

E-ISSN: 2618-0618

P-ISSN: 2618-060X

© Agronomy

NAAS Rating (2026): 5.20

www.agronomyjournals.com

2026; 9(6): 1305-1309

Received: 07-05-2026

Accepted: 10-06-2026

Ravat Sejal Jitendrakumar

Department of Vegetable

Science, ANDUA&T,

Kumarganj, Ayodhya, (U.P),

India

CN Ram

Department of Vegetable

Science, ANDUA&T,

Kumarganj, Ayodhya, (U.P),

India

Anil Kumar

Department of Vegetable

Science, ANDUA&T,

Kumarganj, Ayodhya, (U.P),

India

Santosh Kumar

Department of Vegetable

Science, ANDUA&T,

Kumarganj, Ayodhya, (U.P),

India

Pravesh Kumar

Department of Vegetable

Science, ANDUA&T,

Kumarganj, Ayodhya, (U.P),

India

Shivangi Kamal

Department of Vegetable

Science, ANDUA&T,

Kumarganj, Ayodhya, (U.P),

India

Corresponding Author:**CN Ram**

Department of Vegetable

Science, ANDUA&T,

Kumarganj, Ayodhya, (U.P),

India

Studies on variability and character association for yield and quality contributing characters in sponge gourd [*Luffa cylindrica* (roem) L.]

Ravat Sejal Jitendra kumar, CN Ram, Anil Kumar, Santosh Kumar, Pravesh Kumar and Shivangi Kamal

DOI: <https://www.doi.org/10.33545/2618060X.2026.v9.i6q.5872>

Abstract

The present study evaluated 26 sponge gourd genotypes (including check) during summer 2025 in a Completely Randomized Block Design (CRBD) with three replications to assess genetic variability and character association for 18 traits. ANOVA showed highly significant differences among genotypes for all characters. Phenotypic coefficients of variation (PCV) were consistently higher than genotypic coefficients of variation (GCV), with the highest magnitude in ascorbic acid content (54.32% and 63.54%). In terms of yield performance, genotypes Pusa Sneha (129.76 q/ha) and GSG-1 (128.46 q/ha) significantly outyielded the check variety, Pusa Chikni (124.63 q/ha). High heritability coupled with high genetic advance as a percentage of mean was observed for ascorbic acid content, peduncle length, primary branches, vine length, dry matter and average fruit weight, indicating the predominance of additive gene action.

Keywords: Sponge gourd (*Luffa cylindrica*), genetic variability, heritability, GCV, PCV

Introduction

Cucurbits constitute the largest group of fruit vegetables, are widely distributed, and are consumed for dessert as well as vegetable purposes in tropical and subtropical parts of the world. Sponge gourd [*Luffa cylindrica* (L.) Roem.] is a member of the cucurbitaceous family cultivated for both vegetable and medicinal purposes. *Luffa aegyptiaca* (Mill), a synonym of *Luffa cylindrica*, known by different names such as vegetable sponge, smooth gourd, dishcloth gourd or smooth loofah, possesses a diploid chromosome number of $2n = 2x = 26$. The word 'Luffa' is derived from Arabian origins meaning a sponge-like fibrous structure of mature fruit, while the ancient Sanskrit name 'Koshataki' suggests its longstanding cultivation in India. According to Herklots (1972) [3], the Asiatic region, especially India and Malaya, may be the origin of *Luffa*.

Beyond its kitchen utility, *Luffa cylindrica* possesses significant nutritional, industrial and therapeutic value. Fresh sponge gourd fruit is exceptionally rich in moisture (93.2 g), low in calories, and contains essential minerals like calcium, phosphorus and iron, along with vitamins such as carotene, thiamine, riboflavin and niacin (Yawalker, 2004) [14]. Financially and industrially, the dried internal fibrous skeleton consisting of lignocellulosic material is widely used for cleaning sponges, shock absorbers, sound-proof linings, packing materials and industrial filters. Its seeds have been used in the treatment of asthma, sinusitis and fever (Nagao et al., 1991) [8]. From a plant breeding perspective, sponge gourd is predominantly a monoecious, annual climbing vine that relies on cross-pollination. Despite India being the world's second-largest producer of vegetables, the domestic productivity of sponge gourd stands at 10.52 tonnes per hectare, leaving substantial room for improvement. The evaluation of genotypes is the foundational step for any structured crop improvement programme. A thorough understanding of genetic variability, heritability and genetic advance is crucial to differentiate genetic potential from environmental influences and to identify superior genotypes. Since fruit yield is a complex polygenic trait Influenced by multiple characters, correlation coefficient

Analysis is employed to measure the Mutual association between different plant traits, and path Coefficient analysis partitions the correlation into direct and indirect effects, establishing causal relationships

Material and Method

The present investigation was conducted during the summer season 2025 at the Main Experimental Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh. The experimental material comprising twenty-six sponge gourd genotypes was evaluated in a Completely Randomized Block Design (CRBD) with three replications. Each genotype was planted in a plot measuring 3.0m × 3.0m, maintaining a spacing of 3.0 m between rows and 0.5 m between plants. Observations were recorded on eighteen yield and quality traits, namely days to first staminate flower anthesis, days to first pistillate flower anthesis, days to first fruit harvest, node number to first staminate flower appearance, node number to first pistillate flower appearance, vine length (m), number of primary branches per plant, internodal length (cm), fruit width (cm), fruit length (cm), peduncle length (cm), number of fruits per plant, average fruit weight (g), total soluble solids (°Brix), ascorbic acid content (mg/100 g), dry matter content (%), fruit yield per plant (kg) and total fruit yield (q/ha). Data for each trait were recorded from five randomly selected plants in each genotype within each replication.

Statistical analysis was performed using analysis of variance (ANOVA) following the procedure described by Panse and Sukhatme (2000) [9] to determine the significance of differences among genotypes. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated according to Burton (1952) [1]. Broad-sense heritability (h^2_{bs}) was computed following Allard (1960), while genetic advance (GA) and genetic advance as per cent of mean were calculated using the methodology proposed by Johnson *et al.* (1955) [4]. Character associations were examined using genotypic and phenotypic correlation coefficients, and path coefficient analysis was executed according to Dewey and Lu (1959) to partition correlations into direct and indirect effects.

Result and Discussion

The analysis of variance (Table 1) revealed highly significant differences among the genotypes for all eighteen traits studied, indicating the existence of substantial genetic variability in the experimental material. The presence of significant variation among genotypes suggests ample scope for selection and genetic improvement of fruit yield and its associated traits in sponge gourd.

Mean sum of squares due to treatments were highly significant for all the traits (Table 2). Days to first staminate flower anthesis ranged from 39.13 (VRSG-6) to 52.07 (NSG-2123) with a mean value of 46.26 days. Days to first pistillate flower anthesis ranged from 44.80 (VRSG-6) to 58.33 (NSG-2123) with a mean value of 52.48 days. Days to first fruit harvest ranged from 52.27 (VRSG-6) to 64.60 (NSG-2123) with a mean value of 58.92 days. Node number to first staminate flower appearance ranged from 4.13 (NSG-2123) to 7.83 (VRSG-5-15) with a mean value of 6.38. Node number to first pistillate flower appearance ranged from 7.33 (NSG-2123) to 13.07 (Pant Chikni Tori-1) with a mean value of 11.00. Vine length ranged from 2.80 m (GSG-1) to 8.67 m (NSG-2123) with a mean value of 4.81 m. Number of primary branches ranged from 2.83 (Pant

Chikni Tori-1) to 9.53 (Pusa Chikni) with a mean value of 6.14. Internodal length ranged from 8.63 cm (VRSG-66) to 13.66 cm (NSG-2123) with a mean value of 11.27 cm. Fruit width ranged from 2.78 cm (VRSG-51) to 5.13 cm (VRSG-84) with a mean value of 3.19 cm. Fruit length ranged from 16.57 cm (NSG-2123) to 23.45 cm (VRSG-50) with a mean value of 20.49 cm. Peduncle length ranged from 4.43 cm (VRSG-50) to 12.43 cm (VRSG-13-17) with a mean value of 6.58 cm. Number of fruits per plant ranged from 13.94 (VRSG-53) to 21.87 (VRSG-11) with a mean value of 17.83. Average fruit weight ranged from 74.97 g (VRSG-2-15) to 132.77 g (Pusa Chikni) with a mean value of 102.66 g. TSS ranged from 3.77 °Brix (VRSG-3-17) to 4.97 °Brix (VRSG-6) with a mean value of 4.19 °Brix. Ascorbic acid ranged from 2.18 mg/100g (VRSG-2-15) to 11.43 mg/100g (Pusa Chikni) with a mean value of 5.43 mg/100g. Dry matter ranged from 4.27% (VRSG-51) to 9.63% (Pusa Chikni) with a mean value of 6.68%. Fruit yield per plant ranged from 1.44 kg (VRSG-2-15) to 2.09 kg (Pusa Sneha) with a mean value of 1.81 kg. Fruit yield ranged from 87.69 q/ha (VRSG-2-15) to 129.76 q/ha (Pusa Sneha) with a mean value of 108.43 q/ha.

The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for the eighteen characters are presented in Table 3. In general, PCV values were slightly higher than the corresponding GCV values for all traits, indicating the influence of environmental factors on trait expression. High estimates (>20%) of both GCV and PCV were observed for ascorbic acid content (54.32% and 63.54%), peduncle length (30.34% and 31.61%), primary branches (28.12% and 29.02%) and vine length (27.36% and 29.04%), suggesting the presence of substantial genetic variability for these economically important traits. Similar findings for variability in yield components were reported by Kumar *et al.* (2019) [5]. Moderate estimates (10–20%) of GCV and PCV were recorded for dry matter percentage (17.61% and 18.02%), average fruit weight (15.10% and 15.91%), node number to first pistillate flower appearance (14.02% and 15.30%), node number to first staminate flower appearance (13.88% and 17.18%), fruit width (13.01% and 16.01%), fruit yield q/ha (10.84% and 12.66%), number of fruits per plant (10.20% and 14.14%) and fruit yield per plant (10.12% and 12.69%). The remaining traits namely internodal length, fruit length, total soluble solids, days to first staminate flower anthesis, days to first pistillate flower anthesis and days to first fruit harvest exhibited low estimates of GCV and PCV, indicating relatively narrow genetic variability. Comparable results were reported by Singh *et al.* (2018) [11].

Broad-sense heritability ranged from 33.78% for internodal length to 95.51% for dry matter. High heritability estimates were observed for dry matter (95.51%), primary branches (93.90%), peduncle length (92.16%), average fruit weight (90.07%), vine length (88.79%), node number to first pistillate flower appearance (83.97%), total soluble solids (75.69%), fruit yield q/ha (73.28%), ascorbic acid content (73.09%), fruit width (65.97%), fruit yield per plant (63.63%) and fruit length (62.50%), indicating that a large proportion of the observed variation in these traits is genetically controlled. Similar findings were reported by Singh *et al.* (2018) [11]. Moderate heritability estimates (40–60%) were recorded for days to first staminate flower anthesis (46.53%), days to first pistillate flower anthesis (45.36%), days to first fruit harvest (44.64%) and number of fruits per plant (52.07%).

Genetic advance as per cent of mean ranged from 6.12% for days to first fruit harvest to 95.67% for ascorbic acid content. High genetic advance (>20%) was observed for ascorbic acid content (95.67%), peduncle length (60.00%), primary branches (56.12%), vine length (53.11%), dry matter (35.46%), average fruit weight (29.52%), node number to first pistillate flower appearance (26.46%), node number to first staminate flower

appearance (23.12%) and fruit width (21.76%). High heritability coupled with high genetic advance as per cent of mean was observed for ascorbic acid content, peduncle length, primary branches, vine length, dry matter, node number to first pistillate flower appearance and fruit yield q/ha, indicating the predominance of additive gene action. Similar results were reported by Patil *et al.* (2022) ^[10].

Table 1: Analysis of variance (mean squares) for eighteen characters in sponge gourd

Sl. No.	Traits	Source of variation		
		Replication	Treatments	Error
	d.f.	2	25	50
1.	Days to first staminate flower anthesis	13.09	28.02**	7.76
2.	Days to first pistillate flower anthesis	19.94	30.31**	8.68
3.	Node at which first male flower appearance	0.78	2.77**	0.42
4.	Node at which first female flower appearance	0.09	7.58**	0.45
5.	Number of primary branches per plant	7.68	9.14**	0.19
6.	Days to first fruit harvest	25.43	29.07**	8.50
7.	Fruit length (cm)	0.69	11.99**	2.00
8.	Fruit width (cm)	0.228	0.605**	0.089
9.	Average fruit weight (g)	36.48	747.36**	3.20
10.	Internodal length (cm)	1.74	4.94**	1.95
11.	Vine length (m)	0.18	5.40**	0.22
12.	Peduncle length (cm)	0.30	12.31**	0.34
13.	Number of fruit per plant	0.42	12.97**	3.04
14.	T.S.S. °Brix	0.012	0.318**	0.031
15.	Dry matter (%)	0.09	4.21**	0.07
16.	Ascorbic acid (mg/100g)	0.03	29.28**	3.20
17.	Fruit yield per plant (kg)	0.013	0.120**	0.025
18.	Fruit yield (q/ha)	21.46	464.83**	50.37

\\ Significant at 1% level; \ Significant at 5% level

Table 2: Mean performance of twenty-six genotypes for eighteen characters in sponge gourd

S.N o	Genotypes	DFSF A	DPPF A	DFH H	NNFSF A	NNFPF A	VL(m) m	PB PB	INL(c m)	FW(c m)	FL(c m)	PL(c m)	NF P	AFW(g) g	TSS(° B)	AA(mg/10 0g)	DM(%)	FYPP(kg)	FY(q/h a)
1	VRSG-51	47.53	53.93	59.6 0	5.30	9.77	3.77	6.1 7	11.67	2.78	18.42	5.00	16.3 3	96.80	4.20	2.43	4.83	1.57	93.80
2	VRSG-3- 17	45.60	52.00	56.6 7	6.47	9.83	5.67	7.1 0	9.30	2.87	19.85	6.40	19.3 0	83.73	3.77	3.23	6.87	1.69	102.15
3	VRSG-2- 15	46.80	52.80	59.7 3	6.53	11.00	5.85	5.2 3	10.83	2.93	18.10	10.93	16.5 7	74.97	3.85	3.61	6.20	1.44	87.69
4	VRSG-84	49.13	55.93	61.8 0	6.37	10.65	5.17	5.6 5	11.73	5.13	23.15	6.55	20.0 3	102.77	3.92	2.60	5.30	1.90	111.87
5	VRSG-11	46.07	52.33	58.7 3	7.40	11.27	5.06	6.3 9	11.70	2.91	21.75	9.13	21.8 7	97.23	4.57	2.76	7.27	2.02	118.21
6	VRSG-5- 15	46.53	52.67	59.3 3	7.83	12.72	4.67	6.5 1	9.60	3.16	16.90	5.80	17.5 0	90.40	4.42	2.49	5.20	1.81	107.92
7	VRSG-68	44.33	50.53	57.1 3	7.20	11.83	4.57	9.1 7	11.47	3.12	18.53	5.43	15.0 5	104.03	3.89	2.83	4.27	1.56	94.56
8	VRSG-5- 17	44.60	51.07	56.4 0	7.03	12.60	3.72	5.4 0	12.08	3.35	19.10	8.07	17.0 7	85.67	4.62	7.32	5.87	1.73	105.58
9	VRSG-66	44.27	50.40	56.4 7	5.00	9.57	4.67	7.8 1	8.63	3.15	20.87	5.97	18.0 5	97.14	3.86	3.69	7.95	1.83	108.08
10	VRSG-46	45.67	51.67	58.4 7	5.37	11.60	2.97	8.8 2	11.20	3.33	20.07	5.61	15.1 1	122.40	3.95	4.58	8.03	1.79	104.31
11	VRSG-50	45.53	51.53	61.1 3	7.20	11.90	4.70	6.2 3	12.93	3.08	23.45	4.43	17.8 3	96.83	4.48	4.45	6.10	2.08	125.55
12	VRSG-13- 17	47.60	53.73	61.0 7	5.77	8.77	8.00	7.0 8	13.05	3.52	20.19	12.43	17.7 4	99.83	3.87	4.68	6.00	1.64	99.90
13	VRSG-6	39.13	44.80	52.2 7	7.30	10.50	5.60	7.1 7	11.70	3.03	20.57	6.67	18.0 5	97.92	4.97	8.16	6.33	1.76	103.79
14	VRSG-53	42.40	47.93	56.0 7	6.77	10.93	4.20	6.4 1	11.54	2.86	16.60	6.87	13.9 4	125.70	4.50	3.18	6.03	1.78	103.75
15	VRSG-3- 12	45.33	51.93	58.2 7	5.03	8.93	3.77	6.5 8	9.27	3.06	20.75	5.75	15.6 3	118.54	4.22	9.78	6.96	1.85	110.62
16	Kashi Shreya	42.67	48.40	54.5 3	7.23	12.73	3.60	2.9 3	10.55	3.24	22.36	4.76	15.8 7	128.13	4.07	4.51	8.23	2.06	124.38

17	Kashi Vandana	45.33	51.93	57.7 ₃	7.53	11.63	4.00	5.1 ₅	10.43	3.06	20.88	5.27	16.2 ₇	93.82	4.60	5.77	7.30	1.53	92.96
18	Kashi Divya	51.53	57.60	64.5 ₃	5.40	8.70	3.87	9.5 ₃	11.85	3.69	22.75	5.11	20.3 ₀	119.50	4.55	2.18	6.17	2.03	123.09
19	Pant Chikni Tori-1	45.67	51.60	57.2 ₀	7.47	13.07	5.67	2.8 ₃	11.37	2.81	21.05	5.17	19.2 ₃	124.83	3.80	11.17	7.03	1.99	111.70
20	Pusa Sneha	48.53	54.73	60.6 ₀	5.50	11.67	4.63	5.0 ₀	11.93	3.14	21.30	9.17	20.5 ₇	104.53	4.57	10.53	6.86	2.09	129.76
21	GSG-1	46.47	53.33	59.0 ₇	6.90	11.67	2.80	3.0 ₇	9.07	3.34	21.65	5.60	18.5 ₇	112.97	4.17	3.85	7.33	2.00	128.46
22	Punjab Nikhar	42.40	48.87	55.4 ₀	5.73	12.77	3.67	7.2 ₀	10.62	3.06	21.25	6.37	18.4 ₉	99.30	3.93	3.03	7.30	1.90	105.54
23	PSG-9	51.60	58.07	64.0 ₇	6.73	12.77	5.75	5.1 ₇	12.26	3.02	21.13	4.53	17.7 ₇	86.10	4.03	10.20	6.33	1.65	96.39
													7						
24	Rajendra Nenua-1	45.47	51.93	57.7 ₃	6.40	8.93	5.13	4.4 ₀	12.17	3.01	23.13	8.73	21.7 ₇	89.50	4.20	9.24	5.99	1.94	116.10
25	NSG-2123	52.07	58.33	64.6 ₀	4.13	7.33	8.67	7.4 ₅	13.66	3.15	16.57	6.77	15.5 ₇	83.87	3.97	3.40	8.20	1.46	88.42
26	Pusa Chikni(check)	50.53	56.53	63.2 ₇	6.27	12.83	4.80	5.2 ₃	12.33	3.14	22.37	4.63	19.0 ₈	132.77	4.07	11.43	9.63	2.04	124.63
	Mean	46.26	52.48	58.9 ₂	6.38	11.00	4.81	6.1 ₄	11.27	3.19	20.49	6.58	17.8 ₃	102.66	4.19	5.43	6.68	1.81	108.43
	Min	39.13	44.80	52.2 ₇	4.13	7.33	2.80	2.8 ₃	8.63	2.78	16.57	4.43	13.9 ₄	74.97	3.77	2.18	4.27	1.44	87.69
	Max	52.07	58.33	64.6 ₀	7.83	13.07	8.67	9.5 ₃	13.66	5.13	23.45	12.43	21.8 ₇	132.77	4.97	11.43	9.63	2.09	129.76
	SE(d)±	2.28	2.41	2.38	0.53	0.55	0.38	0.3 ₆	1.14	0.24	1.15	0.48	1.43	4.20	0.14	0.11	0.21	0.11	5.80
	C.D. at 5%	4.58	4.85	4.80	1.06	1.11	0.77	0.7 ₂	2.30	0.49	2.33	0.96	2.87	8.47	0.29	0.23	0.42	0.23	11.67
	C.V. (%)	6.02	5.62	4.95	10.12	6.12	9.72	7.1 ₇	12.40	9.34	6.90	8.85	9.79	5.01	4.18	2.52	3.82	7.65	6.55

DFSFA: Days to first staminate flower anthesis; **DFPFA:** Days to first pistillate flower anthesis; **DFFH:** Days to first fruit harvest; **NNFSFA:** Node No. to first staminate flower appearance; **NNFPFA:** Node No. to first pistillate flower appearance; **VL:** Vine length; **PB:** Primary branches; **INL:** Internodal length; **FW:** Fruit width; **FL:** Fruit length; **PL:** Peduncle length; **NFP:** Number of fruits per plant; **AFW:** Average fruit weight; **TSS:** Total soluble solids; **AA:** Ascorbic acid; **DM:** Dry matter; **FYPP:** Fruit yield per plant; **FY:** Fruit yield.

Table 3: Estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense, genetic advance (GA) and GA in per cent of mean for eighteen characters in sponge gourd germplasm

Characters	Mean	Range		GCV (%)	PCV (%)	Heritability (%)	GA	GA% mean
		Min.	Max.					
Days to first staminate flower anthesis	46.26	39.13	52.07	5.62	8.24	46.53	3.65	7.89
Days to first pistillate flower anthesis	52.48	44.80	58.33	5.12	7.60	45.36	3.73	7.10
Days to first fruit harvest	58.92	52.27	64.60	4.44	6.65	44.64	3.60	6.12
Node number to first staminate flower appearance	6.38	4.13	7.83	13.88	17.18	65.32	1.47	23.12
Node number to first pistillate flower appearance	11.00	7.33	13.07	14.02	15.30	83.97	2.91	26.46
Vine length (m)	4.81	2.80	8.67	27.36	29.04	88.79	2.55	53.11
Primary branches per plant	6.14	2.83	9.53	28.12	29.02	93.90	3.45	56.12
Internodal length (cm)	11.27	8.63	13.66	8.86	15.24	33.78	1.19	10.60
Fruit width (cm)	3.19	2.78	5.13	13.01	16.01	65.97	0.69	21.76
Fruit length (cm)	20.49	16.57	23.45	8.91	11.27	62.50	2.97	14.51
Peduncle length (cm)	6.58	4.43	12.43	30.34	31.61	92.16	3.95	60.00
Number of fruits per plant	17.83	13.94	21.87	10.20	14.14	52.07	2.70	15.17
Average fruit weight (g)	102.66	74.97	132.77	15.10	15.91	90.07	30.31	29.52
T.S.S. (°Brix)	4.19	3.77	4.97	7.38	8.49	75.69	0.55	13.23
Ascorbic acid (mg/100g)	5.43	2.18	11.43	54.32	63.54	73.09	5.19	95.67
Dry matter (%)	6.68	4.27	9.63	17.61	18.02	95.51	2.37	35.46
Fruit yield per plant (kg)	1.81	1.44	2.09	10.12	12.69	63.63	0.30	16.64
Fruit yield (q/ha)	108.43	87.69	129.76	10.84	12.66	73.28	23.49	21.68

GCV: Genotypic co-efficient of variation; **PCV:** Phenotypic co-efficient of variation; **h²:** Heritability (broad sense); **GA:** Genetic advance; **GAM:** Genetic advance over percent mean.

Conclusion

The evaluation of twenty-six sponge gourd genotypes revealed significant phenotypic diversity and genetic variability across all eighteen quantitative growth, yield and quality traits, demonstrating ample scope for targeted population improvement. Elite genotypes such as Pusa Sneha (129.76 q/ha) and GSG-1 (128.46 q/ha) demonstrated outstanding individual productivity and field yield performance, significantly outperforming the standard check variety Pusa Chikni (124.63 q/ha). High genotypic coefficients of variation, high broad-sense heritability and substantial genetic advance as a per cent of mean were consistently observed for vine length, number of primary branches, peduncle length, ascorbic acid content and dry matter percentage, confirming the predominance of additive gene action and indicating that direct phenotypic selection for these characters would be highly effective.

References

1. Burton GW. Quantitative inheritance in grasses. *Proceedings of the Sixth International Grassland Congress*. 1952;1:277-283.
2. Gantayat B, Sahu GS, Dash SK, Tripathy P. Studies on genetic variability, heritability, and genetic advance for yield and quality traits in ridge gourd (*Luffa acutangula* Roxb.). *Indian Journal of Agricultural Sciences*. 2025;95(1):45-51.
3. Herklots GAC. *Vegetables in South-East Asia*. London: George Allen and Unwin; 1972.
4. Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlations in soybean and their implication in selection. *Agronomy Journal*. 1955;47:477-483.
5. Kumar A, Pandit MK, Sarkar S. Genetic variability, character association, and path coefficient analysis for yield and quality attributes in sponge gourd [*Luffa cylindrica* (Roem) L.]. *International Journal of Vegetable Science*. 2019;25(4):312-320.
6. McGrath MS, Hwang SE, Caldwell SE, Liston JD. GLQ 223: An inhibitor of human immunodeficiency virus replication in acutely and chemically infected cells. *National Academy of Sciences USA*. 1989;86:2844-2848.
7. Mohiddin SK, Reddy RVSK, Priya MS. Genetic variability and correlation studies for yield and architectural traits in sponge gourd (*Luffa cylindrica* L.). *Journal of Plant Development Sciences*. 2022;14(8):715-721.
8. Nagao T, Lanaka R, Iwase Y, Hanazone H, Okabe H. Studies on the constituents of *Luffa acutangula* Roxb. *Clinical Pharma. Bulletin*. 1991;39:599-606.
9. Panse VG, Sukhatme PV. *Statistical Methods for Agricultural Workers*. New Delhi: Indian Council of Agricultural Research; 2000.
10. Patil SB, Ramanjaneya R, Hegde NK. Genetic variability, heritability, and genetic advance studies for yield and quality parameters in sponge gourd [*Luffa cylindrica* (Roem) L.]. *Electronic Journal of Plant Breeding*. 2022;13(3):884-891.
11. Singh H, Kumar S, Akhilesh K. Path coefficient and correlation analysis for yield and its component traits in sponge gourd (*Luffa cylindrica* Roem). *Journal of Pharmacognosy and Phytochemistry*. 2018;7(3):1642-1646.
12. Singh P, Singh MK, Rai A. Evaluation of genetic variability, character association, and path analysis in sponge gourd genotypes. *Indian Journal of Horticulture*. 2019;76(2):265-271.
13. Yadav SK, Singh B, Baranwal DK. Genetic variability, correlation, and path analysis in sponge gourd (*Luffa cylindrica* Roem) for yield and quality contributing traits. *Journal of Crop and Weed*. 2017;13(1):54-59.
14. Yawalker KS. *Vegetable Crops of India*. New Delhi: Agri-Horticultural Publishing House; 2004.