*Indian Journal of Agricultural Sciences* **93** (4): 447–451, April 2023/Short Communication
https://doi.org/10.56093/ijas.v93i4.132502

# Genetic diversity analysis in sponge gourd (*Luffa aegyptiaca*)

KOUSTHUBHA V P[1]*, ANITHA P[1], PRADEEP KUMAR T[1], FLEMINE XAVIER[1] and BEENA V I[1]

*College of agriculture, Vellanikkara, Kerala Agricultural University, Thrissur, Kerala 680 656, India*

Received: 21 January 2023; Accepted: 21 March 2023

**Keywords**: Genetic diversity, Heritability, Sponge gourd, Variability

Minor cucurbit landraces need to be extensively collected, conserved and evaluated in order to prevent genetic erosion and discover novel sources of resistance against important biotic and abiotic stresses. Luffa [*Luffa aegyptiaca* Mill] commonly called as sponge gourd, bath sponge or dish cloth gourd, loofa, vegetable sponge, belongs to the family Cucurbitaceae with chromosomes 2n=26. It is an annual summer season vegetable which requires warm summer temperatures. Potential applications of this crop may literally be seen everywhere in the fields including agriculture, medicine, science, engineering, biotechnology however, its cultivation is restricted to a limited areas of Punjab, Bihar, Uttar Pradesh, Delhi, Gujarat, Rajasthan, Haryana and Jharkhand. Thus, there is a huge scope to increase its cultivation to non-conventional areas. Since, it is an underutilized vegetable in Kerala, it is very important to have knowledge on genetic diversity of the crop in formulating crop improvement programme.

The study was carried out at the Department of Vegetable Science, College of Agriculture, Vellanikkara, Kerala Agricultural University, Thrissur, (latitude of 9.62°N and 76.69° E longitude, altitude of 10.78 m amsl), Kerala during February–June 2022 in randomized complete block design with 3 replications. All crop management practices were carried out in accordance with "Package of Practices Recommendations for Crops (2016)" by Kerala Agricultural University (KAU). Twenty sponge gourd genotypes (Table 1) were collected from different ICAR institutes and used in the present study.

*Statistical analysis*: Data on morphological, yield, its components and biochemical traits were subjected to analysis of variance (Panse and Sukhatme 1984), Coefficients of variation, (Burton and de Vane (1953), heritability and genetic advance (Johnson *et al.* 1955) and diversity analysis (Mahalanobis 1928). Biochemical characters like calcium, iron and fibre content were estimated in accordance with Sadasivam and Manickam (1992).

Significant differences existed among 20 sponge gourd genotypes for all the characters studied (Table 2). In general, phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the traits, which showed that environmental effects had more influence on these characters. Fruit yield per plant, fibre content, average fruit weight, node number of first staminate flower, number of primary branches per plant, number of fruits per plant, fruit yield per plant, calcium content, iron content, showed highest magnitude of variability among all the characters. Hence, existence of a broad genetic base for these traits was confirmed, which would be helpful in further

Table 1 Source of sponge gourd genotypes

| Genotype | Source |
|---|---|
| IC-320257 | NBPGR, New Delhi |
| IC-343168 | NBPGR, New Delhi |
| IC-343160 | NBPGR, New Delhi |
| IC-332319 | NBPGR, New Delhi |
| IC-334305 | NBPGR, New Delhi |
| IC-320257 | NBPGR, New Delhi |
| IC-398587 | NBPGR, New Delhi |
| IC-398579 | NBPGR, New Delhi |
| IC-284881 | NBPGR, New Delhi |
| IC-284946 | NBPGR, New Delhi |
| IC-284917 | NBPGR, New Delhi |
| IC-353344 | NBPGR, New Delhi |
| IC-312981 | NBPGR, New Delhi |
| IC-313018 | NBPGR, New Delhi |
| IC-312993 | NBPGR, New Delhi |
| IC-312949 | NBPGR, New Delhi |
| IC-343162 | NBPGR, New Delhi |
| IC-433702 | NBPGR, New Delhi |
| Kashi Shreya | IIVR, Varanasi |
| Local collection | Malappuram, Kerala |

---

[1]College of Agriculture, Vellanikkara, Kerala Agricultural University, Thrissur, Kerala. *Corresponding author email: kousthubha-2020-12-025@student.kau.in

crop improvement through selection. Singh *et al.* (2009), Samaida (2010), Khule *et al.* (2011), Singh *et al.* (2017), Abhijith *et al.* (2018), Kumar *et al.* (2019), Singh *et al.* (2019a), Kumar *et al.* (2020) also reported similar findings.

Magnitude of variability was moderate for node number of first pistillate flower, days to first marketable fruit harvest, fruit length, rind thickness, average fruit weight, total soluble solids and shelf life which confirmed the existence of additive and non-additive gene effects. Therefore, crop improvement for these traits could be achieved by selection, hybridization followed by selection. The current results are in accordance with reports of Samaida *et al.* (2010), Khule *et al.* (2011), Dubey *et al.* (2013), Kumar *et al.* (2013), Kumar *et al.* (2019), Singh *et al.* (2019b) and Som *et al.* (2020).

Magnitude of variability was low for days to first staminate flower, days to first pistillate flower and fruit girth which indicated the narrow genetic base hence, variability must be generated for further improvement. Similar findings were reported by Khule *et al.* (2011), Dubey *et al.* (2013), Kumar *et al.* (2013) and Som *et al.* (2020).

The heritability and genetic advance estimates were categorized [(0–30% = low; 31–60% = moderate; above 60% = high) and (0–10% = low, 10–20% = moderate and above 20% = high)] respectively (Johnson *et al*. 1955). High heritability (>60%) combined with high genetic advance as per cent of mean (>20%) was found in node number to first staminate flower, node number to first pistillate flower, number of primary branches per plant, days to

Table 2 Estimates of variance, heritability and genetic advance as percentage of mean for yield and biochemical traits in sponge gourd

| Character | Range | Mean | GV | PV | EV | CV (%) | GCV | PCV | $h^2$ | GAM% |
|---|---|---|---|---|---|---|---|---|---|---|
| Days to first staminate flower | 39.21-50.33 | 43.67 | 10.24 | 12.44 | 2.20 | 3.39 | 7.32 | 8.07 | 82.3 | 13.69 |
| Days to first pistillate flower | 39.10-52.33 | 44.36 | 16.38 | 20.07 | 3.68 | 4.32 | 9.12 | 10.09 | 81.6 | 16.98 |
| Node number of first staminate flower | 4.33-14.00 | 7.91 | 10.87 | 11.32 | 0.44 | 8.43 | 41.66 | 42.50 | 96.1 | 84.11 |
| Node number of first pistillate flower | 11.66-21.00 | 15.03 | 4.67 | 5.80 | 1.12 | 7.05 | 14.38 | 16.02 | 80.6 | 26.60 |
| Internodal length during flowering | 11.63-16.53 | 14.12 | 1.18 | 4.28 | 3.10 | 12.46 | 7.71 | 14.65 | 27.7 | 8.37 |
| Number of primary branches per plant | 3.33-8.66 | 5.83 | 1.91 | 2.65 | 0.74 | 14.79 | 23.69 | 27.93 | 71.9 | 41.39 |
| Days to first marketable fruit harvest | 44.66-67.00 | 50.93 | 34.18 | 40.28 | 6.09 | 4.84 | 11.47 | 12.46 | 84.9 | 21.78 |
| Fruit length (cm) | 19.80-38.80 | 31.82 | 21.42 | 27.92 | 6.49 | 8.00 | 14.54 | 16.60 | 76.7 | 26.24 |
| Fruit girth (cm) | 5.24-6.22 | 5.68 | 0.03 | 0.14 | 0.11 | 5.83 | 3.47 | 6.79 | 26.2 | 3.66 |
| Rind thickness (mm) | 3.13-5.50 | 3.97 | 0.40 | 0.44 | 0.04 | 5.31 | 15.89 | 16.78 | 89.7 | 31.01 |
| Average fruit weight (g) | 233.33-393.00 | 310.33 | 1896.97 | 2438.11 | 541.10 | 7.40 | 14.03 | 15.91 | 77.8 | 25.50 |
| Number of fruits per plant | 3.66-9.66 | 6.93 | 3.18 | 3.53 | 0.35 | 8.58 | 25.71 | 27.11 | 90.0 | 50.25 |
| Fruit yield per plant (g) | 908.33-3428.22 | 2141.08 | 556845.56 | 581622.00 | 24776.43 | 7.35 | 34.84 | 35.61 | 95.7 | 70.24 |
| Calcium (mg/100 g) | 3.26-13.64 | 7.95 | 8.71 | 8.76 | 0.04 | 2.78 | 37.12 | 37.23 | 99.4 | 76.26 |
| Iron (mg/100 g) | 0.46-1.71 | 0.73 | 0.06 | 0.06 | 0.00 | 7.48 | 34.28 | 35.08 | 95.5 | 68.99 |
| Fibre (mg/100 g) | 190.66-575.66 | 284.5 | 0.01 | 0.01 | 0.00 | 0.00 | 33.95 | 33.95 | 100 | 69.95 |
| Total soluble solids (°Brix) | 2.80-5.00 | 3.48 | 0.30 | 0.31 | 0.00 | 2.03 | 15.88 | 16.01 | 98.4 | 32.46 |
| Shelf life | 6.00-10.66 | 8.15 | 1.84 | 2.67 | 0.83 | 11.18 | 16.66 | 20.07 | 69.0 | 28.51 |

GV, Genotypic variance; PV, Phenotypic Variance; EV, Environmental Variance; CV%, Coefficient of variance; GCV, Genotypic coefficient of variation; PCV, Phenotypic coefficient of variation; $h^2$, heritability in broad sense; GAM, Genetic advance as percentage of mean.

first marketable fruit harvest, fruit length, rind thickness, average fruit weight, number of fruits per plant, fruit yield per plant, calcium, iron, fibre content, total soluble solids and shelf life which indicated that these traits are under the influence of additive gene action and selection could be relied upon for improvement of these traits. The results were in accordance with the findings of Khule *et al.* (2011), Pandey *et al.* (2012), Abhijith *et al.* (2018), Kumar *et al.* (2019), Singh *et al.* (2019a), Kumar *et al.* (2020) and Som *et al.* (2020).

High heritability with moderate genetic advance (10–20%) was evident in days to the first staminate flower and days to the first pistillate flower which showed that these characters are governed by non-additive gene action and the influence of the environment is also high. These results were in confirmation with Khule *et al.* (2011), Kumar *et al.* (2013) and Singh *et al.* (2017).

Low heritability (<30%) accompanied with low genetic advance (<10%) was observed in internodal length during flowering and fruit girth. Therefore, these characters are governed by non-additive gene action and direct selection is not beneficial. Similar result was also reported by Singh *et al.* (2019b) for internodal length during flowering.

Genetic divergence analysis enables us to evaluate the similar and divergent genotypes for use as parents in breeding programmes. Based on Mahalanobis $D^2$ statistics, 20 sponge gourd genotypes were grouped into 7 clusters. Cluster VII had five genotypes (IC-398579, IC-353344, IC-312981, IC-433702, Local collection) cluster VI had four genotypes (IC-398587, IC-343162, Kashi Shreya, IC-284869). Cluster I (IC-320257, IC-343168, IC-334305) and III (IC-343160, IC-332319, IC-312949) had three genotypes each. There were two genotypes in each of clusters IV (IC-284917, IC-313018) and V (IC-284881, IC-312993) and one genotype in cluster II (IC-284946). Intra cluster distance was maximum in cluster VII ($D^2$ = 399.47). Therefore,

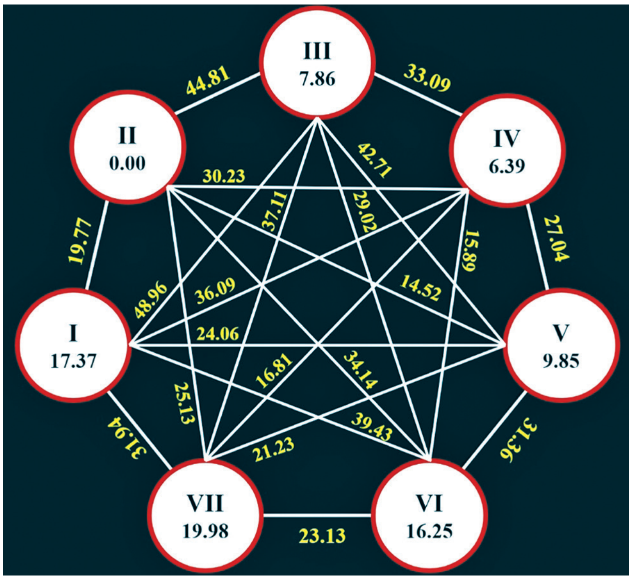

Fig 1 Cluster diagram showing inter and intra cluster distances using D value.

Table 3 Cluster wise performance of characters of sponge gourd

| Character / Cluster | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I | 48.96 | 51.40 | 13.77 | 17.00 | 12.73 | 4.00 | 61.66 | 28.22 | 5.60 | 4.17 | 258.44 | 4.51 | 1009.44 | 7.15 | 0.65 | 360 | 3.35 | 7.99 |
| II | 46.10 | 48.10 | 7.66 | 21.00 | 16.40 | 4.66 | 55.33 | 21.66 | 6.05 | 5.36 | 244.66 | 5.64 | 1400.00 | 13.64 | 0.75 | 250 | 2.80 | 6.00 |
| III | 42.36 | 41.29 | 5.22 | 13.55 | 14.17 | 8.00 | 46.66 | 36.15 | 5.71 | 3.22 | 359.55 | 9.37 | 3405.18 | 8.69 | 0.79 | 300 | 3.63 | 7.88 |
| IV | 41.10 | 41.71 | 8.49 | 12.83 | 15.83 | 5.66 | 47.83 | 33.66 | 5.35 | 4.08 | 313.83 | 7.17 | 2311.08 | 8.57 | 0.59 | 270 | 3.25 | 7.83 |
| V | 41.21 | 42.33 | 7.16 | 14.00 | 15.30 | 4.66 | 47.33 | 34.66 | 5.66 | 4.58 | 351.66 | 4.93 | 1580.55 | 4.99 | 0.59 | 310 | 3.75 | 9.66 |
| VI | 44.58 | 45.33 | 8.41 | 15.16 | 13.09 | 6.41 | 50.41 | 33.85 | 5.79 | 3.94 | 316.58 | 8.16 | 2563.77 | 7.44 | 0.98 | 220 | 2.98 | 8.83 |
| VII | 42.08 | 42.32 | 5.73 | 14.73 | 14.16 | 5.93 | 49.26 | 29.92 | 5.67 | 3.77 | 302.13 | 6.90 | 2028.75 | 8.18 | 0.63 | 260 | 3.98 | 7.79 |

1, Days to anthesis of first staminate flower; 2, Days to anthesis of first pistillate flower; 3, Node number of first staminate flower; 4, Node number of first pistillate flower; 5, Internodal length during flowering (cm); 6, Number of primary branches per plant; 7, Days to first marketable fruit harvest; 8, Fruit length(cm); 9, Fruit girth(cm); 10, Rind thickness (mm); 11, Average fruit weight (g); 12, Number of fruits per plant; 13, Fruit yield per plant (g); 14, Ca content in fruit (mg/100 g); 15, Fe content in fruit (mg/100 g); 16, Fibre content (mg/100 g); 17, Total soluble solids (∘Brix); 18, Shelf life.

greater heterogeneity existed among the genotypes in this cluster. Intra cluster distance was minimum in cluster IV ($D^2$ =40.86) which meant maximum homogeneity existed among the genotypes in this cluster. Inter cluster distance was maximum between cluster I and III ($D^2$ = 2397.99). This indicated that superior hybrids could be obtained by hybridization among the genotypes present in these clusters. Minimum inter cluster distance was recorded between cluster II and V ($D^2$ = 252.77) which indicated low genetic divergence among the genotypes of these clusters. Intra and inter cluster distances are shown in the Fig 1.

Cluster wise means of important characters is presented in the Table 3.The highest mean for days to first staminate flower, days to first pistillate flower, node number to first staminate flower and fibre content was observed in cluster I. The lowest mean days to first staminate flower, days to anthesis of first pistillate flower and node number to first staminate flower was observed in cluster III indicating earliness. Node number to first pistillate flower, internodal length during flowering, days to first marketable fruit harvest, fruit girth, rind thickness and calcium content were highest in cluster II. Number of primary branches per plant, fruit length, average fruit weight, number of fruits per plant, fruit yield per plant were highest in cluster III which indicated that genotypes in this cluster were high yielding. Shelf life was highest in cluster V. Iron content was highest in cluster VI whereas, total soluble solids was highest in cluster VII. Similar results were reported by Singh *et al*. (2019b) and Shilpashree *et al.* (2022).

Sponge gourd is a versatile vegetable having potential applications in diverse industries. However, it is an under exploited vegetable in Kerala. Knowledge on yield, its component characters along with important biochemical characters are most valued pre-requisite before embarking upon on a crop improvement programme. High estimates of GCV and PCV were observed for most of the characters which confirmed the existence of a broad genetic base and would be helpful in further selection for crop improvement. Analysis of genetic diversity showed that inter cluster distance was maximum between cluster I and III. Therefore, for exploitation of heterosis, genotypes should be selected from these clusters. The present investigation showed genotypes IC-343160, IC-332319 and IC-312949 as high yielders.

## SUMMARY

Sponge gourd is versatile summer vegetable having potential applications across many sectors. Twenty sponge gourd genotypes were studied at the Department of Vegetable Science, College of Agriculture, Vellanikkara, Kerala Agricultural University, Thrissur, Kerala for the study of variability in morphological, yield and biochemical traits. Significant difference existed among the genotypes for all the characters under study. In general, Phenotypic Coefficient of Variation (PCV) was higher than Genotypic Coefficient of Variation (GCV) for all the traits evaluated, which indicated the influence of environment on these traits. High estimates of PCV and GCV were recorded for node number of the first staminate flower, number of primary branches per plant, number of fruits per plant, fruit yield per plant, calcium, iron and fibre content. High heritability coupled with high genetic advance as a per cent of the mean were evident in most of the morphological and biochemical traits which suggested the influence of additive gene action for controlling these traits. Genotypes IC-343160, IC-332319 and IC-312949 were high yielders. The sponge gourd genotypes were grouped into seven clusters based on Mahalanobis $D^2$ statistics. Cluster VII had the highest number of genotypes (5) followed by cluster VI (4), and intra cluster distance was maximum in cluster VII. Inter cluster distance was maximum between cluster I and III. Therefore, for exploitation of heterosis, genotypes should be selected from cluster I and cluster III.

## REFERENCES

Abhijeet S K, Yadav N P, Singh V B and Mishra S K. 2018. Genetic variability studies on sponge gourd [*Luffa cylindrical* (L.) Roem.]. *International Journal of Agriculture Environment and Biotechnology* **11**: 941–45.

Burton G W and Devane E H. 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal* **45**: 578–81.

Dubey R K, Singh V and Upadhyay G. 2013. Genetic variability and inter-relationship among some ridgegourd (*Luffa acutangula* L.) accessions under foot hills of Arunachal Pradesh. *Progressive Horticulture* **45**(1): 191–97.

Johnson H W, Robinson H E and Comstock R E. 1955. Estimate of genetic and environmental variability in soybean. *Agronomy Journal* 47: 314–18.

Khule A A, Tikka S B S, Jadhav D J and Kajale D B. 2011. Genetic variability and heritability studies in local collections of sponge gourd (*Luffa cylindrical* Roem). *Asian Journal Bio Science* **6**(1): 119–20.

Kumar J S, Pandit M K and Pathy T L. 2019. Genetic variability, diversity and character association in sponge gourd [*Luffa cylindrica* (Roem.) L.]. *International Journal Current Microbiology and Applied Science* **8**(3): 278–90.

Kumar V, Singh V B, Yadav G C and Maurya D. 2020. Evaluation of genetic variability, heritability and genetic advance in sponge gourd (*Luffa cylindrica* L. Roem.) for various quantitative traits. *International Journal of Chemical Science* **8**(1): 2099–2101.

Kumar R, Ameta K D, Dubey R B and Pareek S. 2013. Genetic variability, correlation and path analysis in sponge gourd (*Luffa cylindrical* Roem.). *African Journal of Biotechnology* **12**(6): 539–43.

Mahalanobis P C. 1928. A statistical study at Chinese head measurements. *Journal of Asiatic Society Bengal* **25**: 301–07.

Panse V G and Sukhatme P V. 1984. *Statistical Methods for Agricultural Workers*. Indian Council of Agricultural Research, New Delhi.

Pandey V, Singh V B and Singh M K. 2012. Selection parameters in sponge gourd (*Luffa cylindrical* Roem.) for yield and yield related component traits. *Environment and Ecology* **30**(2): 412–14.

Sadasivam S and Manickam A. 1992. *Biochemical Methods*, pp. 250. New Age International Publishers, New Delhi.

Samaida D K. 2010. Genetic variability studies and scope of improvement in sponge gourd under hot humid agro-climate. *Indian Journal arid horticulture* **5**(2): 37–39.

Shilpashree N, Anjanappa M, Fakrudin B, Pitchaimuthu M, Ramachandra R K, Shankarappa K S and Aravindkumar J S. 2022. Genetic diversity studies in ridge gourd (*Luffa acutangula* (L.) Roxb.) genotypes. *The Pharma Innovation Journal* **11**(3): 101–05.

Singh R, Singh P K, Choudhary B R, Bhardwaj D R and Rai M. 2009. Genetic variability and component analysis in sponge gourd (*Luffa cylindrica*). *Vegetable Science* **36**(3): 404–05.

Singh P K, Singh V B, Singh C K, Kumar M, Kumar V and Kumar N. 2017. Evaluation of germplasm for PCV, GCV and heritability in luffa (*Luffa cylindrical* Roem.). *International Journal Current Microbiology Applied Sciences* **6**(3): 355–60.

Singh S, Singh V B and Tyagi N. 2019a. Studies on genetic variability of sponge gourd genotypes. *Journal of Pharmacognosy Phytochemistry* **8**(1): 2554–57.

Singh S, Singh V B and Tyagi N. 2019b. Genetic divergence studies in sponge gourd genotypes. *International Journal Chemical Science* **7**(1): 644–47.

Som I, Kunjam K and Thakur R. 2020. Genetic variability of sponge gourd (*Luffa cylindrica* L. Roem.) and it's morphological characterization. *Journal of Pharmacognosy and Phytochemistry* **9**(1): 235–37.