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RESEARCH ARTICLE

# Characterization of primary genepool for enation leaf curl disease resistance and morpho-horticultural traits in okra [*Abelmoschus esculentus* (L.) Moench]

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## Abstract

The present investigation was planned to examine genetic parameters such as GCV, PCV, heritability and GA, along with correlations, diversity, path coefficients and PCA from data on 100 okra genotypes. High GCV and PCV were observed for ELCV (CI), NEB, LA ($^0$) and YPP (g), NH, IL (cm) and NFPP, whereas moderate GCV and PCV were observed for FFN, BA ($^0$), and FL (cm). High heritability coupled with high GAM was observed for almost all the characters studied, except FL (cm), PH (cm), AFW, DFF and DFH show low heritability with low GAM. The YPP, NEB, ELCV (CI), LA ($^0$), NH and IL (cm) showed high genetic advance that helped in effective and reliable selection through these characters for okra improvement. DFF was significantly positively correlated with D50F and DFH. While the negative association with ELCV (CI) was positively correlated with BA (0.397), it was negatively correlated with FL (-0.308), NFPP (-0.627) and NH (-0.535). YPP resulted in a significant positive correlation with AFW, NFPP and NH (0.867) but has a negative correlation with ELCV (CI). The NFPP had a maximum direct effect on AFW (g) followed by FFN and NH and the residual effect of the path analysis was low (0.008), suggesting the inclusion of maximum yield influencing characters in the present study and identified as key traits for developing high fruit yielding genotypes in okra for future breeding program. The genotypes were divided into eight clusters using squared Euclidean distance. The results revealed the presence of considerable genetic diversity in the first three principal components contributed to 53.2% of total variability during the study.

**Keywords:** Diversity, ELCV, Genetic variability and PCA

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## Introduction

Cultivated okra [*Abelmoschus esculentus* (L.) Moench] is a valuable fruit-vegetable of mallow or Malvaceae family, which is widely grown in tropical, subtropical, and mild temperate regions, with its peak production between April to August. This originated from the Hindustani center, i.e., India (Zeven and Zhukovsky 1975). Okra is primarily grown for its tender pods, which are used as green vegetables and soups. Its tender fruit is nutritionally rich in vitamin C (30 mg $100^{-1}$ g), calcium (90 mg $100^{-1}$ g), iron (1.5 mg $100^{-1}$ g) and iodine (97 mg $100^{-1}$ g) (Pal et al. 1952; Karmakar et al., 2022; Mishra et al., 2024). In India, okra contributes more than 72% (6 million tonnes) in terms of global production from the area of 0.5 million hectares NHB (2020) and has vast potential for earning foreign exchange as its significant share in fresh vegetable export APEDA (2020). Seeing the nutritional importance and its production scenario in India, it is a great time to bootup up okra production. But one of the major limiting factors, begomovirus (Family: Geminiviridae), a small satellite DNA b component, caused enation leaf curl virus (ELCV), a major hindrance to quality okra production. 100% Infection of plants in a field is very common and yield losses range from 50 to 94% depending on the stage of crop growth at which infection occurs (Singh et al., 2023). It is quite difficult to control this disease as it is tuff to successfully eliminate the white fly (Kumari et al., 2017). India is the richest country for diverse genotypes of okra. This remarkable variation stems from three key factors, i.e., separation of populations due to geography, genetic obstacles preventing crossbreeding, and divergent evolutionary paths (Haq et al., 2023).

Extensive research initiatives in India have been aimed at creating virus-resistant varieties and hybrids. However, to date, no stable resistance has been identified within the cultivated gene pool. This lack of success is primarily attributed to the emergence of new virus strains or the recombination of existing ones, which enables them to bypass the plant's defense mechanisms. Interspecific hybridization efforts between domesticated and wild okra varieties have achieved limited success due to cross-incompatibility and the infertility of pollen in first-generation hybrids (Nagaraju et al., 2019). So, to enhance the diversity of resistance genes in cultivated varieties and achieve long-lasting, stable resistance, it is important to identify novel sources of ELCV resistance within the available primary gene pool of okra. Understanding the nature and extent of genetic variability and diversity within a base population, as well as the degree of trait transmission, is essential for cultivating desired plant types. Multivariate analysis serves as a powerful method for evaluating the level of divergence among genotypes in a population and the forces at work at various levels (Das et al., 2022). Cluster analysis and principal component analysis (PCA) are commonly used techniques for assessing genetic diversity despite their fundamental differences. Cluster analysis has been extensively utilized to evaluate family relationships (Pandey et al., 2024). Consequently, this study was conducted to examine the nature and magnitude of genetic divergence in okra, as well as to identify the characteristics that play a significant role in its genetic diversity for enation leaf curl virus (ELCV).

## Materials and Methods

### *Evaluation of genotypes for yield and plant architectural traits*

The present experiment was performed in ICAR-Indian Institute of Vegetable Research, Varanasi, during the *rainy* season, 2022 in augmented block design by using a total of 100 advanced line/varieties/hybrid/local cultivars along with five susceptible checks, namely Arka Anamika, Pusa Sawani, Kashi Pragati, VRO-102 and Parbhani Kranti. Observations were recorded for 15 quantitative characters *viz.*, days to first flowering (DFF), days to 50% flowering (D50F), first fruiting node (FFN), days to first harvest (DFH), plant height (cm) (PH), internodal length (cm) (IL), number of effective branches (NEB), branching angle ($^0$) (BA), leaf angle($^0$) (LA), fruit length (cm) (FL), AFW (g) (AFW), number of fruit per plant (NFPP), yield per plant-YPP (g), number of harvests (NH) and incidence of enation leaf curl virus (ELCV). The soil of the plot was sandy loam in texture, having good fertility, properly leveled and well drained. All the agronomic packages and practices were adopted to raise the healthy crop.

### *Estimation of ELCV disease severity in okra genotypes*

Every plant was observed regularly at 15-day intervals (30, 45, 60, 75 and 90) days after seed sowing. All plants were scored on a 0 to 7 scale suggested by Alegbejo (1997) to find out the susceptible and resistant genotypes against ELCV disease. Percent disease incidence (PDI) and coefficient of infection (CI) value were calculated by the procedure coined by (Venkataravanappa et al., 2022).

Formula: $\mathrm{PDI} = \frac{\text{Number of Infected plants}}{\text{Total Number of Plant}} \times 100$

Formula: CI (%) = PDI × RV

Where, PDI = per cent disease Incidence, RV = Response value, CI= Coefficient of infection

### *Statistical Analysis*

The genetic divergence among the okra genotypes was estimated by using $D^2$ statistics Mahalanobis 1936). All genotypes were clustered into different groups accomplished by Tocher's method Rao (1952). The average distance between the cluster and within the cluster was calculated by the statistical procedure given by Singh and Choudhary (1985) by using analysis software, r-studio, SPSS version 16, and Indosat, Hyderabad, India.

## Results and Discussion

### *Grouping of genotypes into different cluster*

Based on $D^2$ values, all the 100 okra genotypes for fifteen quantitative characters could be meaningfully grouped into 8 clusters by utilizing Tocher's method (Figure A andB). Cluster III had a maximum of 20 genotypes, Cluster II and VI had 16 genotypes each, Cluster-IV with 15 genotypes followed by Cluster-VII and VIII with 9 genotypes. While remaining, cluster-I had 5 genotypes. In general, the pattern of distribution of genotypes from diverse geographical regions into different clusters was random. It might be due to the free and frequent exchange of genetic materials among the farmers and breeders of different regions. Therefore, the selection of genotypes for hybridization should be based on genetic divergence rather than geographic diversity. A similar statement has also been observed by (Osekita and Atimokhale, 2024; Temam et al., 2021 and Kumar et al., 2016) in okra.

**Table 1:** Scale for classifying disease reaction in okra to ELCV

| *Symptoms* | *Severity grade* | *Response value* | *CI* | *Reaction* |
|---|---|---|---|---|
| No disease | 0 | 0.00 | 0–4 | HR |
| Top leaves curled | 1 | 0.14 | 4.1–9 | R |
| Top leaves curled and slight stunting of plant | 3 | 0.42 | 9.1–19 | MR |
| All leaves curled, twisting of petiole and slightly stunting of plant | 5 | 0.71 | 19.1–39 | MS |
| Severe curling of leaves, twisting of the petiole, stunting of plant and proliferation of auxiliary branches | 7 | 1.00 | 39.1–69 | S |
| | | | 69.1–100 | HS |

### *Genetic Diversity of the Genotypes Through*

Genetic diversity of the genotypes through multivariate analysis.

### *Intra and Intercluster distance*

The average intra and inter-cluster $D^2$ values estimated as per the procedure given by Singh and Choudhary (1979) are presented in (Table 2). The intra and inter-cluster distance ranged from (2.423–3.006). The maximum intra-cluster distance was found for cluster III (3.006), closely followed by cluster IV (2.946), cluster II (2.933), cluster VII (2.891) and cluster V (2.816). Whereas minimum intra-cluster distance was observed for cluster I (2.423) followed by cluster VIII (2.785) and cluster VII (2.891). As far as inter-cluster distance is concerned, maximum inter-cluster distance was noticed between cluster I and cluster IV (5.487), followed by clusters III and VI (5.055), cluster IV and VII (4.863). In contrast, minimum inter-cluster distance was observed between cluster VI and cluster VIII (2.66), followed by cluster II and V (2.869), cluster III and V (3.294). From cluster mean (Tables 2 and 3), it was estimated that cluster I contributed the lowest yield mean value (108.23), number of fruits per plant (11.74), fruit length (10.26 cm) and highest percent disease incidence (45.76), while cluster III were found highest mean performer for yield per plant (264.57 g), AFW (g) (10.82 g) and number of fruits per plant (24.45) due to comparatively less percent disease incidence (15.66%). Cluster II contains sixteen entries i.e. VRO-220, VRO-224, Arka Abhay, VRO-227, VRO-104, VRO-115, VROT-109, VROT-117, VROB-177, VROB-181, VRO-3, AHRB-55, VRO-5, IC-011702, IC-899726, IC-417231 with less disease incidence. The mean performance of cluster I (264.57) and cluster VII (214.82) was high with respect to yield due to comparatively high mean values for the number of fruits per plant (18.67) and AFW (g) (11.60). From the cluster mean data and inter-cluster distance, it assumed that the hybridization between cluster I and cluster III (inter-cluster distance 5.098) and also cluster II and cluster IV (inter cluster distance 3.358) may produce high-performing hybrids. Therefore, the genotypes VRO-220, VRO-227, VRO-216, VRO-109, VRO-200, VRO-106, VRO-208, VRO-219 and SB-4 may be rewarding entries in the breeding program for the development of high yielding as well as ELCV disease resistant. Similar results have also been observed by (Pattan et al., 2023; Awasthi et al., 2022; Mohammed et al., 2022 and Kumar et al., 2016).

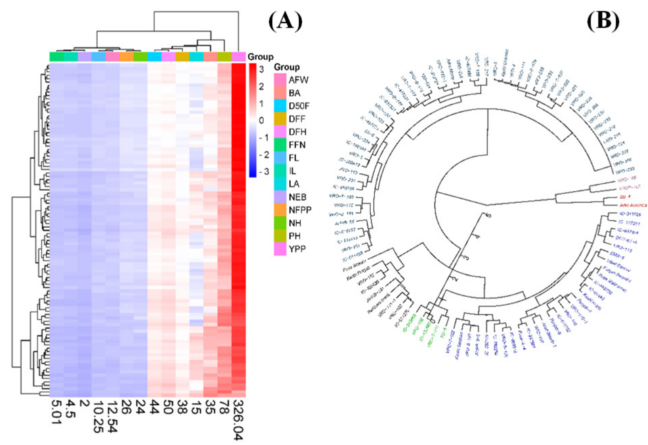


**Figure 1:** Clustering pattern of diverse okra genotypes for yield (A) and ELCV Incidence (B)

### *Genotypic and Phenotypic coefficient of variation*

Estimates for the coefficient of phenotypic and genotypic variation (PCV and GCV, respectively), heritability in a broad sense (H), and genetic advance (GA) as a percent of the mean for all fifteen characters were summarized in (Figures C, D and E). The PCV and GCV values of roughly more than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10 and 20% to be medium (Deshmukh et al., 1996). The genotypic coefficient of variation measures the range of genetic variability shown by the plant characters and helps to compare the genetic variability present in used genotypes for different characters. A high proportion of GCV to PCV is desirable in the selection process because it depicts that the traits are much under genetic control rather than the environment. Close estimates of GCV and PCV were recorded for all the traits under study except FFN, Branching angle ($^0$) and AFW (g) (Figure A). It implies that the contribution towards a final phenotypic expression of these characters is mostly by the genetic makeup of these genotypes rather than the environmental factors. This suggests that selection could be effective on the basis of phenotypic characters along with an equal probability of success in these characters. For correct estimation of the genetic makeup and its contribution to the

**Table 2:** Inter and intra-cluster values for 100 okra genotypes

| *Cluster* | *I* | *II* | *III* | *IV* | *V* | *VI* | *VII* | *VIII* |
|---|---|---|---|---|---|---|---|---|
| I | **2.423** | 3.710 | 5.098 | 5.487 | 3.432 | 3.672 | 5.008 | 3.251 |
| II | | **2.933** | 3.100 | 3.358 | 2.869 | 4.096 | 3.686 | 3.546 |
| III | | | **3.006** | 4.360 | 3.294 | 5.055 | 3.435 | 4.058 |
| IV | | | | **2.946** | 4.607 | 3.712 | 4.863 | 4.058 |
| V | | | | | **2.816** | 4.546 | 4.229 | 3.507 |
| VI | | | | | | **2.778** | 3.771 | 2.660 |
| VII | | | | | | | 2.891 | 3.930 |
| VIII | | | | | | | | 2.785 |

**Table 3:** Cluster mean for 15 different traits in okra

| *Clusters* | *I* | *II* | *III* | *IV* | *V* | *VI* | *VII* | *VIII* |
|---|---|---|---|---|---|---|---|---|
| DFF | 37.8 ± 1.64 | 40.62 ± 2.19 | 40.2 ± 1.47 | 45.27 ± 1.67 | 38.06 ± 1.34 | 43.73 ± 1.42 | 43.22 ± 1.92 | 41.52 ± 1.79 |
| D50F | 44.4 ± 1.82 | 45.56 ± 2.13 | 46 ± 1.49 | 50.53 ± 1.13 | 44.25 ± 1.29 | 49.2 ± 1.89 | 49.11 ± 2.2 | 46.62 ± 2.65 |
| FFN | 5.74 ± 1.27 | 5.41 ± 1.19 | 6.65 ± 1.46 | 7.14 ± 1.84 | 7.08 ± 1.51 | 6.15 ± 1.45 | 6.44 ± 1.4 | 6.86 ± 1.0 |
| DFH | 49.4 ± 1.52 | 51.12 ± 1.75 | 50.55 ± 1.5 | 55.6 ± 1.18 | 48.94 ± 0.93 | 54.41 ± 1.24 | 53.78 ± 1.86 | 52.31 ± 1.34 |
| PH | 76.4 ± 10.53 | 77.56 ± 7.97 | 79.1 ± 8.97 | 84.13 ± 9.26 | 92.25 ± 7.21 | 79.2 ± 8.27 | 79.11 ± 9.96 | 83.96 ± 10.5 |
| IL | 5.3 ± 1.75 | 5.77 ± 1.79 | 5.01 ± 1.22 | 6.57 ± 1.23 | 6.01 ± 1.48 | 3.76 ± 0.69 | 6.98 ± 0.85 | 5.39 ± 1.25 |
| NEB | 1.4 ± 0.89 | 1.5 ± 1.37 | 3.75 ± 1.21 | 1.6 ± 1.35 | 3.31 ± 1.3 | 2.36 ± 1.36 | 2 ± 1.58 | 2.63 ± 1.6 |
| BA | 73 ± 2.74 | 51.31 ± 12.1 | 57.65 ± 11.8 | 47.73 ± 8.61 | 58 ± 9.85 | 67.16 ± 10.3 | 58.33 ± 14.5 | 57.94 ± 10.1 |
| LA | 50.4 ± 9.18 | 26.06 ± 9.62 | 38.8 ± 15.7 | 36.8 ± 16.17 | 36.88 ± 15.5 | 53.77 ± 9.33 | 57.22 ± 10.5 | 35.48 ± 14.2 |
| FL | 10.26 ± 1.24 | 11.48 ± 1.72 | 10.81 ± 2.02 | 11.57 ± 1.31 | 9.89 ± 1.59 | 9.25 ± 1.79 | 8.75 ± 1.49 | 9.11 ± 1.09 |
| AFW | 9.21 ± 0.13 | 9.92 ± 0.98 | 10.82 ± 1.12 | 9.71 ± 1.11 | 9.51 ± 1.18 | 9.71 ± 1.1 | 11.6 ± 0.82 | 10.98 ± 0.97 |
| NFPP | 11.77 ± 3.0 | 17.88 ± 3.88 | 24.45 ± 3.09 | 18.07 ± 3.84 | 17.12 ± 3.65 | 12.52 ± 3.19 | 18.67 ± 3.46 | 10.52 ± 1.92 |
| NH | 13 ± 4.85 | 16.5 ± 3.55 | 23.05 ± 2.68 | 17 ± 3.98 | 17.19 ± 3.51 | 11.48 ± 2.6 | 19.78 ± 3.53 | 9.46 ± 1.98 |
| ELCV | 45.76 ± 14.5 | 14.6 ± 7.48 | 15.66 ± 14. | 19.17 ± 14.0 | 20.28 ± 11.3 | 35.34 ± 20. | 19.74 ± 14.1 | 43.53 ± 15.5 |
| YPP | 108.23 ± 27.01 | 176.17 ± 36.91 | 264.57 ± 43.69 | 174.86 ± 37.82 | 161.51 ± 32.56 | 120.42 ± 30.78 | 214.82 ± 32.02 | 115.62 ± 22.64 |

phenotypic expression of these characters, it is necessary to analysis or evaluation of characters should be conducted in different locations and seasons. In general, the magnitude of PCV was higher than GCV for all the characters under study, indicating that the apparent variation was not only due to genotype but also due to the favorable influence of environment and selection for these traits sometimes may be misleading. The genotypic and phenotypic coefficient of variation of 100 okra genotypes ranged between 1.92 (D50F) to 40.36 (NEB) and 3.61% (D50F) to 67.82% (Coefficient of Infection of ELCV), respectively. The high GCV and PCV values (>20.00 %) were found for a number of effective branches (63.98 and 64.61%), ELCV infection (63.62 and 67.82%), LA (⁰) (40.20 and 41.04%), NH (28.92 and 30.97%) and internodal length (26.12 and 27.86%), respectively. While, low GCV and PCV value was observed in D50F (1.92 and 5.83), Plant Height (9.52 and 12.29%), AFW (g) (4.64 and 12.27) and days to first flowering (5.37 and 7.13%) indicating the potential of simple selection for the improvement of these characters (Figures A and B). This study was supported to (Ola et al., 2021, Barman et al., 2022 and Adiger et al., 2011).

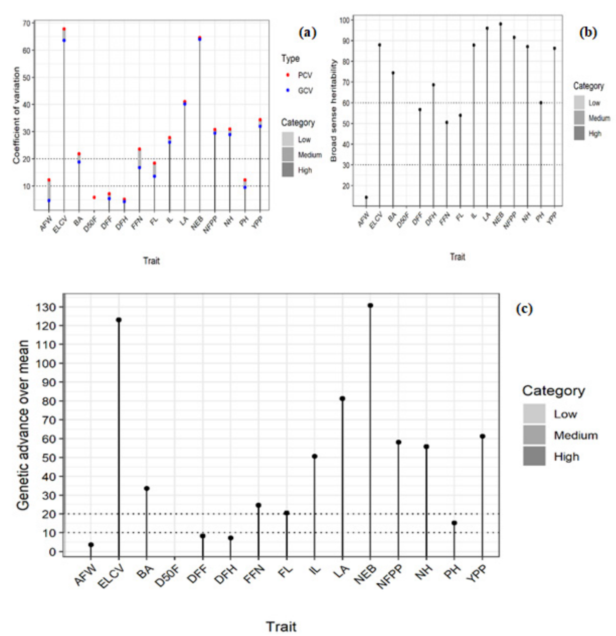


**Figure 2:** Coefficient of Variation (A), Broad Sense Heritability (B), and Genetic advance over mean (C)

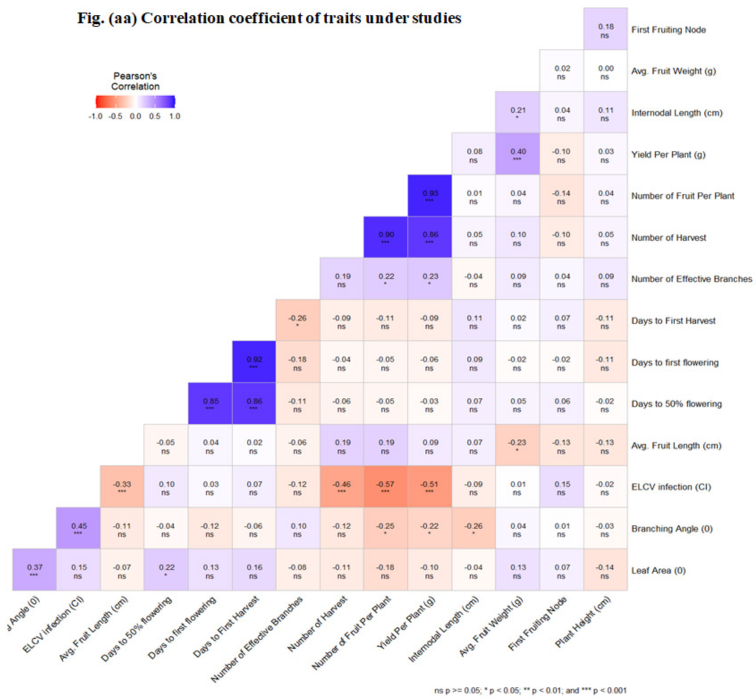


**Figure 3:** Correlation coefficient of traits under studies

### *Heritability (%)*

The estimates of broad sense heritability for all the characters have been described as (Figure C). It was partitioned as high (>60%), moderate (30–60%) and low (<30%). If the heritability of a character is very high, say 80% or more, selection for such characters could be fairly easy (Shaikh et al., 2013; Yonas et al., 2014). Data recorded during investigation, very high broad sense heritability (>80%) was recorded for the character, LA ($^0$) (98.98%), number of effective branches (98.07%), number of fruits per plant (91.58%), ELCV coefficient of infection (87.99%), internodal length (87.89%), followed by NH (87.17%) and yield per plant 87.26% (Figure C). In contrast, low heritability estimates were recorded for AFW (g) and D50F, *i.e.*, (14.27 and 16.23%), respectively. Most of the characters under study showed above-average to very high heritability. The high heritability estimates for quantitative traits are valuable for plant breeders, as they allow selection to be based on phenotypic performance according to (Awasthi et al., 2022 and; Kumar et al., 2016).

### *Genetic Advance (GA)*

Genetic advance depends upon the genetic variability, index of transmissibility, *i.e.*, heritability, and intensity of selection. Estimates of genetic advance at 5% selection intensity range varied from 0.37 (AFW (g)) to 108.51 (YPP). The very high genetic advance was recorded for three characters, *i.e.*, yield per plant (108.51), LA ($^0$) (32.15) and CI of ELCV (29.57). High genetic advance as percent of mean (> 20%) was recorded for the characters Number of effective branches (130.72), CI of ELCV (123.10), LA ($^0$) (81.25), yield per plant (61.19), number of fruits per plant (58.15), NH (55.70), internodal length (50.52), branching angle (33.55), FFN (24.60) and fruit length (20.52). However, days to first flowering (8.34), and days to first harvests (7.28) were observed below average GA as a percent of the mean (Figure C). Moderate genetic advance as a percent of the mean (10–20%) was recorded for the character's plant height (15.22). The above finding gave strong confirmation of the findings of (Temam et al., 2021 and Komoafe et al., 2022).

### *Correlation coefficient*

It helps to identify key traits that can be used for selection to enhance yield. Improving yield might make it easier to increase yield by increasing the smallest yield components on an otherwise high-performing cultivar. The estimates of genotypic and phenotypic correlation coefficients for different characters in 100 okra genotypes are summarized in (Figure 3). Days taken to first flowering were recorded as a highly significant and positive association with D50F and days to first harvesting, *i.e.*, 0.825 to 0.920, respectively. Whereas highly negative but non-significant association was recorded in a number of effective branches (-0.118), which were followed by plant height (-0.105) and NH (-0.062). Similarly, D50F was positively associated with days to the first harvest (0.824). Furthermore, number of fruits per plant was positively associated with the NH (0.907). In continuation, the CI of the enation leaf curl virus was positively correlated with branching angle (0.397), but it was negatively correlated with fruit length (-0.308), number

**Table 4:** Path coefficients showing direct and indirect effects of different characters on fruit yield per plant (g) in cultivated okra

| *Characters* | *DFF* | *D50F* | *FFN* | *DFH* | *PH* | *IL* | *NEB* | *BA* | *LA* | *FL* | *AFW* | *NFPP* | *NH* | *ELCV* | *R with YPP* |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DFF | **-0.0118** | -0.0036 | -0.0004 | 0.0075 | 0.0007 | -0.0006 | -0.0007 | 0.0014 | 0.0023 | 0.0001 | -0.0032 | -0.0680 | -0.0011 | 0.0005 | -0.077 |
| D50F | -0.0098 | **-0.0044** | 0.0009 | 0.0067 | 0.0000 | -0.0006 | -0.0005 | 0.0003 | 0.0034 | -0.0001 | 0.0178 | -0.0329 | -0.0008 | 0.0005 | -0.019 |
| FFN | 0.0002 | -0.0002 | **0.0201** | 0.0005 | -0.0012 | -0.0004 | 0.0002 | 0.0000 | 0.0011 | -0.0004 | 0.0069 | -0.1210 | -0.0017 | 0.0011 | -0.095 |
| DFH | -0.0109 | -0.0036 | 0.0013 | **0.0081** | 0.0006 | -0.0007 | -0.0010 | 0.0008 | 0.0028 | 0.0000 | 0.0100 | -0.1218 | -0.0020 | 0.0008 | -0.116 |
| PH | 0.0013 | 0.0000 | 0.0037 | -0.0008 | **-0.0065** | -0.0008 | 0.0004 | 0.0005 | -0.0021 | -0.0004 | 0.0032 | 0.0232 | 0.0006 | 0.0000 | 0.022 |
| IL | -0.0010 | -0.0003 | 0.0009 | 0.0008 | -0.0007 | **-0.0076** | -0.0001 | 0.0031 | -0.0007 | 0.0002 | 0.0666 | 0.0559 | 0.0017 | -0.0011 | 0.118 |
| NEB | 0.0022 | 0.0005 | 0.0008 | -0.0021 | -0.0006 | 0.0003 | **0.0040** | -0.0012 | -0.0014 | -0.0002 | 0.0306 | 0.1928 | 0.0031 | -0.0009 | 0.228 |
| BA | 0.0014 | 0.0001 | 0.0000 | -0.0005 | 0.0002 | 0.0020 | 0.0004 | **-0.0120** | 0.0057 | -0.0003 | 0.0120 | -0.2146 | -0.0019 | 0.0031 | -0.204 |
| LA | -0.0017 | -0.0009 | 0.0014 | 0.0014 | 0.0008 | 0.0003 | -0.0004 | -0.0042 | **0.0161** | -0.0002 | 0.0409 | -0.1619 | -0.0019 | 0.0012 | -0.109 |
| FL | -0.0004 | 0.0002 | -0.0027 | 0.0001 | 0.0009 | -0.0006 | -0.0003 | 0.0013 | -0.0012 | **0.0030** | -0.0815 | 0.1768 | 0.0032 | -0.0024 | 0.096 |
| AFW | 0.0001 | -0.0002 | 0.0004 | 0.0002 | -0.0001 | -0.0015 | 0.0004 | -0.0004 | 0.0019 | -0.0007 | **0.3488** | 0.0039 | 0.0011 | 0.0004 | 0.354** |
| NFPP | 0.0009 | 0.0002 | -0.0026 | -0.0011 | -0.0002 | -0.0005 | 0.0008 | 0.0028 | -0.0028 | 0.0006 | 0.0015 | **0.9208** | 0.0156 | -0.0048 | 0.931** |
| NH | 0.0008 | 0.0002 | -0.0019 | -0.0009 | -0.0002 | -0.0007 | 0.0007 | 0.0013 | -0.0018 | 0.0006 | 0.0214 | 0.8350 | **0.0172** | -0.0041 | 0.867** |
| ELCV | -0.0007 | -0.0003 | 0.0028 | 0.0009 | 0.0000 | 0.0011 | -0.0004 | -0.0048 | 0.0025 | -0.0009 | 0.0162 | -0.5777 | -0.0092 | **0.0077** | -0.563** |

**Table 5:** Eigen vector, eigen root and associated variation for principal component (PC) in Okra genotypes

| *S. No* | *Parameters* | *$PC_1$* | *$PC_2$* | *$PC_3$* |
|---|---|---|---|---|
| 1 | DFF | -0.178 | -0.533 | -0.029 |
| 2 | D50F | -0.188 | -0.508 | 0.104 |
| 3 | FFN | -0.093 | 0.019 | 0.182 |
| 4 | DFH | -0.210 | -0.524 | 0.001 |
| 5 | PH | 0.049 | 0.065 | 0.094 |
| 6 | IL | 0.044 | -0.131 | -0.039 |
| 7 | NEB | 0.169 | 0.111 | 0.275 |
| 8 | BA | -0.180 | 0.164 | 0.402 |
| 9 | LA | -0.165 | -0.075 | 0.358 |
| 10 | FL | 0.134 | -0.085 | -0.426 |
| 11 | AFW | 0.077 | -0.067 | 0.504 |
| 12 | NFPP | 0.474 | -0.168 | 0.070 |
| 13 | YPP | 0.461 | -0.176 | 0.255 |
| 14 | NH | 0.442 | -0.160 | 0.147 |
| 15 | ELCV | -0.363 | 0.137 | 0.230 |

of fruits per plant (-0.627) and NH (-0.535). Yield per plant resulted significant positive correlation with AFW (g) (0.354), number of fruits per plant (0.931) and NH (0.867) but had a negative correlation between CI of enation leaf curl virus (-0.563). In the other hand, FFN, plant height, internodal length, number of effective branching, leaf area showed no any significant correlation with other characters. This finding was strongly supported to the previous researcher (Lal, 2023; Awasthi et al., 2022; Rana et al., 2020; Neeraja et al., 2022 and Kerure et al., 2017).

### *Path coefficient*

To identify key component characters with direct impacts on fruit yield, researchers partitioned phenotypic correlations of the characters into path coefficients. Table 3 presents the direct and indirect effects of various characters on fruit yield per plant at the phenotypic level. Highest positive direct effect on yield was registered by number of fruits per plant (0.9208) which were followed by AFW (g) (0.3488), FFN (0.0201), NH (0.0172) and leaf area (0.0161). In other hand, negative direct effect on yield was observed in days to first flowering (-0.0118). Residual effect of the path analysis was low (0.00844) suggesting the inclusion of maximum yield influencing characters in the present study which were supported to previous studies by (Kumari et al., 2017; Rathawa et al., 2019; Awasthi et al., 2022 and Nibea et al., 2023).

### *Principal component analysis (PCA)*

Principal component analysis was performed to determine the principal components of growth and yield parameters of the 100 okra genotypes, which best explains the response

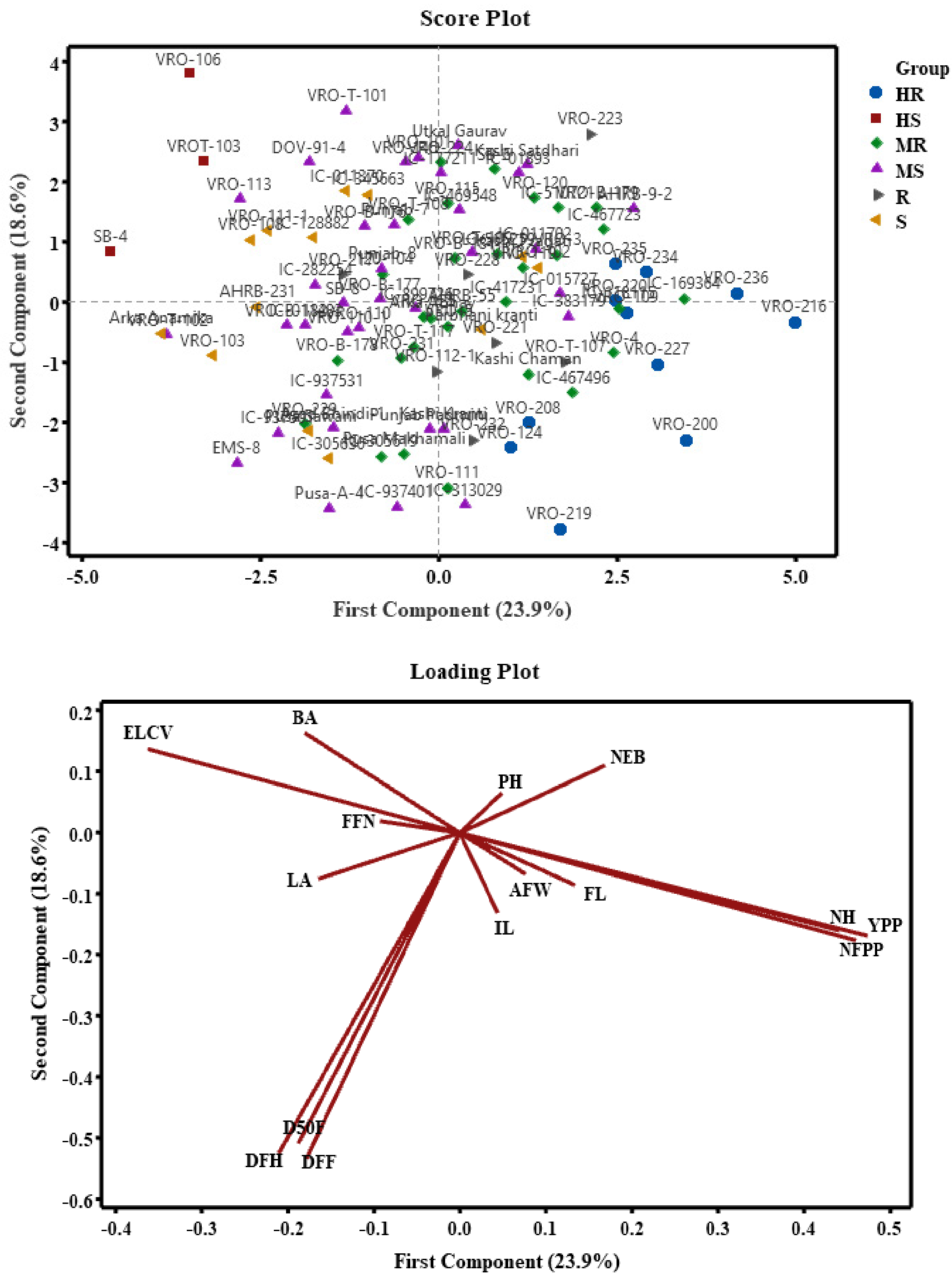


**Figure 4:** Principal component analysis (PCA) showing score plots (A) and loading plots (B) of different attributes of Okra genotypes under field condition

to ELCV for screening resistant okra varieties under field condition. We found that, three principal components, $PC_1$ to $PC_2$, with eigen values greater than one, account for 53.2% of the total variation in the 100 Okra genotypes. $PC_1$ contributes approximately 23.9% to the total variation, followed by $PC_2$ (18.6%) and $PC_3$ (10.7%), indicating appreciable diversity among the genotypes for the studied traits.

Traits that positively contribute to $PC_1$ include PH (0.049), IL (0.044), NEB (0.169), FL (0.134), AFW (0.077), NFPP (0.474), YPP (0.461) and NH (0.442). Similarly, FFN (0.019), PH (0.065), NEB (0.111), BA (0.164) and ELCV (0.137) are significant contributors to $PC_2$, while D50F (0.104), FFN (0.182), DFH (0.001), PH (0.094), NEB (0.275), BA (0.402), LA (0.358), AFW (0.504), NFPP (0.070), YPP (0.255), NH (0.147) and ELCV (0.230) are significant contributors to $PC_3$ (Table 1). The PCA score plot (Figure PA) showed six distinct groups, *i.e.*, highly resistant (HR) genotypes were concentrated further away from the origin in the positive direction along $PC_1$ and highly sensitive (HS) genotypes were scattered along $PC_2$ in the positive direction. The PCA loading plot (Figure PB) showed a better visualization of the relationships and great variation present among all the studied growth and yield parameters. It was revealed that the yield attributes such as NH, YPP and NFPP are strongly and positively correlated to each other and comparatively less positively correlated to AFW, FL, PH, NEB and IL, while all these variables were found negatively correlated with ELCV. The results are in accordance with the findings of (Saleem et al., 2023 and Ranga et al., 2021).

## Conclusion

From this study we concluded that underscores the paramount importance of accessing desirable genetic diversity to meet our current objectives, developing okra varieties that are both high-yielding and resistant to enation leaf curl virus (ELCV). The traits like days to first harvesting, FFN, BA ($^0$), LA ($^0$), and NHs should be given top priority in diverse parent selection for attempting heterotic cross combination and focusing on these traits is essential for achieving the desired outcomes in okra breeding programs.

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## सारांश

वर्तमान शोध वर्षा ऋतु 2022 में भिंडी की 100 जीनोटाइप के साथ उनके आनुवंशिक उन्नति जैसे जीसीवी, पीसीवी, हेरिटैबिलिटी, विविधता, पथ गुणांक, पी.सी.ए. तथा अन्या मापदंडों का पता लगाने के लिए भा.कृ.नु.प.- भारतीय सब्जी अनुसंधान संस्थान, वाराणसी में किया गया था I उच्च जीसीवी और पीसीवी को एनेशन लीफ कर्ल वायरस (संक्रमण का गुणांक), प्रभावी शाखाओं की संख्या, पत्ती कोण ($^0$) और प्रति पौधे की उपज (ग्राम), फल की संख्या, इंटर्नोडल लंबाई (सेमी) और प्रति पौधे फलों की संख्या के लिए पाया गया। लगभग सभी पात्रों के लिए उच्च जी.एए.म. के साथ मिलकर उच्च आनुवांशिकता देखी गई थी , जिसमें फलों की लंबाई (सेमी), पौधे की ऊंचाई (सेमी), औसत फलों के वजन, पहले फलने के दिन और पहले फसल के लिए दिन कम आनुवंशिक अग्रिम माध्य के साथ कम आनुवांशिकता दिखाये हैं। प्रति पौधे की उपज, प्रभावी शाखाओं की संख्या, ई.एल.सी.वी. (सी.आई.), पत्ती कोण ($^0$), फल की संख्या और इंटर्नोडल लंबाई (सेमी) ने उच्च आनुवंशिक अग्रिम दिखाया जो भिंडी सुधार के लिए इन पात्रों के माध्यम से प्रभावी और विश्वसनीय चयन में मदद करता है। प्रति पौधे उपज के परिणामस्वरूप औसत फलों के वजन, प्रति पौधे फलों की संख्या और फसल की संख्या के साथ महत्वपूर्ण सकारात्मक सहसंबंध था, लेकिन ई.एल.सी.वी. (सी.आई.) के बीच नकारात्मक सहसंबंध । प्रति पौधे फलों की संख्या का औसत फल के वजन पर अधिकतम सीधा प्रभाव देखा गया |