches per plant, number of nodes per plant, fruit length, fruit girth, leaf chlorophyll content and mucilage content exerted a high positive direct effect on fruit yield per plant.

Rathava *et al*. (2019) studied 31 genotypes of okra to determine the nature of association among different yield attributes and their direct and indirect contribution towards yield. Fruit yield per plant has exhibited a positive and highly significant correlation with plant height, number of fruits per plant and average fruit length at both genotypic and phenotypic levels. Path coefficient analysis revealed that number of fruits per plant had the maximum direct contribution towards fruit yield, followed by average fruit weight, average fruit diameter and plant height. Average fruit length had the higher negative direct effect on fruit yield per plant, followed by days to 50 % flowering, number of branches and internodal length.

Walling *et al*. (2020) observed the highest PCV and GCV in cumulative leaf area, yield per plant and protein content. The correlation studies indicated that yield per plant showed highly significant positive genotypic correlation coefficients with leaf area index, number of fruits per plant, weight of fruit, fruit length, 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 in 28 okra genotypes.

Ranganayaki *et al*. (2020) conducted correlation and path coefficient analysis in ten genotypes for yield and yield attributing traits. Observations were recorded on eleven yield and yield attributing characters. Fruit yield per plant is positively correlated with fruit weight and number of fruits per plant. Path coefficient analysis revealed that the traits days to first flowering, number of fruits per plant, fruit length, number of ridges per pod and fruit weight have a positive direct effect on fruit yield per plant.

Alam *et al.* (2020) observed that fruit yield per plant showed positive and significant correlation with 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 coefficient in 40 genotypes of okra. The path coefficient analysis indicated a 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 a high but adverse 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.

Janarthanan and Sundaram (2020) conducted a study involving segregants from 2 cross combinations viz., Cross 1 [SKY/DR/RS/107 (P 1) X Tiruchi Local (P 2)] and Cross 2 [IC69257 (P 3) X 770 (P 4)] in which observations were recorded on twelve biometric traits from 250 randomly tagged plants in F_2. Correlation coefficient analysis revealed the importance of number of fruits per plant, plant height at final harvest, number of primary branches at final harvest and internodal length in exercising selection from segregating population of okra as they were found to exert positive and significant association with yield.

Ashraf *et al*. (2020) conducted an experiment to study the correlation and path analysis in the selected okra genotypes. The fruits per plant and fruit weight of different genotypes had a high degree of significant positive association with fruit yield. High positive direct effect indicated that these characters had a significant contribution towards the fruit yield of the genotypes. At the 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, fruit diameter and genotypic level.

2.3 Transgressive segregants

Hybridization often produces progenies with wider phenotypic variation than their parents, which is referred to as transgressive segregation (Rick and Smith, 1953; Devicente and Tanksley, 1993). Unlike heterosis, the extreme phenotypes resulting from transgressive segregation can be fixed after the second filial generation (F_2). The available literature on transgressive segregants in okra is presented below.

Pitchaimuthu *et al*. (2008) identified the transgressive segregants in the population of IIHR-31-1-2 x Arka Anamika BC_3F_1-F_6 generations having various novel characters such as ridgeless fruits (round fruit) and enhanced nodal productivity bearing short internodal length in Okra Selection-1, which was found to be promising for cultivation with high yield and good fruit quality. Okra selection–1 also exhibited smooth fruits, high yield potential and sturdy plant habit.

Shanthkumar and Salimath (2011) conducted an experiment for the selection of productive segregants in the segregating generation of single and double cross F_1 populations in okra. A higher frequency of transgressive segregants was observed in the double cross F_2 population. Among seven populations, the double cross BH 2 × BH 10 recorded the highest number of transgressive segregants.

Somashekhar *et al*. (2011a) evaluated three populations of the okra, viz., biparental mating F_2, single cross F_2 and double cross F_2 populations. Considerable variation was observed in the biparental population compared to single cross F_2 and double cross F_2 populations for most of the characters, number of branches per plant, number of fruits per plant, average fruit weight and fruit yield per plant. It is revealed that intermating in early segregating generations of different individuals leads to the release of additional variability since biparental mating among the segregates in the F_2 of a cross may provide more opportunity for the recombination to occur, break the linkage blocks and mop up desirable genes and as a result gives a higher incidence of transgressive segregants.

Reddy *et al*. (2012b) studied 100 genotypes of okra for all seventeen quantitative characters, which are pertaining to growth, earliness and yield. The use of diverse genotypes from the clusters with high intercluster distance in hybridization is expected to result in high heterosis and throw desirable transgressive segregants.

Akotkar *et al*. (2014) crossed eight okra genotypes in a half-diallel fashion to study the combining ability of the parents and gene action concerning fruit yield and 12 other component characters. The magnitude of GCA variance was higher than the respective SCA variance, indicating the predominance of additive gene action for expressing all the characters. A high × low cross can result in solid transgressive segregants for the desired characters due to the segregation of genes with strong potentials. Crosses involving one parent with a significant gca effect and the other with a poor gca effect would throw up transgressive segregants, giving rise to a new population.

Narkhede *et al*. (2015) assessed 17 genotypes of okra, which were grouped into three clusters, the first comprising 15 genotypes, while the rest of the clusters are solitary clusters with one genotype each. The intercluster distance was maximum between clusters I and III, which indicated that genotypes included in this cluster might give a heterotic response and thus better transgressive segregants and hence may be used for further hybridization programme. Inter-crossing of divergent groups would lead to greater opportunity for crossing over, which releases hidden potential variability by disrupting the undesirable linkages, thus leading to the appearance of desired transgressive segregants.

Paul *et al*. (2017) conducted a study in okra to estimate the magnitude of gene action involved and to identify the good combiner for fruit yield and other yield attributing characters. Fifty five okra hybrids derived by crossing of 11 parents in diallel mating design excluding reciprocals were assessed. The analysis of variance for specific combining ability indicated sufficient variation among cross combinations for yield and related traits. Three top yielding crosses exhibited high sca effects as well as per se performance, having at least one or both parents as a good general combiner for green fruit yield, and it is expected that such type of cross combinations would yield desirable transgressive segregants in later generations.

Priyanka *et al*. (2017) studied 29 genotypes of okra for all eighteen characters pertaining to growth, earliness and yield. The characters fruit length and days to 50% flowering with a high percentage of contribution to total divergence were the potent variables in differentiating the breeding material under study. The use of diverse inbred lines from the divergent clusters with high intercluster distance in hybridization is expected to result in high heterosis and throw desirable transgressive segregants.

Nimbalkar and Totre (2018) evaluated F_2 populations of three okra crosses for yield and yield contributing characters to identify transgressive segregants. Considerable variation was observed in the F_2 populations of the three crosses for most of the characters. Maximum variation among the transgressive segregants was observed for the character viz., plant height followed by green fruit yield per plant in the cross Hisar Navin x Arka Abhay. Among the crosses, the maximum number of transgressive segregants were found in the cross Hisar Navin × Arka Abhay, which indicated its superiority over other crosses.

Patel *et al*. (2020) conducted an experiment to evaluate 35 genotypes in four different environments. The experimental material consisted of 35 genotypes, representing 24 hybrids of 10 diverse parents and commercial hybrid checks. Significant and high estimates of standard heterosis were observed for fruit yield/plant in all environments. Among the hybrids, AOL-16-04 x Parbhani Kranti was consistent with respect to higher heterotic effect for fruit yield/plant across the environments, while cross AOL-16-04 x Arka Anamika was consistent for heterotic effects in few environments. These crosses may be exploited for commercial cultivation and may also be advanced as those would likely yield superior transgressive segregants.

Nanthakumar *et al*. (2021) evaluated 46 genotypes of okra for all the fourteen quantitative characters pertaining to growth, earliness and yield. Forty-six genotypes were grouped into five distinct clusters. The traits viz., yield per plot, plant height, number of seeds per plant, number of fruits per plant and yield per plant were the potent factors in differentiating the germplasm of okra. The use of diverse genotypes from the clusters with high inter-cluster distance in hybridization is expected to result in high heterosis and give desirable transgressive segregants.

Hayati *et al*. (2021) evaluated multiple families of the F_2 populations to select superior families that can be used to produce new cultivars. Results showed variation in each F_2 family in plant height, the number of flowers per plant and the number of fruits per plant. A broad variability of quantitative characters was found for all characters, indicating a high opportunity to obtain valuable traits and desirable segregants in F_2 populations. Variations in qualitative characters were found in stem colour, leaf shape, fruit colour and fruit shape. The selection of plants with specific characters could be maintained with inbreeding or selfing desirable segregants.

MATERIAL AND METHODS

III MATERIAL AND METHODS

The details of materials used, experimental methodology and statistical procedures followed during the present investigation on "Comparative assessment of breeding potential in double cross F_2 populations of okra [*Abelmoschus esculentus* (L.) Moench]" are described in this chapter.

Experiment 1

3.1 Experimental location

The present study was carried out at College of Agriculture, Navile, Shivamogga, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga, India, which is situated at 13.28º North latitude and 75.34º East longitude and an altitude of 617.0 meters above mean sea level during the *Kharif* and *Rabi* season of the year 2022-23. The climate is tropical, wet and dry with red sandy loam soil.

3.2 Experimental material

Four double cross F_2 populations were developed through selfing of the F_1 hybrids of the crosses (Radhika × Shakti), (Mahyco10 × OH-102), (Samrat × SVOK5151) and (NS864 × Arka Nikita). The founder lines or single cross hybrids used to generate the double cross hybrids are listed along with the source in Table 1. Initially, single cross hybrids were synthesized and later used to develop four double cross hybrids, further involved in synthesizing the four double cross F_2 populations.

Table 1: a) List of the commercial hybrids used for the experiment

Sl No.	Hybrid	Source
1.	NS 864	Namdhari seeds
2.	Arka Nikita	IIHR, Bengaluru
3.	Mahyco 10	Mahyco hybrid seeds
4.	OH-102	Syngenta
5.	Raadhika	Advanta
6.	Shakti	Nunhems
7.	Samrat	Nunhems
8.	SVOK 5151	Seminis

b) Parentage of the four double cross F_2 populations

1) (NS864 × Arka Nikita)

↓

F_1

↓ **Selfing**

F_2

2) (Mahyco10 × OH-102)

↓

F_1

↓ **Selfing**

F_2

3) (Radhika × Shakti)

↓

F_1

↓ **Selfing**

F_2

4) (Samrat × SVOK5151)

↓

F_1

↓ **Selfing**

F_2

3.3 Experimental design and layout

A total of 300 F_2 individuals, along with four checks in each double cross F_2 population (viz. SVOK 5151, Raadhika, OH-102 and Mahyco 10) were grown in augmented design with a spacing of 60 × 45 cm. The recommended crop production and protection practices were followed to raise a healthy crop. The summary of the experimental details is presented in Table 2 and the general field view of the experimental plot is depicted in Plate 1(a and b).

Table 2: Summary of the experimental material and field design used to evaluate the double cross F_2 populations generated

1.	Number of F_2 plants (per cross)	300
2.	Experimental design	Augmented
3.	Number of blocks	6
4.	Number of checks	4 (SVOK 5151, Raadhika, NS864, OH-102)
5.	Number of plants in a block	50
6.	Repetition of checks	All checks represented in each block, six repetitions
7.	Spacing between the rows	0.6 m
8.	Spacing between the plants	0.45 m

3.4 Recording of observations

Observations were recorded on all the plants in each of the four double cross F_2 populations for 12 characters. The recorded observations were then used for the statistical analysis. The procedure adopted for recording observations on different characters is given below.

3.4.1 Days to first flowering

The number of days from sowing to the first flowering of plants was counted for each plant and systematically recorded.

3.4.2 Plant height (cm)

The height of each plant was measured from ground level to the tip of the main stem after the vegetative stage and expressed in centimetres.

3.4.3 Number of primary branches

The total number of main branches per plant was counted at the complete maturing stage and recorded as the number of primary branches per plant.

3.4.4 Number of internodes on the main stem

The total number of internodes on the main stem was counted 75 days after sowing.

3.4.5 Internodal length (cm)

The internodal length was measured in centimetres between the sixth and seventh nodes of the plant. The measurement was done 90 days after sowing.

3.4.6 Fruit length (cm)

The length of mature fruit was measured in centimetres from the base of the fruit to the tip of ten randomly chosen fruits from first picking. The mean of these ten fruits was taken to calculate fruit length.

3.4.7 Fruit diameter (cm)

Fruit diameter was recorded at the middle portion of the fruit with the help of digital vernier callipers on the same ten fruits with the same scale used to measure fruit length. The average diameter was calculated and expressed in centimetres.

3.4.8 Average fruit weight (g)

Average fruit weight was calculated by adding the weight of five fruits and dividing by the total number of fruits and expressed in grams per fruit.

3.4.9 Number of fruits per plant

The number of fruits per plant at each harvest was recorded and the total was noted.

3.4.10 Number of seeds per fruit

The number of seeds per fruit in ten random fruits was recorded and the total was noted.

3.4.11 Test weight (g)

A hundred seeds were counted and weighed to determine the test weight in grams.

3.4.12 Fruit yield per plant (g)

The cumulative weight of green fruits over all pickings from each plant was recorded in each of the double cross F_2 populations and parental lines and expressed as grams per fruit.

3.5 Statistical analysis

Observations recorded on individual plants of each of the four double cross F_2 populations, along with checks were used for statistical analysis. Analysis was carried out using R studio version 4.2.0. The analysis of variance, descriptive statistics and genetic parameters were estimated as follows:

3.5.1 Analysis of variance

Analysis of variance was performed to split the total variability into different sources (Federer *et al*., 1961), as mentioned in Table 3.

Table 3: Structure of ANOVA for Augmented design

Sources of variations	Degrees of freedom	Mean sum of squares (MSS)	'F' ratio
Blocks (b)	b – 1	MSS(b)	MSS(b)/ EMSS
Entries (e) (Genotypes + checks)	e – 1	MSS(e)	MSS(e)/EMSS
Genotypes (g)	g – 1	MSS(g)	MSS(g)/EMSS
Checks	c – 1	MSS(c)	MSS(c)/EMSS
Genotypes vs Checks (gc)	1	MSS(gc)	MSS(gc)/EMSS
Error	(b-1) (c-1)	EMSS	

Where,

b = Number of blocks

g = Number of genotypes

c = Number of checks

e = Number of entries (genotypes + checks)

3.5.2 Estimation of mean and range

The mean and range for the observed traits were calculated using the following formula.

The general mean was estimated as,

$$\text{General mean} = \frac{\text{Sum of observations of all plants in each } DCF_2 \text{ population}}{\text{Number of plants}}$$

3.5.2.1 Range (R) was estimated as

The range was mentioned as the lowest and highest values recorded for each trait.

3.5.2.2 The standardized range was estimated as

$$\text{Standardized range} = \frac{\text{Highest value} - \text{lowest value}}{\text{Standard deviation of the respective trait}}$$

The standard deviation was estimated as,

$$\boldsymbol{\sigma} = \sqrt{\frac{\sum(\mathbf{X} - \bar{\mathbf{X}})^2}{\mathbf{n} - \mathbf{1}}}$$

Where,

σ = Standard deviation

X = Each of the values of data

$\bar{X}$ = The mean of X

n = The number of data points

3.5.3 Estimation of genetic parameters

Genetic parameters like GCV, PCV, h^2_{bs}, GA and GAM were estimated using the following formulae for the twelve quantitative traits under consideration.

3.5.3.1 Estimation of phenotypic (PCV) and genotypic coefficient of variation (GCV)

Coefficients of variability at both phenotypic and genotypic levels were estimated for the quantitative characters studied using the following formula given by Burton and De Vane (1953).

- Phenotypic Co-efficient of Variation (PCV)

$$\mathbf{PCV}\ (\%) = \frac{\textbf{Phenotypic standard deviation } (\boldsymbol{\sigma}_{\mathbf{p}})}{\textbf{Grand mean } (\bar{\mathbf{X}})} \times \mathbf{100}$$

- Genotypic Co-efficient of Variation (GCV)

$$\mathbf{GCV}\ (\%) = \frac{\textbf{Genotypic standard deviation}\ (\boldsymbol{\sigma}_{\mathbf{g}})}{\textbf{Grand mean}\ (\overline{\mathbf{X}})} \times \mathbf{100}$$

Estimated PCV and GCV were classified as suggested by Robinson *et al.* (1949)

Scales	Value of GCV and PCV (%)
Low	Less than 10
Moderate	10 – 20
High	More than 20

3.5.3.2 Estimation of heritability in broad sense (h^2_{bs})

Broad sense heritability estimates for the quantitative traits under consideration were estimated according to the formula suggested by Lush (1945).

$$\mathbf{h^2_{bs}} = \frac{\mathbf{V_g}}{\mathbf{V_p}} \times \mathbf{100}$$

Where,

h^2_{bs} = Heritability (Broad sense) expressed in *per cent*

V_g = Genotypic variance

V_p = Phenotypic variance

Estimated heritability values were categorized following Johnson *et al.* (1955),

Scales	Values of heritability in broad sense (%)
Low	Less than 30
Moderate	30 – 60
High	More than 60

3.5.3.3 Estimation of genetic advance (GA)

The extent of the expected genetic advance of the characters at 5 *per cent* selection intensity was computed using the formula suggested by Johnson *et al.* (1955).

$$\mathbf{GA} = \mathbf{h^2_{bs}} \times \boldsymbol{\sigma_p} \times \mathbf{k}$$

Where,

h^2_{bs} = Heritability (broad sense)

σ_p = Phenotypic standard deviation k = Selection differential, which is equal to 2.06 at 5 *per cent* selection intensity (Lush, 1945)

- **Expected Genetic Advance as *per cent* mean (GAM)**

The GAM was calculated as per the formula given by Johnson *et al.* (1955)

$$\mathbf{GAM}\ (\%) = \frac{\mathbf{Genetic\ advance\ (GA)}}{\mathbf{Grand\ mean\ (\bar{X})}} \times 100$$

GAM was categorized following Johnson *et al.* (1955)

Scales	Value of GAM (%)
Low	Less than 10
Moderate	10 – 20
High	More than 20

3.5.4 Estimation of correlation coefficients

The correlation coefficients were computed using the formula given by Al-Jibouri *et al.* (1958) to determine the degree of association of component traits with dependent traits.

$$\mathbf{r_{xy}} = \frac{\mathbf{Cov_{xy}}}{(\sqrt{\mathbf{Var_x}} \cdot \sqrt{\mathbf{Var_y}})}$$

Where,

r_{xy} = Phenotypic correlation coefficient between the characters x and y

Cov_{xy} = Phenotypic covariance between characters x and y

Var_x = Phenotypic variance of the character x

Var_y = Phenotypic variance of the character y

3.5.5 Criteria for inference to assess breeding potential

The criteria used to draw inference is detailed in Table 4. Potential double cross F_2 population(s) were identified following the rank-sum method. Considering the traits *viz*., plant height, number of internodes, internodal length, fruit length, average fruit weight and fruit yield per plant, each population was ranked from 1 to 4 (rank 1 for the population that expressed higher estimate under each of the statistical parameters and through 4 for the population that expressed lower estimate under each of the statistical parameters). Further, ranks were summed across these traits (Kang, 1988) and the population with a lower rank sum was identified as the best population.

Table 4: Criteria for drawing inferences to assess breeding potential.

Statistical parameter	Criteria	Inference
Mean	High	High breeding potential
Standardized range	High	High breeding potential
Coefficient of variation (CV)	High	High breeding potential
Frequency of transgressive segregants	High	High breeding potential

3.5.6 Estimation of frequency of transgressive segregants

Plant breeders consider transgressive segregation an essential tool to bring about crop improvement. Due to segregation and recombination, in some instances, transgressive segregants are produced in F_2 or later generations by the accumulation of favourable genes from both the parents involved in hybridization. The number of plants in each of the double cross F_2 populations registering trait values lower than lower scoring parent and higher than higher scoring parent involved in the construction of the respective double cross F_2 population were counted and designated as transgressive segregants in each of the two categories.

Plate 1(a): Representative view of the experimental plot of DCF_1 populations

Plate 1(b): Representative view of the experimental plot of DCF_2 populations

A. DC_1F_2

B. DC_2F_2

C. DC_3F_2

D. DC_4F_2

Plate 2: Variation in the fruit length, size and diameter among the four double cross F_2 populations of okra

EXPERIMENTAL RESULTS

IV EXPERIMENTAL RESULTS

Plant breeding refers to the process involved in creating the desired genotypes for specific pre-defined purposes through purposeful manipulation of plant species. Plant breeders strive to create a desirable plant with a combination of productivity traits. It has been established that the use of diverse parents produces superior hybrids and desirable recombinants. The success of crop improvement greatly depends upon the magnitude of genetic variability present and the degree of heritability of desirable characters. The double cross derived F_2 populations obtained through diverse single cross combinations are found to yield more genetic variability in comparison with the conventional method of hybridization. Keeping this in view, the present investigation was carried out to assess the potential of double cross F_2 populations in okra. The results obtained for the four double cross F_2 populations are presented under the following heads.

4.1 Analysis of variance for fruit yield and its attributing traits in the four double cross F_2 populations

4.2 Estimation of statistical parameters and components of genetic variability for productivity traits

4.3 Productive transgressive segregants recovered for yield and its component traits

4.4 Breeding potential of the double cross F_2 populations

4.5 Identification of easily field assayable proxy traits to select for fruit yield

4.1 Analysis of variance for fruit yield and its attributing traits in the four double cross F_2 populations

Analysis of variance was carried out for fruit yield and its attributing traits in the four double cross F_2 populations along with four checks. Analysis of variance revealed significant differences among the treatments (genotypes + checks), genotypes, checks and checks vs. genotypes for all the traits in all the four double cross F_2 populations with the exception of days to first flowering in DC_2F_2. This indicated the presence of sufficient genetic variability and the appropriateness of the material for the investigation (Table 5 a, b, c, d).

4.2 Estimation of statistical parameters and components of genetic variability for productivity traits

The mean performance of the eight single cross hybrids used in developing double cross F_2 populations have been compiled in Table 6. Variability was noted for majority of the traits. Mean performance, standard error of mean, standard deviation, range and standardized range, along with components of genetic variability among the

Table 5a: ANOVA for fruit yield and it's component traits in DC_1F_2 (NS864 × Arka Nikita) population of okra

Source of variation	Degrees of freedom	Mean sum of squares											
		DFF	PH	NPB	NI	IL	FL	FD	AFW	NFP	NSF	TW	FYP
Block (eliminating Treatments)	5	1.70	3.46	0.04	0.17	0.13	0.01	0.0008	0.08	0.27	0.47	0.0031	853.45
Genotypes+ Checks(Ignoring Blocks)	303	13.73**	73.95**	0.29**	3.04**	0.46**	0.39**	0.01**	1.17**	5.13**	13.84**	0.07**	3188.81**
Genotypes	299	13.79**	33.83**	0.24**	2.54**	0.25**	0.07**	0.01**	0.12**	4.79**	12.27**	0.01*	2829.28**
Checks	3	12.50	2307.56**	4.71**	46.37**	31.66**	22.48**	0.47**	61.82**	31.89**	106.78**	3.33**	11330.07**
Checks vs. Genotypes	1	22.97**	5401.31**	1.93**	26.48**	1.08*	28.23**	1.06**	134.75**	29.56**	263.48**	10.14**	86576.92**
Error	15	4.17	2.8	0.04	0.24	0.13	0.0039	0.00063	0.03	0.29	1.11	0.0022	539.77

**Significance at 0.01 probability level *Significance at 0.05 probability level

DFF = Days to first flowering PH = Plant height (cm) NPB = Number of primary branches NI = Number of internodes

IL = Internodal length (cm) FL = Fruit length (cm) FD = Fruit diameter (cm) AFW = Average fruit weight (g)

NFP = Number of fruits per plant NSF = Number of seeds per fruit TW = Test weight (g) FYP = Fruit yield per plant (g)

Table 5b: ANOVA for fruit yield and its component traits in the DC_2F_2 (Mahyco10 × OH-102) population of okra

Source of variation	Degrees of freedom	Mean sum of squares											
		DFF	PH	NPB	NI	IL	FL	FD	AFW	NFP	NSF	TW	FYP
Block (eliminating Treatments)	5	11.88	1.35	0.07	0.04	0.14	0.18	0.0003	0.36	0.36	0.34	0.0014	126.19
Genotypes+ Checks(Ignoring Blocks)	303	13.39	31.70**	0.34**	1.95**	1.68**	1.15**	0.03**	1.48**	3.80**	4.20**	0.16**	781.16**
Genotypes	299	16.59	7.29**	0.23**	1.04**	1.23**	0.39**	0.02**	1.41**	3.03**	2.96**	0.08**	462.80*
Checks	3	16.93	2261.55**	9.33**	72.93**	41.62**	38.37**	0.42**	4.80**	50.94**	88.26**	3.91**	32267.34**
Checks vs. Genotypes	1	1.19	637.04**	4.17**	63.59**	32.15**	118.88**	1.56**	14.77**	102.09**	125.35**	13.86**	1066.81*
Error	15	8.96	4.54	0.07	0.26	0.27	0.27	0.0026	0.26	0.34	0.50	0.0039	207.93

**Significance at 0.01 probability level *Significance at 0.05 probability level

DFF = Days to first flowering PH = Plant height (cm) NPB = Number of primary branches NI = Number of internodes

IL = Internodal length (cm) FL = Fruit length (cm) FD = Fruit diameter (cm) AFW = Average fruit weight (g)

NFP = Number of fruits per plant NSF = Number of seeds per fruit TW = Test weight (g) FYP = Fruit yield per plant (g)

Table 5c: ANOVA for fruit yield and its component traits in the DC_3F_2 (Raadhika × Shakti) population of okra

Source of variation	Degrees of freedom	Mean sum of squares											
		DFF	PH	NPB	NI	IL	FL	FD	AFW	NFP	NSF	TW	FYP
Block (eliminating Treatments)	5	1.74	43.51	0.07	0.07	0.01	0.05	0.0026	0.03	0.27	1.10	0.02	35.78
Genotypes+ Checks(Ignoring Blocks)	303	12.89*	136.57**	0.23*	10.30**	0.61**	6.77**	0.04**	7.83**	7.78**	41.74**	0.67**	6567.98**
Genotypes	299	13.06**	116.81**	0.19*	10.01**	0.34**	6.61**	0.03**	8.03**	7.87**	37.77**	0.55**	6385.03**
Checks	3	9.15**	2606.48**	4.17**	55.44**	26.67**	33.03**	0.58**	8.84**	48.11**	60.67**	4.22**	45030.26**
Checks vs. Genotypes	1	5.59	111.87**	0.15*	216.78**	10.67**	2.81**	0.14**	26.33**	47.15**	1367.31**	27.22**	39272.34**
Error	15	4.85	34.31	0.33	0.58	0.02	0.08	0.0018	0.06	0.64	2.17	0.01	226.69

**Significance at 0.01 probability level *Significance at 0.05 probability level

DFF = Days to first flowering PH = Plant height (cm) NPB = Number of primary branches NI = Number of internodes

IL = Internodal length (cm) FL = Fruit length (cm) FD = Fruit diameter (cm) AFW = Average fruit weight (g)

NFP = Number of fruits per plant NSF = Number of seeds per fruit TW = Test weight (g) FYP = Fruit yield per plant (g)

Table 5d: ANOVA for fruit yield and it's component traits in DC_4F_2 (Samrat × SVOK5151) population of okra

Source of variation	Degrees of freedom	Mean sum of squares											
		DFF	PH	NPB	NI	IL	FL	FD	AFW	NFP	NSF	TW	FYP
Block (eliminating Treatments)	5	1.54	1.77	0.34	0.57	0.01	0.39	0.0041	0.06	0.44	0.84	0.0036	20.28
Genotypes+ Checks(Ignoring Blocks)	303	12.29**	241.07**	0.28*	6.45**	1.17**	6.97**	0.04**	7.82**	8.96**	45.66**	0.93**	7700.94**
Genotypes	299	12.44**	217.94**	0.25*	6.00**	0.71**	8.24**	0.04**	7.07**	8.78**	43.13**	0.91**	7184.89**
Checks	3	21.04**	2718.04**	2.15**	59.28**	48.36**	20.46**	0.47**	3.48**	35.93**	78.82**	2.92**	38450.88**
Checks vs. Genotypes	1	4.81	3731.16**	4.94**	4.91**	0.59**	46.57**	0.02*	304.01**	11.90**	721.58**	15.38**	94164.86**
Error	15	1.21	10.91	0.32	0.21	0.02	0.76	0.0029	0.29	0.86	2.35	0.01	151.86

**Significance at 0.01 probability level *Significance at 0.05 probability level

DFF = Days to first flowering PH = Plant height (cm) NPB = Number of primary branches NI = Number of internodes

IL = Internodal length (cm) FL = Fruit length (cm) FD = Fruit diameter (cm) AFW = Average fruit weight (g)

NFP = Number of fruits per plant NSF = Number of seeds per fruit TW = Test weight (g) FYP = Fruit yield per plant (g)

Table 6: Mean performance of parents used in constructing double cross F_2 populations for fruit yield and its component traits in okra

Populations	Parents	Average Plant height (cm)	Number of primary branches	Internodal Length (cm)	Number of internodes	Average fruit length (cm)	Average fruit width (cm)	Average fruit weight (g)	Number of fruits per plant	Test weight (g)	Number of seeds per fruit	Fruit yield per plant (g)
DC_1F_2	NS864	140.29	2.00	10.11	21.00	14.36	1.48	18.29	23.00	7.20	52.16	500.36
	Arka Nikitha	114.65	1.00	7.15	16.00	14.90	1.56	19.21	19.00	7.36	53.74	449.08
DC_2F_2	OH-102	90.83	1.00	10.35	14.00	15.21	1.91	23.32	21.00	6.20	46.30	528.33
	Mahyco10	116.52	2.00	5.10	14.00	13.78	1.39	17.52	16.00	7.62	44.68	366.52
DC_3F_2	Raadhika	96.27	1.00	5.42	15.00	18.62	2.10	26.48	23.00	5.86	48.20	589.15
	Shakti	128.39	1.00	6.33	15.00	16.53	1.62	23.19	21.00	7.72	42.32	453.58
DC_4F_2	Samrat	111.64	1.00	5.06	18.00	15.35	1.45	22.98	21.00	7.36	44.56	532.16
	SVOK5151	142.18	1.00	9.85	20.00	18.60	1.98	25.62	21.00	7.10	38.66	510.78

DC_1F_2 = (NS864 × Arka Nikitha) **DC_2F_2** = (Mahyco10 × OH-102) **DC_3F_2** = (Raadhika × Shakti) **DC_4F_2** = (Samrat × SVOK5151)

four double cross F_2 populations for fruit yield and its component traits, have been tabulated in Table 7. All four double cross F_2 populations which were statistically analysed showed substantial variation for all twelve traits. Genetic variability components estimated were expressed as PCV (phenotypic coefficient of variability), GCV (genotypic coefficient of variability), heritability (h^2_{bs}) and GAM (genetic advance as *per cent* of mean). The Box-Whisker plot depicting the distribution of the twelve traits for these populations are presented in Figures 1-4.

4.2.1.1 Days to first flowering

This trait registered similar mean values and observed range in all the four populations. Population DC_1F_2 registered a standardized range of 6.42, which was the highest among all the populations. In comparison, the populations DC_2F_2 (5.55) and DC_4F_2 (5.77) were found to register similar values of standardized range. Moderate standard deviation was observed for all the populations, of which DC_2F_2 exhibited a comparatively higher value of 4.37.

Although the population DC_1F_2 exhibited low PCV (8.12%) and GCV (6.78%) values for this trait it showed high heritability (69.80%) and moderate GAM (11.69%). Similarly, populations DC_2F_2 (), DC_3F_2 () and DC_4F_2 () also registered low estimates of PCV and GCV. DC_2F_2 (65.97%) and DC_3F_2 (62.84%) showed high heritability. Moderate GAM was observed for DC_3F_2 (10.36%). Similarly, high heritability (90.29%) coupled with moderate GAM (14.44%) was observed in DC_4F_2.

4.2.1.2 Plant height (cm)

The population DC_4F_2 recorded the highest mean plant height of 128.23 cm among all the four populations, followed by DC_1F_2, which recorded a mean of 124.56 cm. The highest range was observed for DC_4F_2, where the values lie between 83.81 cm and 154.14 cm. Correspondingly, similar ranges were observed for the populations DC_1F_2, DC_2F_2 and DC_3F_2. Also, higher standardized range was observed for the populations DC_2F_2 (12.30) followed by DC_1F_2 (9.80). Standard deviation was found to be greater in the populations DC_4F_2 (14.98) and DC_3F_2 (11.19) compared to the other populations.

Moderate estimates of PCV (11.51%) and GCV (11.22%) were observed for the population DC_4F_2, along with high heritability (95.00%) coupled with high GAM (22.56%). The population DC_1F_2, DC_2F_2 and DC_3F_2 exhibited low estimates of PCV and GCV. High heritability (91.72%) was observed for DC_1F_2 with low GAM (8.84%). Similarly, DC_2F_2 registered high heritability (77.65%) coupled with low GAM (1.81%). At the same time, DC_3F_2 showed high heritability (70.62%) coupled with moderate GAM (13.00%).

Table 7: Trait-wise estimation of statistical parameters and genetic variability components for fruit yield among the four double cross F_2 populations of okra

Trait	Parameter / Population	Mean#	SEm	Standard deviation	Range		Standardized range	PCV (%)	GCV (%)	$h^2_{(bs)}$ (%)	GAM (%)
					Lowest	Highest					
Days to first flowering	DC_1F_2	45.57	0.25	3.74	35.50	59.50	6.42	8.12	6.78	69.80	11.69
	DC_2F_2	45.90	0.25	4.37	34.37	58.62	5.55	8.87	6.02	65.97	8.42
	DC_3F_2	45.21	0.21	3.66	37.46	55.21	4.85	7.99	6.34	62.84	10.36
	DC_4F_2	45.50	0.20	3.55	34.79	55.29	5.77	7.75	7.37	90.29	14.44
Plant Height	DC_1F_2	124.56	0.37	6.41	90.94	153.76	9.80	4.67	4.47	91.72	8.84
	DC_2F_2	115.77	0.19	3.40	94.01	135.84	12.30	2.33	1.43	77.65	1.81
	DC_3F_2	121.17	0.67	11.19	94.40	150.58	5.02	8.92	7.50	70.62	13.00
	DC_4F_2	128.23	0.86	14.98	83.81	154.14	4.69	11.51	11.22	95.00	22.56

DC_1F_2 = (NS864 × Arka Nikitha) **DC_2F_2 =** (Mahyco10 × OH-102) **DC_3F_2 =** (Raadhika × Shakti) **DC_4F_2 =** (Samrat × SVOK5151)
Mean of 300 genotypes

Table 7. continued…….

Trait	Parameter / Population	Mean#	SEm	Standard deviation	Range		Standardized range	PCV (%)	GCV (%)	$h^2_{(bs)}$ (%)	GAM (%)
					Lowest	Highest					
Number of primary branches	DC_1F_2	1.53	0.03	0.50	1.40	3.04	3.08	36.56	33.20	82.45	62.19
	DC_2F_2	1.76	0.03	0.52	1.20	3.08	3.61	27.41	23.16	71.39	40.37
	DC_3F_2	1.00	0.03	0.44	0.08	2.17	4.75	43.83	39.56	88.93	46.28
	DC_4F_2	1.51	0.03	0.55	0.17	2.29	3.85	33.22	30.24	91.78	52.33
Number of internodes	DC_1F_2	17.70	0.09	1.62	14.00	26.88	7.95	9.00	8.56	90.48	19.80
	DC_2F_2	14.59	0.06	1.09	13.96	24.96	10.09	7.13	6.16	74.60	10.98
	DC_3F_2	19.75	0.18	3.18	14.50	30.92	5.16	16.02	15.55	94.23	31.14
	DC_4F_2	17.38	0.14	2.46	11.67	23.67	4.88	14.09	13.84	96.48	28.04

DC_1F_2 = (NS864 × Arka Nikitha) **DC_2F_2** = (Mahyco10 × OH-102) **DC_3F_2** = (Raadhika × Shakti) **DC_4F_2** = (Samrat × SVOK5151)
Mean of 300 genotypes

Table 7. continued…….

Trait	Parameter / Population	Mean#	SEm	Standard deviation	Range		Standardized range	PCV (%)	GCV (%)	$h^2_{(bs)}$ (%)	GAM (%)
					Lowest	Highest					
Internodal length (cm)	**DC_1F_2**	8.12	0.02	0.49	5.41	10.30	9.98	4.71	4.46	90.38	9.10
	DC_2F_2	6.56	0.07	1.15	4.78	10.98	5.39	16.92	14.99	78.45	27.38
	DC_3F_2	6.02	0.04	0.62	4.46	9.79	8.59	9.63	9.34	94.05	18.69
	DC_4F_2	7.45	0.05	0.89	5.08	10.44	6.02	11.32	11.15	97.06	22.67
Fruit length (cm)	**DC_1F_2**	14.66	0.02	0.36	14.21	18.64	12.30	1.87	1.82	94.83	3.65
	DC_2F_2	14.31	0.04	0.74	13.06	18.91	7.91	4.36	2.41	70.55	2.75
	DC_3F_2	17.28	0.15	2.56	10.31	20.36	3.92	14.88	14.79	98.79	30.32
	DC_4F_2	17.07	0.17	2.90	8.75	22.14	4.62	16.82	16.02	90.76	31.49

DC_1F_2 = (NS864 × Arka Nikitha) **DC_2F_2 =** (Mahyco10 × OH-102) **DC_3F_2 =** (Raadhika × Shakti) **DC_4F_2 =** (Samrat × SVOK5151)

\# Mean of 300 genotypes

Table 7. continued…….

Trait	Parameter / Population	Mean#	SEm	Standard deviation	Range		Standardized range	PCV (%)	GCV (%)	$h^2_{(bs)}$ (%)	GAM (%)
					Lowest	Highest					
Fruit diameter (cm)	DC_1F_2	1.55	0.04	0.08	1.45	2.11	8.25	4.78	4.50	88.61	8.74
	DC_2F_2	1.57	0.01	0.16	1.29	2.05	4.75	9.99	9.45	89.58	18.46
	DC_3F_2	1.68	0.01	0.19	1.21	2.36	6.05	11.00	10.72	94.83	21.53
	DC_4F_2	1.72	0.01	0.20	1.23	2.52	6.45	11.42	10.99	92.54	21.80
Average fruit weight (g)	DC_1F_2	19.15	0.03	0.56	18.46	24.85	11.41	1.80	1.59	77.60	2.88
	DC_2F_2	23.86	0.07	1.21	19.98	29.12	7.55	4.97	4.50	81.82	8.39
	DC_3F_2	23.01	0.16	2.81	17.63	30.71	4.65	12.31	12.27	99.24	25.21
	DC_4F_2	20.55	0.15	2.66	14.08	28.15	5.29	12.94	12.67	95.96	25.61

DC_1F_2 = (NS864 × Arka Nikitha) **DC_2F_2** = (Mahyco10 × OH-102) **DC_3F_2** = (Raadhika × Shakti) **DC_4F_2** = (Samrat × SVOK5151)
Mean of 300 genotypes

Table 7. continued…….

Trait	Parameter / Population	Mean#	SEm	Standard deviation	Range		Standardized range	PCV (%)	GCV (%)	$h^2_{(bs)}$ (%)	GAM (%)
					Lowest	Highest					
Number of fruits per plant	DC_1F_2	19.53	0.13	2.21	17.67	31.92	6.45	11.21	10.87	93.97	31.73
	DC_2F_2	17.97	0.10	1.78	14.58	26.33	6.60	9.68	9.11	88.62	17.70
	DC_3F_2	22.60	0.16	2.78	17.17	32.67	5.58	12.41	11.90	91.82	23.51
	DC_4F_2	20.43	0.17	2.98	12.96	29.21	5.45	14.51	13.77	90.16	26.98
Number of seeds per fruit	DC_1F_2	52.06	0.20	3.54	43.67	67.92	6.85	6.73	6.42	90.95	12.62
	DC_2F_2	46.14	0.10	1.79	38.83	56.04	9.61	3.73	3.69	95.06	6.93
	DC_3F_2	50.74	0.36	6.22	33.00	65.50	5.23	12.11	11.76	94.26	23.56
	DC_4F_2	49.83	0.38	6.58	30.96	65.46	5.24	13.18	12.81	94.54	25.70

DC_1F_2 = (NS864 × Arka Nikitha) **DC_2F_2** = (Mahyco10 × OH-102) **DC_3F_2** = (Raadhika × Shakti) **DC_4F_2** = (Samrat × SVOK5151)
Mean of 300 genotypes

Table 7. continued…….

Trait	Parameter / Population	Mean#	SEm	Standard deviation	Range		Standardized range	PCV (%)	GCV (%)	$h^2_{(bs)}$ (%)	GAM (%)
					Lowest	Highest					
Test weight (g)	DC_1F_2	7.34	0.01	0.13	5.91	7.82	14.69	1.04	0.82	62.59	1.34
	DC_2F_2	7.46	0.02	0.31	5.91	8.08	7.00	3.79	3.40	83.18	7.43
	DC_3F_2	5.92	0.04	0.76	4.44	8.57	5.43	12.51	12.39	98.08	25.31
	DC_4F_2	6.21	0.05	0.96	4.09	8.63	4.73	15.34	15.23	98.60	31.21
Fruit yield per plant (g)	DC_1F_2	439.90	3.20	55.75	339.47	667.72	5.89	12.09	10.88	80.92	20.19
	DC_2F_2	496.04	1.34	23.29	385.71	581.39	8.40	4.34	3.22	85.07	4.93
	DC_3F_2	519.63	4.60	80.19	363.48	742.29	4.72	15.38	15.10	96.45	30.60
	DC_4F_2	427.20	4.87	84.83	154.20	631.49	5.63	19.84	19.63	97.89	40.07

DC_1F_2 = (NS864 × Arka Nikitha) **DC_2F_2** = (Mahyco10 × OH-102) **DC_3F_2** = (Raadhika × Shakti) **DC_4F_2** = (Samrat × SVOK5151)

Mean of 300 genotypes

4.2.1.3 <u>Number of primary branches</u>

The trait number of primary branches registered a mean value of 1.76 in the population DC_2F_2, which was highest among all the populations. Higher range was displayed by the populations DC_3F_2 (0.08 to 2.17) and DC_4F_2 (0.17 to 2.29). The population DC_3F_2 registered the highest standardized range of 4.75. Also, all the other populations were observed to register similar values.

High values of PCV (36.56%) and GCV (33.20%) were observed in DC_1F_2, which paved way for high heritability (82.45%) together with high genetic GAM (62.19%). Similarly, population DC_2F_2 displayed high PCV (27.41%) and GCV (23.16%), along with high heritability (71.39%) coupled with high GAM (40.37%). High estimates were observed even in the case of populations DC_3F_2 and DC_4F_2. In the population DC_3F_2, high PCV (43.83%) and GCV (39.56%) values were recorded, along with high heritability (88.93%) and GAM (46.28%). Correspondingly, DC_4F_2 registered high PCV and GCV values of 33.22% and 30.24%, which resulted in high heritability (91.78%) and GAM (52.33%).

4.2.1.4 <u>Number of internodes</u>

This trait has a mean value of 19.75, which falls within the observed range of 14.50 and 30.92 in the population DC_3F_2, both of which were highest among all the four populations. The populations DC_1F_2 and DC_4F_2 recorded similar mean values of 17.70 and 17.38, respectively. Highest standardized range of 10.09 was observed for the population DC_2F_2. Low standard deviation was noticed in all the populations.

Low estimates of PCV and GCV were observed for the DC_1F_2 and DC_2F_2. High heritability (90.48%), along with moderate GAM (19.80%), was seen in DC_1F_2. Similarly, DC_2F_2 was found to display high heritability (74.60%) coupled with moderate GAM (10.98%). The populations DC_3F_2 and DC_4F_2 displayed moderate values of PCV (16.02%, 14.09%) and GCV values (15.55%, 13.84%), respectively. This led to high heritability and GAM in both populations. DC_3F_2 recorded heritability and genetic advance estimates of 94.23% and 31.14%, respectively, while DC_4F_2 recorded heritability and GAM of 96.48% and 28.04% respectively.

4.2.1.5 <u>Internodal length (cm)</u>

The mean internodal length in population DC_1F_2 was 8.12 cm, with a range of 5.41 cm to 10.30 cm, which was the highest among all the populations. A similar range of 5.08 cm to 10.44 cm was recorded for the population DC_4F_2. High standardized range was observed for the populations DC_1F_2 and DC_3F_2 being 9.98 and 8.59, respectively. Also, a lower standard deviation was visible in all the populations for this trait.

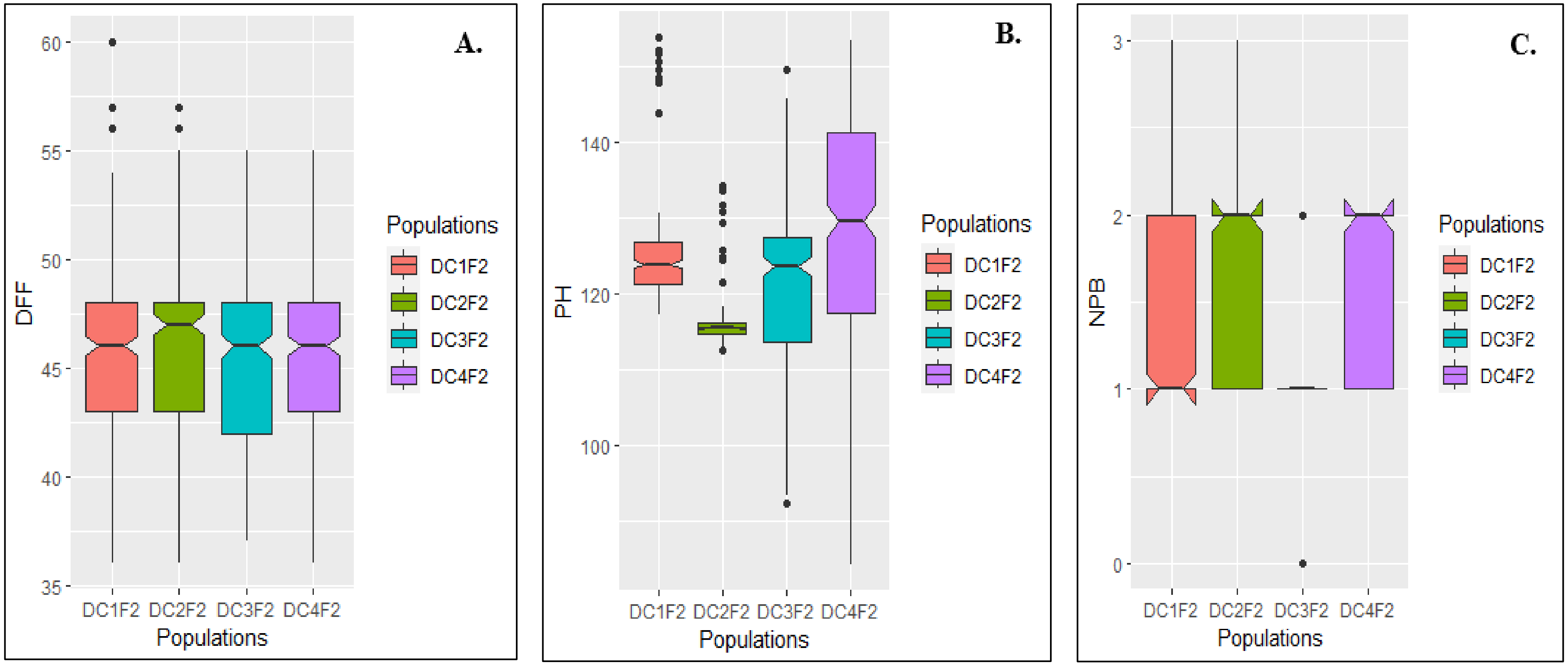

Figure 1: Box whisker plots depicting the distribution of traits, A. Days to first flowering, B. Plant height (cm) and C. Number of primary branches

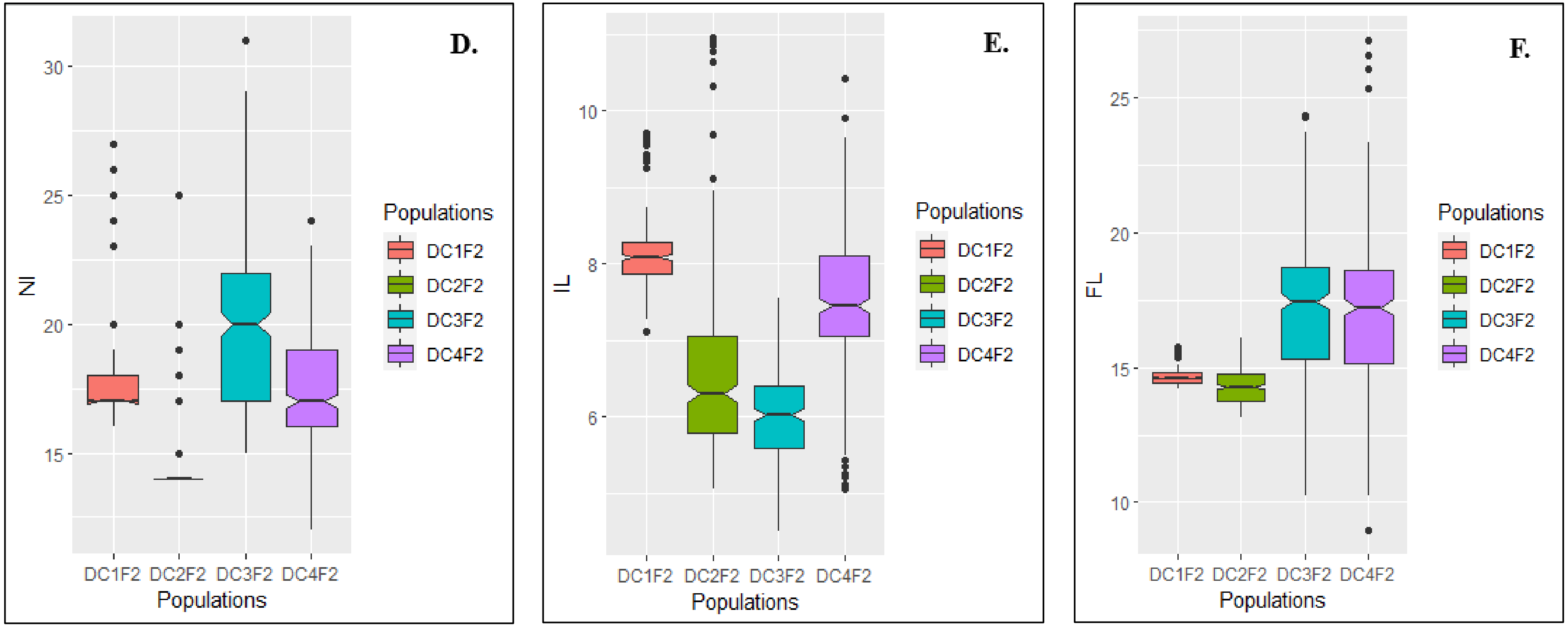

Figure 2: Box whisker plots depicting the distribution of traits, D. Number of internodes, E. Internodal length (cm) and F. Fruit length (cm)

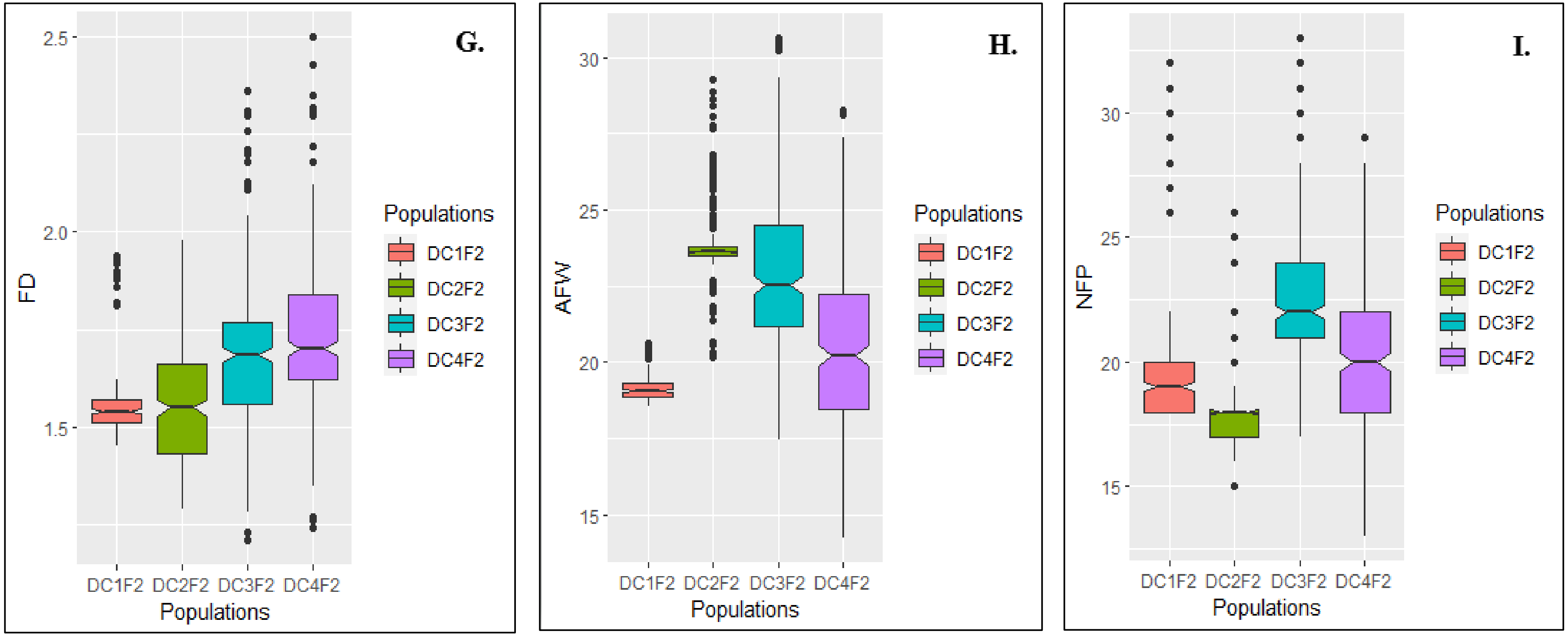

Figure 3: Box whisker plots depicting the distribution of traits, G. Fruit diameter (cm), H. Average fruit weight (g) and I. Number of fruits per plant

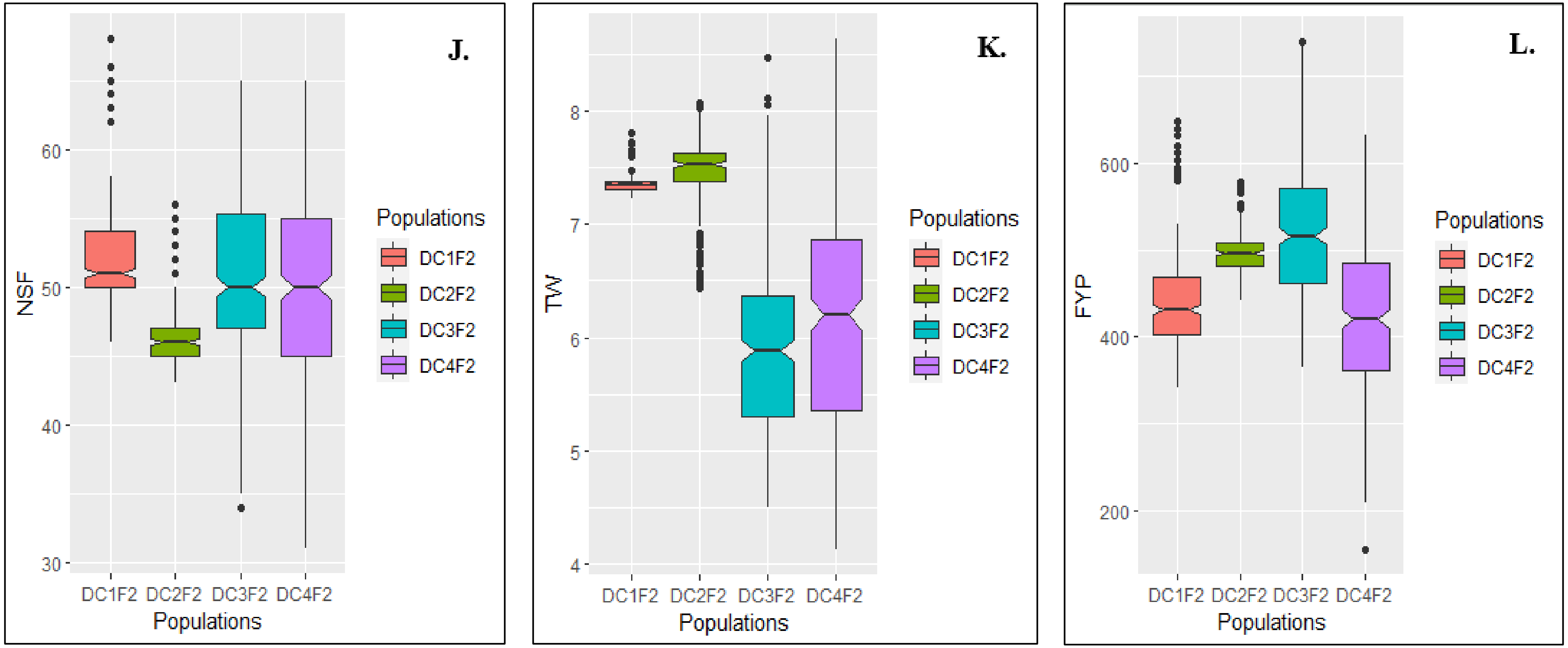

Figure 4: Box whisker plots depicting the distribution of traits, J. Number of seeds per fruit, K. Test weight (g) and L. Fruit yield per plant (g)

DC_2F_2 was observed to have high values of PCV (16.92) and GCV (14.99), which displayed high heritability (78.45%) and GAM (27.38%). Similar findings were registered for the population DC_3F_2, which also showed high heritability (94.05%) coupled with moderate GAM (18.69%). Also, DC_4F_2 recorded moderate PCV (11.32%) and GCV (11.15%) values which led to high heritability (97.06%) and GAM (22.67%). DC_1F_2 displayed low values of PCV and GCV, along with high heritability (90.38%) coupled with low GAM (9.10%).

4.2.1.6 *Fruit length (cm)*

The populations, DC_3F_2 and DC_2F_2, registered high mean performance of 17.28 cm and 17.07 cm, respectively, among all the populations. Similarly, DC_2F_2 had a wide range of 8.75 cm and 22.14 cm. Higher standardized range of 12.30 was observed in the population DC_1F_2 compared to all others. Lower standard deviation was observed in all the populations.

Both populations, DC_3F_2 and DC_4F_2 were found to display moderate values of PCV (14.88%, 16.82%) and GCV (14.79%, 16.02%) respectively. High heritability (98.79%) with high GAM (30.32%) was observed for DC_3F_2. Similarly, DC_4F_2 was observed to exhibit high heritability (90.76%) coupled with high GAM (31.49%). However, low estimates of PCV and GCV were recorded in DC_1F_2 along with high heritability (94.83%) and low GAM (3.55).

4.2.1.7 *Fruit diameter (cm)*

The mean fruit diameter was found to be highest in the population DC_4F_2 (1.72 cm) and all other populations were found to exhibit similar means. The standardized range was calculated to be highest in DC_1F_2, while all the populations displayed nearly similar ranges.

Both DC_3F_2 and DC_4F_2 populations were found to exhibit moderate PCV values viz. (11.00%, 11.42%) along with moderate GCV values (10.72%, 10.99%) respectively. DC_3F_2 was found to register high heritability (94.83%) coupled with high GAM (21.53%). Same findings were observed for the population DC_4F_2 which registered high heritability and high GAM values of 92.54% and 21.80% respectively. All populations displayed high heritability for this trait, while population DC_2F_2 recorded moderate GAM (18.46%) and DC_1F_2 recorded low GAM (8.74%).

4.2.1.8 *Average fruit weight (g)*

This trait exhibited higher mean values in the populations DC_2F_2 (23.86 g) and DC_3F_2 (23.01 g). The standard deviation was observed to be 0.56. While the population DC_1F_2 registered higher standardized range of 11.41. All the populations were found to display similar range while a wider range of 17.63 g to 30.71 g was observed for the population DC_3F_2. Low standard deviation was observed in all the populations.

Populations DC_1F_2 and DC_2F_2 were found to display low PCV and GCV values but high heritability, viz. 77.60% in DC_1F_2 and 81.82% in DC_2F_2 and low GAM (2.88%, 8.39%), respectively, was noticed. Moderate values of PCV (12.31%) and GCV (12.27%) were observed, along with high heritability (99.24%) and high genetic advance (25.21%) in DC_3F_2. Similarly, DC_4F_2 displayed moderate PCV (12.94%) and GCV (12.67%) estimates but high heritability (95.96%) and genetic advance (25.61%).

4.2.1.9 Number of fruits per plant

This trait recorded a mean performance of 22.60 in the population DC_3F_2, which was found to be the highest among all the populations. Higher range was registered in the population DC_4F_2, where the observations lie between 30.96 and 65.46. Also, DC_2F_2 and DC_3F_2 exhibited similar ranges. The standardized range was observed to be highest in the population DC_2F_2 (6.60). DC_3F_2 (2.78) and DC_4F_2 (2.98) registered slightly noticeable standard deviations.

Moderate PCV (11.21%) and GCV (10.87%) estimates were recorded for this trait in the population DC_1F_2 together with high heritability (93.97%) and high GAM (31.73%). In comparison, population DC_2F_2 was found to register low PCV (9.68%) and GCV (9.11%) values but high heritability (88.62%) with moderate GAM (17.70%). Both populations, DC_3F_2 and DC_4F_2, were observed to have moderate PCV and GCV values. DC_3F_2 was recorded PCV and GCV values of 12.41% and 11.90%, respectively along with high heritability (91.82%) and GAM (23.51%). Similar findings were observed in DC_4F_2, where high heritability (90.16%) coupled with high GAM (26.98%) were recorded for the PCV and GCV values of 14.51% and 13.77%, respectively.

4.2.1.10 Number of seeds per fruit

This trait registered a mean of 52.06 in the DC_1F_2 population, which was the highest among all the populations, while similar means of 50.74 and 49.83 were recorded in the populations DC_3F_2 and DC_4F_2. A higher range of 17.17 to 32.67 was observed for the population DC_3F_2, while similar findings were seen in the population DC_1F_2. However, DC_1F_2 (6.45) and DC_2F_2 (6.60) displayed higher standardized range than the rest. Relatively higher standard deviation was recorded in the populations DC_3F_2 (6.22) and DC_4F_2 (6.58).

This trait recorded low PCV and GCV values in both DC_1F_2 and DC_2F_2 populations. DC_1F_2 registered high heritability (90.95%) with moderate GAM (12.62%), while DC_2F_2 was found to exhibit high heritability (95.06%) coupled with low GAM (6.93%). Moderate PCV (12.11%) and GCV (11.76%) values were observed in the population DC_3F_2, which also showed high heritability (94.26%) and high GAM

(23.56%). Similarly, the population DC_4F_2 exhibited moderate estimates of PCV (13.18%) and GCV (12.81%) as well as high heritability (94.54%) coupled with high GAM (25.70%). All the four populations exhibited high heritability for this trait.

4.2.1.11 Test weight (g)

This trait showed higher mean values of 7.34 g and 7.46 g in the DC_1F_2 and DC_2F_2 populations, respectively. Population DC_4F_2 recorded a wider range of 4.09 g to 8.63 g, while similar findings were recorded for DC_3F_2. Also, a higher standardized range of 14.69 was registered in the population DC_1F_2 among all the populations examined. Standard deviation was negligible in all the populations.

The populations DC_1F_2 and DC_2F_2 displayed low values of PCV and GCV along with high heritability (viz. 62.59% and 83.18%, respectively) coupled with low GAM. Moderate values of GCV (12.51%) and PCV (12.39%) were recorded in the population DC_3F_2, along with high heritability (98.08%) and GAM (25.31%). On the same lines, DC_4F_2 registered moderate estimates of PCV (15.34%) and GCV (15.23%), which led to high heritability (98.60%) coupled with high genetic advance (31.21%).

4.2.1.12 Fruit yield per plant (g)

The highest mean values for fruit yield were recorded in the populations DC_2F_2 (496.04 g) and DC_3F_2 (519.63 g). The highest range of 154.20 g to 631.49 g was observed in the population DC_4F_2, followed by DC_3F_2, which recorded a range of 363.48 g to 742.29 g. The standardized range was found to be higher in DC_2F_2 (8.40), while comparable standardized ranges were observed in the populations DC_1F_2 (5.89) and DC_4F_2 (5.63). Standard deviation was noted to be high in all the populations where DC_4F_2 (84.83) and DC_3F_2 (80.19) recorded relatively higher values as compared to other populations.

This trait recorded moderate PCV (12.09%) and GCV (10.88%) values along with high heritability (80.92%) and high GAM (20.19%) for the population DC_1F_2. Low PCV (4.34%) and GCV (3.22%) estimates were observed in the population DC_2F_2, which displayed high heritability (85.07%) with low GAM (4.93%). DC_3F_2 registered moderate PCV and GCV values of 15.38% and 15.10%, respectively, along with high heritability (96.45%) and GAM (30.60%). Similarly, moderate PCV and GCV values of 19.84% and 19.63%, together with high heritability (97.89%) and high GAM (40.07%) were observed for the population DC_4F_2.

4.3 Productive transgressive segregants recovered for the yield and its component traits

The frequency of plants lagging in expression than the lower parent and exceeding the expression of the higher parent are tabulated and indicated in Table 8.

Table 8: Estimates of frequency of transgressive segregants recovered for yield and its component traits among four double cross F_2 populations of okra

Traits	Parents		DC_1F_2 Population (NS864 × Arka Nikita)			Number and percent of transgressive segregants	
	Highest parent value	Lowest parent value	Mean	Highest plant value	Lowest plant value	Superior to better parent (%)	Inferior to lower parent (%)
Days to first flowering	47.00	46.00	45.57	60.00	36.00	101 (33.67)	153 (51.00)
Plant height	134.56	113.42	124.56	153.86	88.64	13 (4.33)	12 (4.00)
Number of primary branches	3.00	1.00	1.33	3.00	0.00	0 (0.00)	6 (2.00)
Number of internodes	20.00	16.00	17.70	27.00	14.00	14 (4.67)	9 (3.00)
Internodal length	9.25	7.00	8.12	10.43	5.34	23 (7.67)	6 (2.00)
Fruit length	15.00	14.21	14.66	18.72	14.23	27 (9.00)	0 (0.00)
Fruit diameter	1.60	1.49	1.55	2.18	1.45	33 (11.00)	7 (2.33)
Average fruit weight	19.30	18.29	19.15	25.19	18.38	92 (30.67)	0 (0.00)
Number of fruits per plant	23.00	18.00	19.53	32.00	18.00	14 (4.67)	0 (0.00)
Number of seeds per fruit	55.32	46.13	52.06	68.00	42.00	41 (13.67)	8 (2.67)
Test weight	7.46	7.20	7.34	7.80	5.86	12 (4.00)	12 (4.00)
Fruit yield per plant	500.36	438.54	439.90	648.52	341.75	39 (13.00)	164 (54.67)

Table 8. Continued……

Traits	Parents		DC_2F_2 Population (OH-102 × Mahyco10)			Number and percent of transgressive segregants	
	Highest parent value	Lowest parent value	Mean	Highest plant value	Lowest plant value	Superior to better parent (%)	Inferior to lower parent (%)
Days to first flowering	44.00	40.00	45.90	57.00	36.00	193 (64.33)	12 (4.00)
Plant height	118.92	88.22	115.77	139.52	92.45	16 (5.33)	0 (0.00)
Number of primary branches	2.00	0.00	1.76	3.00	0.00	14 (4.67)	0 (0.00)
Number of internodes	15.00	14.00	14.29	25.00	14.00	17 (5.67)	0 (0.00)
Internodal length	10.40	5.00	6.56	10.95	5.05	9 (3.00)	0 (0.00)
Fruit length	15.21	13.29	14.31	19.08	13.12	25 (8.33)	8 (2.63)
Fruit diameter	1.91	1.39	1.57	2.12	1.29	20 (6.67)	30 (10.00)
Average fruit weight	24.28	23.28	23.86	39.27	20.19	61 (20.33)	23 (7.67)
Number of fruits per plant	20.00	16.00	17.97	26.00	15.00	27 (9.00)	7 (2.33)
Number of seeds per fruit	49.61	42.56	46.14	56.00	38.00	10 (3.33)	8 (2.67)
Test weight	7.82	6.10	7.46	8.06	5.88	13 (4.33)	7 (2.33)
Fruit yield per plant	523.46	366.52	496.04	578.46	366.84	25 (8.33)	0 (0.00)

Table 8. Continued……

Traits	Parents		DC_3F_2 Population (Raadhika × Shakti)			Number and percent of transgressive segregants	
	Highest parent value	Lowest parent value	Mean	Highest plant value	Lowest plant value	Superior to better parent (%)	Inferior to lower parent (%)
Days to first flowering	44.00	42.00	45.21	55.00	37.00	196 (65.33)	52 (16.67)
Plant height	134.32	95.36	121.17	152.79	89.63	44 (14.67)	6 (2.00)
Number of primary branches	1.00	0.00	1.00	3.00	0.00	2 (0.67)	1 (0.33)
Number of internodes	17.00	15.00	19.75	31.00	14.00	224 (74.67)	3 (1.00)
Internodal length	6.50	5.30	6.02	10.00	4.50	63 (21.00)	31 (10.33)
Fruit length	18.72	16.41	17.28	24.36	10.22	80 (26.67)	117 (39.00)
Fruit diameter	2.12	1.55	1.68	2.36	1.21	11 (3.67)	74 (24.67)
Average fruit weight	26.48	22.29	23.01	30.64	17.46	38 (12.67)	133 (44.33)
Number of fruits per plant	24.00	21.00	22.60	33.00	16.00	59 (19.67)	77 (25.67)
Number of seeds per fruit	49.20	42.32	50.74	65.00	34.00	160 (53.33)	32 (10.67)
Test weight	7.72	5.96	5.92	8.46	4.50	8 (2.67)	164 (54.67)
Fruit yield per plant	589.15	453.58	519.63	739.45	345.16	58 (19.33)	74 (24.67)

Table 8. Continued……

Traits	Parents		DC_4F_2 Population (Samrat × SVOK5151)			Number and percent of transgressive segregants	
	Highest parent value	Lowest parent value	Mean	Highest plant value	Lowest plant value	Superior to better parent (%)	Inferior to lower parent (%)
Days to first flowering	47.00	41.00	45.50	55.00	36.00	85 (28.33)	19 (6.33)
Plant height	148.71	108.16	128.23	153.40	84.23	17 (5.67)	38 (12.67)
Number of primary branches	2.00	1.00	1.51	3.00	0.00	1 (0.33)	5 (1.67)
Number of internodes	22.00	18.00	17.38	24.00	12.00	9 (3.00)	176 (58.67)
Internodal length	9.70	5.50	7.45	10.42	4.93	14 (4.67)	18 (6.00)
Fruit length	19.21	14.92	17.07	27.13	8.96	61 (20.33)	73 (24.33)
Fruit diameter	2.01	1.41	1.72	2.50	1.24	29 (9.67)	11 (3.67)
Average fruit weight	25.62	20.92	20.55	28.26	14.23	15 (5.00)	185 (61.67)
Number of fruits per plant	23.00	20.00	20.43	29.00	13.00	51 (17.00)	123 (41.00)
Number of seeds per fruit	48.23	38.66	49.83	65.00	31.00	166 (55.33)	15 (5.00)
Test weight	7.36	6.86	6.21	8.63	4.13	40 (13.33)	233 (77.67)
Fruit yield per plant	540.30	415.89	427.20	632.48	155.18	35 (11.67)	142 (47.33)

The promising transgressive segregants for the trait fruit yield per plant in the four double cross F_2 populations have been compiled in Table 9.

4.3.1 Days to first flowering

High frequency of transgressive segregants, which were earlier than superior parent were recorded for this trait in the populations DC_1F_2 (51.00%) followed by DC_3F_2 (16.67%). Populations DC_2F_2 (4.00%) and DC_4F_2 (6.33%) registered low frequency of earliness segregants.

4.3.2 Plant height (cm)

High frequency of tall segregants was observed for the population DC_3F_2 (14.67%). While populations DC_1F_2 (4.33%), DC_2F_2 (5.33%) and DC_4F_2 (5.67%) were found to exhibit a low frequency of transgressive segregants for this trait.

4.3.3 Number of primary branches

Low frequency of transgressive segregants for number of primary branches were recovered in the population DC_2F_2 (4.67%) and DC_3F_2 (0.67%). However, DC_4F_2 (0.33%) and DC_1F_2 had close to none transgressive segregants.

4.3.4 Number of internodes

Very high frequency of transgressive segregants with more number of internodes were recovered in the population DC_3F_2 amounting to 74.67%. However, other populations DC_1F_2 (4.67%), DC_2F_2 (5.67%) and DC_4F_2 (3.00%) displayed low frequency of recovery of transgressive segregants for this trait.

4.3.5 Internodal length (cm)

High frequency of transgressive segregants were recorded in the population DC_3F_2 (10.33%). However, populations DC_4F_2 (6.00%) and DC_1F_2 (2.00%) registered a low frequency of transgressive segregants for the trait internodal length. Also, DC_2F_2 recorded no segregants for this trait.

4.3.6 Fruit length (cm)

Populations DC_3F_2 (26.67%) and DC_4F_2 (20.33%) displayed high frequency of productive segregants for fruit length. While DC_1F_2 and DC_2F_2 recorded a low frequency of favourable segregants, viz. 9.00% and 8.33%, respectively.

4.3.7 Fruit diameter (cm)

Population DC_1F_2 recorded 11.00% of productive segregants for the trait fruit diameter, while DC_4F_2 displayed 9.67% segregants for the same. DC_2F_2 and DC_3F_2 showed low frequency of transgressive segregants viz. 6.67% and 3.67%, respectively.

Table 9: Promising transgressive segregants for fruit yield per plant in double cross F_2 population of okra

Population	Plant no.	Fruit yield per plant (g)	% Increase of fruit yield over better parent
DC_3F_2 (Raadhika × Shakti)	214	739.45	25.51
	131	733.65	24.53
	123	718.40	21.94
	185	704.51	19.58
	239	696.25	18.18
	274	695.48	18.05
	192	684.43	16.17
	111	680.35	15.48
	132	673.55	14.32
	40	670.43	13.79
DC_1F_2 (NS864 × Arka Nikitha)	300	648.52	29.61
	215	639.51	27.80
	250	632.56	26.42
	211	619.52	23.81
	123	612.36	22.38
	82	602.27	20.36
	273	594.38	18.79
	30	590.65	18.04
	171	585.61	17.03
	188	579.96	15.90

Note**:** Better parent mean for DC_3F_2 (Raadhika) = 589.15 g
Better parent mean for DC_1F_2 (NS864) = 500.36 g

Table 9. continued……

Population	Plant no.	Fruit yield per plant (g)	% Increase of fruit yield over better parent
DC_4F_2 (Samrat × SVOK5151)	166	632.48	17.06
	167	622.54	15.22
	112	621.84	15.09
	122	616.25	14.06
	168	604.18	11.82
	25	595.18	10.16
	246	588.64	8.94
	201	586.92	8.62
	46	582.61	7.83
	90	580.64	7.46
DC_2F_2 (Mahyco10 × OH-102)	60	578.46	10.51
	264	576.37	10.11
	172	573.39	9.53
	50	568.27	8.56
	201	565.28	7.98
	97	553.74	5.78
	30	549.38	4.95
	110	547.56	4.60
	248	543.71	3.86
	157	538.51	2.87

Note: Better parent mean for DC_4F_2 (Samrat) = 532.16 g
Better parent mean for DC_2F_2 (OH-102) = 528.33 g

4.3.8 Average fruit weight (g)

A high frequency of productive segregants was observed for the populations DC_1F_2 (30.67%), DC_2F_2 (20.33%) and DC_3F_2 (12.67%). However, low frequency of transgressive segregants was observed in the population DC_4F_2 (5.00%).

4.3.9 Number of fruits per plant

Populations DC_3F_2 (19.67%) and DC_4F_2 (17.00%) were found to register a high frequency of segregants for number of fruits per plant. Correspondingly, low frequency of productive transgressive segregants was observed for the populations DC_1F_2 (4.67%) and DC_2F_2 (9.00%).

4.3.10 Number of seeds per fruit

Both populations DC_3F_2 (53.33%) and DC_4F_2 (55.33%), displayed a very high frequency of segregants for number of seeds per fruit. The population DC_1F_2 was observed to record 13.67% of transgressive segregants. But low frequency of productive segregants was observed in the population DC_2F_2 (3.33%).

4.3.11 Test weight (g)

A high frequency of segregants was displayed in the population DC_4F_2 (13.33%). Low frequency of segregants were recorded for this trait in the populations DC_1F_2 (4.00%), DC_2F_2 (4.33%) and DC_3F_2 (2.67%).

4.3.12 Fruit yield per plant (g)

High frequency of transgressive segregants were observed for the trait fruit yield per plant in the population DC_3F_2 (19.33%), DC_1F_2 (13.00%) and DC_4F_2 (11.67%). While the population DC_2F_2 registered 8.33% high yielding segregants.

4.4 Breeding potential of double cross F_2 populations

The trait means, standardized range, coefficient of variation and frequency of transgressive segregants for plant height, number of internodes, internodal length, fruit length, average fruit weight, number of fruits per plant and fruit yield per plant were considered to identify the double cross F_2 populations with high breeding potentials. Rank-sum method was employed to effectively arrive at desirable populations. Trait wise rank and rank-sum for plant height, number of internodes, internodal length, fruit length, average fruit weight, number of fruits per plant and fruit yield per plant for the four double cross F_2 populations have been compiled in Table 10. Cumulative rank-sums of four double cross F_2 populations based on mean, standardized range, coefficient of variation and frequency of transgressive segregants in okra have been recorded in Table 11. Trait mean, standardized range, coefficient of variation and frequency of transgressive segregants were ranked for each of the four populations in such a way that the population having higher value shall be ranked first.

Table 10: Trait wise rank and rank-sum for plant height, number of internodes, internodal length, fruit length, average fruit weight, number of fruits per plant and fruit yield per plant

F_2 Populations	Mean													
	Plant height (cm)	Rank	Number of internodes	Rank	Internodal length (cm)	Rank	Fruit length (cm)	Rank	Average fruit weight (g)	Rank	No. of fruits per plant	Rank	Fruit yield per plant (g)	Rank
DC_1F_2	124.56	2	17.70	2	8.12	4	14.66	3	19.15	4	19.53	3	439.90	3
DC_2F_2	115.77	4	14.29	4	6.56	2	14.31	4	23.86	1	17.97	4	496.04	2
DC_3F_2	121.17	3	19.75	1	6.02	1	17.28	1	23.01	2	22.60	1	519.63	1
DC_4F_2	128.23	1	17.38	3	7.45	3	17.07	2	20.55	3	20.43	2	427.20	4

F_2 populations	Standardized range													
	Plant height	Rank	Number of internodes	Rank	Internodal length	Rank	Fruit length	Rank	Average fruit weight	Rank	No. of fruits per plant	Rank	Fruit yield per plant	Rank
DC_1F_2	9.80	2	7.95	2	9.98	4	12.30	1	11.41	1	6.45	2	5.89	2
DC_2F_2	12.30	1	10.09	1	5.39	1	7.91	2	7.55	2	6.60	1	8.40	1
DC_3F_2	5.02	3	5.16	3	8.59	3	3.92	4	4.65	4	5.58	3	4.72	4
DC_4F_2	4.69	4	4.88	4	6.02	2	4.62	3	5.29	3	5.45	4	5.63	3

DC_1F_2 = (NS864 × Arka Nikitha) **DC_2F_2** = (Mahyco10 × OH-102) **DC_3F_2** = (Raadhika × Shakti) **DC_4F_2** = (Samrat × SVOK5151)

F_2 populations	Coefficient of variation													
	Plant height	Rank	Number of internodes	Rank	Internodal length	Rank	Fruit length	Rank	Average fruit weight	Rank	No. of fruits per plant	Rank	Fruit yield per plant	Rank
DC_1F_2	1.35	4	2.79	3	4.47	2	0.42	4	0.85	4	2.74	3	5.24	1
DC_2F_2	1.85	3	3.57	2	7.77	1	3.60	2	2.12	2	1.53	4	2.91	3
DC_3F_2	4.83	1	3.89	1	2.33	3	1.64	3	1.07	3	3.57	2	2.98	2
DC_4F_2	2.59	2	2.65	4	1.94	4	5.14	1	2.57	1	4.56	1	2.86	4

F_2 populations	Frequency of transgressive segregants (%)													
	Plant height	Rank	Number of internodes	Rank	Internodal length	Rank	Fruit length	Rank	Average fruit weight	Rank	No. of fruits per plant	Rank	Fruit yield per plant	Rank
DC_1F_2	4.33	4	4.67	3	2.00	3	9.00	3	30.67	1	4.67	4	13.00	2
DC_2F_2	5.33	3	5.67	2	0.00	4	8.33	4	20.33	2	9.00	3	8.33	4
DC_3F_2	14.67	1	74.67	1	10.33	1	26.67	1	12.67	3	19.67	1	19.33	1
DC_4F_2	5.67	2	3.00	4	6.00	2	20.33	2	5.00	4	17.00	2	11.67	3

DC_1F_2 = (NS864 × Arka Nikitha) **DC_2F_2** = (Mahyco10 × OH-102) **DC_3F_2** = (Raadhika × Shakti) **DC_4F_2** = (Samrat × SVOK5151)

Table 11: Estimates of rank-sums and cumulative rank-sums of four double cross F_2 populations based on mean, standardized range, coefficient of variation and frequency of transgressive segregants in okra

F_2 populations	Trait mean		Standardized range		Coefficient of variation		Frequency of transgressive segregants		Cumulative rank-sum (a+c+e+g)	Overall rank assigned to DCF_2
	Rank-sum	Rank assigned to DCF_2	Rank-sum	Rank assigned to DCF_2	Rank-sum	Rank assigned to DCF_2	Rank-sum	Rank assigned to DCF_2		
	a	b	c	D	e	f	g	h		
DC_1F_2	21	4	14	2	21	4	20	3	76	3
DC_2F_2	21	3	9	1	17	2	22	4	69	2
DC_3F_2	10	**1**	24	**4**	15	**1**	9	**1**	58	**1**
DC_4F_2	18	2	23	3	17	3	19	2	77	4

DC_1F_2 = (NS864 × Arka Nikitha) **DC_2F_2** = (Mahyco10 × OH-102) **DC_3F_2** = (Raadhika × Shakti) **DC_4F_2** = (Samrat × SVOK5151)

4.4.1 Plant height (cm)

Population DC_4F_2 was ranked 1 for the criteria trait means while DC_1F_2 ranked 2, DC_3F_2 ranked 3 and DC_2F_2 ranked 4. While for the criteria standardized range DC_2F_2 ranked 1 followed by DC_1F_2, DC_3F_2 and DC_4F_2, respectively. For coefficient of variation population, DC_3F_2 was given the rank 1, DC_4F_2 ranked 2, DC_2F_2 ranked 3 and DC_1F_2 ranked 4. Population DC_3F_2 was found to rank first for the criteria frequency of transgressive segregants, followed by populations DC_4F_2, DC_2F_2 ranked third and DC_1F_2 subsequently.

4.4.2 Number of internodes

For the trait number of internodes, the trait means were found to register rank 1 for the population DC_3F_2, rank 2 for DC_1F_2, rank 3 for DC_4F_2 and rank 4 DC_2F_2. Standardized range was found to record rank 1 for the population DC_2F_2 subsequently followed by DC_1F_2, DC_3F_2 and DC_4F_2. DC_3F_2 ranked first for the criteria coefficient of variation while DC_2F_2 ranked second, DC_1F_2 ranked third and DC_4F_2 ranked fourth. The frequency of transgressive segregants was found to record rank 1 for the population DC_3F_2 followed by populations DC_2F_2, DC_1F_2 and DC_4F_2, respectively.

4.4.3 Internodal length (cm)

Population DC_3F_2 was assigned rank 1 for trait mean while DC_2F_2 ranked 2, DC_4F_2 ranked 3 and DC_1F_2 ranked 4. The criteria standardized range registered rank 1 for the population DC_2F_2, rank 2 for DC_4F_2, rank 3 for DC_3F_2 and rank 4 for DC_1F_2. Population DC_2F_2 was observed to record rank 1 for coefficient of variation, followed by populations DC_1F_2, DC_3F_2 and DC_4F_2, respectively. For frequency of transgressive segregants DC_3F_2 ranked first, DC_4F_2 ranked second, DC_1F_2 ranked third and DC_2F_2 ranked fourth.

4.4.4 Fruit length (cm)

For trait mean of fruit length, DC_3F_2 was assigned the rank 1 followed by the populations DC_4F_2, DC_1F_2 and DC_2F_2. DC_1F_2 ranked first for the criteria standardized range, while DC_2F_2 ranked second, DC_4F_2 ranked third and DC_3F_2 ranked fourth. For the coefficient of variation, population, DC_4F_2 registered rank 1, DC_2F_2 ranked 2, DC_3F_2 ranked 3 and DC_1F_2 ranked 4. DC_3F_2 was assigned rank 1 for frequency of transgressive segregants subsequently followed by DC_4F_2, DC_1F_2 and DC_2F_2, respectively.

4.4.5 Average fruit weight (g)

For average fruit weight, the criteria trait mean registered rank 1 for the population DC_2F_2, 2 for DC_3F_2, 3 for DC_4F_2 and 4 for DC_1F_2. For standardized range, DC_1F_2 ranked first while DC_2F_2 ranked second, DC_4F_2 ranked third and DC_3F_2 ranked fourth. DC_4F_2 ranks first in terms of coefficient of variation while DC_2F_2 ranks second,

DC_3F_2 ranks third, and DC_1F_2 ranks fourth. The frequency of transgressive segregants was observed to record rank 1 in the population DC_1F_2 while DC_2F_2 ranked 2, DC_3F_2 ranked 3 and DC_4F_2 ranked 4.

4.4.6 Number of fruits per plant

The population DC_3F_2 ranked 1 for trait mean while DC_4F_2 ranked 2, DC_1F_2 ranked 3 and DC_2F_2 ranked 4. The criteria standardized range recorded rank 1 for the population DC_2F_2, rank 2 for DC_1F_2, rank 3 for DC_3F_2 and rank 4 for DC_4F_2. It was observed that population DC_4F_2 ranked first for coefficient of variation, followed by DC_3F_2, DC_1F_2 and DC_2F_2, respectively. In terms of frequency of transgressive segregants, DC_3F_2 ranked first, DC_4F_2 ranked second, DC_2F_2 ranked third and DC_1F_2 ranked fourth.

4.4.7 Fruit yield per plant (g)

The trait means of fruit yield per plant recorded rank 1 for the population DC_3F_2, rank 2 for DC_2F_2, rank 3 for DC_1F_2 and rank 4 for DC_4F_2. The population DC_2F_2 ranked first for the criteria standardized range while DC_1F_2 ranked second, DC_4F_2 ranked third and DC_3F_2 ranked fourth. For coefficient of variation DC_1F_2 ranked 1, DC_3F_2 ranked 2, DC_2F_2 ranked 3 and DC_4F_2 ranked 4. DC_3F_2 ranks 1 for the frequency of transgressive segregants while DC_1F_2 ranks 2, DC_4F_2 ranks 3 and DC_2F_2 ranks 4.

For trait mean populations DC_1F_2 and DC_2F_2 recorded a rank-sum of 21 for trait mean, while DC_3F_2 and DC_4F_2 recorded rank-sums of 10 and 18, respectively. For standardized range, population DC_1F_2 registered a rank-sum of 14 while DC_2F_2 had a rank-sum of 9, DC_3F_2 had the rank-sum of 24 and DC_4F_2 registered a rank-sum of 23. The populations DC_1F_2, DC_2F_2, DC_3F_2 and DC_4F_2 displayed the rank-sums of 21, 17, 15 and 17 respectively for coefficient of variation. While the frequency of transgressive segregants displayed rank-sums of 9, 19, 20 and 22 for the populations DC_3F_2, DC_4F_2, DC_1F_2 and DC_2F_2 respectively (Table 10).

Cumulative rank sums of 58, 69, 76 and 77 were recorded for the populations DC_3F_2, DC_2F_2, DC_1F_2 and DC_4F_2 respectively (Table 11). This ultimately led to the conclusion that, the population DC_3F_2 ranks 1, DC_2F_2 ranks 2, DC_1F_2 ranks 3 and DC_4F_2 ranks 4 in terms of breeding potential.

4.5 Identification of easily field assayable proxy traits to select for fruit yield

The correlation coefficient proposed by Pearson (1902), helps us to measure both degree as well as direction of association between two or more traits. Green fruit yield is the result of combined effect of several component characters and environment. Understanding the association among the characters is the most important criteria. Correlation explains the nature and magnitude of association between the two metric characters. With this view to understand the nature and magnitude of relationship among the fruit yield and its component traits, the phenotypic correlations were worked out and presented in Table 12.

Plant height showed significant and positive correlation with fruit yield per plant in all the four populations, viz., DC_1F_2 (0.34), DC_2F_2 (0.19), DC_3F_2 (0.44) and DC_4F_2 (0.37). Similarly, number of internodes displayed a significant positive correlation with fruit yield in all the segregating populations DC_1F_2 (0.62), DC_2F_2 (0.40), DC_3F_2 (0.57) and DC_4F_2 (0.45). The trait internodal length was observed to depict significant and positive correlation with fruit yield in the populations DC_1F_2 (0.18) and DC_2F_2 (0.37) while they exhibited significant negative correlation with fruit yield in the populations DC_3F_2 (-0.21) and DC_4F_2 (-0.13). Number of fruits per plant revealed significant and positive correlation with fruit yield per plant in all the populations, viz., DC_1F_2 (0.86), DC_2F_2 (0.75), DC_3F_2 (0.72) and DC_4F_2 (0.62).

Table 12: Estimates of phenotypic correlation coefficients of fruit yield and its component traits among double cross F_2 populations

Statistics	Trait / Population	Plant height (cm)	Number of internodes	Internodal length (cm)	Number of fruits per plant
Fruit yield per plant (g)	DC_1F_2 (NS864 × Arka Nikitha)	0.34**	0.62**	0.18**	0.86**
	DC_2F_2 (Mahyco10 × OH-102)	0.19**	0.40**	0.37**	0.75**
	DC_3F_2 (Raadhika × Shakti)	0.44**	0.57**	-0.21**	0.72**
	DC_4F_2 (Samrat × SVOK5151)	0.37**	0.45**	-0.13*	0.62**

*. Significance at p= 0.05 level.

**. Significance at p= 0.01 level.

DISCUSSION

V DISCUSSION

The success of a breeding programme for the improvement of quantitative attributes depends greatly on the magnitude of genetic variability existing in the germplasm. Burton (1952) suggested that genetic variability along with heritability should be considered for assessing the maximum and accurate effect of selection. High yield can be achieved by the selection of those characters that have high heritability values coupled with high genetic advance. Selection is an indispensable component of the variety development process. Higher the variability in the breeding material, greater would be the chances of selecting the best performing genotypes (Simmonds, 1979). There are multiple approaches to generate variability. One of the most efficient and effective approach amongst them is hybridization. The double cross F_2 populations obtained through diverse single cross combinations are found to yield more genetic variability, in comparison with the conventional method of hybridization. It is revealed that intermating in early segregating generations of different individuals leads to the release of additional variability since biparental mating among the segregates in the F_2 of a cross may provide more opportunity for the recombination to occur, break the linkage blocks and mop up desirable genes and as a result release concealed variability (Somashekhar *et al*., 2011a). Thus, the breeding potential was assessed for the four double cross F_2 populations and the results obtained are discussed in this chapter under the following heads.

5.1 Mean performance of parents

5.2 Variability in the double cross F_2 populations

5.3 Estimation of statistical parameters and genetic components as a measure of variability among the four double cross F_2 populations

5.4 Transgressive segregants for productivity traits among the four double cross F_2 populations

5.5 Breeding potential of the double cross F_2 populations

5.6 Identification of easily field assayable proxy traits to select for fruit yield

5.1 Mean performance of parents

Plant height recorded higher values among the parental single cross hybrids SVOK5151 (142.18 cm) and NS864 (140.29 cm), while a lower value was recorded for the line OH-102 (90.83 cm). More number of primary branches were found in Mahyco10 and NS864 (2.00). OH-102 (10.35 cm) and NS864 (10.11 cm) had higher mean internodal length, while Samrat (5.06 cm) and Mahyco10 (5.10 cm) has lower internodal length. NS864 (21.00) and SVOK5151 (20.00) have more internodes and Mahyco10, along with OH102, have the least number of internodes. Average fruit length was greater for fruits produced by the parents Raadhika (18.62 cm) and SVOK5151 (18.60 cm). Samrat produced relatively narrower fruits (1.45 cm), while Raadhika produced broader fruits (2.10 cm) among the parents. Raadhika (26.48 g) and SVOK5151 (25.62 g) recorded higher average fruit weight. Raadhika (23.00) and NS864 (23.00) produced a greater number of fruits, while the least was produced by Mahyco10 (16.00). Number of seeds per fruit ranged from 53.74 in Arka Nikitha to 38.66 in SVOK5151, while test weight was found to be higher in the line Shakti (7.72 g) and lower in Raadhika (5.86 g). Raadhika (589.15 g), Samrat (532.16 g) and OH-102 (528.33 g) recorded greater fruit yield per plant, while lower value was recorded in Mahyco10 (366.52 g). Owing to the mean performance and variability in the single cross hybrid parents, higher performance was observed for yield and its component traits in the double cross F_2 populations, which is similar to the findings of Somashekhar *et al*. (2011a), Sogaland *et al*. (2012), Medagam *et al*. (2012) Dhankar et al. (2013), and Kumar and Reddy (2016).

5.2 Variability in the double cross F_2 populations

Analysis of variance (ANOVA) revealed significant mean squares attributable to genotypes for the yield contributing characters studied other than days to first flowering in all the four double cross F_2 populations. Mean squares due to genotypes + checks, genotypes, checks and 'genotypes vs. checks' were significant for all the traits other than days to first flowering. Sharma *et al*. (2016), Thulasiram *et al*. (2017), Ranga *et al.* (2021) and Walling *et al.* (2020) also observed similar significant variability in okra. ANOVA is the preliminary step that indicates the presence of variability among the genotypes under investigation. Significant differences among the genotypes justify the quantification of variability in all the populations.

5.3 Estimation of statistical parameters and genetic components as a measure of variability among the four double cross F_2 populations

The information on mean performance of parents and genetic variability parameters becomes necessary for the improvement of productivity traits in crop breeding programmes. The selection of desired genotypes and accomplishment of breeding strategies are aided by the genetic variability present in the breeding material.

In the present investigation, the variability present in the population is split into genotypic and phenotypic variance. Comparison of traits cannot be appropriately made when the absolute range is used as a criterion to assess the genetic variability since these traits have different units of measurement. Hence, standardized range has been used here, as it provides reliable information to compare the traits across each population and thereby, is a better criterion. However, standardized range does not reflect variability in the expression of traits as such. The estimate of coefficient of variation is a measure that uses *per cent* of mean to express variance and can be compared across different traits of various degrees and units. The results obtained are expressed as PCV (phenotypic coefficient of variation), GCV (genotypic coefficient of variation), heritability (h^2_{bs}) and GAM (genetic advance as *per cent* of mean). The utility of estimates of heritability is increased when they are used in conjunction with the selection differential (Johnson *et al.*, 1955). A significant difference was recorded among the test genotypes for various traits.

5.3.1 Statistical parameters as a measure of variability

5.3.1.1 Estimates of mean for yield and its component traits

The arithmetic mean is often used as a measure of central tendency in summarizing the data points. It depicts the tendency of the individuals in the population to congregate in the distribution. The mean values of days to first flowering were similar, i.e. 45 for all four crosses. Estimates of mean plant height ranged between 115.77 cm (DC_2F_2) and 128.23 cm (DC_4F_2). The values of mean plant height were found to be higher in the cross DC_1F_2 and DC_3F_2, which were comparable to that of the cross DC_4F_2. The number of primary branches in all the crosses lies between 1 to 2. The number of internodes in the populations varied from 14.59 in DC_2F_2 to 19.75 in DC_3F_2. The mean values of number of internodes in the crosses DC_4F_2 (17.38) and DC_1F_2 (17.70) were similar. For internodal length, the mean estimates ranged from 6.02 cm in the cross DC_3F_2 and 8.12 cm in DC_1F_2. The mean estimates of fruit length were between 14.31 cm in DC_2 F_2 and 17.28 cm in DC_3F_2, among which the estimates of cross DC_1F_2 were comparable with DC_2F_2, while the estimates of DC_4F_2 were comparable with DC_3F_2. Fruit diameter varied from 1.55 cm in DC_1F_2 to 1.72 cm in DC_4F_2. Further, average fruit weight ranged from 19.15 g in DC_1F_2 to 23.86 g in DC_2F_2. The population DC_3F_2 (23.01 g) had comparable values to that of DC_2F_2. The number of fruits per plant among the populations ranged from 17.97 in DC_2F_2 to 22.60 in DC_3F_2. The number of seeds per fruit varied between 52.06 in the cross DC_1F_2 and 46.14 in the cross DC_2F_2. The mean values of the number of seeds per fruit were comparable in the populations DC_3F_2 and DC_4F_2. The estimates of test weight ranged from 5.92 g in the population DC_3F_2 to 7.46 g in the population DC_2F_2, where the mean values of DC_3F_2 and DC_4 F_2 were comparable. The population DC_3F_2 manifested the higher mean value for fruit yield per plant (519.63 g), while the population DC_4F_2 manifested a lower mean value (427.20 g).

5.3.1.2 Standard deviation for yield and its component traits

Among the measures of dispersion, standard deviation best represents the variability of the traits. Thus, for assessing the potentiality of the double cross F_2 population, this was considered as one of the statistical criteria. It was observed that the magnitude of standard deviation was relatively lesser for the traits days to first flowering, number of primary branches, number of internodes, internodal length, fruit length, fruit diameter, average fruit weight, number of fruits per plant and test weight in all the crosses. A higher magnitude of standard deviation was observed for the trait plant height in the populations DC_3F_2 (11.19) and DC_4F_2 (14.98), while for the trait fruit yield per plant in all the populations where DC_1F_2 (55.75), DC_3F_2 (80.19) and DC_4F_2 (84.83) recorded the highest.

5.3.1.3 Standardized range for yield and its component traits

Absolute range is a measure of dispersion, which represents variability present in the population. However, standardized range is relevant when traits with diverse units of measurement are to be compared within and among segregating populations. Therefore, apart from absolute range, the standardized range was also considered for assessing the breeding potential of the double cross F_2 populations. All the populations exhibited a lower magnitude of standardized range for number of primary branches. Lower magnitude of standardized range might be attributed to oligogenic governance of the traits and the absence of substantial variability for plant height among the parents used in constructing double cross F_2 populations under investigation.

Higher magnitude of standardized range was observed for days to first flowering, plant height, number of internodes, internodal length, fruit length, fruit diameter, average fruit weight, number of fruits per plant, number of seeds per fruit, test weight and fruit yield per plant might be attributed to polygenic governance of the traits. While that for plant height, number of internodes and internodal length may be due to the absence of substantial variability for these traits among the parents used in constructing the double cross F_2 populations under investigation. The traits average fruit weight, number of fruits per plant and fruit yield per plant manifested higher values of standardized range owing to probable governance of these traits by polygenes, which in turn shuffled in the segregants and thereby gave rise to higher variation. Among all the populations, DC_2F_2 expressed higher estimates of standardized range for the trait fruit yield per plant.

5.3.2 Genetic components as a measure of variability.

Phenotypic variability is a measure of dispersion which includes the components of genetic and environmental variability. Thus, the tapered difference between PCV and GCV indicates a relatively lesser influence of environment on the expression of a trait. Therefore, PCV values were higher than GCV values in general, which was in accordance with the findings of Dhankar *et al*. (2013), Rajkumar *et al*. (2014), Sundaram (2015), Khajuria *et al*. (2016) and Jadhav *et al*. (2016). Broad sense heritability, as a variability parameter, enables us to reflect such differences. It is a measure of the magnitude of phenotypic variation due to genotypic factors. Therefore, an estimate of high heritability coupled with high GAM in any population allows effective selection for the trait.

In this context, a narrow difference between PCV and GCV was observed in all four populations for all the traits. High estimates of PCV and GCV were observed for the traits number of primary branches in all the populations, while moderate values of the same were observed for the rest of the traits, which were in line with the findings of Prakash and Pichaimuthu (2010), Yadav *et al*. (2016), and Verma *et al*. (2018). This led to high heritability and GAM for the traits number of primary branches per plant, number of fruits per plant and fruit yield per plant in DC_1F_2. All the traits showed high heritability. Subsequently, moderate GAM was observed for the traits plant height, number of internodes per plant and number of seeds per fruit, while the remaining traits exhibited low GAM in the population DC_1F_2, which was similar to the reports by Sharma *et al*. (2016), Badiger *et al*. (2017) and Rambabu *et al*. (2019).

Similarly, in the cross DC_2F_2, high heritability and GAM were observed for the traits number of primary branches per plant and internodal length. Heritability was found to be high for all the traits. The magnitude of estimates of GAM was discovered to be moderate for the traits number of internodes per plant, fruit diameter and number of fruits per plant, while it was found to be low for the rest of the traits. All these results are in line with the reports of Reddy *et al*. (2012a), Awadhesh *et al*. (2016) and Verma *et al*. (2018).

The cross DC_3F_2 exhibited low estimates of PCV and GCV for the traits days to first flowering, plant height and internodal length, while the magnitude of these estimates was found to be moderate for all other traits. All the traits manifested high heritability, while high heritability coupled with high GAM was observed for the traits number of internodes per plant, fruit length, fruit diameter, average fruit weight, number of fruits per plant, number of seeds per fruit, test weight and fruit yield per plant in the cross DC_3F_2. The traits days to first flowering, plant height and internodal length exhibited moderate GAM.

In the population DC_4F_2, low estimates of PCV and GCV were registered for the trait days to first flowering, while all other traits showed moderate estimates. Subsequently, this manifested high heritability coupled with high GAM for all the traits, suggesting the existence of a wide range of genetic variability for these traits and, thus, the scope for improvement of these characters through simple selection, as reported by Sravanthi (2017), Rathod *et al*. (2019b) and Kumari *et al*. (2019).

5.4 Transgressive segregants for productivity traits among the four double cross F_2 populations

A broad range of phenotypes were detected in double cross F_2 populations. This variation clearly indicates that polygenes administer these characters, which may be additive in nature or due to dominant gene action. It was observed that the populations DC_1F_2 (51.00%) and DC_3F_2 (16.67%) showed a higher proportion of plants recording lower values than the lesser parent for the trait days to first flowering and thereby depicted earliness. The trait plant height recorded a higher frequency of transgressive segregants in the population DC_3F_2 (14.67%), while a lower frequency was recorded in the rest of the populations. Similarly, lower frequency was registered for the trait number of primary branches in all the populations. A very high proportion of segregants was recorded for the trait number of internodes per plant (74.67%) and internodal length (21.00%) in the population DC_3F_2 compared to all other populations, which registered lower proportions for the same. The trait fruit length recorded higher frequency of transgressive segregants in the populations DC_3F_2 (26.67%) and DC_4F_2 (20.33%), while the population DC_1F_2 registered a higher proportion of segregants for the trait fruit diameter (11.00%).

High proportion of productive segregants were recorded for the trait average fruit weight in the populations DC_1F_2 (30.67%), DC_2F_2 (20.33%) and DC_3F_2 (12.67%), whereas the trait number of fruits per plant registered higher frequency in the populations DC_3F_2 (19.67%) and DC_4F_2 (17.00%). For number of seeds per fruit was observed to have greater proportion of segregants in the populations DC_3F_2 (53.33%) and DC_4F_2 (55.33%) while, test weight registered higher frequency in the population DC_4F_2 (13.33%). A significant proportion of productive transgressive segregants was recorded for fruit yield per plant in the crosses DC_1F_2 (13.00%), DC_3F_2 (19.33%) and DC_4F_2 (11.67%). This was in line with the studies of Shanthkumar and Salimath (2011) and Nimbalkar and Totre (2018) who reported transgressive segregants with respect to plant height, number of fruits per plant, average fruit weight and fruit yield per plant in F_2 population of okra.

Recovery of higher percentage of transgressive segregants that surpassed the better parent in the double cross F_2 populations for traits like number of fruits per plant and fruit yield per plant suggested that it is possible to produce inbred lines with these traits transcending the parental limits. The occurrence of transgressive segregants could be attributed to the constellation of complete or incomplete dominant genes that are dispersed among their parents (Chahal and Gosal, 2002). The maximum number of transgressive segregates found in the F_2 population indicated the diverse nature of the parents. Transgressive segregants in F_2 may be caused by dominance × dominance interactions, which are non-fixable and additive × additive interactions, which are fixable, due to the recombination of genes with positive effects. Genetic studies conducted by Risenberg *et al*., (1999) suggest that a combination of alleles from both or multiple parents that have complementary gene effects result in recovery of transgressive segregants with desirable combinations of genes. On receiving positive alleles (or) negative alleles from both parents, segregants are likely to result in obtaining extreme phenotypes.

5.5 Breeding potential of the double cross F_2 populations

Breeders often encounter the issue of limited resources while handling a large number of crosses of bi-parent or multiparent derived populations. However, limited resources can be effectively utilized by identifying potential breeding populations among a set of crosses in terms of higher economic yield and more remarkable recovery of transgressive segregants. Hence, trait means, standardized range, coefficient of variation and frequency of transgressive segregants for plant height, number of internodes, internodal length, fruit length, average fruit weight, number of fruits per plant and fruit yield per plant were considered to arrive at the double cross F_2 population(s) with high breeding potentials (Lakshmi Pathy *et al*., 2018).

Not all the four populations registered higher estimates for all the criteria defined (mean, standardized range, coefficient of variation and frequency of transgressive segregants recovered across productivity traits). Hence, rank-sum method was employed to arrive at the desirable population(s). Double cross F_2 population having a higher estimate of a statistical parameter was assigned with rank 1. Consequently, the F_2 population that expressed lower estimate for statistical parameter received rank 4. A similar method of assigning ranks to the population was followed for each of the criteria. Further, ranks were summed across the traits (Kang, 1988). Considering the rank-sum obtained by each double cross F_2 population across the four statistical parameters criteria, the population DC_3F_2 (with rank-sum 58) was identified as the best potential population. This population ranked highest for the parameters mean, frequency of transgressive segregants and co-efficient of variation. Forwarding such multi parent derived superior populations can assist in the isolation of elite recombinants with multiple target traits. The second best population in terms of breeding potential was identified to be DC_2F_2 (with rank-sum of 69). This population ranked 3 for mean, ranked 2 for standardized range, ranked 2 for coefficient of variation and ranked 4 for frequency of transgressive segregants.

5.6 Identification of easily field assayable proxy traits to select for fruit yield

The development of high yielding lines is particularly reliant on the selection efficiency and the traits under selection which are associated with the yield. Fruit yield is a complex trait and the integrated product of multiple factors known as yield components. Detailed perception of yield and its attributing traits along with study of their interrelationship with yield, is necessary in order to make implicit selection for higher yield. Yield improvement could be attained by carrying out indirect selection for yield and its related traits, whose heritability is high and exhibit a strong association with dependent trait i.e., yield. Hence, correlation coefficients are the best measures to know the interrelationship between the yield attributes and thereby enable selection dependent on positive significant association, which will effectively maximize the yield gain.

In the current investigation, plant height disclosed significant and positive correlation with fruit yield per plant. The findings were in line with the results obtained by Balai *et al*. (2014), Gogineni *et al*. (2015), Pithiya *et al*. (2017), Rajat *et al*. (2018), Karadi *et al*. (2018), Kumar *et al*. (2019), Raval *et al*. (2019), Rathod *et al*. (2019), Rathava *et al*. (2019), Alam *et al*. (2020), and Janarthanan and Sundaram (2020) in okra. Similarly, fruit yield is found to have a significant and positive association with number of internodes. Similar results were reported by Thulasiram *et al*. (2017), Rathod *et al*. (2019), Kelemoge et al. (2019), Kumar *et al*. (2019), Mohammed *et al*. (2020) and Ranganayaki *et al*. (2020) in the populations of okra. Internodal length was found to exhibit significant and positive correlation with fruit yield per plant in the populations DC_1F_2 and DC_2F_2. These results were in accordance with the reports of Nirosha *et al*. (2014), Thulasiram *et al*. (2017), Shuirkar et al. (2018), Rambabu *et al*. (2019), Kelemoge *et al*. (2019), Raval *et al*. (2019) and Rathod *et al*. (2019). While in the populations DC_3F_2 and DC_4F_2 fruit yield was observed to have negative and significant association with internodal length. These results were in agreement with the observations of Mohammad and Marker (2017) and Ranganayaki *et al*. (2020). Number of fruits per plant revealed significant and positive correlation with fruit yield per plant. The results were in accordance with the reports of Gogineni *et al*. (2015), Thulasiram *et al*. (2017), Meena *et al*. (2017), Pithiya *et al*. (2017), Mohammad and Marker (2017), Rajat *et al*. (2018), Rathod *et al*. (2019), Rathava *et al*. (2019), Raval *et al*. (2019), Mohammed *et al*. (2020), Ranganayaki *et al*. (2020), and Al-Juboori (2021).

From the above results, it can be concluded that plant height, number of internodes and number of fruits per plant are the field assayable proxy traits to select for fruit yield.

Conclusion

- The population DC_3F_2 (with rank-sum of 58) displayed highest breeding potential among all the four double cross F_2 populations by exhibiting superior ranking for all the four parameters. The second best population in terms of breeding potential was identified to be DC_2F_2 (with rank-sum 69).

- Correlation coefficient analysis revealed that the traits plant height, number of internodes and number of fruits per plant showed significant and positive correlation with fruit yield and thereby, are the field assayable proxy traits to select for the same.

- High frequency of transgressive segregants were observed for the trait fruit yield per plant in the populations DC_3F_2 (19.33%) and DC_1F_2 (13.00%). Recovery of higher percentage of transgressive segregants that surpassed the higher parent in the double cross F_2 populations suggested that it is possible to produce inbred lines with these traits transcending the parental limits.

Future line of work

- Forwarding the populations DC_3F_2 and DC_2F_2 which registered high breeding potential can assist in isolation of elite recombinants with multiple target traits in advance segregating generations for use in future breeding programmes.

- The traits which have shown high heritability and coupled with high genetic advance as per cent mean could be further improved through simple selection.

- The traits described to exhibit strong positive association with fruit yield in this investigation, can be considered as reliable indices to attain the desired selection response for the same.

- The identified top performing individuals in each of the double cross F_2 populations for fruit yield may be advanced and stabilized to isolate superior breeding lines.

SUMMARY

VI SUMMARY

Genetic variation among economically significant traits is an essential prerequisite for the advancement of any crop. Therefore, it becomes necessary to enhance and quantify the variability by providing room for a greater number of recombination events in relatively wider genomic backgrounds. In this context, double cross F_2 populations developed from crossing two diverse single cross hybrids were considered for investigation. In order to efficiently utilize the limited resources at the breeder's disposal without limiting the number of crosses or reducing the population size, it is desirable to assess the breeding potential of populations at early generations. Hence, the present study was conducted to identify a potential double cross F_2 population among the four populations developed.

The present investigation titled "Comparative Assessment of Breeding Potential in the Double Cross F_2 Populations of Okra [*Abelmoschus esculentus* (L.) Moench]" was carried out during Rabi 2022 at College of Agriculture, Navile, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga, Karnataka, India. The experimental material comprised of four double cross F_2 populations of okra viz. DC_1F_2 (NS864 × Arka Nikita), DC_2F_2 (Mahyco10 × OH-102), DC_3F_2 (Radhika × Shakti) and DC_4F_2 (Samrat × SVOK5151) along with four checks viz. SVOK 5151, Raadhika, NS864 and OH-102.

The experiment was conducted in augmented design with 6 blocks, each block containing 50 plants with a total of 300 plants in each cross. The genotypes were unreplicated while the checks were replicated in all the blocks with the purpose of identifying the populations with high potential, carrying out association studies for the yield attributing traits and recognize transgressive segregants for high yield in okra. Observations were recorded for the traits viz., days to first flowering, plant height, number of primary branches, number of internodes, internodal length, fruit length, fruit diameter, average fruit weight, number of fruits per plant, number of seeds per fruit, test weight and fruit yield per plant.

This study was carried out under the objectives of assessing the breeding potential of the four double cross F_2 populations, correlation studies of field assayable proxy traits viz. plant height, number of internodes, internodal length and number of fruits per plant with fruit yield and isolation of superior transgressive segregants for the trait fruit yield per plant.

Statistical parameters and genetic variability parameters were estimated for all the four populations, while estimates of mean, standardized range, coefficient of variation and frequency of transgressive segregants were together considered as the criteria to assess the breeding potential. To arrive at the population with high breeding potential, rank-sum method incorporating all these statistical parameters was followed. The population DC_3F_2 with the lowest rank-sum (58) was considered to possess high breeding potential. The second best population in terms of breeding potential was found to be DC_2F_2 (69). Also, these populations exhibited substantial variability for most of the traits examined, along with high heritability and GAM.

High frequency of productive transgressive was observed for the trait fruit yield per plant in all the populations. Recovery of a higher percentage of transgressive segregants that surpassed the higher parent in the double cross F_2 populations for traits like number of fruits per plant and fruit yield per plant suggested that it is possible to produce inbred lines with these traits transcending the parental limits. The maximum number of transgressive segregates found in the F_2 population indicated the diverse nature of the parents. Potential segregants which can be forwarded to develop inbred lines have been identified and tabulated.

Correlation coefficient analysis revealed that the traits viz., plant height, number of internodes and number of fruits per plant showed significant and positive correlation with fruit yield and thereby, are the field assayable proxy traits to select for the same. These traits described to exhibit a strong positive association with fruit yield in this investigation, can be considered as reliable indices to attain the desired selection response which will further enable the ease of breeder for focused advancement of the desired lines.

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APPENDIX

VIII APPENDIX

APPENDIX-I

Monthly meteorological data for the experimental period against normal at College of Agriculture, Navile, KSNUAHS, Shivamogga

	Total rainfall of month (mm)			Mean monthly maximum temperature (°C)			Mean monthly Minimum temperature (°C)			Mean monthly Sunshine hours			Mean monthly maximum Relative humidity (%)		
	N	**A**	**D**	**N**	**A**	**D**	**N**	**A**	**D**	**N**	**A**	**D**	**N**	**A**	**D**
July	221.20	378.70	157.50	27.70	27.49	-0.21	21.20	21.41	0.21	2.50	2.12	-0.38	84.00	93.48	9.48
August	197.90	364.10	166.20	27.70	28.05	0.35	22.10	21.34	-0.76	4.00	2.95	-1.05	84.00	94.32	10.32
September	112.00	90.80	-21.20	29.30	28.89	-0.41	21.90	20.93	-0.97	4.80	4.20	-0.60	80.00	92.03	12.03
October	179.40	119.40	-60.00	30.20	29.50	-0.70	21.60	19.85	-1.75	6.30	5.71	-0.59	77.00	86.80	9.80
November	45.80	12.40	-33.40	30.00	29.50	-0.46	19.20	18.26	-0.94	7.10	6.58	-0.52	70.00	83.29	13.29
December	10.40	24.00	13.60	30.00	29.80	-0.20	17.70	17.10	-0.60	8.30	7.40	-0.9	63.00	70.00	7.00
January	1.90	00	-1.90	31.20	30.70	-0.50	16.90	15.10	-1.80	8.90	9.00	0.10	59.00	83.80	24.50
Total	768.6	989.4	-	206.1	203.93	-	140.6	133.99	-	41.9	37.96	-	517	603.72	-

Note:
N- Normal meteorological data (mean of 1986-2021)
A - Actual meteorological data (2022)
D – Deviation from the normal (A-N)