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## GENETIC DIVERSITY ANALYSIS IN SPONGE GOURD [*LUFFA CYLINDRICA* (L.) ROEM.] GENOTYPES

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### ABSTRACT

An experiment was conducted to study the genetic diversity in sponge gourd at Department of Horticulture, M.A.R.S., University of Agricultural Sciences, Dharwad (Karnataka) during *Rabi* season of 2020 with 34 sponge gourd genotypes. Based on Mahalanobis D<sup>2</sup> statistics, genotypes were grouped into six clusters. Cluster I included the higher number of genotypes (24), cluster II had 4 genotypes and cluster V and VI had two genotypes each and remaining two clusters (III and IV) were monogenic groups containing single genotype each. Highest inter cluster distance (976.58) was recorded between the cluster cluster VI and cluster II, indicating the genetic makeup of the genotypes belonging to one cluster differed completely from the genotypes those included in another cluster. In hybridization programme, genotypes present in these clusters could be used as parents to obtain promising segregants. Among the different traits, average fruit weight (34.22%) contributed maximum to the diversity followed by number of fruits per vine (18.00%) and fruit yield per vine (12.30%).

**Key words :** Sponge gourd, Genotypes, Genetic diversity, Cluster.

### Introduction

Sponge gourd [*Luffa cylindrica* (Roem.) L.] (2n=2x=26) is one of the minor cucurbitaceous vegetable crops with old world origin in subtropical Asian region particularly India (Swarup, 2006). It is commonly called as smooth luffa, climbing okra, dishcloth gourd and Chinese okra. Some local names of sponge gourd in India are tuppada heeray kayi (Kannada), chikni turai (Hindi), bhol (Assamese), jhinga (Bengali), janhi (Oriya), gisoda (Gujarati), neti beerakaya (Telugu), peechinga (Malayalam) and pirkanga (Tamil) (Bal *et al.*, 2004).

Most of the cucurbitaceous vegetables, including sponge gourd are usually grown in relatively small area for local consumption and hence exact area and production are unknown. Cucurbits share about 5.6 per cent of the total vegetable production of India (Rai and Rai, 2006). According to FAO estimate, cucurbits are cultivated in an area of about 7.21 lakh ha having annual production of 12.87 lakh tonnes. The productivity of this

crop is 10.52 tonnes per hectare (Anonymous, 2022). The main cucurbits producing countries are China, Korea, India, Japan, Nepal and Central America. In India, major cucurbits growing states are Uttar Pradesh, Punjab, Bihar, Jharkhand, Gujarat, Rajasthan, Haryana and Karnataka.

Sponge gourd is commonly grown for its tender fruits for vegetable purpose. It is a highly nutritive vegetable and it contains moisture of 93.2 g, protein 1.2 g, fat 0.20 g, carbohydrate 2.9 g, vitamins (thiamin 0.02 mg, riboflavin 0.06 mg, niacin 0.4 mg and carotene 120 mg), minerals (calcium 36 mg, phosphorus 19 mg and ferrous 1.1 mg) and fibers 0.20 g per 100 g of edible portion. Sponge gourd fruits contain more protein and carotene than ridge gourd (Gopalan *et al.*, 1999). The mature fruit eases blood circulation and provides relief for rheumatic and arthritic sufferers. It has been found that the consumption of sponge gourd supplies antioxidants like luffin A and luffin B, which are important to human health.

Genetic diversity has been regarded as major factor

in choosing parents for hybridization to achieve high yielding and superior progenies. The  $D^2$  analysis helps to estimate the genetic distance among the lines and also to find traits contributing for genetic divergence. This information can be taken up to compute the genetic divergence so as to identify genetically diverse parents for further breeding programme.

### Materials and Methods

The present investigation was conducted at Olericulture Unit, Department of Horticulture, M.A.R.S., University of Agricultural Sciences, Dharwad (Karnataka) during *Rabi*, 2020. Thirty-four genotypes were evaluated in a randomized block design with two replications. These genotypes were collected from Kittur Rani Channamma College of Horticulture (KRCCH), Arabhavi, Hidakal Research Station (HRES), Hidakal, College of Horticulture (CoH), Mandur, Indian Institute of Vegetable Research (IIVR), Varanasi, Indian Agricultural Research Institute (IARI), New Delhi, local cultivar (Karnataka) and some private varieties (Table 1). All the recommended package of practices was followed for crop raising. Observations on growth and yield parameters were recorded at different stages of crop growth. The genetic divergence was estimated using the  $D^2$  statistics of Mahalanobis (Mahalanobis, 1936) and the population was grouped into cluster by following methods suggested by Tocher's (Rao, 1952). The intra and intercluster distances were calculated formula described by Singh and Choudhary (1977).

## Results and Discussion

### Cluster composition and distance

The analysis of variance indicates significant variation among 34 sponge gourd genotypes for all the characters studied. This indicated that ample variability existed among the genotypes and the analysis of genetic divergence is reasonable. All the genotypes were grouped into six clusters by adopting Tocher's method and it is presented in Table 2. From cluster composition, it reveals cluster I included the maximum number of genotypes (24), cluster II with four genotypes, cluster III and cluster IV had single genotype each, cluster V and VI had two genotypes each.

The intra and inter cluster distance values among six clusters are presented in Table 3 and Fig. 1. The average cluster distance value ranges from 0 to 976.58. The maximum intra cluster distance was recorded in cluster VI (110.91), while the minimum intra cluster distance was reported in clusters III and IV. While, inter cluster distance was lowest between cluster III and cluster I (113.77), showing the genotypes of these cluster were genetically closer. Inter cluster distance was highest between cluster VI and cluster II (976.58), indicating the genetic makeup of the genotypes belonging to one cluster differed completely from the genotypes those included in another cluster. In hybridization programme, genotypes present in these clusters could be used as parents to develop new combinations and further isolate a good recombinant from the segregating population. These

**Table 1 :** List of genotypes used for the experiment.

S. no.	Variety	Source	S. no.	Variety	Source
1	Arabhavi Local	Local cultivar	18	Hunasi Local	Local cultivar
2	COHM-1	CoH, Mandur	19	Kashi Divya	IIVR, Varanasi
3	COHM-2	CoH, Mandur	20	Kashi Shreya	IIVR, Varanasi
4	Dharwad Local	Local cultivar	21	KRCCH-1	KRCCH, Arabhavi
5	HUB-1	HRES, Hidakal	22	KRCCH-2	KRCCH, Arabhavi
6	HUB-2	HRES, Hidakal	23	PSK-1	Private variety
7	HUB-3	HRES, Hidakal	24	PSK-2	Private variety
8	HUB-4	HRES, Hidakal	25	Pusa Chikni (Check)	IARI, New Delhi
9	HUB-5	HRES, Hidakal	26	Pusa Sneha	IARI, New Delhi
10	HUB-6	HRES, Hidakal	27	SG-1	KRCCH, Arabhavi
11	HUB-8	HRES, Hidakal	28	SG-2	KRCCH, Arabhavi
12	HUB-9	HRES, Hidakal	29	SG-4	KRCCH, Arabhavi
13	HUB-10	HRES, Hidakal	30	SG-5	KRCCH, Arabhavi
14	HUB-11	HRES, Hidakal	31	SG-6	KRCCH, Arabhavi
15	HUB-13	HRES, Hidakal	32	Sirsi Local	Local cultivar
16	HUB-14	HRES, Hidakal	33	SRO-3	Private variety
17	HUB-15	HRES, Hidakal	34	Vijaypur Local	Local cultivar

**Table 2 :** Cluster composition of sponge gourd genotypes.

Cluster No.	No. of genotypes	List of genotypes
I.	24	HUB-6, PSK-2, COHM-1, SG-5, KRCCH-2, HUB-2, HUB-5, Kashi Divya, HUB-13, Arbhavi Local, SG-1, SG-4, Pusa Sneha, Dharwad Local, Pusa Chikni, HUB-10, COHM-2, Kashi Shreya, SG-2, SG-6, HUB-14, PSK-1, HUB-9 and HUB-15
II.	4	HUB-1, HUB-3, KRCCH-1 and HUB-8
III.	1	HUB-4
IV.	1	HUB-11
V.	2	SRO-3 and Vijayapur Local
VI.	2	Hunasi Local and Sirsi Local

**Table 3 :** Intra (diagonal) and inter cluster distances for six clusters in sponge gourd genotypes.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	53.87	190.83	113.77	197.23	380.77	498.81
Cluster II		59.74	259.51	425.24	872.95	976.58
Cluster III			0	350.48	430.48	754.99
Cluster IV				0	328.97	252.31
Cluster V					79.55	225.53
Cluster VI						110.91

**Table 4 :** Mean performance of the clusters for different characters in sponge gourd genotypes.

Characters Clusters	X <sub>1</sub>	X <sub>2</sub>	X <sub>3</sub>	X <sub>4</sub>	X <sub>5</sub>	X <sub>6</sub>	X <sub>7</sub>	X <sub>8</sub>	X <sub>9</sub>	X <sub>10</sub>	X <sub>11</sub>	X <sub>12</sub>	X <sub>13</sub>	X <sub>14</sub>
	Cluster I	3.64	47.30	4.62	45.71	14.29	6.57	16.39	14.74	55.44	100.65	11.28	68.81	1.45
Cluster II	4.88	66.91	5.18	41.86	12.96	5.87	21.42	11.97	50.05	106.61	17.05	80.16	2.10	123.12
Cluster III	3.77	47.50	4.58	45.77	17.53	7.90	16.17	8.36	53.91	103.20	11.03	68.49	1.56	75.39
Cluster IV	2.33	35.50	3.12	45.05	15.58	6.97	8.96	34.53	64.55	94.45	6.00	67.69	0.69	65.08
Cluster V	2.01	26.46	2.58	50.09	16.29	9.14	7.49	11.24	66.49	98.00	3.48	46.66	0.32	89.05
Cluster VI	2.00	27.49	2.25	53.77	17.27	7.32	6.30	30.09	69.64	86.75	3.47	55.61	0.40	118.14

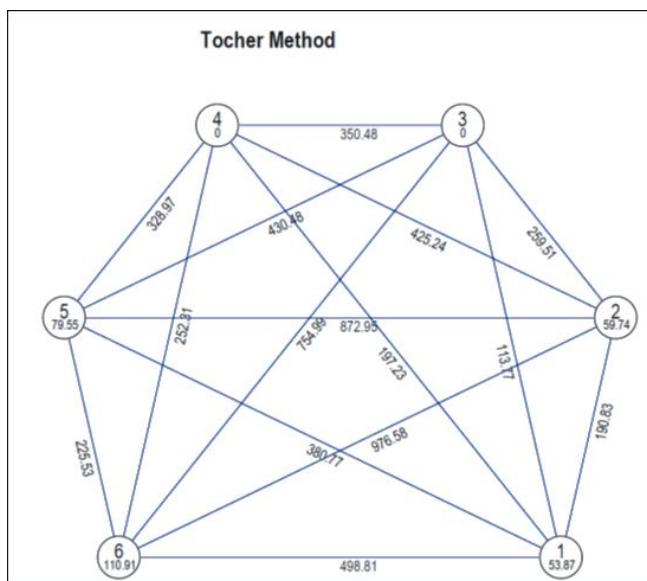
**Note:** X<sub>1</sub>: Vine length (m), X<sub>2</sub>: Number of leaves per vine, X<sub>3</sub>: Number of branches per vine, X<sub>4</sub>: Days to first female flower appearance, X<sub>5</sub>: Node at which first female flower appeared, X<sub>6</sub>: Node at which first male flower appeared, X<sub>7</sub>: Number of female flowers per vine, X<sub>8</sub>: Sex ratio, X<sub>9</sub>: Days to first harvest, X<sub>10</sub>: Days to last harvest, X<sub>11</sub>: Number of fruits per vine, X<sub>12</sub>: Fruit set per cent (%), X<sub>13</sub>: Fruit yield per vine (kg/plant) and X<sub>14</sub>: Average fruit weight (g).

results reflect the findings of previous researchers Debata *et al.* (2017), Saklesh (2016), Khatoon *et al.* (2017), Kumari *et al.* (2017), Methela *et al.* (2018), Pradhan *et al.* (2018), Suresh Kumar *et al.* (2019) and Veerendra *et al.* (2020).

#### Cluster means for different characters

The cluster means for different parameters are given in Table 4 and observed the significant differences between clusters for almost all the parameters studied. Maximum vine length (4.88 m) was recorded in cluster II and minimum (2.00 m) was reported in cluster VI. Highest number of leaves per vine (66.91) was recorded in cluster II and lowest (26.46) was reported in cluster

V. Maximum number of branches per vine (5.18) was reported in cluster II and minimum (2.25) in cluster VI. Less days to first female flower appearance (41.86) showed in cluster II and more days (53.77) was reported in cluster VI. The lowest cluster mean value of node at which first female flower appeared was reported in genotypes of cluster II with mean value of 12.96 and maximum value of 17.53 recorded for genotypes in cluster III. The genotypes found in cluster II had lowest node at which first male flower appeared (5.87), while cluster V had highest node at which first male flower appeared (9.14). The maximum cluster mean value of number of female flowers per vine was reported in genotypes of



**Fig. 1 :** Intra and inter-cluster ( $D^2$ ) values of six clusters of sponge gourd genotypes.

**Table 5 :** Contribution of different characters to diversity in sponge gourd genotypes.

S. no.	Source	Times ranked 1 <sup>st</sup>	Contribution (%)
1	Vine length	3	0.53 %
2	Number of leaves per vine	2	0.36 %
3	Number of branches per vine	5	0.89 %
4	Days to first female flower appearance	1	0.18 %
5	Node at which first female flower appeared	6	1.07 %
6	Node at which first male flower appeared	1	0.18 %
7	Number of female flowers per vine	63	11.23 %
8	Sex ratio	37	6.60 %
9	Days to first harvest	9	1.60 %
10	Days to last harvest	14	2.50 %
11	Number of fruits per vine	101	18.00 %
12	Fruit set per cent	58	10.34 %
13	Fruit yield per vine	69	12.30 %
14	Average fruit weight	192	34.22 %

cluster II with mean value of 21.42 and minimum value of 6.30 recorded for genotypes in cluster VI. Narrow sex ratio (8.36) was reported in cluster III and wider (34.53) was reported in cluster IV.

Cluster II recorded fewer days to first harvest with mean value of 50.05 and more days to first harvest with mean value of 69.64 in cluster VI. Cluster II recorded

highest days to last harvest with mean value of 106.61 and lowest days to first harvest with mean value of 86.75 in cluster VI. The genotypes found in cluster II had maximum number of fruits per vine (17.05), while cluster VI had minimum number of fruits per vine (3.47). The highest cluster mean value of fruit set per cent was reported in genotypes of cluster II with mean value of 80.16% and minimum value of 46.66% recorded for genotypes in cluster V. The genotypes found in cluster II had maximum fruit yield per vine (2.10 kg/plant), while cluster V had minimum (0.32 kg/plant). The highest cluster mean value of average fruit weight was reported in genotype of cluster II with mean value of 123.12 g and minimum value of 65.08 g recorded for genotypes in cluster IV.

Among the clusters, cluster II was diverse with higher values for vine length, number of leaves per vine, number of female flowers per vine, days to last harvest, number of fruits per vine, fruit set per cent, fruit yield per vine, average fruit weight and recorded lower desirable values for days to female flower appearance, node at which first female flower appeared, node at which first male flower appeared and days to first harvest. This research indicated the existence of considerable genetic divergence among the 34 genotypes. Thus, the genotypes of desirable mean performance (for required parameters under consideration from these clusters) are involved in hybridization as better parents for further improvement in sponge gourd (Khatoon *et al.*, 2017). The findings are in line with earlier findings of Waikhom and Kandasamy (2020) and Jitendra *et al.* (2021).

#### Relative contribution of each character towards diversity

The number of times, each character appeared in first rank and its corresponding per cent contribution towards diversity is depicted in Table 5. Among all the characters, average fruit weight recorded higher (34.22%) contribution to the diversity by taking first rank with 192 times out of 561 combinations followed by contribution of number of fruits per vine (18.00%) with 101 times; fruit yield per vine (12.30%) with 69 times; number of female flowers per vine (11.23%) with 63 times; fruit set per cent (10.34%) with 58 times; sex ratio (6.60%) with 37 times; days to last harvest (2.50%) with 14 times; days to first harvest (1.60%) with 9 times; node at which first female flower appeared (1.07%) with 6 times; number of branches per vine (0.89%) with 5 times; vine

length (0.53%) with 3 times; number of leaves per vine (0.36%) with 2 times; days to first female flower appearance and node at which first male flower appeared (0.18%) had contributed one time each to the genetic divergence.

The characters contributed towards diversity from the study are in conformity with Saklesh (2016) for node at which first female flower appeared, fruit cent per cent and fruit yield per vine; Chetariya and Vaddoria (2017) for vine length and sex ratio; Sampath *et al.* (2019) for fruit yield per vine and number of fruits per vine; Singh *et al.* (2019) for node number to anthesis first staminate flower; Suresh Kumar *et al.* (2019) for fruit yield and fruit weight; Rashid (2020) for fruit weight; Ahmad *et al.* (2021) for days to first harvest and average fruit weight and Shilpashree *et al.* (2022) for number of branches per vine.

### Conclusion

Thirty four genotypes showed significant diversity and were classified into six clusters. Cluster I included the higher number of genotypes (24), cluster II had 4 genotypes and cluster V and VI had two genotypes each and remaining two clusters (III and IV) were monogenic groups containing single genotype each. The higher inter cluster distance between the cluster VI and cluster II was recorded by Mahalanobis's method of clustering. Therefore, genotypes from these cluster *viz.*, Hunasi Local and Sirsi Local (cluster VI) and HUB-1, HUB-3, KRCCH-1 and HUB-8 (cluster II) are suggested to include in hybridization activities for obtaining superior recombinants. The characters *viz.*, average fruit weight, number of fruits per vine, fruit yield per vine, number of female flowers per vine and fruit set per cent contributed highest towards diversity.

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