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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) & IV (7.47), whereas, a higher inter-cluster distance was found between clusters III and VI (111.03). The traits *viz*, YVMV incidence (44.67 %) was 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.

*Key words***:** Okra, Himalayan foothill genotypes, divergence, cluster and recombinants.

1.   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

37 Hindustan region. Okra n=12 has a regular series of polyploides with somatic chromosomal

38 numbers 2n=72,109,120,132, and 144 (Raghuwanshi *et al.,* 2019).

39   The root and stems of the okra plant are commonly used to clarify sugarcane juice for the

40 manufacturing of brown sugar and gur (Makur *et al.,* 2019). It is also utilised in the paper

41 industry due to the high mucilage and crude fibre content of the mature stems and fruits

42 (Haruna *et al.,* 2016). Okra has a great medicinal value and is particularly useful in the

43 treatment of genito-urinary disorders such as haemorrhoids, ulcers, chronic dysentery, and

44 spermatorrhoea (Olaniyan and Omoleyomi, 2013). Okra fruits are rich in high iodine content

45 which helps to prevent goitre (Fayaz *et al.,* 2022). Fresh okra vegetable plays a very crucial

46 role in human nutrition, especially as sources of dietary fiber & vitamins (Prasad *et al.,* 2018).

47 The tender green fruit is the potent source of vitamins A, B_1, B_3, B_6, C, folic acid and essential

48 minerals *viz.*, Ca, K, Mg and P have an important role in human diet (Mkhabela *et al.,* 2022).

49   The development of cultivars against target traits such as fruit yield and pest/disease

50 resistance and their promotion is often a more rewarding and appropriate option for the

51 sustainability of smallholder farmers (Sandeep *et al.,* 2022). This is especially relevant in

52 developing and underdeveloped countries, where farmers often do not have the capability to

53 diagnose suitable preventive measures (Kumar *et al.,* 2010). Yellow vein mosaic disease is the

54 most common biotic stress in okra under natural epiphytic conditions. The wild species are

55 widely acknowledged to be a major reservoir of resistance genes, particularly for yellow vein

56 mosaic disease (Gangopadhyay *et al.,* 2017).

57   The concept of linking phenotypes with genotypes is somewhat basic and ubiquitous in plant

58 breeding, as well as in the history of plant domestication, which was accomplished through the

59 selection of superior plants for agricultural use (Kozak *et al.,* 2011). Improving the varieties

60 with desired traits in terms of fruit size, shape and colour and resistance to biotic stress are

61 also very purposeful in the okras' export market. This characterization and genetic diversity

62 analysis was required against this backdrop. Traditionally, a combination of morphological

63 data and phenotypic traits significantly contributed towards the pattern of total genetic

64 diversity present in the population (Oppong-Sekyere *et al.,* 2011). The genetic distances

65 between the lines, determined by using these traits, can be treated as phenotypic similarities

66 between the lines (Kozak *et al.,* 2011).

67   Genetic diversity refers to the heritable variation within and between groups of populations

68 (Alam *et al.,* 2014). The presence of genetic diversity between the genotypes from different

69 geographic regions is attributed to the selection and exchange of okra germplasm between

2

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 a 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.,* 2017).

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 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). 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 is to put a strong basis for the selection and evolving of better recombinants for hybridization and quality improvement programme in the near future

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103 (Prasad *et al.,* 2018; Mkhabela *et al.,* 2022). This research also aims for germplasm
104 conservation and crop improvement for selected indigenous/exotic genotypes grown in
105 Himalayan foothills.
106
107 **2.   MATERIALS AND METHODS**
108   The research was carried out during academic session 2019-2020, at Dholi Farm, Tirhut
109 College Agriculture, a campus of Dr. Rajendra Prasad Central Agricultural University, Pusa,
110 Samastipur- Bihar. Twenty-five genotypes of okra (Table 1), including both indigenous and
111 exotic lines were selected and sown on 25 Jun 2019 in randomized block design with each line
112 consisting of three replications and last observation was taken on plant height at final harvest
113 on 20 September 2019. All the genotypes were procured from Indian Institute of Vegetable
114 Research (IIVR), Varanasi, Uttar Pradesh-India, through materials transfer agreement (Table
115 1). A nationally adapted okra variety "Kashi Kranti" was also included as a check variety. A
116 standardized crop descriptor for okra genotypes was used to measure the various traits under
117 studies (IBPGR, 1991). The data was recorded from five randomly selected plants for different
118 yield attributing traits. The weather data were collected from Department of Agro
119 Meteorology, Tirhut College Agriculture, a campus of Dr. Rajendra Prasad Central
120 Agricultural University, Pusa, Samastipur-Bihar. The weather data was tabulated in (Table 2).
121 The Enlist of the studied phenotypic traits under present study were mention in (Table 3). The
122 description of studied phenotypic traits were summarized below on the following heads.
123
124 **(A). Plant height (cm)**
125   The measurement of plant height of all five selected and tagged plants in each
126 treatment was done using a meter scale, from ground level to the apex of the plant at the final
127 harvest. The measured value was presented in centimetre.
128
129 **(B). Number of primary branches per plant**
130   Primary branches per plant in each genotype of each plot were counted at the time of
131 final harvesting and the average branches per plant were determined.
132
133 **(C). Days to first flowering**
134   The number of days from seed sowing to the anthesis of the first flower was counted.
135
136
137

4

(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 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). 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.

172 **(L). Fruit yield per plant (g)**

173 The fruit yield per plant of the tagged plants was determined by addition of the total fruit

174 weight of all fruit pickings and is shown in grams per plant.

175 2.1. **Genetic divergence**

176 Genetic diversity was determined by Mahalanobis D^2 statistics based on their phenotypic

177 data (Sruthi *et al.,* 2020; Kumar *et al.,* 2021; Vaggar *et al.,* 2022 and Meena *et al.,* 2021).

178

179 2.2. **Cluster Analysis**

180 The genotypes are grouped into various clusters based on their phenotypic similarity (Table-

181 3). D^2 values and Tocher's method were used for grouping of genotypes into different clusters

182 (Kumawat *et al.,* 2020, Kumar *et al.,* 2021; Vaggar *et al.,* 2022).

183

184 2.3. *Average intra and inter-cluster distance* was used to figure out the summation of

185 distances between different genotypes.

186

187 2.4. *Cluster diagram* using "Dendrogram" is used to exhibit inter and intra cluster

188 distances between different clusters-based values of D^2 statistics helped in drawing a diagram.

189 (Yadav, 2020).

190

191 2.5. **Contribution of individual traits towards total divergence**

192 Among all, the combination of genotypes *i.e.* n (n-1)/2, each trait is ranked based on mean

193 difference, where n is the total number of genotypes. Using these ranks, the following table is

194 prepared to work out the percent contribution of each trait to the total divergence (table.5).

195 Percent Contribution by Xp = Number of times appearing first in ranking by Xp $\times$ 100

196 $\qquad\qquad\qquad\qquad\qquad\qquad\qquad$ n (n-1)/2

197 Where, Xp= individual traits

198 $\qquad$ n= number of genotypes

199

200 2.6. **Statistical analysis**

201 The statistical analysis was carried out using Statistical Analysis System [SAS (9.4)] North

202 Carolina State University- United States America, OPSTAT (Operational Statistics-

203 developed by Department Of Mathematics Statistics, Chaudhary Charan Singh Haryana

204 Agricultural University, Hisar, India) and GRAPES software (General R-shiny based

205 Analysis Platform Empowered by Statistics developed by Department of Agricultural

206 Statistics, College of Agriculture, Vellayani, Kerala Agricultural University- India).

207

208 **1.   RESULTS AND DISCUSSION**

209 The mean performance of morphological traits of different genotypes along with check

210 variety (Kashi Kranti) is tabulated in (Table 4). The genotype SKY/DR/RS-13 (136.33 cm &

211 3.10) and IC- 43742 (133.07cm & 3.08) was reported for significantly higher plant height and

212 number of primary branches per plant than the check value (116.67 cm & 2.30). The

213 genotypes VRO-214 (39.03 days & 45.33 days) were observed significantly at par near the

214 check variety (40.57 days & 47.33 days) with respect to days to first flowering and days to

215 first picking. The genotypes namely IC-218872 (68.67) was observed for maximum number of

216 seeds per fruit and VRO-177 (6.87) was recorded significantly superior for maximum number

217 of ridges per plant over the check variety (48.33 & 5.00). The significantly higher fruit length

218 were reported in EC- 015537 (14.53cm), EC-199367 (14.27cm), and VRO-107 (13.83cm),

219 fruit diameter was recorded higher in IC-43742 (1.81cm) than check variety (11.77 cm & 1.60

220 cm). The minimum YVMV incidence (%) was registered in genotypes EC- 199367 (9.33 %)

221 as compare to check variety (17.33 %). The significantly superior genotypes over check

222 variety, Kashi Kranti (11.22 g, 23.67 and 265.67 g) was recorded in VRO-956 (15.63 g)

223 followed by VRO-214 (13.18 g) and EC-199367 (12.91 g) with respect to average fruit

224 weight, IC-43742 (27.50) and EC-199367 (26.70) with respect to maximum number of fruits

225 per plant, IC-43742 (312.33 g) followed by VRO-214 (320.33 g) and EC- 199367 (319.33 g)

226 for higher fruit yield per plant. In the consideration of per se performance of genotype existed

227 vast range of variation for different morphological traits among genotypes of okra under

228 present investigation indicated the evaluation of these genotypes in above respective

229 morphological traits can be more useful in future breeding programme. The similar type

230 results were also reported by some previous researchers (Vaggar *et al.,* 2022).

231 In general, all the okra genotypes displayed relatively wide ranges of variation for all

232 morphological traits evaluated (Oppong-Sekyere *et al.,* 2011). Higher diverse genotypes

233 within the group of population exhibit better heterotic response (Suri *et al.,* 2022). The D^2

234 analysis method is used to group the genotype based on quantitative traits. The genotypes

235 were grouped in different clusters based on the genetic distance between them.

236 The 'cluster patterns', 'clusters mean', 'intra/inter cluster' and 'contribution percentage'

237 were presented in Tables 5, 6, 7 and 8 respectively. The selected (25) genotypes were assessed

238 for genetic divergence followed by division in 6 groups as per the 'Toucher' method (Table

7

239 2). Cluster I had the maximum genotypes (19) followed by cluster IV (2), whereas, Clusters II,

240 III, V, and VI were monogenotypic, *i.e.* consisting of a single genotype. Our result got the

241 support from similar studies attempted earlier by researchers who worked on okra genetic

242 divergence (Prasad *et al.,* 2016; Alemu and Mohammed 2022; Carvalho *et al.,* 2022, and

243 Mohammed *et al.,* 2022).

244 Cluster means for twelve characters of twenty-five genotypes are presented in (Table 3). It

245 was recorded that the maximum cluster mean value for plant height (133.07cm), number of

246 primary branches per plant (3.10), fruit diameter (1.81 cm) and number of fruits per plant

247 (26.00) was recorded in cluster III. It indicates that if a breeding aim is to obtain long plant

248 height, more number of primary branches per plant, fruit diameter and number of fruits per

249 plant then genotypes from these clusters would be selected. The minimum cluster mean value

250 for days to first flowering (40.33 days), days to first picking (47.33 days), number of seeds per

251 fruit (28.33), fruit diameter (1.46 cm) and YVMV incidence (9.33%) was reported in cluster

252 III, cluster II, cluster VI, cluster VI and cluster II respectively. It indicates that if a breeding

253 program aims to obtain desired days to first flowering, days to first picking, numbers of seeds

254 per fruit, fruit diameter and YVMV incidence then genotypes from these clusters would be

255 selected. The maximum cluster mean value for number of seeds per fruit (63.00) and number

256 of ridges per fruit (6.67) was observed in cluster IV and fruit length (14.27cm) and fruit yield

257 per plant (319.33g) was reported in cluster II and average fruit weight (15.63g) was found in

258 cluster V respectively. It reveals that if a breeding program is aimed to obtain desired number

259 of seeds per fruit, number of ridges per fruit, fruit length, fruit yield per plant and average fruit

260 weight, then genotypes from these clusters would be selected. During the investigations, the

261 identified clusters revealed crucial values for various factors under study. Among the clusters

262 (I, II, III, IV, V & VI), the diverse genotypes were compared for higher plant height, early

263 flowering, early picking & fruit yield per plant. Our results find support from the recent

264 reports on genetic divergence of okra crop (Kumar *et al.,* 2021; Vaggar *et al.,* 2022; Alemu

265 and Mohammed 2022 and Mohammed *et al.,* 2022).

266 Average distance in intra-cluster was varied from 7.47 to 13.42 (Table 4). However, cluster

267 number (II, III, V and VI) had zero intra-cluster distance (0.00) indicated as these clusters

268 were monogenotypic *viz.,* having a single genotype while, cluster number I (13.42) and cluster

269 number IV (7.47) indicated maximum intra-cluster distance. The average inter - cluster

270 distance ranged from 14.07 to 111.03. The maximum inter cluster distance reported between

271 cluster number III and cluster number VI (111.03) followed by cluster II and cluster number

VI (90.76), cluster number IV and cluster number VI (90.10), cluster number III and cluster number V (59.44), cluster number I and cluster number VI (48.80), cluster number II and cluster number IV (48.75), cluster number IV and cluster number V (45.24), cluster number II and cluster number V (40.40), cluster number III and cluster number IV (37.75), cluster number V and cluster number VI (33.34). While, minimum inter- cluster distance reported between cluster number II and cluster number III (14.02) followed by cluster number I and cluster number II (23.07), cluster number I and cluster number V (23.63), cluster number I and cluster number III (28.07) and cluster number I and cluster number 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). YVMV incidence (44.67 %) exhibited the highest contribution to the genetic divergence among all the studied traits. As yellow vein mosaic 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).

2. 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, genotype 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 genotypes grown in Himalayan foothills.

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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-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			

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

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

Month	Temperature (^{0}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

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

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

S. No.	Traits	Sampling date
1.	Plant height	
2.	Number of primary branches per plants	
3.	Days to first flowering	
3.	Days to first picking	
5.	Number of seeds per fruits	25 Jun 2019 to 20 September 2019
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)	

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439 **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

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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

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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

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Table 8. Percent contribution of 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

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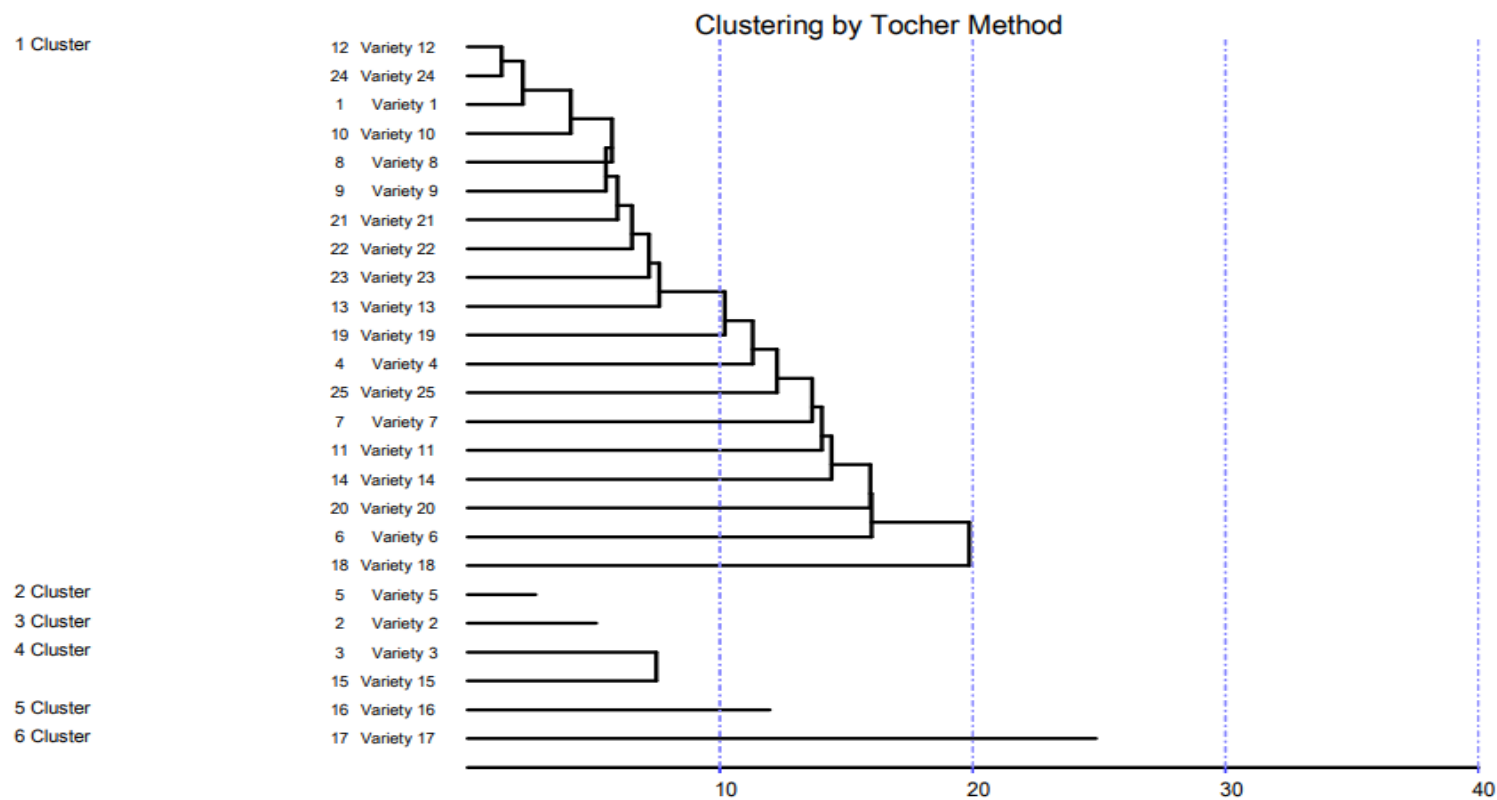
Fig. 1. Clustering pattern of 25 okra genotypes selected for the study.
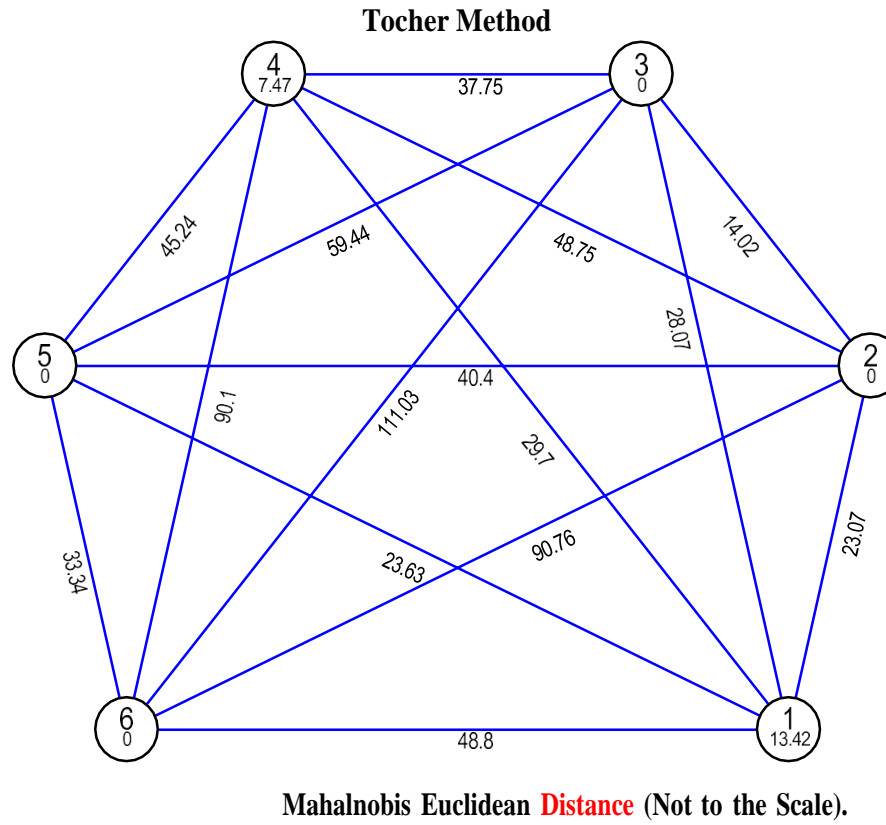
Fig-2. Intra and inter cluster distance (D^2) among six clusters of selected 25 okra genotypes.