

DECIPHERING THE GENETIC ARCHITECTURE OF FRUIT YIELD IN THE UNDERUTILIZED CUCURBIT *SOLENA AMPLEXICAULIS* (LAM.) GANDHI THROUGH VARIABILITY, CORRELATION, AND PATH COEFFICIENT ANALYSES

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ABSTRACT

Solena amplexicaulis (Lam.) Gandhi is an underutilized cucurbitaceous vegetable crop with considerable potential for nutritional and medicinal applications. The present investigation was conducted to evaluate the degree of genetic variability, character association, direct and indirect effects of yield attributing traits among among eighteen breeding lines of *S. amplexicaulis*. The experiment was set up in a randomized block design with three replications, and twelve quantitative characters were assessed. Significant genotype differences were identified by analysis of variance for each attribute under investigation, revealing a high level of genetic diversity. High genotypic coefficient of variation and phenotypic coefficients of variation were recorded for fruit yield per plant (40.93 and 41.11%), number of fruits per plant (35.72 and 35.81%), node number of 1st female flower (24.69 and 25.53%), and fruit length (21.05 and 21.84%), suggesting ample scope for selection. High heritability coupled with high genetic advance as percentage of mean was recorded for fruit yield (99.12% and 83.94%), number of fruits per plant (99.49% and 73.40%), node number of 1st female flower (93.52% and 49.18%), fruit length (92.90% and 41.81%), and average internode length (99.25% and 37.71%), indicating the prevalence of additive gene action. Analysis of genotypic and phenotypic correlations showed a positive and considerable association among the number of fruits per plant ($r_g = 0.991$, $r_p = 0.988$), fruit weight ($r_g = 0.927$, $r_p = 0.904$), fruit length ($r_g = 0.891$, $r_p = 0.858$), and number of primary branches per plant ($r_g = 0.716$, $r_p = 0.648$). The number of fruits per plant had the highest positive direct effect on fruit yield (0.7713), followed by fruit weight (0.1802) and fruit length (0.0485), as shown by path coefficient analysis. The low residual effect (0.0353) suggested that the studied traits accounted for most of the variation in fruit yield. The findings indicate that selection based on fruit weight, fruit length, number of primary branches, and number of fruits per plant would be effective for the genetic improvement of fruit yield in *S. amplexicaulis*.

KEYWORDS: *Solena amplexicaulis*, genetic variability, correlation, heritability, genetic advance, path coefficient analysis, breeding lines.

INTRODUCTION

Solena amplexicaulis (Lam.) Gandhi, is an underexploited perennial vegetable crop belonging to the family Cucurbitaceae. It is commonly known as creeping cucumber, with a chromosome number $2n=24$. The crop is native to India and widely distributed in several South Asian countries including Sri Lanka, Nepal, Bangladesh, Myanmar, Indonesia, Vietnam, and China. In India, it is commonly found growing wild in the deciduous forests and rural regions of Andhra Pradesh, Odisha, Kerala, Maharashtra, and Tamil Nadu. The crop is known by different vernacular names such as Ban Kundari, Tarali, and Amantphool in Hindi, Karolu in Kannada, Thiyyadonda in Telugu, and Karakia in Odia. Despite its wide geographical distribution and traditional importance, *S. amplexicaulis* remains neglected and poorly explored compared to commercially cultivated vegetables. Underexploited vegetable crops have gained considerable attention in recent years because of their potential contribution towards nutritional security, sustainable agriculture, poverty alleviation, and livelihood improvement of rural communities (Padulosi et al., 2013; Mabhaudhi et al., 2022; Ali and Bhattacharjee, 2023). These crops are often rich in essential nutrients and can thrive under marginal environmental conditions with minimal agricultural inputs. *Solena amplexicaulis* is considered an important source of vitamins, minerals, carbohydrates, proteins, fats, and several bioactive compounds that help protect rural populations, especially children, from malnutrition and nutrient deficiency-related disorders (Ali and Bhattacharjee, 2023; Sarkar et al., 2023). Tender fruits are often consumed raw as salads or cooked as vegetables, while the leaves are used as leafy greens in certain parts of India. Being hardy in nature, the crop can tolerate adverse climatic and soil conditions, making it suitable for cultivation in low-input farming systems and under changing climate scenarios. Apart from its nutritional importance, *S. amplexicaulis* possesses remarkable medicinal and therapeutic properties. Different

plant parts have been used in traditional medicine to alleviate various ailments by tribal and rural communities of South India. The Paliyar tribal community of Tamil Nadu traditionally uses leaf extracts of the plant for the treatment of inflammation-related disorders and jaundice in the form of decoction. Additionally, leaf extracts are used to treat skin diseases, lesions, wound healing and possess anti-inflammatory properties. (Aruna et al., 2011; Venkatachalapathi et al., 2011). The tuberous roots are known to possess several medicinal properties including antioxidant, antimicrobial, anti-inflammatory, antinociceptive, and antidiabetic activities. Traditionally, the roots are used in the treatment of anorexia, digestive disorders, asthma, gonorrhoea, spermatorrhoea, and flatulence (Peter, 2007; Karthika and Paulsamy, 2014). Scientific investigations have revealed the presence of several pharmacologically important secondary metabolites in *S. amplexicaulis*, including alkaloids, flavonoids, glycosides, saponins, and terpenoids (Krishnamoorthy and Paulsamy, 2014; Karthika and Paulsamy, 2015). These compounds contribute significantly to the therapeutic potential of the plant. Methanolic extracts of the stem and roots have shown significant antioxidant and antimicrobial activities against various pathogenic microorganisms. Stem bark extracts also exhibited antifungal activity against *Aspergillus ustus*, *Aspergillus niger*, and *Aspergillus ochraceus*, indicating their possible use as antimycotic (Fakruddin et al., 2012; Kabir et al., 2014). Furthermore, several studies have revealed antibacterial, antifungal, antioxidant, cytotoxic, anti-inflammatory, analgesic, and antidiabetic activities in *S. amplexicaulis*, highlighting its considerable pharmacological potential (Kabir et al., 2014; Venkatachalapathi et al., 2019). The whole plant has also been identified as a potential natural source of antioxidant compounds, which may be useful in preventing oxidative stress-related disorders. Despite its immense nutritional and medicinal value, *S. amplexicaulis* has received very little scientific attention. In recent decades, research efforts have mainly focused on commercially important vegetables such as tomato, brinjal, chilli, cucumber, cauliflower, and cabbage, while underutilized crops like *S. amplexicaulis* remain largely unexplored. Moreover, increasing environmental degradation, genetic erosion, habitat destruction and climate change are threatening the natural existence of this valuable crop (Khoury et al., 2022; Mabhaudhi et al., 2022; Dubey et al., 2024; Khundrakpam and Kotiyal, 2024). Therefore, systematic studies on morphological, biochemical, and genetic diversity, along with conservation and sustainable utilization strategies, are urgently required. Such research would not only help in preventing the extinction of this neglected vegetable crop but also contribute towards nutritional security, medicinal applications, climate-resilient agriculture, and livelihood enhancement among rural populations.

MATERIALS AND METHODS

Experimental material and collection of germplasm

18 accessions of *S. amplexicaulis* used in the study were collected from diverse agro-climatic regions of Odisha. Healthy and disease-free planting materials were collected from natural habitats and farmers' fields based on variation in morphological traits such as leaf shape, fruit size, fruit colour, vine vigour, and tuber characteristics. The collected germplasm was maintained in the experimental field of the Central Horticultural Experiment Station, (ICAR-IIHR, Aiginia, Bhubaneswar), India.

Experimental site and climatic conditions

The field experiment was conducted at the Instructional Farm of the Central Horticultural Experiment Station, located at 20°15' N to 20°27' N latitude, 85°40' E to 85°53' E longitude, and an altitude of 25.5-45 m above mean sea level. The experimental site experiences a humid tropical climate with an average annual rainfall of about 1,638 mm, mostly received during the south-west monsoon season.

Experimental design and crop management

The current investigation was laid out in a Randomized Block Design (RBD) with three replications. Each accession were planted at a spacing of 2m × 4m between plants and rows, respectively. Standard agronomic practices including irrigation, weeding, earthing-up etc. were followed uniformly throughout the crop growth period.

Recording of observations

Observations were recorded from 5 randomly selected plants in each replication for various morphological, yield and quality parameters. Data were recorded on number of primary branches, petiole length, node number of 1st female flower, days taken to 1st female flower, average internode length, number of fruits per plant, days from fruit set to maturity, fruit length, fruit diameter, fruit weight, number of seeds per fruit and fruit yield per plant.

Statistical analysis

The experimental data were subjected to analysis of variance (ANOVA) following the procedure outlined by Panse and Sukhatme (1985). The significance of differences among genotypes was tested at 5% probability level. Mean values were compared using critical difference (CD) values wherever the treatment effects were found significant. Statistical analyses were carried out using appropriate statistical software packages.

RESULT AND DISCUSSION

Genetic Variability among Breeding Lines

For all twelve quantitative characteristics examined, the analysis of variance (ANOVA) showed highly significant variations across the eighteen breeding lines of *Solena amplexicaulis*, indicating the existence of significant genetic diversity in the experimental material. Significant variation among genotypes is a prerequisite for effective

selection and crop improvement because it provides opportunities for the identification of superior genotypes possessing desirable traits.

The magnitude of genotypic mean squares was considerably higher than the corresponding error mean squares for most traits, particularly number of fruits per plant, days taken to 1st female flower, node number of 1st female flower, average internode length, number of seeds per fruit, fruit weight and fruit yield. The substantial disparities between treatment and error variances indicate the observed variation was primarily of genetic rather than environmental origin. Similar observations were reported in several cucurbitaceous vegetables, including bottle gourd, ridge gourd, snake gourd and sponge gourd, where significant genotypic differences were observed for yield and yield-contributing characters (Saikia et al., 2017; Rao et al., 2021; Aftab et al., 2024; Kumanan et al., 2024). The significant variability among the breeding lines suggests that the germplasm has a diverse genetic base, making it ideal for future breeding programs aimed at yield optimization and varietal advancement.

Mean Performance of Genotypes

Substantial variation was observed among the eighteen breeding lines for all the characters studied. The population mean values were 5.397 for number of primary branches, 1.518 cm for petiole length, 17.204 for node number of first female flower, 52.152 days for days taken to first female flower, 10.201 cm for average internode length, 179.389 for number of fruits per plant, 7.515 days for fruit set to maturity, 5.368 cm for fruit length, 1.991 cm for fruit diameter, 18.921 g for fruit weight, 15.617 for number of seeds per fruit and 3.429 kg for fruit yield per plant. The wide range of variation observed among the breeding lines further confirms the existence of considerable diversity within the experimental population. Such variability offers opportunities for selecting superior genotypes combining high fruit number, desirable fruit size and enhanced yield potential.

Variability Parameters

The assessments of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), and environmental coefficient of variation (ECV) revealed considerable differences among traits.

High GCV and PCV values were observed for fruit yield per plant (40.93 and 41.11%), number of fruits per plant (35.72 and 35.81%), node number of 1st female flower (24.69 and 25.53%) and fruit length (21.05 and 21.84%). These results indicate that there is an existence of significant variability and suggest that these traits can respond effectively to selection. Similar findings have been reported in ridge gourd and bottle gourd and, where fruit number and fruit yield exhibited high variability and provided greater opportunities for genetic improvement (Varalakshmi et al., 2015; Saikia et al., 2017; Varalakshmi et al., 2018; Rao et al., 2021; Aftab et al., 2024; Kumanan et al., 2024)).

Moderate PCV and GCV values were observed for number of primary branches, average internode length, number of seeds per fruit and days taken from fruit set to maturity. In contrast, petiole length and fruit weight exhibited comparatively lower coefficients of variation, indicating a relatively narrow genetic base for these traits.

PCV values were marginally greater than the corresponding GCV values for each individual character, indicating the impact of environmental influences on trait expression. However, the relatively minor variations between GCV and PCV for the majority of traits indicated that environmental influences were limited and that genetic potential was consistently reflected in phenotypic performance.

Heritability and Genetic Advance

Broad-sense heritability estimates ranged from 8.24% for petiole length to 99.49% for number of fruits per plant. Very high heritability estimates were observed for number of fruits per plant (99.49%), average internode length (99.25%), fruit yield (99.12%), days taken to 1st female flower (98.40%), number of seeds per fruit (97.58%), days from fruit set to maturity (93.55%), node number of 1st female flower (93.52%), fruit weight (92.67%) and fruit length (92.90%). High heritability indicates that a major portion of the observed variability was genetically controlled and could be effectively exploited through selection.

Genetic advance expressed as percentage of mean ranged from 1.48% in petiole length to 83.94% in fruit yield. Fruit yield (83.94%), number of fruits per plant (73.40%), node number of the 1st female flower (49.18%), fruit length (41.81%), average internode length (37.71%), number of seeds per fruit (33.80%), and number of primary branches showed high heritability and high genetic advance.

The combination of high heritability and high genetic advance revealed the predominance of additive gene action and suggests that direct phenotypic selection would be effective for improving these traits (Johnson et al., 1955). Conversely, petiole length exhibited low heritability and low genetic advance, suggesting substantial environmental influence and the possible involvement of non-additive gene action.

The results indicate that number of primary branches, number of fruits per plant, fruit length and fruit represent the most promising traits for genetic improvement in *S. amplexicaulis*.

Genotypic and Phenotypic Correlation Analysis

Correlation analysis study showed that genotypic correlations were generally higher than the corresponding phenotypic correlations which indicates that environmental factors reduced the expression of genetic associations among the traits. Similar trends have been reported in many cucurbit crops.

Fruit yield per plant exhibited strong positive genotypic correlations with the number of fruits per plant (0.991), fruit weight (0.927), fruit length (0.891) and number of primary branches (0.716). Corresponding phenotypic correlations were also positive and high (0.988, 0.904, 0.858 and 0.648, respectively). These findings suggest that these characteristics are the main factors influencing yield and can be used as reliable selection criteria.

The strongest association was observed between number of fruits per plant and fruit yield emphasizing the importance of fruit number in determining productivity. Fruit length and fruit weight also exhibited strong positive relationships with fruit yield, indicating the importance of fruit size attributes.

Fruit yield showed negative correlations with node number of 1st female flower ($r_g = -0.483$; $r_p = -0.465$) and number of seeds per fruit ($r_g = -0.499$; $r_p = -0.490$). The negative association between yield and node number of 1st female flower suggests that genotypes producing female flowers at lower nodes are more productive. Likewise, the negative association between seed number and yield indicated that increased allocation of assimilates to seed formation may reduce fruit growth and yield.

Strong positive interrelationships were also observed among yield attributing traits. Number of fruits per plant showed positive correlations with fruit weight ($r_g = 0.875$; $r_p = 0.841$) and fruit length ($r_g = 0.843$; $r_p = 0.815$), while fruit length exhibited a very strong positive association with fruit weight ($r_g = 0.971$; $r_p = 0.900$). Such positive associations suggests the possibility of simultaneous improvement of these characters through selection.

Path Coefficient Analysis

Path coefficient analysis was conducted to classify the correlation coefficients into direct and indirect effects and to identify traits which had the greatest influence on fruit yield.

The results revealed that number of fruits per plant put forth the highest positive direct effect on fruit yield (0.7713). The strong positive correlation between these two traits was therefore mainly due to the direct contribution of fruit number to yield. This clearly identifies that number of fruits per plant is the most important selection criterion for yield improvement.

Number of fruits per plant was followed by fruit weight and exhibited the second highest positive direct effect (0.1802), followed by fruit length (0.0485), days from fruit set to maturity (0.0261), number of primary branches (0.0193), fruit diameter (0.0061) and days taken to 1st female flower (0.0023). The positive direct effects of these traits indicate that they directly contribution toward yield enhancement.

Negative direct effects were recorded for node number of 1st female flower (-0.0305), average internode length (-0.0138) and petiole length (-0.0059). The negative direct effect of node number of 1st female flower suggests that earlier appearance of female flowers contributes positively to fruit production and overall yield.

In addition to its direct effect, number of fruits per plant exerted substantial positive indirect effects through fruit weight (0.1576) and fruit length (0.0408). Similarly, fruit weight contributed positively through number of fruits per plant (0.6747), whereas fruit length contributed positively through number of fruits per plant (0.6502) and fruit weight (0.1750). These findings explain the strong positive correlations observed among these traits.

The residual effect was observed very low (0.0353), which indicates that approximately 96.47% of the variation in fruit yield was explained by the characters included in the analysis. This demonstrates the adequacy of the path model and confirms the importance of the studied traits in determining fruit yield.

Breeding Implications and Conclusion

The present investigation demonstrated the existence of substantial genetic variability among the breeding lines of *Solena amplexicaulis*. High heritability along with high genetic advance for fruit yield, number of fruits per plant, fruit length, node number of 1st female flower and number of primary branches indicated the prevalence of additive gene action and their effectiveness of direct selection.

Path coefficient and correlation analyses consistently identified number of primary branches, number of fruits per plant, fruit weight and fruit length as the major yield-contributing traits. Among these, number of fruits per plant emerged as the most important component due to its strong positive association and highest direct effect on fruit yield.

Therefore, breeding programmes aimed at improving fruit yield in *S. amplexicaulis* should emphasize selection for increased number of fruits per plant, higher fruit weight, greater fruit length and enhanced branching ability, together with early appearance of female flowers.

Table 1. ANOVA for 12 characters in 18 breeding lines of *Solena amplexicaulis* (Lam) Gandhi.

Sl. No.	Character	Replication MS	Genotype MS	Error MS
1	No. of primary branches	0.321	2.880	0.212
2	Petiole length	0.015	0.020	0.016
3	Node number of 1 st female flower	0.006	55.371	1.249
4	Days taken to 1 st female flower	0.017	105.878	0.572
5	Average internode length	0.001	10.566	0.027
6	Number of fruits per plant	39.801	12340.253	21.229
7	Days from fruit set to maturity	0.132	3.930	0.088
8	Fruit length	0.001	3.930	0.098
9	Fruit diameter	0.002	0.139	0.029
10	Fruit weight	0.090	7.828	0.201
11	Number of seeds per fruit	0.121	20.351	0.167
12	Fruit yield	0.029	5.925	0.018

Sources of Variation

Sl. No.	Source	DF
1.	Replication	2

2.	Genotype	17
3.	Error	34
4.	Total	53

Table 2. Estimates of Variability, Heritability and Genetic advance under selection (5%) for twelve quantitative characters in eighteen genotypes of *Solena amplexicaulis* (Lam.) Gandhi.

Sl. no.	Characters	Range	Mean	GCV (%)	PCV (%)	ECV (%)	Heritability(H ²) (%)	GA	GA (% of Mean)
1	No. primary branches	4.333-7.267	5.397	17.4737	19.447	8.5354	0.8074	1.75	32.3435
2	Petiole length	1.347-1.620	1.518	2.5004	8.7093	8.3426	0.0824	0.002	1.4788
3	Node no. 1st female flower	7.467-23.133	17.204	24.6889	25.5295	6.4971	0.9352	8.46	49.1845
4	Days taken 1st female flower	41.133-60.800	52.152	11.3606	11.4528	1.4501	0.984	12.11	23.2145
5	avg. internode length	7.463-13.283	10.201	18.3734	18.4429	1.5995	0.9925	3.85	37.7066
6	No. of fruits per plant	60.533-237.533	179.389	35.7216	35.8139	2.5689	0.9949	131.67	73.397
7	Days fruit set to maturity	5.577-9.477	7.515	15.0593	15.5699	3.9547	0.9355	2.25	30.0047
8	fruit length	3.567-7.400	5.368	21.0547	21.8439	5.8185	0.929	2.24	41.8057
9	fruit diameter	1.667-2.367	1.991	9.6099	12.8604	8.5463	0.5584	0.29	14.7929
10	Fruit weight	16.267-21.913	18.921	8.4271	8.754	2.3701	0.9267	3.16	16.7114
11	No. seeds per fruit	11.233-21.267	15.617	16.6095	16.814	2.6148	0.9758	5.28	33.7993
12	Fruit yield	0.977-5.200	3.429	40.9284	41.1099	3.8587	0.9912	2.88	83.9403

Note: GCV = Genotypic Coefficient of Variation, PCV = Phenotypic Coefficient of Variation, ECV = Environmental Coefficient of Variation, H² = Broad-sense Heritability, GA = Genetic Advance at 5% Selection Intensity, GAM = Genetic Advance as Percent of Mean

Note: Heritability (H²) is expressed in broad sense. Genetic Advance (GA) was estimated at 5% selection intensity. GA as percent of mean (GAM) was used to assess the expected improvement through selection.

Table 3. Classification of Heritability and GAM

Trait	Heritability (%)	Category	GAM (%)	Category
No. of primary branches/plant	80.74	High	32.34	High
Petiole length	8.24	Low	1.48	Low
Internodal length	93.52	High	49.18	High
Days to first male flower anthesis	98.40	High	23.21	High
Average fruit weight	99.25	High	37.71	High
No. of fruits/plant	99.49	High	73.40	High
Days to first harvest	93.55	High	30.00	High
Fruit length	92.90	High	41.81	High
Fruit diameter	55.84	Moderate	14.79	Moderate
Fruit girth/width	92.67	High	16.71	Moderate

No. of seeds/fruit	97.58	High	33.80	High
Fruit yield/plant	99.12	High	83.94	High

Table 4. Combined genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among twelve quantitative characters in eighteen breeding lines of *Solena amplexicaulis* (Lam.) Gandhi.

Characters	NPB	PL	NFFF	DFFF	AIL	NFP	DFM	FL	FD	FW	NSF	FY
NPB	1.000	- 0.207	-0.424	-0.267	0.044	0.629	0.153	0.783	0.282	0.866	- 0.426	0.716
PL	0.129	1.000	0.221	0.235	0.701	0.178	- 0.167	0.772	1.127	0.445	0.189	0.232
NFFF	- 0.376	0.027	1.000	0.079	0.269	- 0.456	0.278	- 0.321	- 0.200	- 0.435	0.130	- 0.483
DFFF	- 0.234	0.084	0.069	1.000	- 0.082	- 0.038	0.232	0.151	- 0.121	0.001	- 0.153	- 0.022
AIL	0.044	0.198	0.268	-0.081	1.000	0.046	0.015	0.269	- 0.022	0.228	0.170	0.065
NFP	0.569	0.068	-0.439	-0.038	0.045	1.000	- 0.065	0.843	- 0.013	0.875	- 0.496	0.991
DFM	0.119	- 0.075	0.279	0.220	0.020	- 0.066	1.000	0.029	- 0.444	0.094	0.133	- 0.012
FL	0.669	0.241	-0.297	0.140	0.258	0.815	0.016	1.000	0.195	0.971	- 0.420	0.891
FD	0.096	0.109	-0.072	-0.091	- 0.002	- 0.002	- 0.303	0.141	1.000	0.068	- 0.019	0.011
FW	0.773	0.091	-0.402	0.008	0.221	0.841	0.093	0.900	0.062	1.000	- 0.478	0.927
NSF	- 0.357	0.106	0.123	-0.148	0.166	- 0.488	0.113	- 0.402	0.000	- 0.455	1.000	- 0.499
FY	0.648	0.073	-0.465	-0.021	0.063	0.988	- 0.014	0.858	0.012	0.904	- 0.490	1.000

Note 1: Values above the diagonal represent Genotypic Correlation Coefficients (G), whereas values below the diagonal represent Phenotypic Correlation Coefficients (P).

Note 2: NPB-Number of Primary Branches, PL-Petiole Length, NFFF- Node Number of First Female Flower, DFFF- Days Taken to First Female Flower, AIL- Average Internode Length, NFP- Number of Fruits per Plant, DFM- Days from Fruit Set to Maturity, FL- Fruit Length, FD- Fruit Diameter, FW- Fruit Weight, NSF- Number of Seeds per Fruit, FY- Fruit Yield per Plant

Table 5. Direct and indirect effects of eleven component characters on fruit yield per plant estimated through genotypic path coefficient analysis in eighteen breeding lines of *Solena amplexicaulis* (Lam.) Gandhi.

Character	NPB	PL	NFF F	DF F	AIL	NFP	DFM	FL	FD	FW	NSF
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NPB	0.019 3	0.001 2	0.013 0	- 0.000 6	- 0.000 6	0.485 3	0.004 0	0.038 0	0.001 7	0.156 1	- 0.001 4
PL	- 0.004 0	- 0.005 9	- 0.006 8	0.000 5	- 0.009 7	0.137 0	- 0.004 4	0.037 4	0.006 9	0.080 1	0.000 6
NFFF	- 0.008 2	- 0.001 3	- 0.030 5	0.000 2	- 0.003 7	- 0.351 7	0.007 3	- 0.015 6	- 0.001 2	- 0.078 5	0.000 4
DFFF	- 0.005 2	- 0.001 4	- 0.002 4	0.002 3	0.001 1	- 0.029 1	0.006 1	0.007 3	- 0.000 7	0.000 1	- 0.000 5
AIL	0.000 9	- 0.004 1	- 0.008 2	- 0.000 2	- 0.013 8	0.035 2	0.000 4	0.013 1	- 0.000 1	0.041 1	0.000 6
NFP	0.012 2	- 0.001 1	0.013 9	- 0.000 1	- 0.000 6	0.771 3	- 0.001 7	0.040 8	- 0.000 1	0.157 6	- 0.001 6
DFM	0.003 0	0.001 0	- 0.008 5	0.000 5	- 0.000 2	- 0.050 3	0.026 1	0.001 4	- 0.002 7	0.016 9	0.000 4
FL	0.015 1	- 0.004 6	0.009 8	0.000 4	- 0.003 7	0.650 2	0.000 8	0.048 5	0.001 2	0.175 0	- 0.001 4
FD	0.005 5	- 0.006 7	0.006 1	- 0.000 3	0.000 3	- 0.010 2	- 0.011 6	0.009 5	0.006 1	0.012 2	- 0.000 1
FW	0.016 7	- 0.002 6	0.013 3	0.000 0	- 0.003 1	0.674 7	0.002 4	0.047 1	0.000 4	0.180 2	- 0.001 5
NSF	- 0.008 2	- 0.001 1	- 0.004 0	- 0.000 4	- 0.002 3	- 0.382 8	0.003 5	- 0.020 3	- 0.000 1	- 0.086 2	0.003 2

Note: NPB-Number of Primary Branches, PL-Petiole Length, NFFF- Node Number of First Female Flower, DFFF- Days Taken to First Female Flower, AIL- Average Internode Length, NFP- Number of Fruits per Plant, DFM- Days from Fruit Set to Maturity, FL- Fruit Length, FD- Fruit Diameter, FW- Fruit Weight, NSF- Number of Seeds per Fruit, FY- Fruit Yield per Plant

Table 6. Ranking of Characters for Selection

Rank	Character	Basis for Ranking
1	No. fruits per plant	Highest direct effect and highest correlation with yield
2	Fruit weight	Strong direct effect and strong yield association
3	Fruit length	High correlation and positive direct effect
4	No. primary branches	Positive association with yield
5	Average internode length	High heritability and GAM
6	Node no. 1 st female flower	High variability but negative association with yield
7	No. seeds per fruit	High heritability but negative correlation with yield
8	Fruit diameter	Moderate heritability and weak association
9	Petiole length	Low heritability and low GAM

Table 7. Breeding Implications and Selection Criteria

Character	Variability	Heritability	GAM	Yield Correlation	Direct Effect	Breeding Value
No. fruits per plant	High	High	High	Positive	High	Excellent
Fruit weight	Moderate	High	Moderate	Positive	High	Excellent
Fruit length	High	High	High	Positive	Moderate	Excellent
No. primary branches	Moderate	High	High	Positive	Moderate	Very Good

Average internode length	Moderate	High	High	Positive	Negative	Good
Node no. 1st female flower	High	High	High	Negative	Negative	Useful for earliness
Fruit diameter	Moderate	Moderate	Moderate	Weak	Low	Moderate
Petiole length	Low	Low	Low	Weak	Negative	Poor
Fruit yield	High	High	High	—	—	Selection Target

REFERENCES

1. Aftab, O., Nazir, G., Gautam, A., Hussain, K., et al. (2024). Evaluation of genetic variability for yield improvement in bitter gourd (*Momordica charantia* L.) genotypes. *Journal of Advances in Biology & Biotechnology*, 27(6), 736–745.
2. Ali A and Bhattacharjee B (2023). Nutrition security, constraints, and agro-diversification strategies of neglected and underutilized crops to fight global hidden hunger. *Frontiers in Nutrition* 10: 1144439.
3. Aruna A, Rajkumar N and Brindha P (2011). Ethnomedicinal uses of wild edible plants among tribal communities of Tamil Nadu. *Indian Journal of Traditional Knowledge* 10: 98-102.
4. Deepa Devi N, Mariappan S, Arumugam T and Anandakumar CR (2017). Genetic variability, heritability, correlation and path analysis in snake gourd (*Trichosanthes cucumerina* L.). *Electronic Journal of Plant Breeding* 8: 566-571.
5. Dubey RK, Singh V and Pandey S (2024). Underexploited vegetables of Northeastern region. *Indian Horticulture* 68: 50-54.
6. Fakruddin M, Hossain MN and Ahmed MM (2012). Antimicrobial and antioxidant activities of *Solena amplexicaulis* extracts. *Journal of Medicinal Plants Research* 6: 3441-3445.
7. Johnson HW, Robinson HF and Comstock RE (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal* 47: 314-318.
8. Kabir MSH, Hossain MM and Rahman MM (2014). Antifungal activity of stem bark extracts of *Solena amplexicaulis* against selected fungal pathogens. *International Journal of Pharmaceutical Sciences and Research* 5: 1452-1457.
9. Karthika K and Paulsamy S (2014). Traditional knowledge on medicinal plants used by tribal people in Tamil Nadu, India. *Asian Pacific Journal of Tropical Disease* 4(Suppl. 1): S45-S50.
10. Karthika K and Paulsamy S (2015). TLC and HPTLC fingerprints of various secondary metabolites in the stem of the traditional medicinal climber *Solena amplexicaulis* (Lam.) Gandhi. *Indian Journal of Pharmaceutical Sciences* 77: 111-116.
11. Khoury CK, Brush S, Costich DE, Curry HA, de Haan S, Engels JMM, et al. (2022). Crop genetic erosion: Understanding and responding to loss of crop diversity. *New Phytologist* 233: 84-118.
12. Khundrakpam R and Kotiyal A (2024). Unveiling the impact of climate change on underutilized fruit crops: A review. *International Journal of Advanced Biochemistry Research* 8: 552-558.
13. Krishnamoorthy K and Paulsamy S (2014). Phytochemical profiling of leaf, stem and tuber parts of *Solena amplexicaulis* (Lam.) Gandhi using GC-MS. *International Scholarly Research Notices* 2014: Article ID 567409.
14. Kumanan, K., Vijayalatha, K.R. and Ahamed, A.S. (2024). Genetic variability and heritability in bitter gourd for better yield and quality under sodic soil. *Journal of Advances in Biology & Biotechnology*, 27(12), 264–270
15. Mabhaudhi T, Hlahla S, Chimonyo VGP, Henriksson R, Chibarabada TP, Murugani VG, et al. (2022). Diversity and diversification: Ecosystem services derived from underutilized crops and their co-benefits for sustainable agricultural landscapes and resilient food systems in Africa. *Frontiers in Agronomy* 4: 859223.
16. Padulosi S, Thompson J and Rudebjer P (2013). *Fighting Poverty, Hunger and Malnutrition with Neglected and Underutilized Species: Needs, Challenges and the Way Forward*. Bioversity International, Rome, Italy.
17. Panse VG and Sukhatme PV (1985). *Statistical Methods for Agricultural Workers*. 4th Edition. Indian Council of Agricultural Research, New Delhi, India.
18. Peter KV (2007). *Underutilized and Underexploited Horticultural Crops*. Volume 3. New India Publishing Agency, New Delhi, India.
19. Rao, P.G., Behera, T.K., Gaikwad, A.B., Munshi, A.D., Srivastava, A. and Vinod (2021). Genetic analysis and QTL mapping of yield and fruit traits in bitter gourd (*Momordica charantia* L.). *Scientific Reports*, 11, 4109.
20. Saikia, J., Phookan, D.B. and Talukdar, P. (2017). Studies on genetic variability in ivy gourd [*Coccinia grandis* (L.) Voigt]. *Indian Journal of Horticulture*, 74(1), 119–123. (Still one of the most cited variability studies in ivy gourd.)
21. Sarkar T, Salauddin M, Roy S, Chakraborty R, Rebezov M, Shariati MA, Thiruvengadam M and Rengasamy KRR (2023). Underutilized green leafy vegetables: frontier in fortified food development and nutrition. *Critical Reviews in Food Science and Nutrition* 63: 11679-11733.

22. Singh A, Bundela AK and Abhilash PC (2023). Nutritional, ethnomedicinal and agricultural significance of neglected and underutilized crops from Eastern Uttar Pradesh, North India. *Agronomy* 13: 2318.
23. Varalakshmi, B., Pitchaimuthu, M., Rao, E.S., Manjunath, K.S.S. and Swathi, S.H. (2015). Genetic variability, correlation and path analysis in ridge gourd (*Luffa acutangula* (Roxb.) L.). *Journal of Horticultural Sciences*, 10(2): 154–158.
24. Varalakshmi, B., Pitchaimuthu, M. and Rao, E.S. (2018). Genetic variability, correlation and path analysis in bottle gourd (*Lagenaria siceraria* (Mol.) Standl.) germplasm. *Journal of Horticultural Sciences*, 13(2): 131–136.
25. Venkatachalapathi A, Paulsamy S and Senthilkumar K (2011). Traditional medicinal plants used by tribal communities in Tamil Nadu for wound healing and skin diseases. *Journal of Medicinal Plants Research* 5: 3523-3529.