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Genetic variability, heritability and genetic advance for yield and quality traits in sponge gourd [*Luffa cylindrica* (L.) M. Roem.]

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Abstract

Genetic variability, heritability and genetic advance were estimated for twenty morphological, yield and quality characters in sponge gourd [*Luffa cylindrica* (L.) M. Roem.] using 10 parents, 45 F₁ hybrids and 45 F₂ populations evaluated in Randomized Block Design with three replications during Kharif 2025-26 at Chandra Shekhar Azad University of Agriculture and Technology, Kanpur (U.P.), India. Analysis of variance revealed highly significant ($p < 0.01$) differences among genotypes for all twenty characters in all three populations. High genotypic coefficient of variation (GCV) coupled with high broad-sense heritability (h^2_B) and high genetic advance as percentage of mean (GAM) was recorded for fruit yield per plant (GCV: 26.94%; h^2_B : 96.51%; GAM: 54.60%), fruit yield per plot (26.84%; 93.75%; 53.61%), number of fruits per plant (18.97%; 94.89%; 38.12%), shelf life (15.84%; 96.34%; 32.08%) and fruit length (15.73%; 96.99%; 31.96%) in parents, indicating additive gene action and high responsiveness to direct selection. Node number of first male flower, total soluble solids and ascorbic acid showed low GCV with low GAM, limiting early-generation selection for these traits. The findings provide a comprehensive framework for designing efficient selection and hybridization strategies in sponge gourd.

Keywords: *Luffa cylindrica*, genotypic coefficient of variation, phenotypic coefficient of variation, broad-sense heritability, genetic advance, additive gene action

Introduction

Sponge gourd [*Luffa cylindrica* (L.) M. Roem.], commonly referred to as smooth luffa or ghiya tori, is a major cucurbitaceous vegetable cultivated extensively across tropical and subtropical regions of Asia, Africa and Latin America. In India, its cultivation is concentrated in Uttar Pradesh, Bihar, West Bengal, Andhra Pradesh and Maharashtra, primarily during the Kharif season. The crop occupies a dual economic position: the immature fruits serve as a nutritious culinary vegetable rich in carbohydrates, proteins, calcium and ascorbic acid (Whitaker and Davis, 1962) [30], while the dried fibrous skeleton of mature fruits finds wide application as a natural sponge, loofah pad, industrial filter and handicraft raw material. Despite these attributes, sponge gourd remains comparatively underexploited in terms of systematic genetic improvement relative to bottle gourd, bitter gourd and ridge gourd. The foundation of any successful crop improvement programme rests on the magnitude and nature of genetic variability present in the breeding material. The genotypic and phenotypic coefficients of variation (GCV and PCV) are widely used indices to quantify the extent of genetic and total phenotypic variation among genotypes (Burton, 1952; Singh and Chaudhary, 1985) [8, 26]. A close correspondence between GCV and PCV indicates minimal environmental influence on trait expression. Heritability in broad sense (h^2_B), defined as the proportion of total phenotypic variance attributable to genetic factors (Allard, 1960) [2], determines the efficiency with which phenotypic selection reflects underlying genetic differences. However, heritability alone does not predict actual selection gain, since high heritability may arise from non-additive gene effects not fixable by selection (Lush, 1940) [19]. Genetic advance as percentage of mean (GAM), when interpreted jointly with heritability, provides a reliable indicator of gene action: high heritability with high GAM points to additive effects and ensures productive mass or pedigree selection, while

high heritability with low GAM implies dominance and epistatic variance (Johnson *et al.*, 1955) [12]. Although several workers have estimated genetic parameters in sponge gourd, comprehensive simultaneous evaluation of parents, F₁ hybrids and F₂ populations for all major morphological, yield and quality characters remains limited. (Gantayat *et al.*, 2025) [10] and Billur *et al.*, (2025) [6] recently reported variability parameters in sponge gourd, while (Annigeri *et al.*, 2020, Bisen *et al.*, 2016) [4, 7] and (Abhijeet *et al.*, 2018) [1] have contributed important baseline data. Quality-related traits such as sugar fractions, ascorbic acid and shelf life remain comparatively less studied relative to yield traits. The present investigation was undertaken to estimate GCV, PCV, h^{2B}, GA and GAM for twenty characters across three populations, with the aim of identifying traits amenable to direct selection and providing a quantitative basis for designing breeding strategies in sponge gourd.

Materials and Methods

The experiment was conducted at the Vegetable Research Farm, Department of Vegetable Science, CSAUA&T, Kanpur (latitude 26°28'N, longitude 80°19'E, altitude 126 m), Uttar Pradesh, India during Kharif 2025-26. Ten genetically diverse sponge gourd parents were selected for the study: Kashi Divya, Kashi Kalyani, VRSG-1716, VRSG-1731, Kashi Vandana, Kashi Shreya, VRSG-175, VRSG-1710 and VRSG-196 were procured from ICAR-Indian Institute of Vegetable Research (IIVR), Varanasi, while Kalyanpur Hari Chikni was a locally adapted variety sourced from CSAUA&T, Kanpur. These ten parents were crossed in all possible combinations under a half-diallel mating design (Griffing, 1956; Method II, Model I) [5] to generate 45 F₁ hybrids, which were subsequently self-pollinated to produce 45 F₂ populations. All 100 entries (10 parents + 45 F₁ + 45 F₂) were evaluated in Randomized Block Design with three replications. Each entry was sown in a single row of 4.5 m with row-to-row spacing of 0.75 m and plant-to-plant spacing. Plants were allowed to trail freely on the ground along the bed. Standard agronomic practices and recommended fertilizer doses (100:60:60 kg NPK/ha) were followed uniformly.

Observations were recorded on five randomly selected competitive plants per entry per replication for twenty characters: days to first male flower (DFMF), days to first female flower (DFFF), node number of first male flower (NNMF), node number of first female flower (NNFF), days to first harvest (DFH), vine length (VL), number of primary branches per plant (NPB), average fruit weight (AFW), fruit length (FL), fruit diameter (FD), number of fruits per plant (NFP), fruit yield per plant (FY), fruit yield per plot (FYPP), dry matter content (DM), total soluble solids (TSS), non-reducing sugar (NRS), reducing sugar (RS), total sugar (TS), ascorbic acid (ASC) and shelf life (SL). Analysis of variance was performed following Panse and Sukhatme (1985). Genotypic (σ^2_g) and phenotypic (σ^2_p) variances, GCV and PCV (Burton, 1952) [8], heritability in broad sense $h^{2B} (\%) = (\sigma^2_g / \sigma^2_p) \times 100$ (Allard, 1960) [2] and genetic advance at 5% selection intensity $GA = k \times \sqrt{\sigma^2_p} \times h^{2B}$, $k = 2.063$ (Johnson *et al.*, 1955) [12] were estimated. GCV and PCV were classified as low (<10%), moderate (10-20%) or high (>20%) (Sivasubramanian and Madhavamenon, 1973) [27], and GAM as low (<10%), moderate (10-20%) or high (>20%) (Johnson *et al.*, 1955) [12].

Results and Discussion

Analysis of variance (Table 1 and Figure 1) revealed highly significant ($p < 0.01$) differences among genotypes for all twenty characters studied in parents, F₁ hybrids and F₂ populations of sponge gourd, confirming the existence of adequate genetic variability amenable to selection. Mean squares due to replications were non-significant for the overwhelming majority of trait-population combinations, confirming experimental precision and uniformity of field management. Detailed estimates of variability parameters are presented in (Table 2 and Figure 2) discussed below. Similar highly significant differences among genotypes for all quantitative traits were reported by (Abhijeet *et al.*, 2018) [1], (Singh *et al.*, 2019) [25], (Kumar *et al.*, 2022) [18] and (Sashi Suman *et al.*, 2024) [23] in sponge gourd.

Phenological and Vegetative Characters

Days to first male flower (DFMF) ranged from 31.50 to 38.12 days (mean 35.29) in parents, with low GCV (6.47%) and PCV (6.80%), indicating narrow phenotypic and genotypic variability for this trait. Despite the limited range, heritability was very high ($h^{2B} = 90.47\%$) with moderate GAM (12.70%), confirming that the observed variability, though small, is predominantly genetic and additive in origin. In F₁ hybrids, DFMF ranged from 31.12 to 36.86 days (mean 34.29; $h^{2B} = 69.38\%$; GAM = 7.03%), while F₂ populations showed h^{2B} of 61.33% and GAM of 7.15%. The gradual decline in heritability across generations reflects some contribution of dominance variance in hybrid populations. Similar low GCV with high heritability for DFMF was reported by (Gantayat *et al.*, 2025) [10] and (Billur *et al.*, 2025) [6] in sponge gourd. Low GCV for days to first male flower was also reported by (Kasera *et al.*, 2018) [13] and (Prabakaran *et al.*, 2025) [21] in sponge gourd, while (Abhijeet *et al.*, 2018) [1] noted that node number at first staminate flower recorded the highest GCV (36.20%), indicating greater variability when flowering is measured by node position rather than days.

Days to first female flower (DFFF) in parents ranged from 36.53 to 44.33 days (mean 40.55), with low GCV (5.70%), high h^{2B} (81.96%) and moderate GAM (10.65%). The narrow GCV-PCV difference across all three generations confirms minimal environmental modification of flowering time. In F₁ hybrids, DFFF ranged from 36.58 to 42.20 days (mean 39.43; $h^{2B} = 66.25\%$), and F₂ populations recorded h^{2B} of 56.88%, reflecting reduced additive variance in segregating populations. Node number of first male flower (NNMF) showed low GCV (3.31%) and PCV (4.42%) with moderate h^{2B} (56.11%) and low GAM (5.11%) in parents, declining sharply to h^{2B} of 34.95% in F₁ and 16.47% in F₂, with consistently very low GAM. This pattern indicates the predominance of non-additive gene action for NNMF, making early-generation selection ineffective. Node number of first female flower (NNFF) showed a comparable decline from 61.23% (parents) to 32.42% (F₂), confirming substantial dominance variance. Hybridization-based approaches are more appropriate for improving these traits, consistent with observations of (Annigeri 2020) [4].

High heritability with moderate genetic advance for days to first female flower was similarly observed by (Kasera *et al.*, 2018) [13] with $h^2 = 90.4\%$ and Saudamini (Ray *et al.*, 2021) [24] in sponge gourd. Days to first harvest (DFH) ranged from 43.50 to 53.67 days (mean 48.79) in parents, with low GCV (8.07%) but very high h^{2B} (94.30%) and moderate

GAM (16.16%), indicating strong additive genetic control. This pattern persisted across generations: F_1 $h^2B = 79.69\%$ and F_2 $h^2B = 71.24\%$, confirming that selection for early harvest will be reliable. Vine length (VL) showed moderate h^2B (71.39%) and moderate GAM (12.36%) in parents, declining to 43.73% in F_2 , suggesting partial non-additive contribution in segregating populations. Number of primary branches (NPB) recorded high h^2B (90.54%) and moderate GAM (15.86%) in parents, declining to 44.36% in F_2 , consistent with involvement of dominance variance in branching habit. High heritability for days to first harvest was corroborated by (Prabakaran *et al.*, 2025) [21] and (Priyanka *et al.*, 2025) [22] in sponge gourd.

Yield and Yield-Contributing Characters

Average fruit weight (AFW) ranged from 113.72 to 168.29 g (mean 140.38 g) in parents, with moderate GCV (10.96%), high h^2B (80.68%) and high GAM (20.31%), collectively indicating additive gene action and good scope for mass selection. In F_1 hybrids, AFW showed h^2B of 65.46% and GAM of 11.24%, and F_2 populations recorded h^2B of 54.67% and GAM of 10.55%. The slight decline reflects modest inbreeding depression and some non-additive contribution. These results are in agreement with (Gantayat *et al.*, 2025) [10] and Aslam *et al.*, (2024) [5]. High heritability coupled with high genetic advance for average fruit weight was similarly documented by (Abhijeet *et al.*, 2018) [1], (Kasera *et al.*, 2018) [13] with $h^2 = 89.4\%$ and $GA\% = 49.85\%$, (Singh *et al.*, 2019) [25], (Annigeri 2020) [4] with $h^2 = 71.8\%$ and $GA\% = 33.6\%$, (Kumar *et al.*, 2020) [16], (Sashi Suman *et al.*, 2024) [23] and (Prabakaran *et al.*, 2025) [21] in sponge gourd.

Fruit length (FL) emerged as one of the most selection-responsive traits. Parents showed high GCV (15.73%), very high h^2B (96.99%) and very high GAM (31.96%) the most favourable combination for selection response. In F_1 hybrids, h^2B was 87.18% and GAM 19.99%, while F_2 populations recorded h^2B of 82.82% and GAM of 19.87%. The uniformly high estimates across all generations confirm strong additive genetic control and predict rapid, consistent gains from selection for fruit length. Fruit diameter (FD) showed high h^2B in parents (82.28%) but low GAM (11.18%), declining sharply in F_1 (56.20%; GAM 5.42%) and F_2 (46.10%; GAM 5.36%), indicating notable dominance variance that limits early-generation selection utility. Very high heritability and high genetic advance for fruit length were similarly reported by (Singh *et al.*, 2019) [25] [25], (Kumar *et al.*, 2020) [16], (Kumar *et al.*, 2022) [18] and (Prabakaran *et al.*, 2025) [21] in sponge gourd.

Number of fruits per plant (NFP) is a primary yield determinant in sponge gourd. In parents, NFP ranged from 12.53 to 23.67 (mean 18.17), with high GCV (18.97%), very high h^2B (94.89%) and very high GAM (38.12%), providing compelling evidence for additive inheritance. In F_1 hybrids, h^2B was 81.43% and GAM 21.38%, and F_2 populations showed h^2B of 70.92% and GAM of 20.91%. The persistent high heritability and GAM across all three generations confirm the effectiveness of early-generation selection for NFP. (Abhijeet *et al.*, 2018) [1] and (Bisen *et al.*, 2016) [7] similarly reported high GCV and heritability for this trait. High heritability and high genetic advance for number of fruits per plant were reported by (Kasera *et al.*, 2018) [13] with $h^2 = 92.8\%$ and $GA\% = 49.83\%$, (Singh *et al.*, 2019) [25] with $h^2 = 80.1\%$ and $GA\% = 39.2\%$, (Annigeri 2020) [4]

with $h^2 = 76.4\%$ and $GA\% = 38.2\%$, (Kumar *et al.*, 2020) [16] with $h^2 = 92.49\%$, (Kumar *et al.*, 2022) [18], (Kousthubha *et al.*, 2023) [14] and (Prabakaran *et al.*, 2025) [21] in sponge gourd.

Fruit yield per plant (FY) recorded the highest GAM among all characters: 26.94% GCV, 96.51% h^2B and 54.60% GAM in parents, the most desirable combination a plant breeder can encounter, confirming overwhelming additive genetic control and predicting substantial gains from selection. In F_1 hybrids, FY ranged from 2.05 to 4.06 kg (mean 2.89 kg; $h^2B = 85.41\%$; GAM = 31.59%), and F_2 populations recorded h^2B of 77.02% and GAM of 30.55%. The uniformly high GAM (>30%) across all generations strongly supports direct selection for FY in any generation. Fruit yield per plot (FYPP) closely mirrored FY (parents: GCV = 26.84%; $h^2B = 93.75\%$; GAM = 53.61%), as expected. These findings are consistent with Billur *et al.*, (2025) [6], Abhijeet *et al.*, (2018) [1] and Bisen *et al.*, (2016) [7]. These findings conform with Singh *et al.*, (2019) [25] reporting $h^2 = 82.4\%$ and $GA\% = 37.8\%$; Annigeri (2020) [4] with GCV = 29.6% and PCV = 34.8%; Saudamini Ray *et al.*, (2021) [24] with $h^2 = 84.3\%$; (Kumar *et al.*, 2022) [18]; Sashi Suman *et al.*, (2024) [23] with GCV = 24.96%; and (Prabakaran *et al.*, 2025) [21] and (Gantayat *et al.*, 2025) [10] in sponge gourd, all reporting high GCV, heritability and genetic advance for fruit yield per plant.

Quality Characters

Dry matter content (DM) showed moderate GCV (10.92%), high h^2B (90.72%) and high GAM (21.45%) in parents, indicating additive gene effects and good scope for selection. Both F_1 ($h^2B = 74.87\%$; GAM = 12.13%) and F_2 ($h^2B = 68.76\%$; GAM = 11.93%) maintained relatively high heritability, suggesting persistent genetic control across generations. Total soluble solids (TSS) showed low GCV (3.88%) and moderate h^2B (61.40%) in parents, but heritability declined steeply to 26.53% in F_1 and 29.84% in F_2 , with very low GAM throughout (2.36-6.27%), clearly indicating substantial non-additive gene influence and environmental sensitivity. Selection for TSS in early generations is therefore unlikely to be productive. High heritability for dry matter content was similarly noted by (Kumar *et al.*, 2019) [15] and (Kumar *et al.*, 2022) [18] in sponge gourd.

Non-reducing sugar (NRS) showed a favourable pattern with high h^2B (87.61%) and moderate GAM (19.94%) in parents, persisting at high levels in F_1 (73.14%) and F_2 (66.29%), suggesting predominantly additive genetic control. Total sugar (TS) similarly showed high h^2B (87.31%) and moderate GAM (16.30%) in parents. Reducing sugar (RS) showed moderate h^2B in parents (75.38%) declining progressively in F_1 (49.32%) and F_2 (47.51%), indicating partial dominance involvement. Ascorbic acid content (ASC) showed moderate h^2B (59.49%) with low GAM (6.66%) in parents, declining further in F_1 (43.60%) and F_2 (36.97%), confirming the influence of non-additive gene action and environmental factors on this biochemical trait. Marker-assisted selection in advanced generations would be more appropriate for ASC improvement. High heritability for sugar fractions was corroborated by (Kumar *et al.*, 2019) [15] in sponge gourd, indicating the scope for simultaneous improvement of yield and quality characters.

Shelf life (SL) emerged as one of the most promising traits for direct selection: high GCV (15.84%), very high h^2_B (96.34%) and very high GAM (32.08%) in parents, remaining high in F_1 (h^2_B = 83.80%; GAM = 18.85%) and F_2 (h^2_B = 80.84%; GAM = 18.87%). The consistently high heritability and high GAM across all three populations confirm additive gene control of shelf life and predict

excellent response to selection. Genotypes with SL exceeding 8 days would be particularly valuable for distant market supply chains. These results corroborate the findings of (Gantayat *et al.*, 2025)^[10] and (Amulya *et al.*, 2025)^[3]. Comparable high heritability estimates for fruit quality traits were reported by (Sashi Suman *et al.*, 2024)^[23], (Yadav *et al.*, 2024)^[29] and (Vidya *et al.*, 2025)^[28] in sponge gourd.

Table 1: Analysis of Variance (Mean Sum of Squares) for twenty characters in sponge gourd — Parents, F_1 Hybrids and F_2 Populations (Kharif 2024-25)

S. No.	Characters	Parents			F_1 Hybrids			F_2 Populations		
		Replications (df = 2)	Treatments (df = 9)	Error (df = 18)	Replications (df = 2)	Treatments (df = 44)	Error (df = 88)	Replications (df = 2)	Treatments (df = 44)	Error (df = 88)
1	Days to First Male Flower Appearance	0.649	16.196**	0.549	2.011	6.767**	0.868	2.391	8.592**	1.492
2	Days to First Female Flower Appearance	2.465	17.218**	1.177	0.955	6.879**	0.998	0.531	8.906**	1.796
3	Node No. of First Male Flower	0.024	0.304**	0.063	0.067	0.128**	0.049	0.031	0.165*	0.104
4	Node No. of First Female Flower	0.041	0.750**	0.131	0.047	0.337**	0.091	0.006	0.449**	0.184
5	Days to First Harvest	0.330	47.411**	0.936	1.942	18.781**	1.470	1.404	22.629**	2.684
6	Vine Length (m)	0.016	0.300**	0.035	0.008	0.185**	0.048	0.182	0.216**	0.065
7	No. of Primary Branches per Plant	0.268*	1.393**	0.047	0.093	0.748**	0.162	0.149	0.684**	0.202
8	Average Fruit Weight (g)	37.544	767.131**	56.715	9.380	302.964**	45.315	3.530	336.425**	72.847
9	Fruit Length (cm)	2.545**	33.590**	0.344	0.351	14.590**	0.682	2.461	14.617**	0.945
10	Fruit Diameter (cm)	0.003	0.135**	0.009	0.094**	0.054**	0.011	0.023	0.068**	0.019
11	No. of Fruits per Plant	0.121	36.291**	0.640	0.316	18.640**	1.316	0.590	16.428**	1.975
12	Fruit Yield per Plant (kg)	0.021	1.463**	0.017	0.008	0.728**	0.039	0.013	0.578**	0.052
13	Fruit Yield per Plot (kg)	0.763	52.824**	1.148	0.304	26.199**	1.411	0.472	20.820**	1.883
14	Dry Matter Content (%)	0.033	1.441**	0.048	0.017	0.631**	0.063	0.144	0.667**	0.088
15	Total Soluble Solids (°Brix)	0.001	0.090**	0.016	0.025	0.049**	0.024	0.048	0.058**	0.025
16	Non-reducing Sugar (%)	0.113	1.243**	0.056	0.011	0.582**	0.063	0.026	0.685**	0.099
17	Reducing Sugar (%)	0.022	0.171**	0.017	0.013	0.083**	0.021	0.000	0.090**	0.024
18	Total Sugar (%)	0.061	2.069**	0.096	0.129	0.858**	0.118	0.694*	0.916**	0.156
19	Ascorbic Acid (mg/100 g)	0.004	0.952**	0.176	0.066	0.478**	0.144	0.038	0.699**	0.253
20	Shelf Life (days)	0.215*	2.936**	0.037	0.068	1.284**	0.078	0.041	1.301**	0.095

** : Significant at 1% probability level; * : Significant at 5% probability level; values without marker: non-significant.

Table 2: Estimates of genetic variability, heritability and genetic advance in sponge gourd [*Luffa cylindrica* (L.) M. Roem.] for twenty characters across Parents, F_1 Hybrids and F_2 Populations

Character	Gen.	Max.	Min.	Mean	SE(m)±	GCV (%)	PCV (%)	h^2_B (%)	GA	GAM (%)
Days to First Male Flower (days)	Parents	38.12	31.50	35.29	0.43	6.47	6.80	90.47	4.48	12.70
	F_1 Hybrids	36.86	31.12	34.29	0.54	4.09	4.91	69.38	2.41	7.03
	F_2 Populations	37.90	31.95	34.78	0.71	4.42	5.65	61.33	2.49	7.15
Days to First Female Flower (days)	Parents	44.33	36.53	40.55	0.63	5.70	6.30	81.96	4.32	10.65
	F_1 Hybrids	42.20	36.58	39.43	0.58	3.55	4.36	66.25	2.35	5.96
	F_2 Populations	43.39	36.88	40.09	0.77	3.84	5.09	56.88	2.40	5.97
Node No. of First Male Flower	Parents	9.00	8.00	8.57	0.14	3.31	4.42	56.11	0.44	5.11
	F_1 Hybrids	8.73	7.94	8.38	0.13	1.93	3.27	34.95	0.20	2.36
	F_2 Populations	8.95	7.92	8.47	0.19	1.69	4.15	16.47	0.12	1.41
Node No. of First Female Flower	Parents	12.00	10.33	11.13	0.21	4.08	5.22	61.23	0.73	6.59
	F_1 Hybrids	11.77	10.20	10.92	0.17	2.62	3.81	47.40	0.40	3.73
	F_2 Populations	12.04	10.23	11.03	0.25	2.69	4.73	32.42	0.35	3.16
Days to First Harvest (days)	Parents	53.67	43.50	48.79	0.56	8.07	8.31	94.30	7.88	16.16
	F_1 Hybrids	52.24	42.48	47.24	0.70	5.08	5.70	79.69	4.42	9.36
	F_2 Populations	53.90	42.63	47.91	0.95	5.38	6.38	71.24	4.49	9.37
Vine Length (m)	Parents	4.70	3.78	4.19	0.11	7.09	8.39	71.39	0.52	12.36
	F_1 Hybrids	5.30	4.21	4.70	0.13	4.56	6.50	49.07	0.31	6.58
	F_2 Populations	4.95	3.84	4.38	0.15	5.12	7.75	43.73	0.31	6.99
No. of Primary Branches/Plant	Parents	9.46	7.26	8.29	0.13	8.08	8.49	90.54	1.31	15.86
	F_1 Hybrids	9.87	7.97	8.95	0.23	4.94	6.68	54.60	0.67	7.52
	F_2 Populations	9.44	7.50	8.37	0.26	4.79	7.19	44.36	0.55	6.58
Avg. Fruit Weight (g)	Parents	168.29	113.72	140.38	4.35	10.96	12.20	80.68	28.51	20.31
	F_1 Hybrids	161.94	117.42	137.63	3.89	6.73	8.32	65.46	15.47	11.24
	F_2 Populations	160.24	111.27	135.57	4.93	6.91	9.35	54.67	14.30	10.55

Fruit Length (cm)	Parents	27.00	15.43	21.16	0.34	15.73	15.97	96.99	6.76	31.96
	F ₁ Hybrids	25.76	16.28	20.74	0.48	10.38	11.12	87.18	4.15	19.99
	F ₂ Populations	25.52	15.66	20.17	0.56	10.58	11.63	82.82	4.01	19.87
Fruit Diameter (cm)	Parents	3.73	3.22	3.43	0.05	5.97	6.59	82.28	0.38	11.18
	F ₁ Hybrids	3.71	3.16	3.40	0.06	3.51	4.68	56.20	0.18	5.42
	F ₂ Populations	3.72	3.06	3.33	0.08	3.83	5.64	46.10	0.18	5.36
No. of Fruits/Plant	Parents	23.67	12.53	18.17	0.46	18.97	19.48	94.89	6.93	38.12
	F ₁ Hybrids	26.21	15.99	20.92	0.66	11.49	12.73	81.43	4.47	21.38
	F ₂ Populations	23.72	14.09	18.24	0.81	12.04	14.29	70.92	3.81	20.91
Fruit Yield/Plant (kg)	Parents	3.84	1.72	2.58	0.08	26.94	27.43	96.51	1.41	54.60
	F ₁ Hybrids	4.06	2.05	2.89	0.11	16.57	17.93	85.41	0.91	31.59
	F ₂ Populations	3.58	1.77	2.48	0.13	16.87	19.22	77.02	0.76	30.55
Fruit Yield/Plot (kg)	Parents	23.05	10.32	15.46	0.62	26.84	27.72	93.75	8.29	53.61
	F ₁ Hybrids	24.34	12.30	17.35	0.69	16.57	17.93	85.41	5.48	31.59
	F ₂ Populations	21.46	10.62	14.89	0.79	16.87	19.22	77.02	4.55	30.55
Dry Matter Content (%)	Parents	7.44	4.94	6.25	0.13	10.92	11.46	90.72	1.34	21.45
	F ₁ Hybrids	7.44	5.51	6.40	0.14	6.80	7.86	74.87	0.77	12.13
	F ₂ Populations	7.43	5.34	6.30	0.17	6.97	8.41	68.76	0.75	11.93
Total Soluble Solids (°Brix)	Parents	4.40	3.87	4.06	0.07	3.88	4.95	61.40	0.25	6.27
	F ₁ Hybrids	4.42	3.92	4.16	0.09	2.22	4.32	26.53	0.09	2.36
	F ₂ Populations	4.39	3.80	4.11	0.09	2.53	4.63	29.84	0.12	2.85
Non-reducing Sugar (%)	Parents	7.31	5.15	6.09	0.14	10.33	11.03	87.61	1.21	19.94
	F ₁ Hybrids	7.18	5.22	6.25	0.15	6.65	7.78	73.14	0.73	11.73
	F ₂ Populations	7.20	5.07	6.12	0.18	7.22	8.87	66.29	0.74	12.13
Reducing Sugar (%)	Parents	3.87	3.14	3.50	0.07	6.48	7.46	75.38	0.41	11.61
	F ₁ Hybrids	3.94	3.28	3.59	0.08	4.00	5.70	49.32	0.20	5.80
	F ₂ Populations	3.90	3.17	3.55	0.09	4.17	6.05	47.51	0.21	5.93
Total Sugar (%)	Parents	11.18	8.50	9.59	0.18	8.46	9.05	87.31	1.56	16.30
	F ₁ Hybrids	10.92	8.66	9.83	0.20	5.05	6.14	67.65	0.84	8.57
	F ₂ Populations	10.63	8.38	9.70	0.23	5.19	6.60	61.81	0.82	8.41
Ascorbic Acid (mg/100 g)	Parents	13.21	11.01	12.14	0.24	4.19	5.43	59.49	0.81	6.66
	F ₁ Hybrids	13.15	11.66	12.39	0.22	2.69	4.08	43.60	0.45	3.67
	F ₂ Populations	13.06	11.22	12.21	0.29	3.16	5.19	36.97	0.48	3.96
Shelf Life (days)	Parents	8.45	5.12	6.21	0.11	15.84	16.14	96.34	1.99	32.08
	F ₁ Hybrids	8.11	5.29	6.35	0.16	9.98	10.90	83.80	1.19	18.85
	F ₂ Populations	8.00	5.22	6.23	0.18	10.17	11.32	80.84	1.18	18.87

GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation; h^{2B} : Broad-sense Heritability; GA: Genetic Advance; GAM: Genetic Advance as% of Mean. $k = 2.063$ (5% selection intensity). Green cells: GAM $\geq 20\%$ (high); Yellow: 10-20% (moderate). Bold GCV: $\geq 20\%$; Bold h^{2B} : $\geq 60\%$; Bold GAM: $\geq 20\%$.

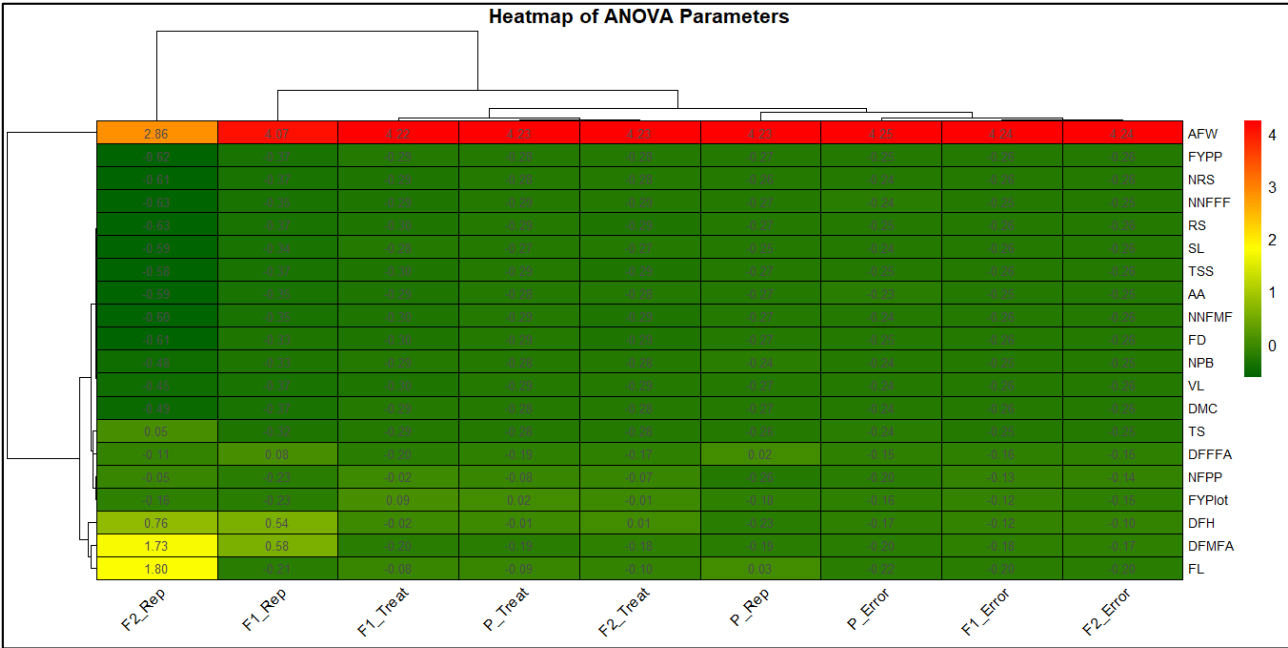


Fig 1: Analysis of Variance (Mean Sum of Squares) for twenty characters in sponge gourd Parents, F₁ Hybrids and F₂ Populations (Kharif 2024-25)

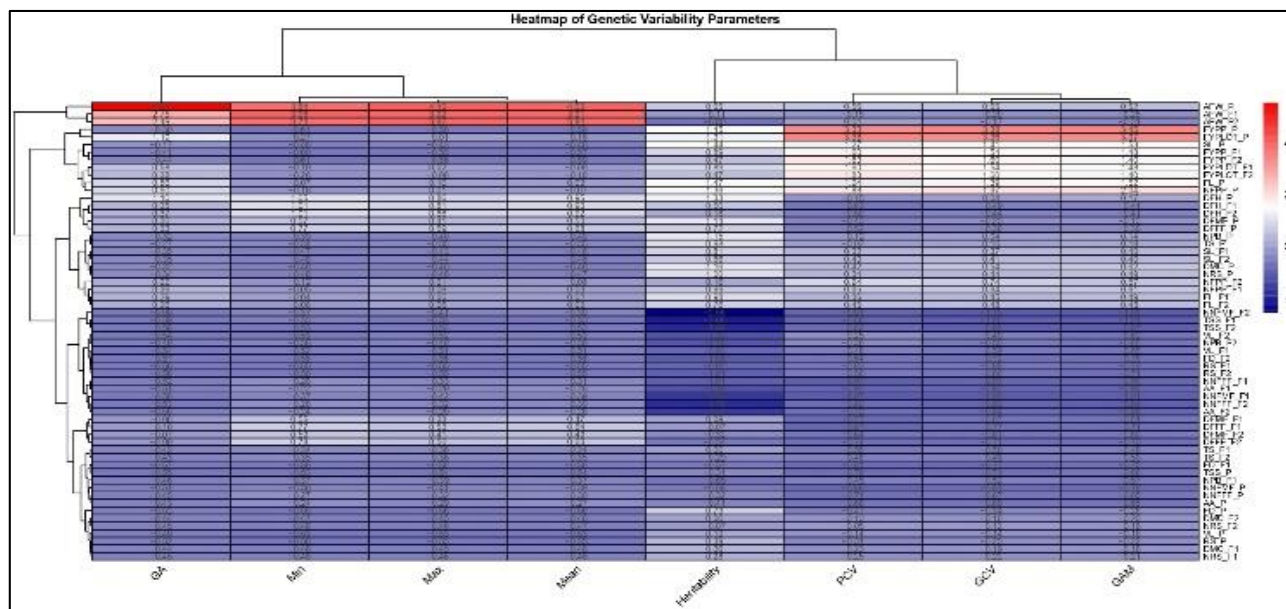


Fig 2: Estimates of genetic variability, heritability and genetic advance in sponge gourd [*Luffa cylindrica* (L.) M. Roem.] for twenty characters across Parents, F₁ Hybrids and F₂ Populations

Conclusion

The present investigation demonstrated the presence of substantial genetic variability among 100 sponge gourd genotypes for twenty morphological, yield and quality characters. High broad-sense heritability combined with high genetic advance as percentage of mean was recorded for fruit yield per plant ($h^2_B = 96.51\%$; GAM = 54.60%), fruit yield per plot (93.75%; 53.61%), number of fruits per plant (94.89%; 38.12%), shelf life (96.34%; 32.08%) and fruit length (96.99%; 31.96%), confirming additive gene action and high scope for direct selection. Dry matter content, average fruit weight, non-reducing sugar and total sugar showed high heritability with moderate GAM, suggesting partial non-additive involvement. Node number of first male and female flower, total soluble solids and ascorbic acid content exhibited low to moderate heritability with low GAM, limiting early-generation selection; hybridization breeding and progeny testing in advanced generations are recommended for these traits. Collectively, the genetic parameters provide a robust quantitative framework for designing effective selection-based and hybridization-based improvement strategies for sponge gourd [*Luffa cylindrica* (L.) M. Roem.].

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