

## RESEARCH ARTICLE

# Genetic Variability, Character Association and Path Coefficient Analysis in Satputia (*Luffa acutangula* var. *hermaphrodita*)

Nangsol Dolma Bhutia<sup>1,2</sup>, Amish Kumar Sureja<sup>3\*</sup>, Rakesh Bhardwaj<sup>4</sup>, Manjusha Verma<sup>4</sup>  
and Anilabha Das Munshi<sup>3</sup>

### Abstract

A study was carried out to assess the genetic architecture of 36 genotypes of satputia. Fruit yield and fourteen yield contributing traits were recorded from five plants at random. The mean performances of 36 satputia genotypes for yield and its attributing traits showed wide variation. The difference between the genotypic and phenotypic correlation coefficients was narrow for various traits. This indicates lesser influence of the environment in the expression of these traits and the presence of a strong inherent association among the traits. High heritability (%) estimates coupled with high genetic gain (%) were observed for fruit yield per plant (88.27, 72.08), number of fruits per plant (87.83, 53.60), average fruit weight (87.17, 45.41), number of primary branches (91.25, 46.73) and fruit diameter (79.15, 43.13), indicated that these traits are under additive gene effects, hence are more reliable for effective selection. The highest positive significant direct effect on yield was recorded by fruit length, followed by number of clusters per plant, node number of the first hermaphrodite flower and number of fruits/plant at both genotypic and phenotypic levels. Therefore, direct selection for these traits would be worthwhile for the improvement of yield in satputia.

**Keywords:** Correlation, GCV, *Luffa*, PCV, Path coefficient, Satputia

<sup>1</sup>College of Horticulture, Central Agricultural University, Bermiok, 737134, Sikkim, India.

<sup>2</sup>The Graduate School, ICAR-Indian Agricultural Research Institute, New Delhi, 110012, India.

<sup>3</sup>ICAR-Indian Agricultural Research Institute, New Delhi, 110012, India.

<sup>4</sup>ICAR-National Bureau of Plant Genetic Resources, New Delhi, 110012, India.

**\*Author for correspondence:**  
aksureja@gmail.com

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### Introduction

The rising global demand for nutritious crops has led to an increasing need for exploring underutilised crops and constant breeding programs aimed at producing new and improved varieties that satisfy both societal and economic requirements. Satputia (*Luffa acutangula* var. *hermaphrodita*) is an underutilized vegetable crop belonging to the Cucurbitaceae family. It is grown in the north-eastern part of Uttar Pradesh and adjoining areas as a mixed crop and as a mono-crop in both summer and rainy seasons (Choudhary *et al.*, 2007). It bears hermaphrodite flowers in clusters and is economically important for its tender fruits. Fruits of satputia are nutritious and are good sources of vitamin A, iron, phosphorus, ascorbic acid and zinc.

Despite its economic importance and presence of considerable variability, limited systematic information is available on the genetic characterization of satputia and its genetic improvement. Key genetic parameters, such as genotypic (GCV) and phenotypic (PCV) coefficients of variation,

play a pivotal role in facilitating crop improvement (Das *et al.*, 2012). The quantitative characters are very much prone to environmental influence, which necessitates the partitioning of overall variances as heritable and non-heritable components for an efficient breeding programme. To clearly comprehend the link between yield and its components, as well as their direct and indirect consequences, correlation and path analysis are useful tools for understanding the association. Heritability of characters can be relied upon, as it enables the plant breeder to decide the extent of selection pressure to be applied under a particular environment, which separates out the environmental influence from the total variability. The estimation of heritability has a greater role to play in determining the effectiveness of selection for a character, provided it is considered in conjunction with the predicted genetic advance as suggested by Johnson *et al.*, (1955), as the heritability is influenced by biometrical method, generation of hybrid, sample size of experimental material and environment. The findings of this investigation are anticipated to provide important insights into the genetic architecture of satputia for the selection of superior genotypes. This will be accomplished by bridging the information gap between yield and its constituent traits.

## Materials And Methods

The investigation was carried out at the research farm of

the Division of Vegetable Science of ICAR-Indian Agricultural Research Institute, New Delhi, which lies at 28.63° N, 77.15° E, 228 MSL. The climate of Delhi is semi-arid with hot summers and cool winters. The study material comprised of thirty six germplasm lines of Satputia collected from various parts of India and maintained in the Division of Vegetable Science (Table 1). The experiment was laid out in Randomized Block Design with three replications. Two to three seeds of each genotype were sown in the hills on the ridges at a spacing of 3.5 m × 75 cm. All the recommended practices were followed to grow a successful crop. Fruit yield and fourteen yield contributing traits were recorded (Table 2) from five plants at random.

The statistical analysis for each observed trait under the study was performed using MS-Excel, OPSTAT and Statistical Analysis System (SAS). The mean values of data recorded for the traits for the genotypes were subjected to analysis of variance as described by Gomez and Gomez (1983) for Randomised Block Design. The genotypic and phenotypic coefficients of variability were calculated as per the formulae given by Burton and De-Vane (1953). Heritability in the broad sense was calculated by the formula as suggested by Allard (1960). Genetic gain expressed as per cent ratio of genetic advance and population mean was estimated by the method given by Johnson *et al.*, (1955). The genotypic and phenotypic correlations were calculated as per Al-Jibouri *et al.*, (1958) by using analysis of variance and

**Table 1:** List of thirty-six genotypes of satputia used in the investigation

Genotype	Source	Genotype	Source
DSat-1	Muzaffarpur, Bihar	DSat-23	Gorakhpur, Uttar Pradesh
DSat-1-2	Muzaffarpur, Bihar	DSat-63	Jhargra, West Bengal
DSat-2	Bhubaneswar, Odisha	DSat-103	Sundergarh, Odisha
DSat-3	Jamshedpur, Jharkhand	DSat-112	Dhenkanal, Odisha
DSat-4	Ranchi, Jharkhand	DSat-112-1	Angul, Odisha
DSat-4-1	Madhubani, Bihar	DSat-113	Midnapore, West Bengal
DSat-4-12	Begusarai, Bihar	DSat-115	Midnapore, West Bengal
DSat-5	Koderma, Jharkhand	DSat-116	Jamshedpur, Jharkhand
DSat-7	Hazaribagh, Jharkhand	DSat-120	Sambalpur, Odisha
DSat-8	Pusa, Bihar	DSat-121	Hajipur, Bihar
DSat-9	Gumla, Jharkhand	DSat-122	Barabanki, Uttar Pradesh
DSat-9-1	Sitamarhi, Bihar	DSat-123	Ranchi, Jharkhand
DSat-10	Varanasi, Uttar Pradesh	DSat-124	Tezu, Arunachal Pradesh
DSat-11	Samastipur, Bihar	DSat-125	Purulia, West Bengal
DSat-11-1	Samastipur, Bihar	DSat-126	Dewariya, Uttar Pradesh
DSat-14	Gaya, Bihar	DSat-128	Bahraich, Uttar Pradesh
DSat-15	Barauni, Bihar	Kashi Khushi	IIVR, Varanasi
DSat-19	Sambalpur, Odisha	Swarna Sawani	ICAR Complex for Eastern Region Regional Center, Ranchi

**Table 2:** ANOVA and estimates of genetic variability for yield and its attributing traits in satputia genotypes

Trait	Range Min-Max	Mean	Coefficient of Broad sense variability (%) heritability advance			Genetic as (%)	Mean sum of square		
			GCV (%)	PCV (%)	(%) of mean		Replica- tion	Geno type	Error
Days to first female flower anthesis	33.75-50.17	40.64	12.58	12.76	97.21	32.75	0.27	2761.57**	52.29
Days to 50% flowering	36.74-55.00	43.98	8.50	9.14	86.36	20.84	0.73	3315.81**	153.66
Days to first fruit set	38.80-56.19	48.06	10.71	11.20	91.32	27.01	4.19	2872.12**	176.4
Node number of first hermaphrodite flower	4.08-8.09	5.77	14.85	22.52	43.00	25.84	6.72	109.82**	66.44
Number of primary branches	3.13-6.58	4.49	18.53	19.40	91.25	46.73	0.07	74.37**	4.6
Vine length (m)	1.30-2.77	1.89	16.45	25.35	42.07	28.16	0.55	14.70**	9.25
Number of fruits per cluster	3.10-6.95	5.38	8.44	19.93	17.95	9.45	2.01	55.03**	66.44
Number of clusters per plant	2.36-4.98	3.93	13.93	20.98	44.04	24.40	22.01	45.11**	26.84
Days to first fruit harvest	44.66-60.33	54.10	6.87	7.56	82.66	16.50	23.35	1559.03**	203.74
Fruit length (cm)	6.09-9.83	8.41	9.92	15.70	39.96	16.56	3.63	110.44**	73.7
Fruit diameter (mm)	15.93-32.37	22.28	18.37	20.64	79.15	43.13	5.25	1895.24**	305.97
Average fruit weight (g)	43.17-96.53	60.88	18.42	19.73	87.17	45.41	38.84	13628.41**	1274.66
Number of fruits/plant	9.80-25.57	17.31	21.66	23.12	87.83	53.60	75.94	1541.90**	136.1
100 Seed weight (g)	6.53-13.53	8.85	15.76	18.84	69.98	34.80	0.40	229.98**	57.54
Fruit yield per plant (kg)	0.57-2.06	1.05	29.06	30.93	88.27	72.08	164.11	10007.67**	849.24

\*\*Significant at 1% level of probability

covariance matrix in which total variability was split into replications, genotypes and errors. The genotypic and phenotypic correlation coefficients were used to find out their direct and indirect contribution towards yield per plot. The direct and indirect paths were obtained by following Dewey and Lu (1959).

## Results and Discussion

The improvement in crop yield depends upon the extent of genetic variability available in breeding materials and the extent to which the major yield contributing traits are heritable from generation to generation. The genetic variability can be a choice for selecting suitable parents. Analysis of variance showed that the mean sum of squares for genotypes was highly significant for all traits, indicating the existence of a high degree of genetic variability in the germplasm.

Nevertheless, the analysis of variance is not sufficient and conclusive to elucidate all the inherent genotypic variance in the collections. Therefore, it becomes necessary to split the observed variability into phenotypic variation (PV) and genotypic variation (GV) and subsequently GCV and PCV, which indicates the extent of variability existing for various traits. Moderate GCV and PCV variation (>20%) were observed for fruit yield per plant (kg) and number of fruits per plant (Table 2). Similar results were also obtained by Karuppaiah *et al.*, (2002) in ridge gourd. It indicated the presence of moderate variability in the germplasm for selection, and further, the differences between PCV and GCV values were minimum indicating that the traits under study were less influenced by the environment. Hence, these characters can be relied upon, and simple selection can be practiced for further improvement.

**Table 3:** Phenotypic and genotypic correlations among different quantitative traits in thirty-six genotypes of satputia

Traits	DFA	DFS	NNHF	NPB	VL	NOFC	NCPP	DTFHH	FL	FD	AFW	NOFPP	100SW	FYPP
	(P)	(G)	(P)	(G)	(P)	(G)	(P)	(G)	(mm)	(g)	(g)	(g)	(kg)	(g)
D50F	0.989*	0.653*	0.215*	-0.004	0.033	0.18*	-0.05	0.536*	-0.111	-0.040	-0.035	-0.163*	-0.164*	-0.266*
DFA	0.960*	0.629*	0.143*	0.011	0.060	0.11*	-0.06	0.506*	-0.059	-0.030	-0.007	-0.146*	-0.134*	-0.199*
DFS		0.692*	0.194*	0.032	0.067**	0.22*	-0.04	0.545*	-0.081	-0.038	-0.005	-0.158*	-0.139*	-0.264*
NNHF		0.671*	0.136*	0.051	0.099**	0.13*	-0.03	0.529*	-0.055	-0.031	0.008	-0.148*	-0.124*	-0.205*
NPB			0.047	0.174*	-0.008	0.130	-0.05	0.890**	0.073	-0.120*	0.087	-0.064	-0.009	-0.173*
VL(m)			0.039	0.171*	-0.026	0.07	-0.04	0.825*	0.043	-0.111*	0.077	-0.060	-0.010	-0.152*
NOFC				-0.412**	0.072*	-0.17**	-0.44**	0.138*	0.096*	0.048	0.269*	-0.390**	-0.176*	0.101*
NCPP				-0.281*	0.118*	-0.10**	-0.22*	0.115*	0.195*	0.037	0.245*	-0.313*	-0.123*	0.137*
DTFHH					-0.105*	0.44*	0.04	0.064	0.063	-0.034	0.075	0.090**	0.189*	-0.325*
FL(cm)					-0.153*	0.36*	0.06	0.050	0.021	-0.048	0.057	0.092**	0.175*	-0.325*
FD(mm)						-0.17**	-0.10	-0.040	-0.379*	0.090**	-0.006	0.042	0.033	-0.116*
AFW(g)						-0.10**	0.03	-0.061	-0.216*	0.095**	-0.020	0.060	0.043	-0.151*
NOFPP								0.010	0.041	-0.254*	-0.204*	0.451**	0.293*	-0.217**
100SW(g)								0.008	0.073	-0.137*	-0.112*	0.346*	0.238*	-0.087**
								-0.151*	0.125	-0.011	-0.018	0.635**	0.490**	0.135*
								-0.170*	0.029	-0.052	0.012	0.511*	0.408*	0.132*
									0.115	-0.075	0.098	-0.130*	-0.055	-0.086*
									0.076	-0.064	0.077	-0.122*	-0.060	-0.116*
										-0.056	0.237*	0.086	0.175**	0.257*
										-0.045	0.165*	0.044	0.101**	0.149*
											0.270*	-0.413**	-0.166*	-0.073*
											0.229*	-0.370*	-0.155*	-0.104*
												-0.095**	0.561*	-0.002
												-0.090**	0.561*	-0.022
													0.751*	0.097*
													0.754*	0.104*
														0.055
														0.056

\*Significant at 5% level of probability; \*\*Significant at 1% level of probability (P: Phenotypic correlation; G: Genotypic correlation)

D50F: Days to 50% flowering, DFA: Days to first female flower anthesis, DFS: Days to first fruit set, NNHF: Node number of first hermaphrodite flower, NPB: Number of primary branches, VL: Vine length (m), NOFC: Number of fruits per cluster, NCPP: Number of clusters per plant, DTFHH: Days to first fruit harvest, FL: Fruit length (cm), FD: Fruit diameter (mm), AFW: Average fruit weight (g), NOFPP: Number of fruits/ plant, 100 SW: 100 seed weight (g), FYPP: Fruit yield per plant (kg).

**Table 4:** Path coefficient analysis for different traits in satputia genotypes

Trait	D50F	DFA	DFS	NNHF	NPB	VL (m)	NOFC	NCPP	DTEFH	FL (cm)	FD (mm)	AFW (g)	NOFPP	100 SW (g)	Phenotypic correlation with fruit yield
Days to 50% flowering	-1.710	1.580	-0.177	0.042	0.001	-0.006	-0.060	-0.006	0.125	-0.019	0.001	0.023	0.064	-0.124	-0.266*
Days to first female flower anthesis	-1.691	1.597	-0.188	0.038	-0.007	-0.013	-0.072	-0.005	0.127	-0.013	0.001	0.003	0.062	-0.105	-0.264*
Days to first fruit set	-1.116	1.105	-0.272	0.009	-0.038	0.002	-0.043	-0.006	0.208	0.012	0.004	-0.056	0.025	-0.007	-0.173*
Node number of first hermaphrodite flower	-0.368	0.310	-0.013	0.196	0.090	-0.013	0.057	-0.051	0.032	0.016	-0.001	-0.175	0.153	-0.133	0.101*
Number of primary branches	0.008	0.051	-0.047	-0.081	-0.218	0.020	-0.147	0.004	0.015	0.011	0.001	-0.048	-0.035	0.143	-0.325*
Vine length (m)	-0.057	0.107	0.002	0.014	0.023	-0.187	0.056	-0.011	-0.009	-0.063	-0.003	0.004	-0.016	0.025	-0.116*
Number of fruits per cluster	-0.311	0.344	-0.035	-0.034	-0.096	0.031	-0.333	0.021	0.002	0.007	0.008	0.133	-0.177	0.222	-0.217**
Number of clusters per plant	0.089	-0.065	0.013	-0.086	-0.008	0.018	-0.061	0.117	-0.035	0.021	0.000	0.012	-0.250	0.370	0.135*
Days to first fruit harvest	-0.916	0.870	-0.242	0.027	-0.014	0.007	-0.003	-0.018	0.234	0.019	0.002	-0.064	0.051	-0.042	-0.086*
Fruit length (cm)	0.190	-0.129	-0.020	0.019	-0.014	0.071	-0.014	0.015	0.027	0.167	0.002	-0.154	-0.034	0.132	0.257*
Fruit diameter (mm)	0.068	-0.061	0.033	0.010	0.007	-0.017	0.085	-0.001	-0.018	-0.009	-0.031	-0.176	0.163	-0.125	-0.073*
Average fruit weight (g)	0.060	-0.008	-0.024	0.053	-0.016	0.001	0.068	-0.002	0.023	0.040	-0.008	-0.650	0.038	0.424	-0.002
Number of fruits/plant	0.279	-0.252	0.017	-0.077	-0.020	-0.008	-0.150	0.074	-0.031	0.014	0.013	0.062	-0.393	0.568	0.097*
100 Seed weight (g)	0.280	-0.222	0.003	-0.035	-0.041	-0.006	-0.098	0.057	-0.013	0.029	0.005	-0.364	-0.296	0.756	0.055

Residual effect: 0.69. Direct effect= Bold diagonals.

\*Significant at 5% level of probability; \*\*Significant at 1% level of probability

D50F: Days to 50% flowering, DFA: Days to first female flower anthesis, DFS: Days to first fruit set, NNHF: Node number of first hermaphrodite flower, NPB: Number of primary branches, VL: Vine length (m), NOFC: Number of fruits per cluster, NCPP: Number of clusters per plant, DTEFH: Days to first fruit harvest, FL: Fruit length (cm), FD: Fruit diameter (mm), AFW: Average fruit weight (g), NOFPP: Number of fruits/plant, 100 SW: 100 seed weight (g).

Lower difference of PCV over GCV were observed in satputia genotypes for traits, viz., days to first female flower anthesis, days to 50% flowering, days to first fruit set, days to first fruit harvest, number of primary branches, fruit length, fruit diameter, average fruit weight, number of fruits per plant, 100 seed weight and fruit yield per plant, thereby indicating that these traits were less influenced by environment and mostly attributed to genotype. Thus, phenotypic variability may be a good measure of genotypic variability for these traits in satputia. Similar results were also obtained by Koppad *et al.*, (2015) in ridge gourd.

High heritability (>60%) estimates along with high genetic advance as a percentage of mean (>40%) were recorded for fruit yield per plant, number of fruits per plant, average fruit weight, number of primary branches and fruit diameter, thereby indicating the predominance of additive gene component. Thus, there is ample scope for improving these traits with direct selection. Besides, high heritability coupled with moderate genetic gain was noted for days to first female flower anthesis, days to 50% flowering, days to first fruit set and days to first fruit harvest, indicating that these traits are under non-additive gene effects and selection for these traits will be less effective. Similar findings were also reported by Sureja *et al.*, (2010) in ash gourd, Kumar *et al.*, (2013) in sponge gourd and Koppad *et al.*, (2015) in ridge gourd.

Variability studies provide information on the extent of improvement to be achieved in different traits, but they do not throw light on the extent and nature of the relationship existing between various characters. Therefore, for a rational approach towards the improvement of yield, selection has to be made for the components of yield, since there may not be genes for yield *per se*, but only for various yield components (Grafius, 1959). Further, many of these yield contributing characters may interact in desirable and undesirable directions. Hence, knowledge regarding the association of various characters among themselves and with economic characters is essential. In the present study, the genotypic and phenotypic correlation coefficients were worked out for yield and its attributing components. The difference between the genotypic and phenotypic correlation coefficients was narrow for various traits in the present findings, and this indicates the lesser influence of environment in the expression of these traits and the presence of strong inherent association among the traits (Table 3).

Fruit yield per plant was found to be positively and significantly (at  $P=0.05$ ) associated with node number of first hermaphrodite flower ( $rg= 0.137$ ), number of

clusters per plant ( $rg= 0.132$ ), fruit length ( $rg= 0.149$ ) and number of fruits per plant ( $rg= 0.104$ ) at the genotypic level. Hence, direct selection for these traits could be made for improving yield. Based on the overall results of phenotypic and genotypic correlation, it is possible to breed desirable satputia varieties combining high fruit yield with superior quality attributes.

The analysis of correlation indicates the association pattern of component traits with yield, and it simply represents the general association of a particular trait with yield rather than providing cause and effect relationship. The technique of path coefficient analysis, developed by Wright (1921) and demonstrated by Dewey and Lu (1959), facilitates partitioning the correlation coefficients into direct and indirect involvement of various characters on yield. As such, it measures the direct influence of one variable upon another. Such information would be of immense value in enabling the breeder to exclusively identify important component traits of yield and utilize the genetic stock for improvement in a planned way. In the present investigation, 15 traits were selected for path analysis, and the traits that showed significant positive correlation with yield are fruit length (0.257), number of clusters per plant (0.135), node number of first hermaphrodite flower (0.101), and number of fruits per plant (0.097) (Table 4). Therefore, direct selection for these traits would be worthwhile for the improvement of yield in satputia.

## Conclusion

In this study, the variability parameters, heritability, genetic advance, correlation and path analysis for yield and yield contributing traits were assessed in thirty-six genotypes of satputia. The results indicated a moderate to high range of variability in the majority of the traits. High heritability estimates along with high genetic advance as a percentage of the mean were recorded for fruit yield per plant, number of fruits per plant, average fruit weight, number of primary branches and fruit diameter, thereby indicating the predominance of additive gene component. Fruit yield per plant was found to be positively and significantly associated with a number of yield contributing traits, thereby indicating that direct selection of these traits will be effective for yield improvement in satputia.

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