Genetics of quantitative traits from interspecific crosses between *Luffa hermaphrodita* × *Luffa cylindrica*

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Abstract

Generation mean analysis study in sponge gourd was undertaken to estimate the gene action operating in the inheritance of quantitative traits using six basic generations of two interspecific crosses, namely SATPUTIA × SG 282 and SATPUTIA × PSG 9. The F2 and backcross generations showed high genetic variance for vine length, fruit weight and fruits per vine. Additive, dominant, additive x additive, additive × dominance and dominance x dominance effects significantly influenced most of the traits. The additive effect significantly contributed to fruit length and weight in both crosses. Dominance effects were significant for almost all the traits in both crosses. Additive × dominance type of interactions contributed significantly for female bud length, ovary length, style length, node to first flower, fruit diameter, fruit weight, fruits per vine and yield per vine. Duplicate effects influenced all the traits in both the crosses except for fruit length in SAT × PSG 9. For further improvement in interspecific progenies, the pedigree method can be applied to exploit additive variance to develop improved inbreds. However, transgressive segregates can further be used to exploit the presence of dominance, additive × dominance and dominance × dominance interactions.

Keywords: Sponge gourd, Satputia, inter-specific cross, genetics, dominance, epistasis.

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Introduction

Sponge gourd (*Luffa cylindrica* L., 2n = 26.), a cucurbitaceous vegetable, is widely cultivated in the summer and kharif seasons in India's tropical and sub-tropical parts. It is the main crop among gourd vegetables that originated in the subtropical region of Asia, particularly India (Kalloo 1993). Genus *Luffa* mainly comprised of nine species. Among these, *Luffa acutangula* L., *L. aegyptiaca* Mill., *L. echinata* Roxb., *L. graveolens* Roxb., *L. hermaphrodita* Singh and Bhandari, including two debatable species, *L. tuberose* Roxb., and *L. umbellate* M. Roem found distributed in India. However, *L. quinquefida* and *L. operculata* are new world species that were found distributed from Mexico to Nicaragua and Panama as well as to Southern Brazil (Chakravarty 1982, Jeffrey 1992). It is a cross-pollinated diploid species that bears monoecious flowers and smooth fruits on long trailing vines. The anthesis of its deep yellow flowers occurs in the morning (6.00 to 8.00 a.m.). Its fast growth, short duration and photo-insensitive nature make it suitable for raising in summer as well as in *kharif* season. However, its yield potential mainly depends upon the female: male ratio of the flowers. The occurrence of male and female flowers on vines further varies with the genotype, season of cultivation, microclimate of the vines, and water and nutrient management during its cultivation.

Interspecific hybridization combines many traits of two wide species. The segregation, selection and utilization of different traits from a wide cross mainly depend upon the genetics of different traits. Generation mean analysis developed by Hayman (1958) for the estimation of genetic components of induced variation has proved to be an important technique. It uses different generations and provides information about the different genetic parameters and epistatic interactions involved in the expression of different traits. Many traits are governed by additive, non-additive and epistatic effects among the genes. The precise knowledge of the nature and magnitude of these effects for different characters related to productivity helps in the choice of effective breeding methods and accelerates the pace of genetic improvement of target crop. Therefore, the present investigation was planned to explore the genetics of different quantitative traits from interspecific cross between *Satputia* and sponge gourd.

Materials and Methods

The plant material for the present investigation involved two different interspecific crosses (SAT × PSG 9 and SAT × SG 282) between two species developed in 2018. The F2 and backcross generations (BC1P1 and BC1P2) with the respective parents of each cross were developed in summer 2019. The parents were maintained and the seed of F_1 crosses was also multiplied. The experiment consists of six generations of each of the cross viz. P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2. The seedlings were raised in artificial media in plug trays. The 10 seedlings for each parent and F_1, 50 for each backcross and 100 for each F2 population in each of three replications were transplanted in randomized block design at the vegetable farm of Punjab Agricultural University, Ludhiana during the summer season of 2020. Crop was raised as per recommended cultivation practices (Anonymous 2019). The seedlings were transplanted at 60 cm spacing on both sides of three metre wide beds. Individual plant data of each generation of each cross in all three replications was recorded for vine length at first harvest, internodal length (cm), leaf length (cm), leaf width (cm), days to flowering, node of 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 (no.), yield per vine (kg) and compiled replication-wise for the statistical analysis.

   The mean values, standard errors and variances of the different generations were subjected to weighed least-squares analysis using the scaling test (Mather 1949) and the joint scaling test to estimate gene effects. The genetic effects were estimated using the models suggested by Mather and Jinks (1982) and Jinks and Jones (1958). The significance of the scales and gene effects were tested by using the t-test. The significance of A and B scales provided the indication for the presence of additive x additive (i), additive x dominance (j) and dominance x dominance (l) type gene interactions. The significance of only C scale provided the importance of dominance (h) and dominance x dominance (l) effects. The complementary and duplicate type of epistasis was ascertained from the same and different signs for h and l, respectively. The fitment of additive dominance model (ADM) or six-parameter model was ascertained through chi square (χ^2) analysis.

Results and Discussion

The results for mean performance and variance of the six basic generation viz., P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2 of crosses *SATPUTIA* × SG 282 and *SATPUTIA* × PSG 9 for fifteen quantitative traits is presented in Table 1 and 2, respectively. The results show the differences of variances for each trait in different generations. Vine length displayed the highest variance among various quantitative traits followed by fruit weight and fruits per vines in F_2 and two backcrosses of each cross. The segregating generation of two interspecific crosses displayed maximum variability in vine length, fruit weight and fruits per plant and these traits formed the most important selection parameters for crop improvement in sponge gourd. These F_2 and backcross populations can further be used to develop short vines for intensive cultivation. In sponge gourd, fruit weight and fruits per vines directly influence the yield potential. Therefore, these segregating generations can provide the transgressive segregates carrying short vines, good average fruit weight, and more fruits per vine, ultimately enhancing the yield potential. Similar results for high genetic variability for various vines and yield traits were confirmed in the studies of Singh *et al.* (2002) and Rathore *et al.* (2017) in ridge gourd.

   For the generation mean analysis of two interspecific crosses in sponge gourd, the results for A, B and C scales revealed the inadequacy of the simple Additive Dominance Model for most of the traits under investigation (Table 3). The non-significance of all the scales for ovary width in the first cross (SAT × SG 282) highlighted the involvement of ADM for trait expression. However, the significance of all the scales for internodal length, leaf width, female bud length, ovary length, style length, fruit length, fruit weight and fruits per vine, A and C scales for vine length and yield per vine, only A scale for node to first female bud and only B scale for fruit diameter indicated the involvement of epistatic interactions for their expression in the segregating generations of this cross. The results for SAT × PSG 9 cross also highlighted the inadequacy of ADM for all the traits because of the significance of A, B and C scales for female bud length, ovary length, style length, days to first flower, fruit length and fruit weight, A and C scales for the traits vine length, leaf length, leaf width, ovary width, node to first female bud and yield per vine, only A scale for fruits per vine and only C scale for

Table 1: Means and variances for different traits in all generations of *SATPUTIA* × SG 282

Traits	SATPUTIA		SG 282		SATPUTIA × SG 282		F_2(SATPUTIA × SG 282)		(SATPUTIA × SG 282) × SATPUTIA		(SATPUTIA × SG 282) × SG 282	
	Mean	Variance	Mean	Variance	Mean	Variance	Mean	Variance	Mean	Variance	Mean	Variance
VL (cm)	64.75	1.06	70.80	1.44	131.67	1.14	70.15	24.65	83.00	9.53	108.20	18.12
IL (cm)	6.90	0.04	7.12	0.05	4.62	0.09	6.33	0.02	9.66	0.06	7.19	0.02
LL (cm)	7.18	0.05	7.22	0.05	4.60	0.10	6.33	0.02	9.64	0.06	7.19	0.02
LW (cm)	9.40	0.09	13.68	0.10	10.86	0.04	8.60	0.02	10.73	0.04	10.26	0.02
FBL(mm)	47.17	0.99	75.13	1.07	69.52	0.96	47.93	0.46	37.09	0.62	58.09	1.28
OL (mm)	37.12	0.98	64.57	0.97	56.32	0.64	35.83	0.36	29.04	0.59	45.99	1.06
OW (mm)	9.25	0.06	5.55	0.007	7.60	0.03	7.18	0.02	8.43	0.04	6.60	0.03
SL (mm)	5.89	0.14	11.17	0.10	11.79	0.11	7.27	0.03	9.61	0.02	8.73	0.04
DFF	45.97	0.03	3550	0.27	23.93	0.08	40.00	0.25	34.71	0.07	37.35	0.26
NFFB	6.03	0.07	9.97	0.06	9.00	0.02	8.76	0.05	10.58	0.10	9.53	0.08
FL (cm)	4.78	0.01	28.25	0.06	16.87	0.11	10.39	0.05	8.31	0.04	16.53	0.07
FD (cm)	2.80	0.008	2.71	0.002	4.09	0.02	3.57	0.003	3.32	0.003	3.94	0.004
FW (g)	25.83	0.52	115.03	0.37	77.13	1.05	59.51	20.68	37.33	8.73	84.57	7.14
FPP	58.00	0.87	14.77	0.10	67.60	0.79	43.31	2.98	32.94	2.50	38.21	3.30
YPP (kg)	1.50	0.006	1.70	0.002	5.23	0.07	2.58	0.02	1.22	0.009	3.19	0.04

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 female flower, NFFB-node to first female bud, FL-fruit length, FD-fruit diameter, FW-fruit weight, FPV-fruits per vine, YPPV-yield per plant

Table 2: Means and variances for different traits in all generations of *SATPUTIA* × PSG 9

Traits	SATPUTIA		PSG 9		SATPUTIA × PSG 9 (F1)		(SATPUTIA × PSG 9) (F_2)		(SATPUTIA × PSG 9) × SATPUTIA (BC1P1)		(SATPUTIA × PSG 9) × PSG 9 (BC1P1)	
	Mean	variance	Mean	variance	Mean	variance	Mean	variance	Mean	variance	Mean	variance
VL (cm)	61.98	1.90	107.34	1.08	124.00	1.84	76.89	29.51	117.65	26.59	115.36	28.10
IL (cm)	6.90	0.04	7.55	0.08	9.53	0.10	6.31	0.01	8.52	0.03	8.86	0.03
LL (cm)	7.25	0.06	8.86	0.02	10.28	0.05	6.60	0.01	7.51	0.01	9.33	0.02
LW (cm)	9.40	0.09	12.18	0.06	14.14	0.09	9.24	0.02	10.00	0.02	13.19	0.05
FBL (mm)	47.17	0.99	51.19	0.80	53.14	0.69	48.38	0.61	32.98	0.68	27.30	1.25
OL (mm)	37.12	0.98	42.02	0.87	44.16	0.96	38.64	0.52	35.96	1.06	46.71	0.98
OW (mm)	9.25	0.06	6.36	0.02	7.48	0.09	6.83	0.01	7.15	0.03	6.58	0.01
SL (mm)	5.89	0.14	9.36	0.05	11.12	0.09	7.60	0.02	9.13	0.02	9.02	0.08
DFF	45.97	0.03	61.20	0.20	37.57	0.35	40.49	0.20	35.28	0.04	40.89	0.32
NFFB	6.03	0.07	16.33	0.05	7.60	0.05	8.85	0.04	11.46	0.11	11.63	0.10
FL (cm)	4.78	0.01	23.57	0.03	16.00	0.11	12.18	3.08	8.64	0.05	17.95	0.10
FD (cm)	2.79	0.007	2.98	0.00	4.70	0.01	3.90	0.30	3.39	0.04	4.33	0.06
FW (g)	25.83	1.52	105.60	1.35	107.13	1.20	64.67	20.47	31.23	12.80	79.57	12.99
FPP	58.00	1.87	11.33	0.04	56.23	0.51	49.04	5.00	40.31	3.05	37.83	3.91
YPP (kg)	1.50	0.006	1.20	0.00	6.02	0.02	3.10	0.03	1.29	0.01	3.05	0.04

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 female flower, NFFB-node to first female bud, FL-fruit length, FD-fruit diameter, FW-fruit weight, FPV-fruits per vine, YPPV-yield per plant

Table 3: Estimates of scaling tests for various quantitative traits of SAT × SG 282 and SAT × PSG 9 cross in sponge gourd

| Traits | SAT × SG 282 | | | $\chi2_{ADM}$ | SAT × PSG 9 | | | $\chi2_{ADM}$ |
	A	B	C		A	B	C	
VL	-30.40 ± 9.50**	13.94 ± 10.72	-118.27 ±15.08**	91.48**	41.31 ± 11.67**	18.02± 13.24	-99.12 ± 12.59**	112.17**
IL	7.79 ± 0.62**	2.55 ± 0.49**	1.96 ± 0.89*	184.25**	0.60 ± 0.53	0.64 ±0.55	-8.29 ± 0.85**	221.90**
LL	7.50 ± 0.63**	2.56 ± 0.49**	1.72 ± 0.89	171.24**	-2.52 ± 0.40**	-0.48 ± 0.39	10.27 ± 0.68**	280.28**
LW	1.21 ± 0.55*	-4.02 ± 0.46**	-10.41 ± 0.79**	244.64**	-3.53 ± 0.51**	0.07 ± 0.59	-12.90 ± 0.90**	268.16**
FBL	-42.52± 2.34**	-28.47± 2.85**	-69.63 ± 4.16**	411.53**	-34.35± 2.10**	10.26± 2.55**	-11.14 ± 37.89**	305.56**
OL	-35.36± 2.23**	-28.91±2.61**	-71.02 ± 3.77**	415.69**	-9.35 ± 2.49**	7.24 ± 2.40**	-12.88 ± 3.74**	40.33**
OW	0.015 ± 0.48	0.052 ± 0.37	-1.27 ± 0.66	4.693	-2.43 ± 0.52**	-0.69 ± 0.39	-3.25 ± 0.79**	26.71**
SL	1.55 ± 0.57**	-5.50 ± 0.62**	-11.56 ± 1.05**	272.55**	1.27 ± 0.57*	-2.44 ± 0.67**	-7.07 ± 0.95**	123.79**
DFF	-0.39 ± 0.63	15.26 ± 0.12**	33.03 ± 2.15**	359.70**	-15.59± 0.73**	-17.45± 1.35**	-30.58± 2.20**	504.28**
NFFB	6.13 ± 0.71**	0.10 ± 0.65	1.04 ± 0.98	74.22**	9.29 ± 0.75**	-0.68 ± 0.71	-2.17 ± 0.96*	177.22**
FL	-5.03 ± 0.52**	-12.06± 0.68**	-25.20 ± 1.13**	598.61**	-3.50 ± 0.57**	-3.67 ± 0.72**	-11.65± 1.31**	96.26**
FD	-0.25 ± 0.19	1.07 ± 0.18**	0.57 ± 0.34	52.93**	-0.71 ± 0.19**	0.99 ± 0.19**	0.44 ± 0.31	61.02**
FW	-23.50± 4.95**	-17.90± 5.00**	-52.43 ± 9.64**	34.37**	-60.43 ± 3.99**	-37.60± 4.06**	-85.50 ± 7.43**	312.40**
FPV	-62.41 ±3.56**	-9.10 ± 3.75*	-34.74 ± 7.27**	315.61**	-33.69± 3.82**	6.35 ± 4.02	16.72 ± 0.92	87.69**
YPV	-4.20 ± 0.33**	-0.39 ± 0.48	-3.31 ± 0.76**	188.64**	-4.52 ± 0.04**	-0.70 ± 0.43	-1.97 ± 0.77*	301.18**

*, ** Significant at 5% and 1% levels, respectively

Note: 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 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.

internodal length. In F_2 and backcrosses of SAT × SG 282, the genotypes can be selected by carrying forward their progenies for fixation of traits in homozygous conditions in advanced generations. Thus, the expression of this trait can easily be improved through the pedigree method as suggested in earlier reports of Tewari *et al.* (1998) in bitter gourd. On the other hand, the significance of the scaling test for most of the traits further highlighted that the genetics of these traits from interspecific crosses could not be explained through a simple additive dominance model because the epistatic interactions had affected their expression in F2 and backcross generations. Our results for scaling tests were in line with the findings of Singh *et al.* (2000), Pallavi *et al.* (2019) in bottle gourd and cowpea.

The analysis of six parameter model further partitioned the main gene effects (additive and dominance) of quantitative traits of both the crosses, SAT × SG 282 and SAT × PSG 9, into various types of gene interactions(Table 4). It explained the expression of different traits under investigation through additive, dominance, additive × additive, additive × dominance and dominance × dominance effects. In SAT × SG 282 cross, the dominance component was on higher side than the additive component for all the traits except for fruit length and weight. Also, the dominance × dominance types of interactions were significant for all the traits except for days to first flower. Additive × additive type of interactions were also significant for most of the traits

except female bud length, ovary length, fruit diameter, fruit weight and yield per vine and additive × dominance types of interactions were significant for all the traits except fruit weight. The opposite sign of [h] and [l] components revealed the involvement of duplicate epistasis for expressing all the traits in this cross. However, in SAT × PSG 9 cross, the dominant component was on higher side than the additive component for all the traits except for ovary width and fruit length. Among epistatic interactions, dominance × dominance effects were significant for most of the traits except for ovary length, fruit length and fruit diameter, additive × additive gene actions were significant for most of the traits except ovary width, days to first flower, fruit diameter and fruit weight and also additive × dominance behaviors were significant for most of the traits except for vine length, internodal length, days to first flower and fruit length. The opposite sign of [h] and [l] components for most of the traits revealed the involvement of duplicate type of epistasis for their expression. However, similar sign for [h] and [l] components of fruit length confirmed complementary epistasis in this cross. For further improvement in most of the traits, the occurrence of dominance and dominance × dominance effects in cross SAT × SG 282, signified the importance of selection through heterosis breeding as well as the prevalence of additive × additive can be exploited through hybridization and selection through pedigree method resulting in transgressive segregates. The duplicate

Table 4: Estimates of six parameter model for various quantitative traits of SAT × SG 282 and SAT × PSG 9 cross of sponge gourd

Traits	SAT × SG 282						
	m	d	h	i	j	l	Epistasis
VL	-34.04 ±13.94*	-3.02 ± 3.02	251.06 ± 37.48**	101.81±13.60**	-44.34 ± 12.13**	-85.35 ± 25.88**	Duplicate
IL	-1.32 ± 0.82	-0.16 ± 0.16	24.66 ± 2.13**	8.38 ± 0.80**	5.25 ± 0.65**	-18.72 ± 1.45**	Duplicate
LL	-1.14 ± 0.82	-0.02 ± 0.16	24.15 ± 2.14**	8.34 ± 0.80**	4.94 ± 0.66**	-18.41 ± 1.46**	Duplicate
LW	3.94 ± 0.75**	-2.14 ± 0.21**	11.69 ± 1.93**	7.60 ± 0.72**	5.23 ± 0.65**	-4.78 ± 1.27**	Duplicate
FBL	62.51± 3.95**	-13.98± 0.72**	-65.33 ±10.24**	-1.36 ± 3.88	-14.05 ± 3.11**	72.35 ± 6.91**	Duplicate
OL	44.09 ± 3.58**	-13.73 ± 0.70**	-45.28 ± 9.40**	6.75 ± 3.51	-6.45 ± 2.92*	57.51 ± 6.37**	Duplicate
OW	-	-	-	-	-	-	
SL	0.91 ± 0.85	-2.64 ± 0.25**	14.54 ± 2.13**	7.62 ± 0.81**	7.05 ± 0.70**	-3.66 ± 1.44*	Duplicate
DFF	58.89 ± 2.32**	5.23 ± 0.27**	-38.26 ± 5.35**	-18.16 ± 2.31**	-15.65 ± 1.27**	3.29 ± 3.15	Duplicate
NFFB	2.81 ± 1.23*	-1.97 ± 0.18**	17.60 ± 3.17**	5.19 ± 1.22**	6.03 ± 0.94**	-11.41 ± 1.99**	Duplicate
FL	8.41 ± 1.10**	-11.73 ± 0.14**	-0.51 ± 2.70	8.11 ± 1.09**	7.04 ± 0.72**	8.98 ± 1.75**	Duplicate
FD	2.50 ± 0.58**	0.04 ± 0.05	2.67 ± 0.69**	0.25 ± 0.27	-1.32 ± 0.20**	-1.08 ± 0.48*	Duplicate
FW	59.41 ± 8.17**	-44.60 ±0.69**	-12.64 ± 19.98	11.03 ± 8.15	-5.60 ± 5.04	30.37 ± 13.67**	Duplicate
FPV	73.16 ± 8.45**	21.62 ± 0.70**	-113.84 ±20.12**	-36.77 ± 8.42**	-53.31 ± 5.02**	108.28 ± 12.06**	Duplicate
YPV	2.88 ± 0.70**	-0.10 ± 0.04*	-3.53 ± 1.75*	-1.28 ± 0.70	-3.82 0.45**	5.88 ± 1.17**	Duplicate
	SAT × PSG 9						
	m	d	h	i	j	l	Epistasis
VL	-79.10 ± 18.32**	-9.36 ± 2.18**	420.88 ± 51.74**	158.44± 18.19**	23.30± 16.66	-217.77 ±34.55**	Duplicate
IL	-2.31 ± 0.71**	-0.32 ± 0.18	22.61 ± 1.88**	9.53 ± 0.68**	-0.03 ± 0.62	-10.77 ± 1.33**	Duplicate
LL	0.78 ± 0.57	-0.81 ± 0.14**	13.78 ± 1.46**	7.27 ± 0.56**	-2.04 ± 0.46**	-4.28 ± 1.00**	Duplicate
LW	1.35 ± 0.77	-1.39 ± 0.19**	18.77 ± 2.01**	9.44 ± 0.75**	-3.59 ± 0.65**	-5.98 ± 1.38**	Duplicate
FBL	62.13 ± 4.24**	-2.01 ± 0.67**	-46.04 ± 10.65**	-12.96 ± 4.19**	-44.61 ± 3.09**	37.05 ± 6.727**	Duplicate
OL	28.80 ± 4.11**	-2.45 ± 0.68**	24.00 ± 10.56*	10.77 ± 4.05**	-16.59 ±3.16**	-8.65 ± 6.82	Duplicate
OW	7.67 ± 0.63**	1.44 ± 0.13**	-3.18 ± 1.63	0.13 ± 0.62	-1.74 ± 0.50**	2.99 ± 1.15**	Duplicate
SL	1.72 ± 0.90	-1.74 ± 0.21**	14.12 ± 2.37**	5.90 ± 0.87**	3.70 ± 0.77**	-4.73 ± 1.60**	Duplicate
DFF	56.04 ± 2.16**	-7.62 ± 0.24**	-53.96 ± 5.14**	-2.45 ± 2.15	1.86 ± 1.28	35.49 ± 3.24**	Duplicate
NFFB	0.41 ± 1.24	-5.15 ± 0.17**	26.57 ± 3.27**	10.77 ± 1.23**	9.97 ± 0.99**	-19.38 ± 2.10**	Duplicate
FL	9.70 ± 1.35**	-9.39 ± 0.10**	3.61 ± 3.22	4.48 ± 1.35**	0.16 ± 0.79	2.69 ± 2.01	Complementary
FD	3.03 ± 0.31**	-0.09 ± 0.05*	1.81 ± 0.78*	-0.15 ± 0.30	-1.70 ± 0.23**	-0.14 ± 0.52	Duplicate
FW	78.25 ± 7.96**	-39.88± 0.85**	-81.68 ± 19.39**	-12.53 ± 7.91	-22.83 ± 5.10**	110.56 ± 12.16**	Duplicate
FPV	78.76 ± 10.44**	23.33 ± 0.69**	-93.97 ± 24.04**	-44.10 ± 10.41**	-40.04 ± 5.45**	71.44 ± 14.00**	Duplicate
YPV	4.60 ± 0.86**	0.15 ± 0.04**	-7.04 ± 2.01**	-3.25 ± 0.86**	-3.82 ± 0.47**	8.47 ± 1.20**	Duplicate

type of epistasis suggested a mild and intense selection in earlier and later generations, respectively, for all the traits in SAT × SG 282 cross. While for further improvement of all the traits, heterosis breeding can be employed due to the preponderance of dominance and dominance × dominance component for most of the traits in this cross. The prevalence of additive, dominance, additive × additive and additive × dominance type of interactions for different traits in SAT ×

PSG 9 cross suggested the improvement in inbreds through recurrent selection and use of heterosis breeding for better expression in future generations. Similar findings were reported by Lawande and Patil (1990), Singh *et al.* (2000) and Pallavi *et al.* (2019) in bitter gourd, bottle gourd and cowpea.

In was concluded from the present investigation that there was high genetic variation for vine length, fruit weight and fruits per vine in the F_2 and two backcrosses for each

interspecific cross in the sponge gourd. The generation mean analysis of both the crosses indicated the influence of epistatic interactions among the genes involved in most traits' expression. Therefore, further improvement requires transgressive segregation of additive effects of traits into desired genotypes and their utilization in heterosis breeding to exploit dominance as well as dominance $\times$ dominance effects. The utilization of these interspecific derivatives would be highly helpful in crop improvement of sponge gourd for intensive cultivation and yield potential.

References

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

Hayman BI (1958) Separation of epistatic from additive and dominance variation in generation means. Heredity 12:371–390.

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

Jinks JL and Jones RM (1958) Estimation of components of heterosis. Genetics 43:223–234.

Kalloo G and Bergh BO (ed) (1993). *Genetic improvement of vegetable crops* pp 265-266.

Lawande KE, Gadakh SR, Kale PN and Joshi VR (1994) Generation mean analysis in bitter gourd. J Maharashtra Agric Univ 19:126-127.

Mather K (1949) *Biometrical genetics*. Dover publication, Inc., New York.

Mather K and Jinks JL (1982) *Biometrical Genetics*. Chapman and Hall, London.

Pallavi, Singh A and Chaudhary S (2019) Generation mean analysis using six parameters genetic model for quantitative traits in cowpea [[*Vigna unguiculata (L.) Walp.*]. Int J Curr Microbiol App Sci 8:1967-73.

Rathore JS, Collis JP, Singh G, Rajawat KS and Jat BL (2017) Studies on genetic variability in ridge gourd (*Luffa acutangula* L. Roxb.) genotypes in Allahabad agro-climate conditions. *Int J Curr Microbiol Appl Sci* 6:317-338.

Singh PK, Kumar JC and Sharma JR (2000) Genetic estimates (gene action) in long fruited bottle gourd. Veg Sci 27:162-64

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

Tewari D, Ram HH and Jaishwal HR (1998) Gene effects for various horticultural traits in bitter gourd *(Momordica charantia* L.). Veg Sci 25:159-161.

सारांश

चिकनी तोरई में दो अन्तर्राप्रजातीय संकरण 'सतपुतिया ग एस.जी.-282 एवं सतपुतिया ग पी.एस.जी.-9 द्वारा 6 पीढ़ी पद्धति से मात्रात्मक गुणों के वंशागतित्व के जीन प्रक्रिया को ज्ञात करने के लिए पीढ़ी माध्य विश्लेषण किया गया। एफ-2 एवं पश्च संकरण पीढ़ी में लता की लम्बाई, फल भार तथा प्रति पौध फलों की संख्या हेतु उच्च अनुवांशिक विविधता पाया गयी। योज्य, प्रभावी योज्य ग योज्य, योज्य ग प्रभावी तथा प्रभावी ग प्रभावी का प्रभाव अधिकांश गुणों के लिये सार्थक पाया गया। फल की लम्बाई एवं फल भार का दोनों संकरणों में योज्य प्रभावी का योगदान सार्थक रहा। दोनों संकरणों में लगभग सभी गुणों हेतु प्रभावी का प्रभाव सार्थक रहा। योज्य ग प्रभावी का आपसी प्रक्रिया मादा कलिका की लम्बाई, अण्डाशय की लम्बाई, स्टाइल की लम्बाई, पुष्पन का प्रथम पार्श्व, फल व्यास, फल भार, प्रति लता फलों की संख्या एवं उपज प्रति पौध के प्रति सार्थक योगदान पाया गया। दोनों संकरणों में डुप्लीकेट प्रभाव सभी गुणों पर पाया गया केवल सतपुतिया ग पी.एस.जी.-9 के फल लम्बाई को छोड़कर। आगे अन्तर्राप्रजातिय से विकसित संततियों के सुधार हेतु वंशावली विधि को अपनाकर योज्य विविधता का उपयोग कर अंतजार्तीय सुधार किया जा सकता है। जबकि अतिक्रामी पृथक्करण का उपयोग आगे प्रभावी, योज्य ग प्रभावी तथा प्रभावी ग प्रभावी परस्पर क्रिया में किया जा सकता है।