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Genetic Divergence for Different Yield Attributing Traits in Okra [*Abelmoschus Esculentus* (L.) Moench] Genotypes Grown in Himalayan Foothills Region

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ABSTRACT

The Himalayan foothills region of India is rich in the genetic diversity of okra, which is yet to be explored for its genetic divergence. To envisage the genetic diversity of this un-explored varietal collection, the genetic divergence among 25 genotypes of okra was estimated using Mahalanobis D^2 statistic. The indigenous and exotic lines were grouped into 6 clusters using Tocher's methods. Results revealed that a higher number of genotypes were recorded under cluster I (19) and cluster IV (2), while cluster II, III, V and VI were mono-genotypic. A higher intra- cluster distance was observed between clusters I (13.42) and IV (7.47), whereas, a higher inter-cluster distance was found between clusters III and VI (111.03). The traits *viz*, Yellow Vein Mosaic Virus (YVMV) incidence (44.67 %) were contributing the highest towards the total genetic divergence. The present study revealed the detailed genetic divergence for different yield-attributing traits in okra. This study presents a strong basis for the selection and evolving of better recombinants for hybridization and quality improvement programme. This research bear utility in the form of germplasm conservation and crop improvement for selected indigenous/exotic genotypes grown in Himalayan foothills.

Keywords: Cluster and recombinants, Himalayan foothill genotypes, Yellow Vein Mosaic Virus.

INTRODUCTION

Okra [*Abelmoschus esculentus* (L.) Moench] is the most significant nutritive vegetable crop in India (Temam *et al.,* 2021). During the rainy and spring-summer seasons, okra is predominantly grown in the tropics and subtropics of the world for immature fragile green fruits as well as processed products (Temam, N., 2020). The okra crop, which belongs to the Malvaceae family and the genus *Abelmoschus*, is said to have originated in Ethiopia (Mohammed *et al.,* 2022). Although according to Sonwani *et al.* (2022) it originated in the Hindustan region. Okra (n= 12) has a regular series of polyploides with somatic chromosomal numbers 2n= 72, 109, 120, 132, and 144 (Raghuwanshi *et al.,* 2019).

The root and stems of the okra plant are commonly used to clarify sugarcane juice for the manufacturing of brown sugar and gur (Makur *et al.,* 2019). It is also utilised in the paper industry due to the high mucilage and crude fibre content of the mature stems and fruits (Haruna *et al.,* 2016). Okra has a great medicinal value and is particularly useful in the treatment of genito-urinary disorders such as haemorrhoids, ulcers, chronic dysentery, and spermatorrhoea (Olaniyan and Omoleyomi, 2013). Okra fruits are rich in high iodine content, which helps to prevent goitre (Fayaz *et al.,* 2022). Fresh okra vegetable plays a very crucial

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role in human nutrition, especially as sources of dietary fiber and vitamins (Prasad *et al.,* 2018). The tender green fruit is the potent source of vitamins A, B_1, B_3, B_6, C, folic acid and essential minerals *viz*., Ca, K, Mg and P have an important role in human diet (Mkhabela *et al.,* 2022).

The development of cultivars against target traits such as fruit yield and pest/disease resistance is often a more rewarding and appropriate option for the sustainability of smallholder farmers (Sandeep *et al.,* 2022). This is especially relevant in developing and underdeveloped countries, where farmers often do not have the capability to diagnose suitable preventive measures (Kumar *et al.,* 2010). Yellow vein mosaic disease is the most common biotic stress in okra under natural epiphytic conditions. The wild species are widely acknowledged to be a major reservoir of resistance genes, particularly for yellow vein mosaic disease (Gangopadhyay *et al.,* 2017).

The concept of linking phenotypes with genotypes is somewhat basic and ubiquitous in plant breeding, as well as in the history of plant domestication, and has been used for selection of superior plants for agricultural use (Kozak *et al.,* 2011). Improving the varieties with desired traits in terms of fruit size, shape and colour, and resistance to biotic stress are also very purposeful in the okras' export market. This characterization and genetic diversity analysis was required against this backdrop. Traditionally, a combination of morphological data and phenotypic traits significantly contributed towards the pattern of total genetic diversity present in the population (Oppong-Sekyere *et al.,* 2011). The genetic distances between the lines, determined by using these traits, can be treated as phenotypic similarities between the lines (Kozak *et al.,* 2011).

Genetic diversity refers to the heritable variation within and between groups of populations (Alam *et al.,* 2014). The presence of genetic diversity between the genotypes from different geographic regions is attributed to the selection and exchange of okra germplasm between farmers from different geographic locations and between ethnic groups. The duplications in the germplasm due the migrant farmers often carry seeds from their original growing location to their new growing locations (Oppong-Sekyere *et al.,* 2011). Genetic diversity exploits essential work in vegetable breeding because hybrids from diverse sources of germplasm exhibited more opportunity for F_1 hybrids development than closely related species (Alam *et al.,* 2014).

Genetic divergence has been an important topic in plant breeding in recent decades, and still is. It should be defined as the divergence of the gene pool of a population from the gene pools of other populations, which can occur as a result of mutation, genetic drift, and selection. The basis of morphological and genotypic divergences or similarities could be viewed as a complicated genetic system (Kozak *et al.,* 2011). Differences across the varieties of the same or different species may be linked to allelic variation and variable gene expression associated with morphological and non-physiological features, in addition to the genotype-by-environment interaction of each locus (Kozak *et al.,* 2011 and Kyriakopoulou *et al.,* 2014).

The D^2 statistics provides a magnitude estimate of diversity between two genotypes (Sruthi *et al.,* 2020). In okra, F_1 hybrids are more widespread, and new genotypes for heterosis are constantly being selected (Sandeep *et al.,* 2022). As a result, genetic divergence among existing genotypes must be investigated, and germplasm must be collected for identification (Sanwal *et al.,* 2012). When identifying relevant parental lines for heterosis breeding, grouping genotypes based on D^2 analysis will be advantageous (Mohammed *et al.,* 2022).

The clustering pattern indicated the existence of diverse forms in collections made from the close geographic location, indicating more opportunity to select the most desirable genotypes (Oppong-Sekyere *et al.,* 2011, Gangopadhyay *et al.,* 2017). A cluster diagram obtained from the

phynotypic descriptors of genotypes based on the simple matching coefficient (Oppong-Sekyere *et al.,* 2011).

The Pusa Region of Bihar, India, represents Himalayan Foothill Plain, and is well known for its distinctive soil, slope, altitudes, climate, and ecological diversity of okra germplasm, which are yet un-explored for diversity trait in this region (Koku *et al.,* 2020). The genetic diversity of okra in this region is very high (Sonwani *et al.,* 2022) and there is a necessity of developing high-yielding, better nutrition, post-harvest quality and biotic/abiotic resistant okra germplasm for this region.

The objective of the present study was to put a strong basis for the selection and evolving of better recombinants of okra for hybridization and quality improvement program in the near future (Prasad *et al.,* 2018; Mkhabela *et al.,* 2022). This research also aimed for germplasm conservation and crop improvement for selected indigenous/exotic genotypes grown in Himalayan foothills.

MATERIALS AND METHODS

The research was carried out during academic session 2019-2020, at Dholi Farm, Tirhut College Agriculture, a Campus of Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur-Bihar. Twenty-five genotypes of okra (Table 1), including both indigenous and exotic lines, were selected and sown on 25 Jun 2019. Design was randomized block with each line consisting of three replications. The last observation was taken on plant height at final harvest on 20 September, 2019. All the genotypes were procured from Indian Institute of Vegetable Research (IIVR), Varanasi, Uttar Pradesh-India, through materials transfer agreement (Table 1). A nationally adapted okra variety "Kashi Kranti" was also included as a check variety. A standardized crop descriptor for okra genotypes was used to measure the various traits under studies (IBPGR, 1991). The data was recorded from five randomly selected plants for different yield attributing traits. The weather data were collected from Department of Agro Meteorology, Tirhut College Agriculture, a Campus of Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur-Bihar. The weather data are tabulated in Table 2. The enlist of the studied phenotypic traits under present study are mention in Table 3. The description of studied phenotypic traits are summarized below:

(A). Plant Height (cm)

The measurement of plant height of all five selected and tagged plants in each treatment was done using a meter scale, from ground level to the apex of the plant at the final harvest. The measured value was presented in centimetre.

(B). Number of Primary Branches per Plant

Primary branches per plant in each genotype of each plot were counted at the time of final harvesting and the average branches per plant were determined.

(C). Days to First Flowering

The number of days from seed sowing to the anthesis of the first flower was counted.

(D). Days to First Picking

The cumulative number of days from seed sowing to harvesting of the first fruit was recorded.

(E). Number of Seeds per Fruit

Five dried fruits were randomly collected from tagged plants in each plot and seeds were extracted. The number of seeds were counted for the average.

(F). Number of Ridges per Fruit

Ridges per fruit were counted during the third pickings of each genotype in each plot and the average number of ridges per fruit were calculated.

(G). Fruit Length (cm)

The marketable fruits of each genotype were selected in each plot and the length of these fruits, excluding fruit stalk, was

Table 1. List of genotypes with their source of procurement for the study.

S. No.	Genotypes	Source	S. No.	Genotypes	Source
1.	IC-43735	IIVR[a]-Varanasi, India	14.	VRO-196	IIVR-Varanasi, India
2.	IC-43742	IIVR-Varanasi, India	15.	VRO-177	IIVR-Varanasi, India
3.	IC-218872	IIVR-Varanasi, India	16.	VRO-956	IIVR-Varanasi, India
4.	IC-105667	IIVR-Varanasi, India	17.	VRO-433	IIVR-Varanasi, India
5.	EC-199367	IIVR-Varanasi, India	18.	VRO-214	IIVR-Varanasi, India
6.	EC-015537	IIVR-Varanasi, India	19.	VRO-320	IIVR-Varanasi, India
7.	SKY/DR/RS-13	IIVR-Varanasi, India	20.	VRO-107	IIVR-Varanasi, India
8.	SKY/DR/RS-107	IIVR-Varanasi, India	21.	VRO-173	IIVR-Varanasi, India
9.	VRO-454-10-1	IIVR-Varanasi, India	22.	VRO-404	IIVR-Varanasi, India
10.	VRO-232-10-1	IIVR-Varanasi, India	23.	VRO-40	IIVR-Varanasi, India
11.	VRO-132-10-1,2	IIVR-Varanasi, India	24.	VRO-37	IIVR-Varanasi, India
12.	VRO-304-10-1	IIVR-Varanasi, India	25.	Kashi Kranti	IIVR-Varanasi, India
13.	VRO-109-1	IIVR-Varanasi, India			

[a] IIVR: Indian Institute of Vegetable Research, Varanasi, Uttar Pradesh- India. https://iivr.icar.gov.in/.

Table 2. Average monthly weather data on the field location during the okra-growing season.

Month	Temperature (°C)		Humidity (%)		Wind speed (Km h^{-1})	Rainfall (mm)	Evaporation (mm)
	Max	Min	Morning	Evening			
Jun-2019	36.7	26.3	81	57	6.3	0.0	6.3
July-2019	30.4	25.2	92	76	4.2	138.7	4.2
August-2019	33.6	26.3	90	76	5.2	100.7	5.2
September-2019	32.4	25.9	89	80	2.8	74.2	2.8

Source: Department of Agro Meteorology, Tirhut College Agriculture, a campus of Dr. Rajendra Prasad Central Agricultural University, Pusa, Samastipur, Bihar-India.

Table 3. Enlist of the studied phenotypic traits under present study.

S. No.	Traits	Sampling date
1.	Plant height	25 Jun 2019 to 20 September 2019
2.	Number of primary branches per plants	
3.	Days to first flowering	
3.	Days to first picking	
5.	Number of seeds per fruits	
6.	Number of ridges per fruits	
7.	Fruit length (cm)	
8.	Fruit diameter (cm)	
9.	YVMV incidence (%)	
10.	Average fruit weight (g)	
11.	Number of fruits per plants	
12.	Fruit yield per plant (g)	

measured with meter scale and the mean length per pod was calculated.

(H). Fruit Diameter (cm)

Five fruits of each genotype were randomly selected in each plot and diameter was measured at the base of fruits with the help of venire caliper.

(I). Yellow Vein Mosaic Virus (YVMV) Incidence (%)

Under natural disease pressure conditions, all the plants in each plot were recorded for the appearance of YVMV incidence percentage. Numbers of plants affected by YVMV were counted at 30, 45, 60 and 75 days after sowing of crop in each genotype. The percent incidence was determined based on the total number of plants per plot.

$$\text{YVMV infestation of plants (\%)} = \frac{\text{Number of YVMV infected plants} \times 100}{\text{Total number of plants}}$$

(J). Average Fruit Weight (g)

Five edible fruits were selected randomly from tagged plants in each plot and their weight (g) was taken using weighing balance.

(K). Number of Fruits per Plant

The number of fruits picked from all tagged plants in each picking were added and it measured the total number of fruits per plant.

(L). Fruit Yield per Plant (g)

The fruit yield per plant of the tagged plants was determined by addition of the total fruit weight of all fruit pickings and is shown in grams per plant.

Genetic Divergence

Genetic diversity was determined by Mahalanobis D^2 statistics based on their phenotypic data (Sruthi *et al.,* 2020; Kumar *et al.,* 2021; Vaggar *et al.,* 2022; Meena *et al.,* 2021).

Cluster Analysis

The genotypes were grouped into various clusters based on their phenotypic similarity (Table 3). D^2 values and Tocher's method were used for grouping of genotypes into different clusters (Kumawat *et al.,* 2020, Kumar *et al.,* 2021; Vaggar *et al.,* 2022).

Average Intra and Inter-Cluster Distance was used to figure out the summation of distances between different genotypes.

Cluster diagram by "Dendrogram" was used to exhibit inter and intra cluster distances between different clusters-based values of D^2 statistics (Yadav, 2020).

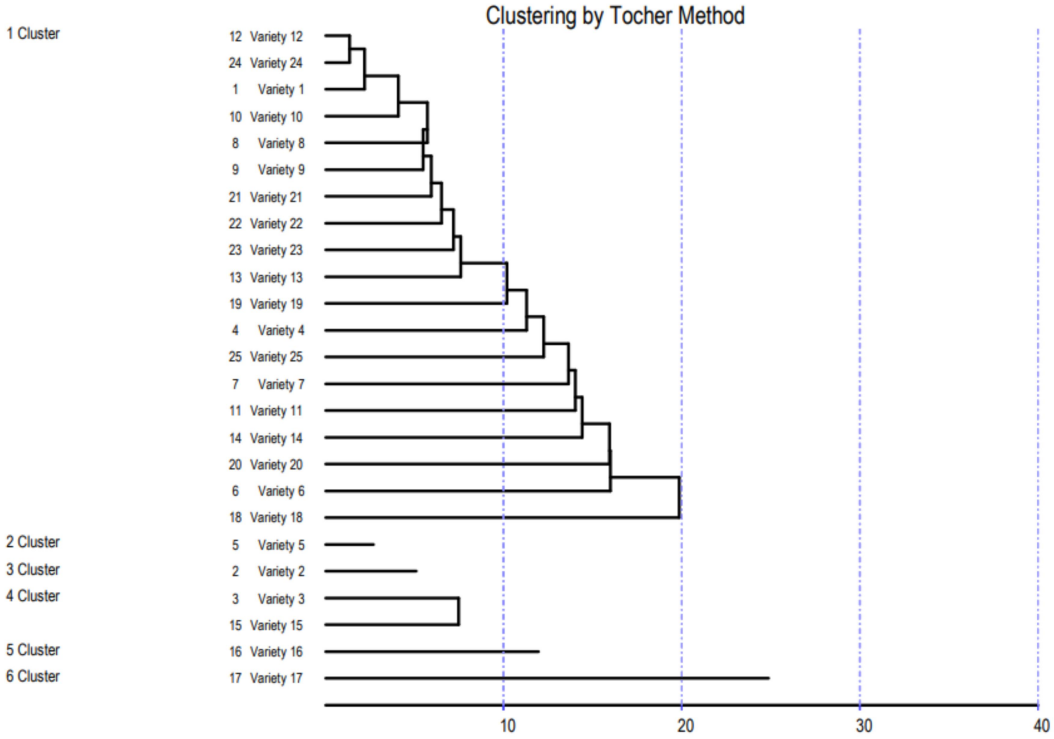

Figure 1. Clustering pattern of 25 okra genotypes selected for the study.

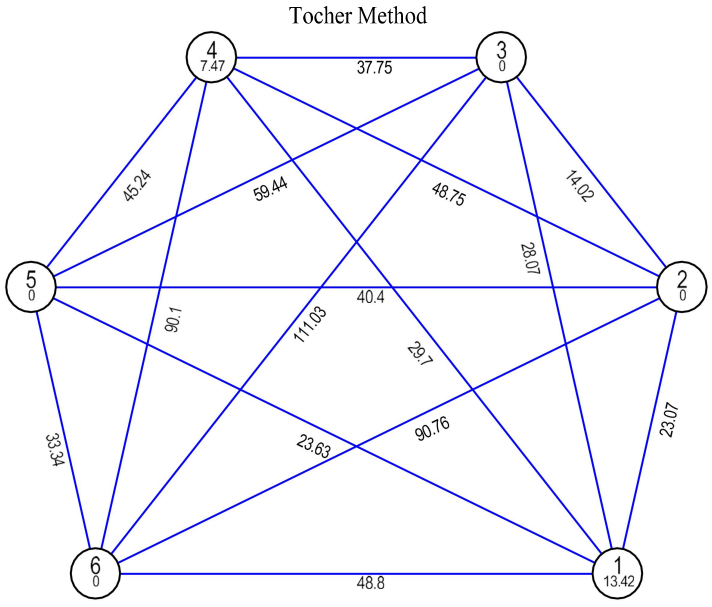

Figure 2. Intra and inter cluster Distance (D^2) among six clusters of the selected 25 okra genotypes.

Contribution of Individual Traits towards Total Divergence

Among all, the combination of genotypes *i.e.* n (n-1)/2, each trait was ranked based on mean difference, where n is the total number of genotypes. Using these ranks, the following table was prepared to work out the percent contribution of each trait to the total divergence (Table 4).

Percent contribution by Xp = Number of times appearing first in ranking by Xp×100

n (n-1)/2

Where, Xp= Individual traits, and n= Number of genotypes.

Statistical Analysis

The statistical analysis was carried out using Statistical Analysis System [SAS (9.4)] North Carolina State University- United States America, OPSTAT (Operational Statistics- developed by Department Of Mathematics Statistics, Chaudhary Charan Singh Haryana Agricultural University, Hisar, India) and GRAPES software (General R-shiny based Analysis Platform Empowered by Statistics developed by Department of Agricultural Statistics, College of Agriculture, Vellayani, Kerala Agricultural University- India).

RESULTS AND DISCUSSION

The mean performance of morphological traits of different genotypes along with check variety (Kashi Kranti) is tabulated in Table 5. The genotype SKY/DR/RS-13 (136.33 cm & 3.10) and IC-43742 (133.07 cm and 3.08) was reported for significantly higher plant height and number of primary branches per plant than the check value (116.67 cm and 2.30). The genotypes VRO-214 (39.03 and 45.33 days) were observed significantly at par near the check variety (40.57 and 47.33 days) with respect to days to first flowering and days to first picking. The genotypes IC-218872 (68.67) were observed for maximum number of seeds per fruit and VRO-177 (6.87) was recorded significantly superior for maximum number of ridges per plant over the check variety (48.33 and 5.00). The significantly higher fruit length were reported in EC-015537 (14.53 cm), EC-199367 (14.27 cm), and VRO-107 (13.83 cm), fruit diameter was recorded higher in IC-43742 (1.81 cm) than check variety (11.77 and 1.60 cm). The minimum YVMV incidence (%) was registered in genotypes EC-199367 (9.33 %) as compare to check variety (17.33 %). The significantly superior genotypes over check variety, Kashi Kranti (11.22, 23.67 and 265.67 g) was recorded in VRO-956 (15.63 g) followed by VRO-214 (13.18 g) and EC-199367 (12.91 g) with respect to average fruit weight, IC-43742 (27.50) and EC-199367 (26.70) with respect to maximum number of fruits per plant, IC-43742 (312.33 g) followed by VRO-214 (320.33 g) and EC- 199367 (319.33 g) for higher fruit yield per plant (Table 4). In the consideration of per se performance of genotype existed vast range of variation for different morphological traits among genotypes of okra under present investigation indicated the evaluation of these genotypes in above respective morphological traits can be more useful in future breeding program. The similar type results were also reported by some previous researchers (Vaggar *et al.,* 2022).

In general, all the okra genotypes displayed relatively wide ranges of variation for all morphological traits evaluated (Oppong-Sekyere *et al.,* 2011). Higher diverse genotypes within the group of population exhibit better heterotic response (Suri *et al.,* 2022). The D^2 analysis method was used to group the genotype based on quantitative traits. The genotypes were grouped in different clusters based on the genetic distance between them.

The ‘cluster patterns’, ‘clusters mean’, ‘intra/inter cluster’ and ‘contribution percentage’ are presented in Tables 5, 6, 7, and 8, respectively. The selected (25) genotypes were assessed for genetic

Table 4. Mean performance of morphological traits of twenty five okra genotypes.

Genotypes	Plant height (cm)	Number of primary branches per plant	Days to first flowering	Days to first picking	Number of seeds per fruit	Number of ridges per plant	Fruit length (cm)	Fruit diameter (cm)	YVMV incidence (%)	Average fruit weight (g)	Number of fruits per plant	Fruit yield per plant (g)
IC- 43735	107.40	1.97	44.00	50.33	52.67	5.00	10.23	1.62	36.28	11.51	20.33	254.00
IC- 43742	133.07	3.08	40.33	48.00	56.67	5.00	12.00	1.81	12.33	12.07	27.50	312.33
IC- 218872	108.33	2.20	42.33	53.00	68.67	6.47	10.13	1.68	27.67	11.78	21.97	265.33
IC- 105667	114.87	2.25	41.73	48.30	54.67	5.00	10.97	1.52	21.67	10.34	24.33	261.67
EC- 199367	117.20	2.57	41.33	47.33	39.33	5.00	14.27	1.63	9.33	12.91	26.70	319.33
EC- 015537	130.33	3.07	39.63	46.33	43.33	5.07	14.53	1.50	19.13	11.17	24.67	275.67
SKY/DR/RS- 13	136.33	3.10	43.17	48.67	52.00	5.13	11.33	1.58	27.12	11.19	25.67	286.88
SKY/DR/RS- 107	110.00	2.27	41.27	47.67	42.33	5.00	10.63	1.71	33.33	11.55	22.00	256.67
VRO-454-10-1	100.00	2.27	41.33	48.67	48.00	5.00	10.03	1.53	38.12	11.23	21.50	250.00
VRO-232-10-1	95.67	1.90	43.33	51.00	51.33	5.00	9.23	1.62	24.83	10.52	21.00	255.00
VRO-132-10-1,2	116.33	2.25	40.83	48.67	35.33	5.13	13.67	1.64	21.00	10.96	25.67	296.67
VRO-304-10-1	91.33	1.87	42.50	52.33	52.67	5.00	9.62	1.80	32.45	11.73	20.00	247.67
VRO-109-1	101.00	1.90	44.33	49.67	37.67	5.00	9.60	1.58	34.78	11.05	19.00	236.67
VRO-196	119.33	2.40	41.33	47.33	42.33	5.00	13.00	1.68	15.18	11.98	24.00	285.33
VRO-177	96.67	1.77	47.33	55.33	57.33	6.87	10.53	1.72	27.76	10.33	20.67	230.67
VRO-956	107.67	2.08	42.40	49.67	44.00	5.13	13.17	1.69	37.39	15.63	20.67	287.67
VRO-433	118.33	2.73	42.93	50.67	28.33	5.00	10.90	1.46	51.67	11.35	22.33	266.00
VRO-214	133.00	3.00	39.03	45.33	46.00	5.13	12.50	1.79	14.67	13.18	24.00	320.33
VRO-320	120.07	2.80	41.37	48.00	47.00	5.07	10.13	1.72	24.33	11.77	24.00	283.33
VRO-107	119.00	2.53	40.47	47.33	30.67	5.00	13.83	1.49	25.00	11.80	25.33	302.67
VRO-173	122.67	2.37	46.00	53.00	48.33	5.07	10.17	1.64	30.97	11.43	24.33	282.67
VRO-404	111.67	2.25	41.67	47.00	54.00	5.00	10.70	1.59	41.00	11.73	20.60	256.67
VRO-40	121.00	2.43	44.33	50.33	40.33	5.07	10.83	1.49	29.71	10.67	22.67	238.67
VR0- 37	102.00	2.00	41.33	49.33	50.00	5.00	9.43	1.74	32.11	11.80	19.67	253.33
Kashi Kranti	116.67	2.30	40.57	47.33	48.33	5.00	11.77	1.60	17.33	11.22	23.67	265.67
CD (5%)	15.04	0.39	3.83	4.69	6.76	0.60	2.00	0.21	5.04	1.67	2.58	40.12

Table 5. Clustering pattern of okra genotypes selected for the study.

Cluster	Number of genotypes	Genotypes in cluster
I	19	VRO-304-10-1, VRO-37, IC-43735, VRO-232-10-1, SKY/DR/RS-107, VRO-454-10-1, VRO-173, VRO-404, VRO-40, VRO-109-1, VRO-320, IC-105667, Kashi Kranti, SKY/DR/RS-13, VRO-132-10-1,2, VRO-196, VRO-107, EC-015537, VRO-214
II	1	EC-199367
III	1	IC-43742
IV	2	IC-218872, VRO-177
V	1	VRO-956
VI	1	VRO-433

Table 6. Cluster mean for studied attributes of okra genotypes based on phenotypic similarity.

Characters	Mean of cluster					
	I	II	III	IV	**V**	**VI**
Plant height (cm)	114.14	117.20	133.07	102.50	107.67	118.33
Number of primary branches per plant	2.36	2.57	3.10	1.98	2.08	2.73
Days to first flowering	42.01	41.33	40.33	44.83	42.40	42.93
Days to first picking	48.77	47.33	48.00	54.17	49.67	50.67
Number of seeds per fruit	46.16	39.33	56.67	63.00	44.00	28.33
Number of ridges per fruit	5.04	5.00	5.00	6.67	5.13	5.00
Fruit length (cm)	11.17	14.27	12.00	10.33	13.17	10.90
Fruit diameter (cm)	1.62	1.63	1.81	1.70	1.69	1.46
YVMV incidence (%)	27.32	9.33	12.33	27.71	37.39	51.67
Average fruit weight (g)	11.41	12.91	12.10	11.06	15.63	11.35
Number of fruits per plant	22.76	25.00	26.00	21.32	20.67	22.33
Fruit yield per plant (g)	268.92	319.33	312.33	248.00	287.67	266.00

Table 7. Mean intra and inter cluster Distance (D^2) among six clusters of okra.

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	13.42	23.07	28.07	29.70	23.63	48.80
Cluster II		0.00	14.02	48.75	40.40	90.76
Cluster III			0.00	37.75	59.44	111.03
Cluster IV				7.47	45.24	90.10
Cluster V					0.00	33.34
Cluster VI						0.00

divergence followed by division in 6 groups as per the 'Toucher' method (Figure 1). Cluster I had the maximum genotypes (19) followed by cluster IV (2), whereas, Clusters II, III, V, and VI were monogenotypic, *i.e.* consisting of a single genotype. Our result got the support from similar studies attempted earlier by researchers who worked on okra genetic divergence (Prasad *et al.,* 2016; Alemu and Mohammed 2022; Carvalho *et al.,* 2022, and Mohammed *et al.,* 2022).

Cluster means for twelve characters of twenty-five genotypes are presented in Table 3. It was recorded that the maximum cluster mean value for plant height (133.07 cm),

Table 8. Percent contribution of the studied phenotypic attributes towards total genetic divergence in okra.

Traits	Times ranked first	% Contribution
Plant height	14	4.67
Number of primary branches per plants	23	7.67
Days to first flowering	2	0.67
Days to first picking	0	0.00
Number of seeds per fruits	59	19.67
Number of ridges per fruits	30	10.00
Fruit length (cm)	8	2.67
Fruit diameter (cm)	2	0.67
YVMV incidence (%)	134	44.67
Average fruit weight (g)	18	6.00
Number of fruits per plants	7	2.33
Fruit yield per plant (g)	3	1.00

number of primary branches per plant (3.10), fruit diameter (1.81 cm) and number of fruits per plant (26.00) was recorded in cluster III. It indicates that if a breeding aim is to obtain long plant height, more number of primary branches per plant, fruit diameter and number of fruits per plant, genotypes from these clusters would be selected. The minimum cluster mean value for days to first flowering (40.33 days), days to first picking (47.33 days), number of seeds per fruit (28.33), fruit diameter (1.46 cm) and YVMV incidence (9.33%) was reported in cluster III, II, VI, VI, and II, respectively. It indicates that if a breeding program aims to obtain desired days to first flowering, days to first picking, numbers of seeds per fruit, fruit diameter and YVMV incidence, genotypes from these clusters would be selected. The maximum cluster mean value for number of seeds per fruit (63.00) and number of ridges per fruit (6.67) was observed in cluster IV, and fruit length (14.27 cm) and fruit yield per plant (319.33 g) was reported in cluster II, while maximum average fruit weight (15.63 g) was found in cluster V. It reveals that, if a breeding program is aimed to obtain the desired number of seeds per fruit, number of ridges per fruit, fruit length, fruit yield per plant, and average fruit weight, genotypes from these clusters would be selected. During the investigations, the identified clusters revealed crucial values for various factors under study. Among the clusters (I, II, III, IV, V and VI), the diverse genotypes were compared for higher plant height, early flowering, early picking and fruit yield per plant. Our results find support from the recent reports on genetic divergence of okra crop (Kumar *et al.,* 2021; Vaggar *et al.,* 2022; Alemu and Mohammed 2022; Mohammed *et al.,* 2022).

Average distance in intra-cluster varied from 7.47 to 13.42 (Figure 2). However, cluster number (II, III, V and VI) had zero intra-cluster distance (0.00), as these clusters were monogenotypic *viz.,* having a single genotype, while cluster number I (13.42) and cluster number IV (7.47) indicated maximum intra-cluster distance. The average inter-cluster distance ranged from 14.07 to 111.03. The maximum inter-cluster distance reported between cluster number III and VI (111.03) followed by cluster II and VI (90.76), cluster number IV and VI (90.10), cluster number III and V (59.44), cluster number I and VI (48.80), cluster number II and IV (48.75), cluster number IV and V (45.24), cluster number II and V (40.40), cluster number III and IV (37.75), cluster number V and VI (33.34). The minimum inter-cluster distance reported was between cluster number II and III (14.02) followed by cluster number I and II (23.07), cluster number I and V (23.63), cluster number I and III (28.07), and cluster number I and IV (29.70). Similar findings were

reported by Carvalho *et al.* (2022), Alemu and Mohammed (2022), and Mohammed *et al.* (2022) while working on cluster distance for genetic divergence of okra crop.

The contribution of each character to 'overall genetic divergence' is presented in Table 5. Yellow Vein Mosaic Virus (YVMV) incidence (44.67 %) exhibited the highest contribution to the genetic divergence among all the studied traits. This virus is a threat to okra cultivation all over India, the higher percentage of its contribution to the 'overall genetic divergence' could be an opportunity to identify the genotype immunity/resistance to it (Carvalho *et al.,* 2022).

CONCLUSIONS

Present study revealed the detailed genetic divergence for different yield attributing traits in okra genotypes grown in Himalayan foothills. This study presents a strong basis for the selection and evolving of better recombinants for hybridization and quality improvement programmes. Based on the present investigation, it can be concluded that for the character multiple branches per plant, genotypes can be selected from cluster III for the development of hybrids. Similarly, to improve high yield per plant with lowest incidence of yellow vein mosaic virus, genotypes from cluster II are ideal for crossing or their derivatives for further selection. This research bears utility in the form of germplasm conservation and crop improvement for selected indigenous/exotic okra genotypes grown in Himalayan foothills.

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واگرایی ژنتیکی برای صفات مختلف منتسب به عملکرد در ژنوتیپ‌های بامیه [*Abelmoschus Esculentus (L.) Moench*] کشت شده در منطقه کوهپایه‌های هیمالیا

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چکیده

منطقه کوهپایه های هیمالیا درهند سرشار از تنوع ژنتیکی بامیه است که هنوز به دلیل واگرایی ژنتیکی آن مورد بررسی قرار نگرفته است. برای پیش بینی تنوع ژنتیکی این مجموعه از ارقام ناشناخته، واگرایی ژنتیکی بین ۲۵ ژنوتیپ بامیه با استفاده از آماره Mahalanobis D^2 برآورد شد. لاین های بومی و خارجی (exotic)با استفاده از روش‌های توچر(Tocher's methods) در ۶ خوشه دسته بندی شدند. نتایج نشان داد که تعداد بیشتری از

ژنوتیپ ها در خوشه I (۱۹) و خوشه IV (۲) بود ولی خوشه II، III، V و VI تک ژنوتیپی بودند. فاصله درون خوشه ای بالاتری بین خوشه های I (۱۳.۴۲) و IV (۷.۴۷) مشاهده شد، در حالی که، فاصله بین خوشه ای بالاتر بین خوشه های III و VI (۱۱۱.۰۳) مشاهده شد. صفات مربوط به شیوع ویروس موزاییک ورید زرد (YVMV) (۴۴/۶۷ درصد)، بیشترین سهم را در واگرایی ژنتیکی کل داشتند. این پژوهش واگرایی ژنتیکی دقیق را برای صفات مختلف منتسب به عملکرد در بامیه نشان داد. این پژوهش مبنایی قوی برای انتخاب و تکامل نوترکیب‌های بهتر برای هیبریداسیون و برنامه بهبود کیفیت بامیه ارائه می‌کند و در قالب حفاظت از ژرم پلاسم و بهبود محصول برای ژنوتیپ‌های بومی/خارجی منتخب کشت شده در دامنه‌های هیمالیا مفید است.