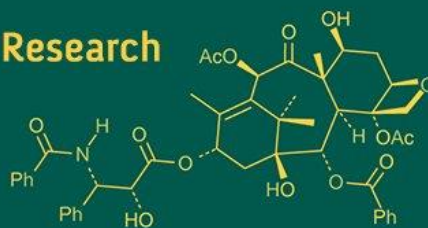
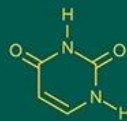
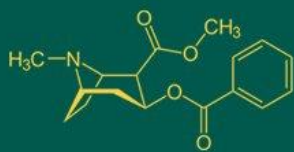


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Priyanka C Billur
Department of Vegetable
Science, College of
Horticulture, UHS, Bagalkot,
Karnataka, India

Sanjeevraddi G Reddi
Department of Agronomy,
College of Horticulture, UHS,
Bagalkot, Karnataka, India

Raveendra S Jawadagi
Department of Vegetable
Science, College of
Horticulture, UHS, Bagalkot,
Karnataka, India

Shashikanth Evoor
Department of Vegetable
Science, College of
Horticulture, UHS, Bagalkot,
Karnataka, India

Satish D
Department of Genetics and
Plant Breeding, College of
Horticulture, UHS, Bagalkot,
Karnataka, India

Corresponding Author:
Priyanka C Billur
Department of Vegetable
Science, College of
Horticulture, UHS, Bagalkot,
Karnataka, India

Unraveling genetic variability and heritable components governing growth, flowering and yield traits in F₂ population of sponge gourd (*Luffa cylindrica* (L.) Roem.)

Priyanka C Billur, Sanjeevraddi G Reddi, Raveendra S Jawadagi, Shashikanth Evoor and Satish D

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Abstract

Sponge gourd (*Luffa cylindrica* (L.) Roem.; $2n = 2x = 26$) is a nutritionally rich yet underexploited cucurbitaceous vegetable cultivated across 7.21 lakh hectares in India, primarily in Uttar Pradesh, Bihar, Gujarat, Punjab, Rajasthan, Jharkhand, Haryana and Karnataka. The crop's tender fruits are valued for their high moisture (93.2 g/100 g), protein (1.2 g), carbohydrates (2.9 g), carotene (120 mg), vitamins and minerals, while mature fruits and antioxidant compounds like luffin A and B contribute to medicinal uses. Despite its nutritional significance, sponge gourd has received limited breeding attention and systematic germplasm improvement efforts are lacking. The present study, conducted during 2025 at the College of Horticulture, Bagalkot (University of Horticultural Sciences, Bagalkot) utilized an F₂ population derived from the hybrid cross KRCCH-3 × Samreen to evaluate genetic variability, heritability, and genetic advance for key growth, flowering, yield, and quality traits. Observations on vine length, branching, flowering behavior, fruit yield and total soluble solids were analyzed using genotypic and phenotypic coefficients of variation (GCV and PCV), broad-sense heritability (h^2) and genetic advance as percent of mean (GAM). Results indicated substantial variability within the F₂ population, with GCV values lower than PCV for all traits, suggesting environmental influence. High GCV and PCV were observed for node at first male flower appearance, while fruit length, fruit diameter, number of fruits per vine and average fruit weight exhibited high heritability with high GAM, implying the predominance of additive gene effects and suitability for direct selection. In contrast, traits like days to flowering and harvest showed low GCV and GAM, indicating narrow variability and the necessity of hybridization or heterosis breeding for improvement. Overall, the study highlights significant genetic diversity in sponge gourd and identifies promising traits for effective selection and cultivar development. Sponge gourd (*Luffa cylindrica* (L.) Roem.; $2n = 2x = 26$) is a nutritionally rich yet underexploited cucurbitaceous vegetable cultivated across 7.21 lakh hectares in India, primarily in Uttar Pradesh, Bihar, Gujarat, Punjab, Rajasthan, Jharkhand, Haryana, and Karnataka. The crop's tender fruits are valued for their high moisture (93.2 g/100 g), protein (1.2 g), carbohydrates (2.9 g), carotene (120 mg), vitamins, and minerals, while mature fruits and antioxidant compounds like luffin A and B contribute to medicinal uses. Despite its nutritional significance, sponge gourd has received limited breeding attention, and systematic germplasm improvement efforts are lacking. The present study, conducted during 2025 at the University of Horticultural Sciences, Bagalkot, utilized an F₂ population derived from the hybrid cross KRCCH-3 × Samreen to evaluate genetic variability, heritability, and genetic advance for key growth, flowering, yield, and quality traits. Observations on vine length, branching, flowering behavior, fruit yield, and total soluble solids were analyzed using genotypic and phenotypic coefficients of variation (GCV and PCV), broad-sense heritability (h^2), and genetic advance as percent of mean (GAM). Results indicated substantial variability within the F₂ population, with GCV values lower than PCV for all traits, suggesting environmental influence. High GCV and PCV were observed for node at first male flower appearance, while fruit length, fruit diameter, number of fruits per vine, and average fruit weight exhibited high heritability with high GAM, implying the predominance of additive gene effects and suitability for direct selection. In contrast, traits like days to flowering and harvest showed low GCV and GAM, indicating narrow variability and the necessity of hybridization or heterosis breeding for improvement. Overall, the study highlights significant genetic diversity in sponge gourd and identifies promising traits for effective selection and cultivar development.

Keywords: Sponge gourd, variability, heritability and genetic advance

Introduction

Sponge gourd (*Luffa cylindrica* (L.) Roem.; $2n = 2x = 26$) is a minor cucurbitaceous vegetable and is known by various regional names such as *tuppada heeray kayi* (Kannada),

chikni turai (Hindi), *jhinga* (Bengali) and *pirkanga* (Tamil) (Wehner *et al.*, 2020) [31]. Which is cultivated on roughly 7.21 lakh hectares, producing around 12.87 lakh tonnes at an average yield of 10.52 t/ha, with major production in Uttar Pradesh, Punjab, Bihar, Gujarat, Rajasthan, Jharkhand, Haryana and Karnataka (Halder *et al.*, 2022) [9].

The crop is valued for its tender fruits, rich in water (93.2 g/100 g), protein (1.2 g), carbohydrates (2.9 g), carotene (120 mg), vitamins (thiamine 0.02 mg, riboflavin 0.06 mg, niacin 0.4 mg) and minerals (calcium 36 mg, iron 1.1 mg, phosphorus 19 mg) (Gopalan *et al.*, 1999) [8]. Compared to ridge gourd, it has higher protein and carotene content. Mature fruits are traditionally used to improve blood circulation and manage rheumatism and arthritis. Additionally, sponge gourd contains antioxidants such as luffin A and B, which support human health. Currently, there is no structured strategy for improving sponge gourd cultivars. Despite its nutritional significance, the crop has received limited attention from plant breeders, with little systematic effort in germplasm collection, evaluation or conservation at national or international levels. The substantial genetic diversity within India remains largely underutilized, emphasizing the need for a focused and organized crop improvement program.

The F_2 population is genetically important because it helps scientists comprehend the pattern of trait inheritance and how genetic variation is distributed. It is created by crossing two F_1 individuals, which are the first-generation offspring from different parent lines. In the F_2 generation, alleles segregate and recombine according to Mendelian laws, allowing researchers to observe patterns like the classic 3:1 ratio for simple traits and to uncover recessive traits that might be hidden in the F_1 . F_2 populations are also vital for genetic mapping, helping to pinpoint gene locations on chromosomes and identify quantitative trait loci (QTLs) that control complex traits. This genetic diversity within the F_2 is crucial for breeding, as it provides a pool of varied individuals from which breeders can select plants or animals with desirable characteristics. Overall, the F_2 generation offers a detailed insight into genetic variation and inheritance, making it a key resource in genetics and breeding studies.

Materials and Methods

The research was carried out at the University of Horticultural Sciences, Bagalkot, specifically at the College of Horticulture, Bagalkot, Karnataka, India, from January to April 2025. Hybrid KRCCH-3 x Samreen were chosen to create the experimental material needed for the variability studies in the F_2 generation. Following selfing of this hybrid, F_2 seeds were obtained and used for the main experiment focusing on variability studies. Seeds sown in trays filled with coco peat. Seedlings were transplanted to the main field 16 days after germination with 2m x 1m spacing. All the recommended package of practices was followed to raise a healthy crop.

Observations were made on various parameters including growth and flowering metrics such as vine length at final harvest (m), the number of primary branches at final harvest, days to first male and female flowering, the node of first male and female flowering. Yield parameters includes the number of fruits per vine, fruit length (cm), average fruit weight (g), fruit diameter (mm), days to first harvest and days to last harvest, fruit yield per vine (kg). Quality

parameter measured was TSS. The observations are detailed in the below tables.

To measure the degree of variation in the F_2 population, estimates of mean, range, genotypic variance (GV), phenotypic variances (PV), genotypic (GCV) and phenotypic coefficients of variations (PCV), broad-sense heritability (h^2), genetic advance (GA) and also GAM, were worked out for growth, flowering and yield-related traits and the outcomes are given in the Table 1. In order to facilitate interpretation, the GAM estimates were grouped into three different categories, namely low (0-10%), moderate (10-20%) and high (>20%). Likewise, heritability were arranged into low (0-30%), moderate (30-60%) and high (>60%) classes.

Results and Discussion

All the parameters shows considerable variation within population and GCV is smaller than PCV for all traits, which indicates the environmental impact and role of different variability parameters. Table 1. Shows genetic variability estimates for growth, flowering, yield and quality parameters in F_2 population of sponge gourd (KRCCH-3 x Samreen).

Higher estimates of GCV and PCV were recorded for the character node at first male flower appearance (GCV: 26.75%; PCV: 31.42%). Such high values reflect the presence of a wide genetic base within the population. The close association between GCV and PCV further indicates that environmental influence on its expression is limited. Therefore, this trait offers considerable potential for genetic improvement through simple selection. Comparable results in ridge gourd were also reported by Khatoun *et al.* (2016) [13].

Moderate levels of GCV and PCV were noted for the traits such as node at first female flower appearance (GCV: 13.07%; PCV: 15.52%), vine length at final harvest (GCV: 11.95%; PCV: 15.33%), fruit length (GCV: 13.41%; PCV: 14.04%), fruit diameter (GCV: 13.41%; PCV: 14.22%), number of fruits per vine (GCV: 17.86%; PCV: 18.34%), average fruit weight (GCV: 14.10%; PCV: 14.41%), fruit yield per vine (GCV: 17.76%; PCV: 18.62%) and total soluble solids (GCV: 17.81%; PCV: 18.35%). These result revealed that the traits had medium genetic root ability. Similar results were observed by Varalakshmi *et al.* (2015) [29], Singh *et al.* (2020) [25], Arvindkumar *et al.* (2011) [3], Panda *et al.* (2022) [19] and Hegade *et al.* (2009) [11] in ridge gourd; Rajput *et al.* (2012) [21], Rathod (2007) [23] and Kutty and Dharmatti (2004) [15] in bitter gourd; Narayanankutty *et al.* (2006) [18] in snake gourd, Sachidanand K (2015) [24] in bottle gourd.

Moderate GCV along with high PCV were recorded for the trait primary branches per vine (GCV: 19.82%; PCV: 23.70%). This suggests that the observed variability may be influenced by diverse genetic factors such as polygenic control, epistasis interactions, genetic mutations or allelic differences. Similar findings were reported by Dubey *et al.* (2013) [16] and Choudary and Kumar, 2011 [5].

Low GCV and PCV values were obtained for the traits such as days to first female flower (GCV: 7.16%; PCV: 8.01%), days to first male flower (GCV: 7.32%; PCV: 8.15%), days to first fruit picking (GCV: 5.55%; PCV: 7.38%) and days to last fruit picking (GCV: 4.65%; PCV: 6.51%). Similar observations have been reported by Methela *et al.* (2019) [17], Thulasiram *et al.* (2022) [28], Ram *et al.* (2006) [22],

Choudhary and Kumar (2011) ^[5], Koppad *et al.* (2015) ^[14], Singh *et al.* (2017) ^[26], Sravani *et al.* (2021) ^[27], Durga *et al.* (2021) ^[7] and Vidya *et al.* (2025) ^[30]. This reflects a narrow genetic base, indicating that variability for these characters needs to be created through hybridization to obtain transgressive segregants or by employing mutation breeding.

High heritability combined with high GAM were recorded for traits such as node at first female flower appearance (h^2 : 70.85%; GAM: 22.83%), node at first male flower appearance (h^2 : 72.48%; GAM: 46.91%), primary branches per vine (h^2 : 69.16%; GAM: 19.09%), fruit length (h^2 : 91.14%; GAM: 26.37%), fruit diameter (h^2 : 88.93%; GAM: 26.37%), fruits number per vine (h^2 : 94.86%; GAM: 35.83%), average fruit weight (h^2 : 95.66%; GAM: 28.40%), fruit yield (h^2 : 91.00%; GAM: 34.90%) and total soluble solids (h^2 : 94.22%; GAM: 35.61%). This reflects the major role of additive gene effects in governing these traits, suggesting that direct selection would be highly effective for their improvement. Similar findings have been also reported by Purushottama (2022) ^[20], Ram *et al.* (2006) ^[22], Singh *et al.* (2017) ^[26], Choudhary and Kumar (2011) ^[5], Dubey *et al.*

(2013) ^[16], Varalakshmi *et al.* (2015) ^[29], Harshitha *et al.* (2019a) ^[10], Thulasiram *et al.* (2022) ^[28], Sachidanand (2015) ^[24] and Annigeri (2020) ^[2] in different crops.

High heritability with moderate genetic advance as percent of mean (GAM) was recorded for traits such as days to first female flower (h^2 : 79.89%; GAM: 13.18%), days to first male flower (h^2 : 80.66%; GAM: 13.54%) and vine length (h^2 : 60.16%; GAM: 19.09%). This indicates that additive gene effects predominantly govern the expression of these traits, suggesting that direct selection would be effective for their improvement. Similar outcomes were reported by Thulasiram *et al.* (2022) ^[28], Manoj *et al.* (2018) ^[16], Kannan *et al.* (2019) ^[12] and Akhila and Singh (2020) ^[1] in different crops.

Moderate heritability with low GAM was also observed for days to first (h^2 : 56.52%; GAM: 8.59%) and last picking of fruits (h^2 : 51.14%; GAM: 6.86%) which indicates the predominance of non additive gene action, suggesting limited scope of improvement through direct selection. Hence, heterosis breeding would be more effective for the improvement of these traits (Bhargava *et al.*, 2017) ^[4].

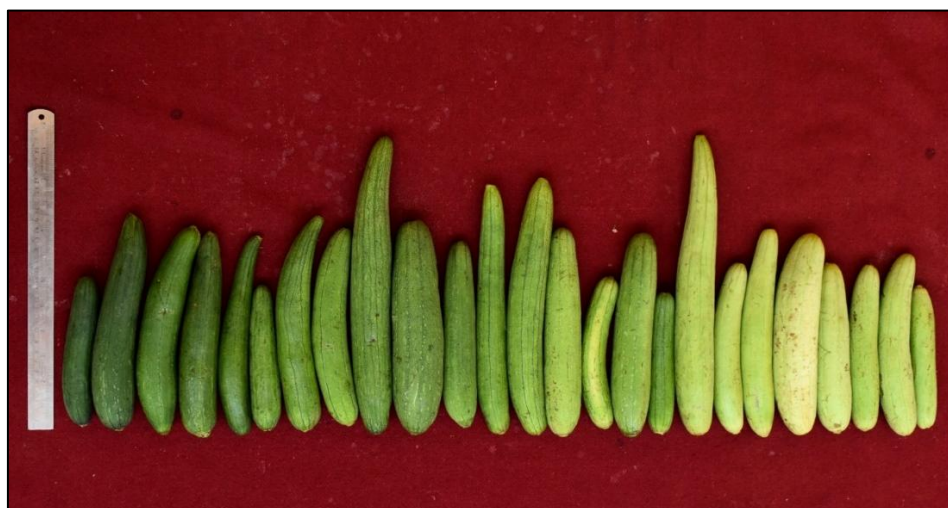


Plate 1: Variability in the F₂ population

Table 1: Genetic variability estimates for growth, flowering, yield and quality parameters in F₂ population of sponge gourd (KRCCH-3 × Samreen)

Sl. No.	Character	Mean	Range		GCV (%)	PCV (%)	h^2 (%)	GAM
			Min	Max				
1	Days to first female flower appearance	46.35	37	57	7.16	8.01	79.89	13.18
2	Node at first female flower appears	11.43	8	17	13.07	15.52	70.85	22.83
3	Days to first male flower appearance	39.18	33	49	7.32	8.15	80.66	13.54
4	Node at first male flower appears	5.24	3	11	26.75	31.42	72.48	46.91
5	Vine length at final harvest (m)	5.41	3.5	8	11.95	15.33	60.16	19.09
6	Number of primary branches per vine at final harvest	4.68	2	8	19.82	23.70	69.97	34.16
7	Fruit length (cm)	20.01	13	29.43	13.41	14.04	91.14	26.37
8	Fruit diameter (cm)	3.34	2.19	4.6	13.41	14.22	88.93	26.05
9	Number of fruits per vine	21.11	10	32	17.86	18.34	94.86	35.83
10	Average fruit weight (g)	132.40	69	190	14.10	14.41	95.66	28.40
11	Days to first picking	57.14	47	65	5.55	7.38	56.52	8.59
12	Days to last picking	106.99	85	125	4.65	6.51	51.14	6.86
13	Fruit yield per vine (kg)	2.53	0.8	3.88	17.76	18.62	91	34.90
14	Total soluble solids ($^{\circ}$ B)	3.93	2.2	6	17.81	18.35	94.22	35.61

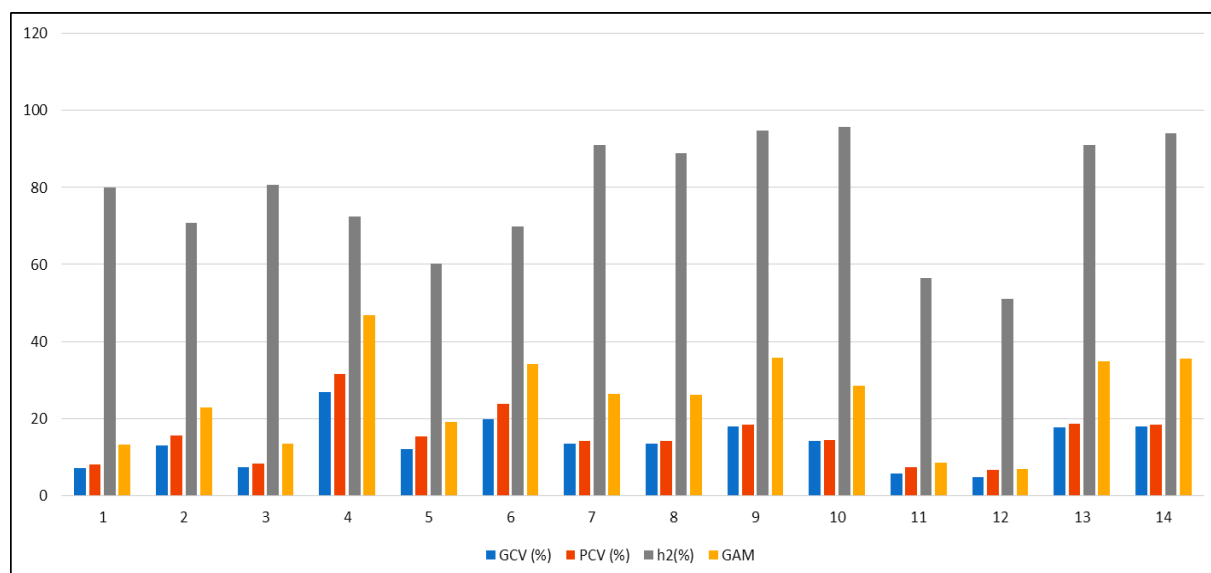


Fig 1: Estimates of genetic variability traits in the F₂ population

- | | | |
|--|--|------------------------------|
| 1-Days to first female flower appearance | 6-Number of primary branches per vine at final harvest | 11-Days to first picking |
| 2-Node at first female flower appears | 7-Fruit length | 12-Days to last picking |
| 3-Days to first male flower appearance | 8-Fruit diameter (cm) | 13-Fruit yield per vine (kg) |
| 4-Node at first male flower appears | 9-Number of fruits per vine | 14-Total soluble solids |
| 5-Vine length at final harvest (m) | 10-Average fruit weight (g) | |

Conclusion

The F₂ population of sponge gourd displayed substantial genetic variability for key growth and yield traits. Traits such as node at first male and female flower, number of primary branches, fruit size, fruit number, average fruit weight, total yield and TSS exhibited high heritability and genetic advance, highlighting the predominance of additive gene effects, indicating that these traits can be effectively improved through direct selection. Conversely, traits like days to first flowering and vine length showed lower variability and moderate genetic advance, reflecting a stronger influence of non-additive gene action, where recurrent selection may be more appropriate. Overall, these findings provide a strong basis for targeted breeding to enhance the genetic potential of sponge gourd.

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