P. ISSN: 0971-8184 II E. ISSN: 0976-1926
DOI: 10.61949/0976-1926.2025.v38i01.05

Indian Journal of
Plant Genetic Resources

RESEARCH ARTICLE

Genetic Variability and Breeding Potential in the F_2 and Backcross Populations of Interspecific Crosses between *'Satputia'* (*Luffa hermaphrodita* Singh and Bhandari) and Sponge Gourd (*Luffa cylindrica* (Roem.) L.)

MK Sidhu*, Sahil Chaudhary and Madhu Sharma

Abstract

The genetic divergence between two parents creates the potential populations carrying a good selection efficiency of different qualitative and quantitative traits, for which a breeder seeks improvement in a particular crop. The genetic potential displayed through genetic variability, heritability, and genetic advance of the quantitative traits usually describe the breeding values of a cross. In the present investigation, we evaluated the F_2 and backcross populations of two interspecific crosses between '*Satputia*' and sponge gourd for genetic variability. All the traits of these wide cross populations had a wide range of variability. GCV, PCV, heritability, and genetic advance remained on the higher side for leaf length, leaf width, and internodal length, while moderate for fruit length, fruit weight, and fruits per plant. Most of the other traits carried a low expression of genetic variability with a high influence of the environment. The vine yield was positively and significantly correlated with fruits per vine and fruit weight in all the populations. However, the association of other traits varied in different F_2 and backcrosses populations. It was concluded that BC_1P_2 populations of both the crosses had been most appropriate for crop improvement concerning the quantitative horticultural traits and yield potential.

Keywords: Sponge gourd, *'Satputia'*, Inter-specific cross, Genetic components, Correlation analysis.

Department of Vegetable Science, Punjab Agricultural University, Ludhiana, Punjab, India.

***Author for correspondence:**

mksidhu@pau.edu

Received: 04/04/2023 **Revised:** 05/09/2024

Accepted: 06/09/2024

How to cite this article: Sidhu MK, S Chaudhary and M Sharma (2025). Genetic Variability and Breeding Potential in the F_2 and Backcross Populations of Interspecific Crosses between 'Satputia' (*Luffa hermaphrodita* Singh and Bhandari) and Sponge Gourd (*Luffa cylindrica* (Roem.) L.). *Indian J. Plant Genet. Resour*. 38(1), 44-52. **DOI:** 10.61949/0976-1926.2025.v38i01.05

Introduction

Sponge gourd (*Luffa cylindrica* L., 2n = 26.) is a cucurbitaceous gourd vegetable of the Summer and *Kharif* seasons in the tropical and sub-tropical parts of India. It belongs to the genus *Luffa* that originated in the sub-tropical region of Asia particularly in India (Kalloo and Bergh, 1993). This small genus of the family *Cucurbitaceae* is mainly comprised of nine species. Among these, *L. acutangula* L., *L. aegyptica* Mill. (syn *L. cylindrica* L.), *L. echinata* Roxb., *L. graveolens* Roxb., *L. hermaphrodita* Singh and Bhandari, including two debatable species, *L. tuberosa* Roxb., and *L. umbellata* M. Roem. are found distributed in India (Chakravarty, 1982). However, *L. quinquefida* and *L. operculata* are new-world species that are found distributed from Mexico to Nicaragua and Panama as well as to Southern Brazil (Jeffrey, 1992; Singh *et al*., 1991). A species *L. saccata* has been reported from Australia (Telford *et al*., 2011)

Sponge gourd is a cross-pollinated diploid species that bears monoecious flowers and smooth fruits on long trailing vines. Its deep yellow flowers open in the morning (6.00–8.00 a.m.). Its fruits carry black or white seeds. Its fast growth, short duration, and photo-insensitive nature make it suitable for growing in the Summer and the *Kharif* seasons. However, the yield potential mainly depends upon the female-to-male ratio of the flowers.

The occurrence of male and female flowers on the vines further varies with the genotype, season of cultivation, the microclimate of the vines, and also on water and nutrient management during its cultivation (Choudhary *et al*., 2014).

The genetic improvement of yield in monoecious sponge gourd is mainly based on a selection of the genotypes with a high female-to-male ratio (Chaubey *et al*., 2014). Inter-specific hybridization with related species bearing more fruits per vine can also enhance the yield potential of this crop. Among various *Luffa* species, '*Satputia'* (*L. hermaphrodita*), a bisexual, semi-wild species, exclusively bears many flowers and fruits in clusters (Choudhary *et al*., 2009). Successful inter-specific hybridization between sponge gourd and this species can unlock the transfer of many traits, such as a high female: male ratio, hermaphrodism, and cluster bearing as well as can lead to antioxidant improvement in sponge gourd (Singh, 1991, Karmakar *et al*., 2013). Recently, it has been found to be cross-compatible with cultivated sponge gourd (Sidhu, 2019; Sidhu and Kaur, 2021). As the appearance of genetic variability depends upon the genetic distance between the parents used for hybridization, there is a need to explore the segregating populations of interspecific crosses between two species for different morphological traits. Furthermore, heritability, genetic advance, and correlation coefficient of different traits with the yield per vine in different segregating populations can also help in the selection of appropriate traits for increasing the female-to-male ratio as well as yield potential of this crop. Because of this, the present investigation was carried out to highlight the breeding potential through genetic variation and correlation analysis of different traits for yield in the F_2 and backcross populations derived from two different interspecific crosses in sponge gourd (*L. cylindrica* (Roem.) L.).

Materials and Methods

Plant Material

The present investigation was carried out with the F_2 and two backcross populations of each of two interspecific crosses between sponge gourd and '*Satputia'*. One genotype, '*PSG-9'* from sponge gourd, had a low female-to-male ratio and poor yield potential along with more vegetative growth, while the other genotype, SG-282 had a high female-to-male ratio and high yield potential and had short vines as compared to the former. '*Satputia'* (*L. hermaphrodita*) is a bisexual, semi-wild species that bears many flowers and fruits in clusters (Singh, 1991). The crosses between the *'Satputia'* genotype SAT-1 and sponge gourd were attempted in the *Kharif* season of 2018. The seed of the F_2 and backcross populations was multiplied during the Summer season of 2019.

Experimental Details

All the segregating populations derived from two different interspecific crosses between '*Satputia'* and sponge gourd were sown in plug trays in February 2020. About 80 plants for each F_2 and 50 plants for each backcross population were transplanted in the field during March 2020 using a randomized complete block design with three replications. The experiment was conducted at the Vegetable Research Farm of Punjab Agricultural University, Ludhiana, which is located at 30° 54′ North (latitude) and 75° 48′ East (longitude) at a height of 247 m above sea level. This region has a sub-tropical climate having hot summers associated with desiccating winds during April-June, rainfall (average 700 mm) during July-September, and frost in December-January. The soil of the experimental plot was mainly sandy loam in texture with 0.4% organic carbon, 0.076 ds/m electrical conductivity, and neutral soil pH (7.06).

The crop was raised as per recommended cultivation practices (Anonymous, 2019). Individual plant data for vine length at first harvest, internodal length (cm), leaf length (cm), leaf width (cm), days to female flowering, the node of the first female flower, female bud length (cm), ovary length (mm), ovary width (mm), style length (mm), fruit length (cm), fruit diameter (cm), fruit weight (g), fruits per vine (number), yield per vine (kg) were recorded in three replications of each population of two crosses. The vernier caliper was used to measure the flower traits. The data was compiled replication-wise for the statistical analysis.

Statistical Analysis

The replicated data of all the populations were compiled and subjected to analysis of variance. The different components of genetic variation, such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in a broad sense, and genetic advance for each trait, were calculated for the assessment of the breeding potential of six populations derived from two interspecific crosses. The different components of genetic variation and correlations from replicated data of different quantitative traits were analyzed population-wise through the statistical software SPAR 2.0 (Ahuja *et al*., 2008).

Results and Discussion

Genetic Variability in F_2 Population

In two F_2 populations derived from sponge gourd × *'Satputia'*, the data for different components of genetic variation in 15 quantitative traits are presented in Table 1. In the F_2 population of cross SAT-1 × SG 282, PCV was higher than its respective GCV for all traits under investigation, which ranged from 21.34 to 91.05% and 4.27 to 35.04%, respectively. Although the yield per vine recorded the highest PCV (91.05%), internodal length displayed the greatest GCV (35.04%) in this population. The other traits, such as leaf length (26.27 and 24.64%), and leaf width (26.15 and 24.59%), also showed high PCV and GCV, respectively. However, the vine length, ovary length, ovary width, fruit

Table 1: Components of genetic variation for different traits in F_2 populations of *Satputia* × sponge gourd

Traits	F_2 (SAT-1 × SG 282)							F_2 (SAT-1 × PSG 9)						
	Range	Mean	GCV (%)	PCV (%)	H_B (%)	G A	GA (PM)	Range	Mean	GCV (%)	PCV (%)	H_B (%)	G A	GA (PM)
VL (cm)	20.12-146.35	70.15	18.62	53.26	34.96	0.72	1.03	15.25-150.03	76.89	12.99	47.68	27.24	0.56	0.73
IL (cm)	2.74-14.08	6.33	35.04	38.10	91.97	1.89	29.93	2.44-13.50	6.31	34.39	40.26	85.42	1.76	27.89
LL (cm)	3.31-11.56	6.33	24.64	26.27	93.80	1.93	30.52	2.55-12.58	6.60	25.44	27.40	92.85	1.91	28.98
LW (cm)	4.22-14.55	8.60	24.59	26.15	94.03	1.94	22.52	3.50-14.84	9.24	23.26	25.13	92.56	1.91	20.64
FBL (mm)	20.32-79.74	47.93	5.49	24.63	22.29	0.46	0.96	26.15-74.83	48.38	13.40	28.02	47.82	0.99	2.04
OL (mm)	14.40-68.61	35.83	14.44	28.95	49.88	1.03	2.87	16.14-83.07	38.64	14.63	32.23	45.39	0.94	2.42
OW (mm)	3.63-14.44	7.18	11.58	30.55	37.91	0.78	10.88	3.37-14.89	6.83	9.77	28.65	34.10	0.70	10.29
SL (mm)	2.61-13.81	7.27	7.03	38.60	18.21	0.38	5.16	3.12-15.56	7.60	4.41	33.74	13.07	0.27	3.54
DFF	26.00-52.00	40.00	4.74	21.34	22.21	0.46	1.14	30.00-65.00	40.49	4.49	20.40	22.01	0.45	1.12
NFFB	3.00-18.00	8.76	6.80	42.28	16.08	0.33	3.78	4.00-21.00	8.85	10.11	38.87	26.01	0.54	6.05
FL (cm)	3.15-20.10	10.39	10.50	36.39	28.85	0.59	5.72	3.25-25.05	12.18	19.26	39.55	48.70	1.00	8.24
FD (cm)	2.01-6.44	3.57	4.27	26.14	16.34	0.34	9.43	1.75-6.54	3.90	5.96	24.55	24.28	0.50	12.82
FW (g)	10.00-117.00	59.51	16.39	47.60	34.43	0.71	1.19	10.00-110.00	64.67	10.92	41.82	26.11	0.54	0.83
FPV	7.00-168.00	43.31	9.68	69.07	14.01	0.29	0.67	5.00-157.00	49.04	28.62	78.74	36.35	0.75	1.53
YPV (kg)	0.14-10.50	2.58	13.84	91.05	15.20	0.31	12.14	0.21-9.85	3.10	38.85	98.55	39.42	0.81	26.20

VL-vine length, IL- internodal length, LL-leaf length, LW-leaf width, FBL-female bud length, OL-ovary length, OW-ovary width, SL-style length, DFF-days to the female flower, NFFB-node to first female bud, FL-fruit length, FD-fruit diameter, FW-fruit weight, FPV-fruits per vine, YPV-yield per vine. GCV-genotypic coefficient of variation, PCV-phenotypic coefficient of variation, H_b-heritability in the broad sense, GA-genetic advance, GA (PM)-genetic advance as percent length, fruit weight, and yield per vine in the F_2 population of this cross established a moderate degree of GCV (10–20%). Among all the traits under investigation, leaf width (94.03 and 22.52%), followed by leaf length (93.80 and 30.52%) and internodal length (91.97 and 29.93%) explained the high level of heritability along with high genetic advance (PM), respectively. Vine length, ovary length, ovary width, and fruit weight showed moderate heritabilities, while yield per vines carried moderate genetic advance (PM). All the other traits carried a lower magnitude of both the components in this cross.

The F_2 population of cross SAT × PSG 9 also carried higher PCVs than respective GCVs of all traits under investigation, which ranged from 20.40 to 98.55% and 4.41 to 38.85%, respectively. Among the different traits of this cross, the yield per vine achieved the highest PCV (98.55%), as well as GCV (38.85%). In this cross population, the internodal length (40.26 and 34.39%), leaf length (27.40 and 25.44%), leaf width (25.13 and 23.26%), fruits per vine (78.74 and 28.62%) also carried high PCV and GCV, respectively. However, the vine length, female bud length, ovary length, node to first female bud, fruit length, and fruit weight unveiled the moderate order of GCVs (10–20%). Leaf length (92.85 and 28.98%, respectively), leaf width (92.56 and 20.64%, respectively), and internodal length (85.42% and 27.89%, respectively) in F_2 of SAT-1 × PSG 9 showed a high level of heritabilities coupled with moderate genetic advances. Fruit length (48.70%), female bud length (47.82%). Ovary length (45.39%), fruits per vine (36.35%) and ovary width (34.10%) showed moderate heritabilities with low genetic advance. However, fruit yield per vine (39.42%) had moderate heritabilities but showed considerable genetic advances (26.20%) in the F_2 of this cross.

Genetic Variability in BC_1P_1 Population

The components of genetic variation for different quantitative traits in two BC_1P_1 populations of sponge gourd × *'Satputia'* are presented in Table 2. In the BC_1P_1 population of the first cross (SAT × SG 282), PCVs and GCVs ranged from 9.26 to 94.52% and 2.62 to 27.81%, respectively. PCV of each trait was higher than its respective GCV. Fruit yield per vine described the highest PCV (94.52%), whereas internodal length carried the highest GCV (27.81%). Among various traits, internodal length (31.59 and 27.81%), leaf length (23.69 and 21.45%) and leaf width (23.34 and 21.56%) provided the higher order of PCVs and GCVs, respectively and vine length, ovary length, node to first female bud, fruit length, fruit weight and yield per vine revealed the moderate degree (10–20%) of GCV's. The remaining traits carried a moderate to a high degree of PCV's but a low level of GCVs. The internodal length (88.03 and 18.77%), leaf length (90.54 and 19.35%), and leaf width (92.37 and 17.73%) presented high heritabilities accompanied by moderate genetic advances, respectively, in the BC_1P_1 population of cross SAT-1 × SG 282, while ovary length, node to first female bud and fruit diameter exhibited moderate heritabilities (30–60%). Many traits of this backcross, such as vine length, female bud length, stigma length, days to first female flowers, fruit length, fruit weight, fruits per vine, and yield per vine had lower values for heritabilities and genetic advances.

In the BC_1P_1 population of second cross SAT-1 × PSG 9, PCVs for all the traits were higher than their respective GCVs. For this backcross, PCV's and GCV's ranged from 6.96 to 87.29% and 0.74 to 24.85%, respectively. The highest value of PCV was obtained for yield per vine (87.29%), while the highest GCV was achieved for internodal length (24.85%). The higher order of PCVs and GCVs was observed for internodal length (30.06 and 24.85%, respectively) and yield per vine (87.29 and 24.29%, respectively). The middle order of GCV (10–20%) was observed for vine length, leaf length, leaf width, ovary length, node to first female bud, fruit weight, and fruits per vine. The high heritabilities accompanied by moderate genetic advances were revealed respectively for internodal length (82.67 and 19.99%), leaf length (82.57 and 22.65%), and leaf width (88.54 and 18.24%) in the BC_1P_1 population of cross SAT-1× PSG 9. Ovary length and fruit weight displayed moderate heritabilities with low genetic advance (PM). Although yield per vine had the lower side heritability, but it had high genetic advance. All the other traits in this backcross also displayed low heritabilities and genetic advances.

Genetic Variability in BC_1P_2 Population

The components of genetic variation for different quantitative traits in two BC_1P_2 crosses of *'Satputia'* × sponge gourd are presented in Table 3. In the BC_1P_2 population of the first cross (SAT-1 × SG 282), PCVs for all traits were higher than their respective GCVs. Among all the traits, PCVs and GCVs ranged between 14.89 to 74.79% and 2.57 to 22.25%, respectively. The yield per vine had the highest PCV (74.79%) and the internodal length attained the greatest GCV (22.25%). Only internodal length (24.96 and 22.25%) and yield per vine (74.69 and 20.68%) disclosed the higher order of PCVs and GCVs, respectively in the BC_1P_2 population of this cross. However, leaf length (14.89 and 11.92%) and leaf width (16.48 and 13.24%) achieved the medium range of PCVs and GCVs, respectively. Internodal length (89.14 and 25.54%), leaf length (80.05 and 22.94%), and leaf width (80.34 and 16.13%) established the high heritabilities accompanied with moderate genetic advances, respectively. Ovary length, fruit length, fruit diameter and fruit weight showed moderate heritabilities (>30%).

In the BC_1P_2 population of cross SAT-1 × PSG 9, PCVs for all traits under investigation were higher than their respective GCVs, which ranged from 16.94 to 76.64% and 1.64 to 22.09%, respectively. Among all the traits, internodal length (22.09 and 23.99%) and yield per vine (20.21 and 76.64%) in this population of this cross carried the higher

Table 2: Components of genetic variation for different traits in BC_1P_1 populations of *Satputia* × sponge gourd

	BC_1P_1-(SAT-1 × SG 282) ×SAT-1							BC_1P_1-(SAT-1 × PSG 9) ×SAT-1						
Traits	Range	Mean	GCV (%)	PCV (%)	H_B (%)	G A	GA (PM)	Range	Mean	GCV (%)	PCV (%)	H_B (%)	G A	GA (PM)
VL (cm)	26.35-161.13	83.00	13.43	45.56	29.48	0.61	0.73	12.25-368.02	117.65	13.32	65.33	20.39	0.42	0.36
IL (cm)	3.10-15.50	9.66	27.81	31.59	88.03	1.81	18.77	4.80-17.25	8.52	24.85	30.06	82.67	1.70	19.99
LL (cm)	3.21-13.36	9.64	21.45	23.69	90.54	1.87	19.35	4.50-12.45	7.51	15.11	18.30	82.57	1.70	22.65
LW (cm)	5.13-15.86	10.73	21.56	23.34	92.37	1.90	17.73	5.51-14.24	10.00	15.53	17.54	88.54	1.82	18.24
FBL (mm)	17.88-60.10	37.09	5.42	26.08	20.78	0.43	1.15	16.30-69.46	32.98	7.33	30.73	23.85	0.49	1.49
OL (mm)	12.25-50.90	29.04	10.76	32.45	33.16	0.68	2.35	13.40-65.55	35.96	10.73	35.06	30.60	0.63	1.75
OW (mm)	4.60-13.02	8.43	4.07	27.95	14.56	0.30	3.56	3.92-13.33	7.15	6.08	30.89	19.68	0.41	5.67
SL (mm)	6.33-13.39	9.61	4.60	17.80	25.84	0.53	5.54	6.11-13.65	9.13	2.33	21.09	11.05	0.23	2.49
DFF	31.00-44.00	34.71	2.62	9.26	28.29	0.58	1.68	32.00-54.00	35.28	0.74	6.96	10.63	0.22	0.62
NFFB	3.00-20.00	10.58	12.29	37.32	32.93	0.68	6.41	4.00-22.00	11.46	10.20	36.15	28.22	0.58	5.07
FL (cm)	4.35-17.77	8.31	16.07	78.48	20.48	0.42	5.08	4.15-15.25	8.64	8.29	32.82	25.26	0.52	6.02
FD (cm)	1.13-4.70	3.32	6.49	20.03	32.40	0.67	20.10	1.64-5.68	3.39	5.08	35.15	14.45	0.30	8.78
FW (g)	15.00-62.00	37.33	15.18	50.96	29.79	0.61	1.64	10.00-50.00	31.23	18.89	56.60	33.37	0.69	2.20
FPV (no.)	7.00-125.00	32.94	9.38	61.24	15.32	0.32	0.96	6.00-105.00	40.31	13.80	53.08	26.00	0.54	1.33
YPV (kg)	0.14-6.20	1.22	10.60	94.52	11.21	0.23	18.94	0.12-4.55	1.29	24.29	87.29	27.83	0.57	44.44

VL-vine length, IL- internodal length, LL-leaf length, LW-leaf width, FBL-female bud length, OL-ovary length, OW-ovary width, SL-style length, DFF-days to the female flower, NFFB-node to first female bud, FL-fruit length, FD-fruit diameter, FW-fruit weight, FPV-fruits per vine, YPV-yield per vine. GCV-genetic coefficient of variation, PCV-phenotypic coefficient of variation, H_b-heritability in a broad sense, GA-genetic advance, GA (PM)-genetic advance as percent of mean

Table 3: Components of genetic variation for different traits in BC_1P_2 populations of *Satputia* × sponge gourd

Traits	BC_1P_2-(SAT-1 × SG 282) × SG 282							BC_1P_2-(SAT-1 × PSG 9) × PSG 9						
	Range	Mean	GCV (%)	PCV (%)	H_B (%)	G A	GA (PM)	Range	Mean	GCV (%)	PCV (%)	H_B (%)	G A	GA (PM)
VL (cm)	11.20-300.21	108.20	5.50	48.19	11.41	0.24	0.22	14.25-520.05	115.36	12.09	53.81	22.47	0.46	0.40
IL (cm)	3.74-12.24	7.19	22.25	24.96	89.14	1.84	25.54	5.25-13.65	8.86	22.09	23.99	92.08	1.90	21.41
LL (cm)	5.50-11.33	7.19	11.92	14.89	80.05	1.65	22.94	4.05-13.50	9.33	18.18	19.08	95.28	1.96	21.04
LW (cm)	7.41-14.10	10.26	13.24	16.48	80.34	1.66	16.13	5.50-17.34	13.19	19.37	20.27	95.56	1.97	14.92
FBL (mm)	31.52-100.15	58.09	5.75	24.32	23.64	0.49	0.84	35.88-99.33	27.30	4.83	23.86	20.24	0.42	1.53
OL (mm)	20.53-85.35	45.99	8.57	27.36	31.32	0.65	1.40	26.89-84.69	46.71	6.34	25.93	24.45	0.50	1.08
OW (mm)	2.86-12.77	6.60	5.83	29.52	19.75	0.41	6.16	4.45-9.08	6.58	1.64	19.73	8.31	0.17	2.60
SL (mm)	3.48-14.68	8.73	4.39	29.75	14.76	0.30	3.48	4.20-20.45	9.02	6.76	38.00	17.79	0.37	4.06
DFF	26.00-56.00	37.35	2.57	16.73	15.36	0.32	0.85	27.00-60.00	40.89	2.94	16.94	17.36	0.36	0.87
NFFB	4.00-18.00	11.51	4.65	33.50	13.88	0.29	2.48	7.00-24.00	10.00	2.99	33.88	8.83	0.18	1.82
FL (cm)	7.25-23.40	16.53	8.73	20.64	42.30	0.87	5.27	9.41-28.10	17.95	6.01	21.13	28.44	0.59	3.26
FD (cm)	2.11-6.26	3.94	7.83	20.62	37.97	0.78	19.85	2.24-6.98	4.33	4.72	21.86	21.59	0.44	10.27
FW (g)	45.00-110.00	84.57	7.63	21.41	35.64	0.73	0.87	40.00-95.00	79.57	9.40	24.17	38.89	0.80	1.01
FPV	12.00-154.00	37.22	11.47	60.72	18.89	0.39	1.05	9.00-133.00	37.83	16.27	65.53	24.83	0.51	1.35
YPV (kg)	0.70-9.24	3.19	20.68	74.79	27.65	0.57	17.86	0.45-10.64	3.05	20.21	76.64	26.37	0.54	17.81

VL-vine length, IL- internodal length, LL-leaf length, LW-leaf width, FBL-female bud length, OL-ovary length, OW-ovary width, SL-style length, DFF-days to the female flower, NFFB-node to first female bud, FL-fruit length, FD-fruit diameter, FW-fruit weight, FPV-fruits per vine, YPV-yield per vine. GCV-genetic coefficient of variation, PCV-phenotypic coefficient of variation, H_b-heritability in a broad sense, GA-genetic advance, GA (PM)-genetic advance as percent of mean order of GCVs and PCVs, respectively. However, leaf length (18.18%) and leaf width (19.37%), fruits per vine (16.27%), and vine length (12.09%) achieved the medium range of GCV's. Internodal length (92.08 and 21.41%), leaf length (95.28 and 21.04%), and leaf width (95.56 and 14.92%) in this population unveiled high heritabilities accompanied with moderate genetic advances that indicated the presence of additive gene action. Fruit yield per vine carried low heritabilities (26.37%) with moderate genetic advance (17.81%).

In the present scenario of sponge gourd breeding, we usually seek improvement in various fruit and yield traits. Two interspecific crosses between *Satputia* and sponge gourd presented a high genetic diversity through a wide range of variation in different traits (Figure 1D). Each trait showed a high level of variation due to greater genetic divergence between the parents involved in the crosses (Figure 1A, B, C). During the investigation of various populations of two interspecific crosses, the observations on internodal length, leaf length, and leaf width presented the smaller differences between the PCVs and GCVs. It highlighted a lower degree of environmental influence on the phenotypic expression of these traits especially in the progenies developed from these interspecific crosses. We can select smaller internodes and leaves to reduce the excessive vegetative growth from the progenies of these crosses. In sponge gourd, the longer internodes generally appear in lengthy vines that are very difficult to manage in the field without proper staking. The selection of internodal length in a negative direction would reduce the vine length and also minimize the area required for a single vine. Thus, this crop can also come under intensive cultivation by changing the plant architecture and reducing the plant spacing. Therefore, these characters would be more effective selection indices involving diverse *Luffa* species in future breeding programs.

The higher magnitude of the differences between the genotypic and phenotypic coefficients of variation for other traits reflected the greater influence of the environment on the expression of these traits. Medium to high order of GCVs for fruits per vine and yield per vine in the F_2 and backcross generations of both crosses also revealed their importance in selection. Medium order of GCVs for female bud length, ovary length, fruit length and fruit weight in the F2 of both the crosses and node to first female bud in BC_1P_1 of both the crosses also highlighted their importance as selection criteria from these progenies in the future. Similarly, the importance of GCV in the selection of the genotypes has also been reported in ridge gourd (Singh *et al*., 2002), bitter gourd (Prasanth *et al.,* 2020) and sponge gourd (Pandey *et al*., 2012; and Singh *et al*., 2017).

Further, the high heritabilities accompanied by high genetic advances for the internodal length, leaf length, and leaf width in the $F_{2,}$ as well as the backcross populations of both the crosses, indicated that the additive genes most likely governed these traits. The moderate genetic advances for fruit yield per vine in the different generations of two crosses also highlighted the importance of this trait for the selection of high-yielding genotypes in future generations of this cross. These populations have an exploitable amount of variation, and pedigree selection can be the most effective method of improvement. The low heritabilities accompanied by low genetic advances would make ineffective selections in the progenies in many traits from these crosses. The importance of heritabilities and genetic advances in an effective selection of traits has already been highlighted by many researchers in different crops (Chowdhury and Sharma, 2002). Similarly, the divergent values of heritabilities and genetic advances were also reported in cauliflower genotypes (Singh *et al*., 2023).

Correlation Analysis

The results for correlation analysis of different traits with yield potential in two F_2 and their respective backcrosses are presented in Table 4. In the F_2 as well as backcross populations of both the crosses, the positive and highly significant correlation of fruit yield was established with fruit weight (r = 0.46–0.85) and fruits per vine (r = 0.72–0.93). The fruit yield in the F_2 of cross SAT × SG 282 was also significantly and negatively correlated with the node to first female bud (r = -0.17) as well as significantly and positively correlated

Figure 1: Interspecific hybridization for genetic variability in sponge gourd: A. SG-282, B. Satputia, C. fruits of parents and F_1 hybrid and D. fruit variability in F_2 population

Table 4: Correlation of different traits with fruit yield in the F_2 and backcross populations of both crosses in sponge gourd

Traits	SAT-1 × SG 282			SAT-1 × PSG 9		
	F_2	BC_1P_1	BC_1P_2	F_2	BC_1P_1	BC_1P_2
VL (cm)	-0.01	-0.01	-0.50	0.08	0.45**	0.53**
IL (cm)	-0.03	0.03	-0.60	0.05	0.61**	0.65**
LL (cm)	-0.06	-0.06	0.01	0.02	0.61**	0.66**
LW (cm)	0.035	-0.02	0.00	0.04	0.59**	0.66**
FBL (mm)	-0.06	-0.03	0.04	0.13*	0.59**	0.63**
OL (mm)	-0.02	-0.02	-0.03	0.05	0.50**	0.61**
OW (mm)	0.07	0.01	-0.16*	0.03	0.63**	0.64**
SL (mm)	0.026	0.04	0.11	-0.10	0.61**	0.61**
DFF	-0.05	-0.13*	0.01	-0.09	0.62*	0.64**
NFFB	-0.17*	0.21*	-0.01	-0.09	0.54**	0.62**
FL (cm)	0.12*	-0.06	-0.13*	0.17*	0.67**	0.66**
FD (cm)	-0.03	0.18*	0.04	0.14*	0.65**	0.65**
FW (gm)	0.53**	0.59**	0.50**	0.46**	0.85**	0.76**
FPV(no.)	0.78**	0.72**	0.91**	0.80**	0.88**	0.93**

VL-vine length, IL- internodal length, LL-leaf length, LW-leaf width, FBL-female bud length, OL-ovary length, OW-ovary width, SL-style length, DFF-days to the female flower, NFFB-node to first female bud, FL-fruit length, FD-fruit diameter, FW-fruit weight, FPV-fruits per vine, YPV-yield per vine.

with fruit length (r = -0.12). In the BC_1P_1 of cross SAT × SG 282, the fruit yield was also positively and significantly associated with the node to first female flower (0.21) and fruit diameter (0.18) and negatively affected with the days to first harvest (-0.13). However, BC_1P_2 of the same cross showed a negative and significant association of fruit yield with ovary width and fruit length. In the F_2 of cross SAT × PSG 9, the fruit yield was also significantly and positively affected by female bud length, fruit length, and diameter. However, in both the backcrosses of this cross, the yield was positively and significantly associated with all the traits under investigation.

In the present investigation, the correlation of all the traits with fruit yield per vine indicated a differential display of trait association in six segregating populations developed from two crosses. The overall observation for trait association from F_2 of both the crosses indicated the high influence of fruit weight and the number of fruits per plant on fruit yield. In the first cross (SAT× SG 282), the earliness of the node to the first female flower and days to the first harvest also improved the yield, respectively, in the F_2 and BC_1P_1. Mainly, the association of fruit length with yield played a different role in different populations. Increased fruit length along with augmented fruit weight as well as fruits per vine was more important in $F_{2,}$ while fruit diameter influenced the yield in $BC_1P_{1.}$ The decreasing trend of fruit length, along with increased fruit weight and number, influenced the yield per vine in BC_1P_1. There was a wide genetic variation between sponge gourd and *Satputia* for fruit traits, where the backcross with second had contributed towards the thick and short fruits. Although the results of association with vine length, internodal length, and leaf dimensions were non-significant, the negative sign indicated that the selection could be practiced for short vine and internodal length along with less vegetative growth in this cross. These traits were also important for crop improvement in sponge gourd. In both the backcrosses of the second cross (SAT× PSG 9), the yield was significantly influenced by all the traits under investigation. The population-specific trait association in these crosses can further be used for yield improvement in sponge gourd. Our results were in agreement with the findings of Cruz *et al*., (1997), Chowdhury and Sharma (2002), Choudhary *et al*., (2014), and Touthang *et al*., (2021).

Conclusion

It was concluded from the present investigation that F_2 as well as backcross populations of interspecific crosses between *Satputia* and sponge gourd had a wide range of genetic variability for different quantitative traits affecting the yield potential. The excessive vegetative growth of vines and leaves has also become an undesirable trait for the intensive cultivation of this crop. High genotypic coefficients of variation and heritabilities as well as moderate genetic advances for internodal length, leaf length, and leaf width, suggested that it can be improved for short vine and less vegetative growth also by practicing selection in the negative direction. Secondly, the traits such as ovary length, ovary width, and fruit weight in the F_2 population of the first cross, female bud length, ovary length, female bud length, fruit length, fruits per vine and yield per vine in the F_2 population of the second cross had moderate to high level of genotypic coefficient of variations along with moderate heritabilities as well as genetic advances and suggested the possible improvement through these selection indices. The short vines with early bearing more number of small fruits per vine can also contribute towards the yield potential in sponge gourd. Similarly, the moderate genetic coefficient of variations for fruits per vine and moderate heritabilities for various fruit traits in both the backcrosses involving cultivated species (BC_1P_2) made these populations most reliable for the improvement of horticultural fruit traits in sponge gourd. The selection for more fruit weight and fruits per vine can be helpful in increasing the yield in all the populations developed from interspecific hybridization in this investigation. Similarly, the negative association of node to the first female flower in the first F_2 cannot be ignored as it brings earliness as well as augmentation in the yield potential. The yield potential in both the backcrosses of the second cross was influenced significantly by all the traits under investigation. Therefore, due consideration can be given to all such traits for crop improvement from the particular cross combination.

References

Ahuja S, PK Malhotra, VK Bhatia and R Parsad (2008) Statistical Package for Agricultural Research (SPAR 2.0). *J. Indian Soc. Agric. Stat.* 62:65-74.

Chakravarty HL (1982) Fascicles of Flora of India: Fascicle 11. Cucurbitaceae. In: *Botanical Survey of India*, Howrah, West Bengal, India, pp 85-116.

Chaubey T, DK Upadhay and B Singh (2014) Genetic improvement of gourds: sponge gourd [*Luffa cylindrica* (L.) Roem.]. *Adv. Res. J. Crop Improv.* 5: 215-217.

Choudhary BR, S Kumar and SK Sharma (2014) Evaluation and correlation for growth, yield and quality traits of ridge gourd (*Luffa acutangula*) under arid conditions. *Indian J. Agric. Sci.* 84: 498–502.

Choudhary BR, S Pandey and R Singh (2009) Genetic diversity evaluation in *Satputia* (*Luffa hermaphrodita*). *Proceedings of International Conference on Horticulture, Bangalore,* Karanataka, India, pp 379-382.

Chowdhury D and KC Sharma (2002) Studies on variability, heritability, genetic advance and correlation in ridge gourd (*Luffa acutangula* Roxb.). *Hort. J.* 15**:** 53-8.

Cruz VMV, MIS Tolentino, NC Altoveros, MLH Villavicencio, LB Siopongco, AC Dela Vina and RP Laude (1997) Correlations among accessions of Southeast Asian *Luffa* genetic resources and variability estimated by morphological and biochemical methods. *Philipp. J. Crop Sci.* 22: 131-140.

Jeffrey C (1992) Names of indigenous Neotropical species of *Luffa* Mill. (Cucurbitaceae). *Kew Bulletin* 47: 741-742.

Kalloo G and BO Bergh (1993) Loofah-Luffa spp. In: *Genetic improvement of vegetable crops*. Oxford Pergamon Press Ltd. United Kingdom. pp 265-266.

Karmakar P, AD Munshi, TK Behera, R Kumar, C Kaur and BK Singh (2013) Hermaphrodite inbreds with better combining ability improve antioxidant properties in ridge gourd [*Luffa acutangula* (Roxb.) L.]. *Euphytica* 191: 75–84. DOI 10.1007/s10681-013-0862-x

Prasanth K, AT Sadashiva, M Pitchaimuthu and B Varalakshmi (2020) Genetic diversity, variability and correlation sudies in bitter gourd (*Momordica charantia* L.) *Indian J. Plant Genet. Resour.* 33(2): 102–105.

Pandey V, VB Singh and MK Singh (2012) Selection parameters in sponge gourd (*Luffa cylindrica* Roem.) for yield and yield related component traits. *Environ. Ecol.* 30: 412-414.

Sidhu MK (2019) Pre-breeding of clustered and bisexual traits through interspecific hybridization between sponge gourd (*Luffa cylindrica* L.) and *Satputia* (*Luffa hermaphrodita*). *Proceedings of First Vegetable Science Congress on Emerging Challenges in Vegetable Research and Education*, 1-3 February 2019, Agriculture University, Jodhpur, Rajasthan, India, 50 p.

Sidhu MK and J Kaur (2021) Inter-specific hybridization between sponge gourd (*Luffa cylindrica* L.) and '*Satputia*' (*Luffa hermaphrodita* Singh & Bhandari) for pre-introgression of cluster bearing, high yield, and gynoecism, *J. Genet.* 100:73. https://doi.org/10.1007/s12041-021-01323-0

Singh BP (1991) Inter-specific hybridization in between new and old-world species of Luffa and its phylogenetic implications. Cytologia 56, 359–365. https://doi.org/10.1508/cytologia.56.359

Singh J, A Shrama, P Shrama and N Kumar (2023) Genetic variability and association studies in mid-late and late group of cauliflower (*Brassica oleracea* L. var. botrytis). (2023). *Indian J. Plant Genet. Resour.* 36(01): 45-51. https://doi.org/10.5958/0976-1926.2023.00036.1.06

Singh PK, VB Singh, CK Singh, M Kumar, V Kumar and N Kumar (2017) Evaluation of germplasm for PCV, GCV, and heritability in Luffa (*Luffa cylindrica* Roem.). *Int. J. Curr. Microbiol. Appl. Sci.* 6**:**355-360.

Singh RP, J Mohan and D Singh (2002) Study on genetic variability and heritability in ridge gourd *(Luffa acutangula)*. *Agric. Sci. Dig.* 22: 279-280.

Telford I, H Schaefer, W Greuter and SS Renner (2011) A new Australian species of *Luffa* (Cucurbitaceae) and typification of two Australian *Cucumis* names, all based on specimens collected by Ferdinand Mueller in 1856. *Phyto Keys* 5: 21-29. https://doi.org/10.3897/phytokeys.5.1395

Touthang L, H Kalita, B Makdoh, T Angami and R Singh (2021) Agro-morphological characterization, genetic variation and heritability analysis of rice landraces (*Oryza sativa* L.) of Arunachal Pradesh, Northeast India (2021). *Indian J. Plant Genet. Resour.* 34 (02), 185–195. https://doi.org/10.5958/0976-1926.2021.00017.6.