**Analysis of Genetic Variability and Potential for Genetic Improvement in Sponge Gourd [*Luffa cylindrica* (L.) Roem.] through Heritability and Genetic Advance**

**ABSTRACT**

This study assessed the genetic variability, heritability, and genetic progress of 25 genotypes of sponge gourd [*Luffa cylindrica* L. (Roem.)]. In this randomized block design experiment with three replications, twenty yield and quality characteristics were evaluated. The significant differences between genotypes discovered by the analysis of variance demonstrate the high level of genetic diversity. Traits like dry matter content, chlorophyll content, vine length, and number of primary branches showed high genotypic and phenotypic coefficients of variation, heritability, and genetic advancement, suggesting their potential for effective selection and genetic advancement. Certain genotypes, such as VRSG-517 and NDSG-23-1, showed superior performance in yield from that of the check variety (Pusa Chikni). The findings indicate that traditional breeding operations can consistently address these traits to produce improved cultivars of sponge gourd.

*Key words: GCV, PCV, genetic advance, genetic variability, heritability, Sponge gourd.*

1. **INTRODUCTION**

Sponge gourd [*Luffa cylindrical* (L.) Roem.], a climbing vine belonging to the Cucurbitaceae family having chromosome number of 2n = 2x = 26 is said to have originated in Africa. It goes by several names, including Egyptian cucumber, vegetable sponge, and dishcloth gourd (Cho *et al*., 2015; Gong *et al.,* 2024). It is widely grown throughout Asia and Africa and is prized for its gastronomic and therapeutic properties; the mature fruits are used as natural sponges, while the younger ones are eaten as vegetables.

There are seven tropical species in the genus Luffa. Among these, *L*. *cylindrica* is showing great promise, particularly in India, where cultivation most likely started. There are 825 species and 118 genera in the Cucurbitaceae family (Kallo, 1993).

The highest producer of sponge gourd in the world is China. India is also a major producer, ranking second globally. Sponge gourd is typically farmed in a somewhat limited area for locals in India, taking up around 7.21 lakh hectares and yielding 12.87 lakh tons of fruit annually. This crop yields 10.52 tons per hectare **(**Anonymous, 2022**).** India is a major producer of sponge gourd, with significant cultivation in states like Uttar Pradesh, Bihar and West Bengal**.**

Sponge gourd’s nutritional and medicinal values make it an attractive crop to enhance and diversity food systems and improve food and nutrition security. However, it remains an undervalued, underutilized, and neglected cucurbit crop due to poor research and investment support **(**Kumari *et al*., 2019**).** However, there is increased interest in the cultivation of sponge gourd due to high market demand (Mim *et al*., 2021). The escalating demand and niche potential of the crop will require the development of high-yielding and locally adapted varieties with consumer and market-preferred traits.

1. **MATERIALS AND METHOD**

The present investigation was carried out during the summer season of 2023-2024 at the Main Experimental Station, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.), India using 25 sponge gourd genotypes. The experiment followed the Randomized Block Design (RBD) with three replications.

Sponge gourd is propagated through seeds. The seeds are sown in raised beds, furrows and pits. The seeds are soaked in water for 12-24 hours before sowing to hasten the germination. In this investigation, spacing of 3.0m x 0.5m is maintained with a plot size of 3.0 x 3.0 m2. In order to ensure good crop growth, the cultivation followed the tactics and guidelines that were recommended. Five randomly chosen plants from each plot were taken into consideration for recording observations for sixteen different yield and quality traits. The data were statistically analysed using analysis of variance (ANOVA), methodology outlined by (Panse and Sukhatme, 2000) and using the formula developed by (Burton and De Vane 1953), the genotypic and phenotypic coefficients of variability for each trait were calculated. According to the guidelines of (Weber and Moorthy, 1952) broad sense heritability was estimated and the genetic gain was computed using the method recommended by (Johnson *et al*.,1955).

1. **RESULTS AND DISCUSSION**

The analysis of variance, conducted in accordance with the method outlined by Panse and Sukhatme (2000), revealed highly significant differences among the genotypes for all the traits evaluated, indicating substantial genetic variability within the experimental material.

The variance analysis revealed significant differences among several genotypes, suggesting that the genotypes used in the experiment exhibited a high degree of variability across a range of attributes. They are eligible for the further genetic research because of their diversity (Table-1). The relative differences in variability between, several attributes are listed (Table-2). Comprehensive results are provided for each of the twenty traits, including a average values, range, phenotypic and genotypic coefficients of variation (PCV and GCV), broad-sense heritability (h2), and predicted genetic advancement as a percentage of the mean (GAM).

**Table 1: Analysis of variance (mean squares) for twenty characters in sponge gourd.**

|  |  |  |
| --- | --- | --- |
| **Sl. No.** | **Traits** | **Source of variation** |
| **D.F.** | **Replication** | **Treatments** | **Error** |
| **2** | **24** | **48** |
| 1. | Days to first staminate flower anthesis | 2.77 | 49.53\*\* | 3.55 |
| 2. | Days to first pistillate flower anthesis | 5.99 | 44.52\*\* | 4.18 |
| 3. | Node number of the first staminate flower appearance  | 0.104 | 0.705\*\* | 0.134 |
| 4. | Node number of the first pistillate flower appearance  | 0.008 | 0.568\*\* | 0.256 |
| 5. | Number of primary branches per plant  | 0.075 | 1.359\*\* | 0.069 |
| 6. | Internodal length (cm) | 1.193 | 0.868\*\* | 0.457 |
| 7. | Petiole length (cm) | 0.05 | 1.11\*\* | 0.39 |
| 8. | Days to first fruit harvest  | 3.28 | 47.35\*\* | 10.14 |
| 9. | Fruit length (cm) | 0.32 | 19.09\*\* | 1.76 |
| 10. | Fruit width (cm)  | 0.072 | 0.299\*\* | 0.054 |
| 11. | Average fruit weight (g) | 11.16 | 92.20\*\* | 46.70 |
| 12. | Number of fruit per plant  | 0.238 | 6.453\*\* | 0.562 |
| 13. | Vine length (m) | 0.004 | 2.196\*\* | 0.130 |
| 14. | T.S.S 0B  | 0.019 | 1.116\*\* | 0.030 |
| 15. | Dry matter % | 0.093 | 7.044\*\* | 0.073 |
| 16. | Moisture content % | 0.084 | 7.036\*\* | 0.080 |
| 17. | Ascorbic acid (mg/100) | 0.073 | 0.471\*\* | 0.014 |
| 18. | Chlorophyll content (mg/g) | 0.014 | 0.870\*\* | 0.016 |
| 19. | Yield per plant (kg) | 0.022 | 0.137\*\* | 0.014 |
| 20. | Yield (q/ha) | 47.99 | 479.06\*\* | 50.70 |

The genotype VRSG-154 showed early for days to first staminate flower anthesis (30.67 days), earliest days for anthesis of first pistillate flower was recorded in genotype VRSG-68 (38.33), node no. for first staminate flower appearance was highest in genotype VRSG-11 (5.40), node no. for first pistillate flower appearance was highest in genotype Manipur (local), Maximum primary branches per plant was recorded in NDSG-23-8 (5.03), highest value of internodal length was noticed for NDSG-23-4 (9.50 cm), maximum petiole length was reported in the genotype VRSG-68-1 (9.09cm), days to first fruit harvest was earliest in the genotype VRSG-68 (48.17 days), Highest fruit length was noticed in Pusa Chikni (28.65 cm), Highest fruit width was observed significantly in the genotype VRSG-66 (4.37cm) , average fruit weight was highest in VRSG-2-15 (142gm), highest number of fruits plant-1 was noticed in NDSG-23-1 (14.95), longest vine was observed at NDSG-23-4 (6.16m), highest T.S.S 0B was observed in Manipur (local) (6.13), maximum amount of dry matter was observed from the genotype Manipur (local) (9.01), maximum amount of moisture content was observed from the genotype NDSG-23-8 (96.40), the ascorbic was recorded highest in the genotype VRSG-84 (3.93), the chlorophyll content was found to be the highest in the genotype (NDSG-3) 3.62, the highest yield per plant was found in the genotype VRSG-5-17 (2.03 Kg), the highest yield (q/ha) was observed in the genotype VRSG-5-17 (122.49) . Similar findings were reported by Abhijeet *et al.,* (2018), Sharma *et al.,* (2023), Madhavi *et al.,* (2023), Mohiddin *et al.,* (2022), Dubey *et al.,* (2022), Annigeri *et al.,* (2023).

**Table.2. Estimates of range, grand mean, 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 twenty characters in sponge gourd germplasm.**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Characters** | **Mean** | **Range** | **GCV (%)** | **PCV (%)** | **Heritability****(%)** | **GA** | **GA% mean** |
| **Min** | **Max** |
| Days to first staminate flower appearance  | 36.83 | 30.67 | 43.67 | 10.63 | 11.80 | 81.18 | 7.27 | 19.73 |
| Days to first pistillate flower appearance  | 44.34 | 38.33 | 50.59 | 8.27 | 9.47 | 76.27 | 6.60 | 14.88 |
| Node number to first staminate flower appearance  | 4.74 | 3.53 | 5.40 | 9.21 | 12.02 | 58.71 | 0.69 | 14.54 |
| Node number to first pistillate flower appearance  | 7.63 | 6.67 | 8.51 | 4.22 | 7.86 | 28.81 | 0.36 | 4.66 |
| Number of primary branches  | 3.63 | 2.83 | 5.03 | 18.07 | 19.47 | 86.13 | 1.25 | 34.54 |
| Internodal length (cm)  | 8.28 | 7.32 | 9.50 | 4.47 | 9.31 | 23.09 | 0.37 | 4.43 |
| Petiole length (cm)  | 8.14 | 6.70 | 9.09 | 6.06 | 9.74 | 38.62 | 0.63 | 7.75 |
| Days to first fruit harvest  | 54.25 | 48.17 | 60.59 | 6.49 | 8.75 | 55.04 | 5.38 | 9.92 |
| Fruit length (cm)  | 21.96 | 18.17 | 28.65 | 10.94 | 12.50 | 76.64 | 4.33 | 19.73 |
| Fruit width (cm) | 3.99 | 3.32 | 4.37 | 7.15 | 9.22 | 60.21 | 0.46 | 11.44 |
| Average fruit weight (g)  | 132.58 | 121.00 | 142.00 | 2.94 | 5.93 | 24.51 | 3.97 | 3.00 |
| Number of fruit per plant  | 12.08 | 9.53 | 14.95 | 11.60 | 13.15 | 77.73 | 2.54 | 21.06 |
| Vine length (m)  | 4.37 | 2.91 | 6.16 | 18.99 | 20.71 | 84.09 | 1.57 | 35.88 |
| T.S.S (0B) | 4.84 | 3.87 | 6.13 | 12.42 | 12.93 | 92.26 | 1.19 | 24.58 |
| Dry matter (%)  | 5.80 | 3.60 | 9.01 | 26.30 | 26.71 | 96.96 | 3.09 | 53.34 |
| Moisture content (%)  | 94.20 | 90.99 | 96.40 | 1.62 | 1.64 | 96.65 | 3.08 | 3.27 |
| Ascorbic acid (mg/100g)  | 3.13 | 2.50 | 3.93 | 12.49 | 13.05 | 91.59 | 0.77 | 24.62 |
| Chlorophyll content (mg/g)  | 2.68 | 1.66 | 3.62 | 19.89 | 20.42 | 94.84 | 1.07 | 39.90 |
| Yield per plant (kg)  | 1.60 | 1.26 | 2.03 | 12.68 | 14.61 | 72.25 | 0.36 | 22.65 |
| Yield (q/ha)  | 95.84 | 73.68 | 122.49 | 12.47 | 14.51 | 73.80 | 21.15 | 22.07 |

* 1. **Genotypic and Phenotypic coefficient of variation**

The estimates of phenotypic coefficients of variations (PCV) were higher than genotypic coefficient of variations (GCV) for all the characters. The highest (>20%) phenotypic as well as genotypic coefficients of variation were observed in dry matter % (26.71% and 26.30%). Moderate (10-20%) estimates of PCV and GCV were estimated for days to first staminate flower appearance (11.80% and 10.63%), node number to first staminate flower anthesis (12.02% and 9.21%), number of primary branches (19.47% and 18.07%) , fruit length (12.50% and 10.94%), number of fruit per plant (13.15% and 11.60%), T.S.S. (12.93% and 12.42%), ascorbic acid (13.05% and 12.49%), yield per plant (14.61% and 12.68%), and yield (q/ha) (14.51 % and 12.47% ). The phenotypic and genotypic coefficients of variations were lower (<10%) for days to first pistillate flower anthesis (9.47% and 8.27%), node number of first pistillate flower anthesis (7.86% and 4.22%), internodal length (9.31% and 4.47), petiole length (9.74% and 6.06%), days to first fruit harvest (8.75% and 6.49%), fruit width (9.22% and 7.15%), average fruit weight (5.93% and 2.94%), moisture content (1.64% and 1.62%). Similar results have been reported by Som *et al.,* (2020).

**Fig. 1. Effect of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) for fourteen characters of sponge gourd**

* 1. **Heritability and genetic advance**

High estimates of heritability (>80%) were recorded in the characters days to first staminate flower anthesis (81.18%), number of primary branches (86.13%), vine length (84.09%), T.S.S 0B (92.26%), dry matter (96.96%), moisture content (96.65%), ascorbic acid (91.59%), chlorophyll content (94.84%). The moderate heritability (>60% and <80%) was recorded in following characters: fruit width (60.21%), yield (q/ha) (73.80%), days to first pistillate flower anthesis (76.27%), fruit length (76.64%), no. of fruits plant-1 (77.73%), and yield (q/ha) (75.25%). Lower heritability (<60%) was recorded in the following characters : node number to frist pistillate flower anthesis ( (28.81%), internodal length (23.09%), petiole length (38.62%) and average fruit weight (24.51%), node number to first staminate flower anthesis (58.71%) , days to first fruit harvest (55.04%). The result are conformity with the study of Singh *et al*., (2023) , the high estimates of heritability in broad sense (>80%) were observed for node number to first pistillate flower (96%), node number to first staminate flower anthesis (91%), vine length at last harvest (91%), marketable fruit yield per plant (90%), no. of fruits plant-1 (87%), marketable fruit yield per plant (90%), average fruit weight (87%), number of primary branches per vine at last harvest (86%), whereas moderate heritability in broad sense (>60% and 80%) were noticed for days to first pistillate flower anthesis (70%), and number of nodes per vine at last harvest (78%). Days to first fruit harvest and fruit diameter (54%) showed low heritability (<50%).

Highest value of genetic advance in percent of mean was shown by dry matter (53.34%). While average fruit weight exhibited the lowest value (3.00%) for this parameter. The characters which observed very high estimates of genetic advance was yield (q/ha) (21.15) and lowest genetic advance was estimated for fruit yield per plant (0.36) and node number to first pistillate flower anthesis (0.36). Similar result was also reported by Yadav *et al*., (2024). They recorded high genetic advance as per cent of mean in fruit yield per plant (73.84%), followed by number of fruits per plant (56.32%), and internodal length (41.73%) while low genetic advance in per cent of mean found in days to first fruit harvest (9.83%) followed by days to first male flower appearance (9.81%) and days to first female flower appearance (12.93%). Similar result was also reported by Yadav *et al*., (2024) for traits like number of fruits per plant and yield (q/ha).

1. **CONCLUSION**

The current study showed that the experimental material had a significant exploitable variability in twenty yield and quality related traits. The phenotypic coefficient of variation (PCV) was generally higher than the genotypic coefficient of variation (GCV), indicating the presence of both genetic and environmental influences, though the relatively small difference suggests that genetic factors had a predominant role in the expression of the traits. Certain genotypes, such as VRSG-517 and NDSG-23-1, showed superior performance in yield from that of the check variety (Pusa Chikni). Overall, the genetic variability, high heritability, and substantial genetic advance observed in traits like dry matter, chlorophyll content, vine length, number of primary branches per plant, suggest that these traits offer significant potential for improvement through conventional breeding methods in sponge gourd.

Disclaimer (Artificial intelligence)

Option 1:

We declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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