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## Genetic variability studies in F<sub>2</sub> segregating population of chilli (*Capsicum annuum* L.)

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### Abstract

The present investigation was carried out during *khariif* 2018-19 at Horticultural Research Station, Lam farm, Guntur to estimate the genetic variability, heritability and genetic advance for twelve quantitative traits in F<sub>2</sub> population of two crosses namely *viz.*, LCA-764 x LCA-315 and MS-276A x LCA-801. The PCV was higher than GCV and the difference between PCV and GCV was narrow for most of the characters revealing little influence of the environment in the expression of these traits. High magnitude of PCV and GCV were observed for number of fruits per plant, number of seeds per fruit and dry fruit yield per plant suggesting the existence of wide range of genetic variability in the both crosses for these traits and thus the scope for improvement of these characters through simple selection would be better. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, fruit diameter, number of fruits per plant and dry fruit yield per plant indicating these characters are governed by additive gene action making the simple selection more effective.

**Keywords:** *Capsicum annuum*, GCV, PCV, heritability, genetic advance

### Introduction

Chilli (*Capsicum annuum* L.) is one of the most important commercial crop of India and it is grown worldwide as spice cum vegetable crop. Its introduction is believed to be through the Portuguese in the 16th century in India. Indispensable spice of chilli, due to its pungency, taste, appealing colour and flavor. It is an important ingredient in daily cuisine in India and is also used in the preparation of pickles, chutneys, sauces *etc.* The fruits of chilli are rich source of carbohydrates, proteins, minerals, ascorbic acid and vitamins C, A and E. Capsaicin is a crystalline acrid volatile alkaloid and it is responsible for pungency of chilli, which is present in the placenta of fruit. It has diverse therapeutic and prophylactic uses in allopathic and ayurvedic medicine. It is also a good source of oleoresin which has varied uses in processed food and beverage industries and got high export potential. The natural colour extracts are also finding increased value in chilli which replace the artificial colours in the food items especially in developed countries.

The productivity of the crop is low due to many limiting factors such as lack of superior genotypes or improved cultivars for use in breeding programme to develop potential hybrids. So, there is need for development of new varieties and hybrids with high productivity. The critical assessment of nature and magnitude of variability in the germplasm stock is one of the important pre-requisites for formulating effective breeding methods (Krishna *et al.*, 2007). Improvement in any crop is proportional to the magnitude of its genetic variability present in germplasm. Greater the variability in a population, there are the greater chance for effective selection for desirable types (Vavilov, 1951). Heritability is the portion of phenotypic variation which is transmitted from parent to progeny. Higher the heritable variation, greater will be the possibility of fixing the characters by selection. Hence, heritability studies are of foremost importance to judge whether the observed variation for a particular character is due to genotype or due to environment. Heritability estimates may not provide clear predictability of the breeding value. Thus, estimation of heritability accompanied with genetic advance is generally more useful than heritability alone in prediction of the resultant effect for selecting the best individuals (Johnson *et al.*, 1955)<sup>[6]</sup>.

Therefore, the present investigation was carried out with a view to study the genetic variability, heritability and genetic advance for yield and yield component characters in F<sub>2</sub> population of two crosses namely *viz.*, LCA-764 x LCA-315 and MS-276A x LCA-801 chilli.

**Material and methods**

The experiment was carried out at Horticultural Research Station, Lam farm, and Guntur during *Kharif* 2018-19 in F<sub>2</sub> population of two crosses namely *viz.*, LCA-764 x LCA-315 and MS-276A x LCA-801. The crop received timely management practices as per recommended package of practices. The crop was maintained properly till last harvest and observations on yield as well as yield contributing characters was noted on F<sub>2</sub> populations along with parents. From each cross 240 plants were studied and taken data from all the plants.

The observation were recorded for 12 characters, plant height (cm), plant spread (cm), number of branches per plant, days to 50% flowering, days to first picking, fruit length(cm), fruit diameter (cm), average dry fruit weight (g), number of fruits per plant, number of seeds per fruit, test weight (g) and dry fruit yield per plant (g).

Genotypic and phenotypic coefficient of variation were calculated as per the formula suggested by Burton and Devane (1952). Heritability and expected genetic advance were calculated as per formula given by Johnson *et al.* (1955) [6].

$$\text{Genotypic variance } (V_g \text{ or } \sigma_g^2) = \frac{\text{Genotype MSS}-\text{Error MSS}}{r}$$

$$\text{Environmental variance } (V_e \text{ or } \sigma_e^2) = \frac{\text{Error MSS}}{r}$$

r = number of replications

Phenotypic variance (V<sub>p</sub> or σ<sup>2</sup><sub>p</sub>) = V<sub>g</sub>+ V<sub>e</sub>

$$\text{PCV} = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

$$\text{GCV} = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

Where,

- σ<sub>g</sub><sup>2</sup> = Genotypic variance
- σ<sub>e</sub><sup>2</sup> = Environment variance
- σ<sub>p</sub><sup>2</sup> = Phenotypic variance
- $\bar{X}$  = General mean

PCV and GCV were classified as shown below (Sivasubramanian and Menon 1973) [22].

- Less than 10% = Low
- 10-20% = Moderate
- More than 20% = High

Heritability in broad sense was estimated as per the formulae suggested by Allard (1960) [1].

$$h^2(b) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

- h<sup>2</sup>(b) = Heritability estimates in broad sense
- σ<sub>g</sub><sup>2</sup> = Genotypic variance
- σ<sub>p</sub><sup>2</sup> = Phenotypic variance

The heritability (h<sup>2</sup>(b)) was categorised as suggested by Johnson *et al.* (1955) [6].

- 0-30% = Low
- 31-60% = Medium
- 61% and above = High

This was estimated as per formula proposed by Allard (1960) [1]

$$GA = K \times \sigma_p \times h^2(b)$$

Where,

K = Selection differential at 5 per cent selection intensity which accounts to a constant value 2.06

- h<sup>2</sup>(b) = Heritability in broad sense
- σ<sub>p</sub> = Phenotypic standard deviation

Genetic advance over mean (GAM) was calculated using the following formula and was expressed in percentage.

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where,

- GA = genetic advance
- $\bar{X}$  = general mean of the character

The genetic advance as per cent over mean was categorized as mentioned below (Johnson *et al.*, 1955) [6].

- Less than 10% = Low
- 10-20% = Moderate
- More than 20% = High

**Results and discussion**

The results of variability, heritability and genetic advance are presented in the table 1 and 2. The variability analysis revealed that the magnitude of GCV and PCV were closer in both the crosses *viz.* cross-1 (LCA-764 x LCA-315) and cross-2 (MS-276A x LCA-801) for majority of the characters. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters in both crosses (Table 1 & 2) and the difference between PCV and GCV was narrow indicating the little influence of environment on the expression of these characters and considerable amount of variation was observed for all the characters. These results were suggesting that, little contribution of environmental effect on population. Similar findings were observed by Pandit and Adhikary (2014) [13], Vijaya *et al.* (2014) [25], Janaki *et al.* (2015) [5], Satish *et al.* (2016) [18], Singh *et al.* (2017) [21], Zehra *et al.* (2017) [26], Mopidevi *et al.* (2018), Syed *et al.* (2020).

**Table 1:** Mean, GCV, PCV, heritability, genetic advance and per cent mean of genetic advance in F<sub>2</sub> population of cross-1 (LCA-764 x LCA-315)

S. No.	Character	Mean	GCV (%)	PCV (%)	h <sup>2</sup> (b) (%)	GA @ 5%	GAM @ 5%
1	Plant height (cm)	77.49	15.59	18.41	71.71	21.08	27.20
2	Plant spread (cm)	75.23	18.27	22.58	65.52	22.92	30.47
3	No.of branches per plant	2.82	22.00	43.43	25.67	0.65	22.96
4	Days to 50% flowering	34.25	4.12	5.84	49.88	2.05	6.00
5	Days to first picking	66.44	2.39	3.15	57.52	2.48	3.74

6	Fruit length(cm)	16.58	10.77	13.55	63.17	2.92	17.64
7	Fruit diameter (cm)	5.47	15.40	19.17	64.55	1.39	25.49
8	Average dry fruit weight (100 fruits/g)	118.09	19.04	20.02	90.46	44.06	37.31
9	Number of fruits per plant	144.96	37.84	45.51	69.14	93.96	64.82
10	Number of seeds per fruit	60.03	20.79	28.56	52.97	18.71	31.17
11	Test weight (g)	10.37	89.54	91.52	95.70	18.71	180.44
12	Dry fruit yield per plant (g)	118.49	44.18	56.01	62.22	85.07	71.80

In the cross LCA-764 x LCA-315, results showed that the genotypic coefficient of variation was observed highest for test weight (89.54%) followed by yield per plant (44.18%), number of fruits per plant (37.84%), number of branches per plant (22.00%), number of seeds per fruit (20.79%), while moderate in average dry fruit weight (19.04%) followed by plant spread (18.27), plant height (15.59%), fruit diameter (15.40%), fruit length (10.77%). whereas the lowest was found in days to 50% flowering (4.12%) followed by days to first picking (2.39%).

The highest phenotypic coefficient of variation was observed highest for test weight (91.52%) followed by yield per plant (56.01%), number of fruits per plant (45.51%), number of branches per plant (43.43%), number of seeds per fruit (28.56%), plant spread (22.58%), average dry fruit weight (20.02%), While moderate in fruit diameter (19.17%), plant height (18.41%), fruit length (13.55%). Whereas the lowest was found in days to 50% flowering (5.84%) followed by days to first picking (3.51%).

Higher GCV and PCV were recorded for characters like number of primary branches per plant, number of fruits per plant, number of seeds per fruit, test weight and yield per plant, and indicating higher magnitude of variability for these characters. In general, higher names of genotype coefficient of variation was lower than the phenotypic coefficient of variation for all the traits implying the possible role of the environment on these traits. These findings were similar to Pandit and Adhikary (2014) [13], Vijaya *et al.* (2014) [25], Janaki *et al.* (2015) [5], Satish *et al.* (2016) [18], Kranthi *et al.* (2016) [8], Meena *et al.* (2016) [11], Singh *et al.* (2017) [21], Zehra *et al.* (2017) [26], Nagarju *et al.* (2018) [12] and Syed *et al.* (2020).

Heritability in broad sense was high for plant height (71.71%), plant spread (65.52%), fruit length (63.17%), fruit diameter (64.55%), and average dry fruit weight (90.46%), number of fruits per plant (69.14%), test weight (95.70%) and fruit yield per plant (62.22%). While days to 50% flowering (49.88), days to first picking (57.52%), number of seeds per fruit (52.97%) and number of primary branches per fruit (25.57%) recorded lowest broad sense heritability value.

Genetic advance as per cent mean was high for all the characters under study *viz.*, plant height (27.20%), plant spread (30.47%), number of primary branches (22.96%), fruit diameter (25.49%), average dry fruit weight (25.49%), number of fruits per plant (64.82%), number of seeds per fruit (31.17%), test weight (180.44%) and fruit yield per plant (71.80%) except for fruit length (17.64%) showed moderate and days to 50% flowering (6.00%), days to first picking (3.74%) was low.

Heritability estimates along with genetic advance are more useful than heritability value alone in predicting the selection of best individuals. In the present investigation High estimates of heritability with high genetic advance as percent over mean were recorded for yield per plant, test weight, number of fruits per plant, average dry fruit weight, fruit diameter, fruit length, plant spread and plant height. These findings are similar to Mahantesh *et al.* (2013) [10], Amit *et al.* (2014) [2], Pandit and Adhikary (2014) [13], Vijaya *et al.* (2014) [25], Ajith and Manju (2015) Janaki *et al.* (2015) [5], Satish *et al.* (2016) [18], Kranthi *et al.* (2016) [8], Rosamaina *et al.* (2016) [17], Singh *et al.* (2017) [21], Zehra *et al.* (2017) [26], Nagaraju *et al.* (2018) [12] and Syed *et al.* (2020). It might be assigned to be under the control of additive genes and phenotypic selection for their improvement could be achieved by simple breeding methods.

**Table 2:** Mean, GCV, PCV, heritability, genetic advance and per cent mean of genetic advance in F<sub>2</sub> population of cross-2 (MS-276A x LCA-801)

S. No.	Character	Mean	GCV (%)	PCV (%)	h <sup>2</sup> (b) (%)	GA @ 5%	GAM @ 5%
1	Plant height (cm)	75.90	26.04	27.50	89.69	38.56	50.81
2	Plant spread (cm)	107.90	11.50	15.21	57.17	19.32	17.91
3	No.of branches per plant	4.10	12.44	24.27	26.26	0.54	13.13
4	Days to 50% flowering	34.30	7.64	8.02	90.82	5.15	15.01
5	Days to first picking	67.10	3.33	3.75	78.88	4.08	6.09
6	Fruit length(cm)	17.61	20.72	22.02	88.50	7.07	40.15
7	Fruit diameter (cm)	5.68	40.28	42.00	92.00	4.52	79.59
8	Average dry fruit weight (100 fruits/g)	57.80	16.30	14.81	-21.08	-3.72	-6.43
9	Number of fruits per plant	267.00	20.22	25.35	63.63	88.72	33.23
10	Number of seeds per fruit	50.16	18.98	28.65	43.91	13.00	25.91
11	Test weight (g)	16.83	19.17	22.94	69.79	5.55	32.98
12	Dry fruit yield per plant (g)	132.40	52.10	56.36	85.46	131.38	99.23

In the cross, MS-276A x LCA-801 results showed that the genotypic coefficient of variation was observed highest for yield per plant (52.10%) followed by fruit diameter (40.28%), plant height (26.04%), fruit length (20.72%) and number of fruits per plant (20.22%), while moderate test weight (19.17%) followed by number of seeds per fruit (18.98%), average dry fruit weight (16.30%), number of branches per plant (12.44%), plant spread (11.50%) whereas the lowest

was found in days to 50% flowering (7.64%) followed by days to first picking (3.33%).

The highest phenotypic coefficient of variation was recorded for observed highest for yield per plant (56.01%) followed by fruit diameter (42.00%), number of seeds per fruit (28.65%), plant height (27.50%), number of fruits per plant (25.35%), number of primary branches per plant (24.27%), test weight (22.94%), fruit length (22.02%), while moderate in plant

spread (15.21%) and average dry fruit weight (14.81%). Whereas the lowest was found in days to 50% flowering (8.02%) followed by days to first picking (3.75%).

Higher GCV and PCV were recorded for characters like plant height, fruit length, and fruit diameter, number of fruits per plant and yield per plant and indicating higher magnitude of variability for these characters. In general, higher values of genotype coefficient of variation was lower than the phenotypic coefficient of variation for all the traits implying the possible role of the environment on these traits. These findings were similar to Pandit and Adhikary (2014)<sup>[13]</sup>, Vijaya *et al.* (2014)<sup>[25]</sup>, Janaki *et al.* (2015)<sup>[5]</sup>, Satish *et al.* (2016)<sup>[18]</sup>, Kranthi *et al.* (2016)<sup>[8]</sup>, Meena *et al.* (2016)<sup>[11]</sup>, Singh *et al.* (2017)<sup>[21]</sup>, Zehra *et al.* (2017)<sup>[26]</sup>, Nagaraju *et al.* (2018)<sup>[12]</sup> and Syed *et al.* (2020).

Heritability in broad sense was high for plant height (89.69%), plant spread (65.52%), days to 50% flowering (90.82%), days to first picking (78.88%), fruit length (88.50%), fruit diameter (92.00%), number of fruits per plant (63.63%), test weight (69.79%) and fruit yield per plant (85.46%). While number of seeds per fruit (43.91%) was moderate and number of primary branches per fruit (26.26%) and average dry fruit weight (21.08%) recorded lowest broad sense heritability value.

Genetic advance as per cent mean was high for plant height (50.81%), fruit length (40.15%), fruit diameter (79.59%), number of fruits per plant (33.23%), number of seeds per fruit (25.91%), test weight (32.98%) and fruit yield per plant (99.23%), while moderate in plant spread (17.91%), number of branches per plant (13.13%), days to 50% flowering (15.01%) whereas days to first picking (6.09%) and average dry fruit weight (6.43%) was low.

Heritability estimates along with genetic advance are more useful than heritability value alone in predicting the selection of best individuals. In the present investigation High estimates of heritability with high genetic advance as percent over mean were recorded for yield per plant, test weight, number of fruits per plant, fruit diameter, fruit length, days to 50% flowering and plant height. These findings are similar to Mahantesh *et al.* (2013)<sup>[10]</sup>, Amit *et al.* (2014)<sup>[2]</sup>, Pandit and Adhikary (2014)<sup>[13]</sup>, Vijaya *et al.* (2014)<sup>[25]</sup>, Ajith and Manju (2015) Janaki *et al.* (2015)<sup>[5]</sup>, Satish *et al.* (2016)<sup>[18]</sup>, Kranthi *et al.* (2016)<sup>[8]</sup>, Rosamaina *et al.* (2016)<sup>[17]</sup>, Singh *et al.* (2017)<sup>[21]</sup>, Zehra *et al.* (2017)<sup>[26]</sup>, Nagaraju *et al.* (2018)<sup>[12]</sup> and Syed *et al.* (2020). It might be assigned to be under the control of additive genes and phenotypic selection for their improvement could be achieved by simple breeding methods.

The findings indicate that there exists adequate genotypic variation in the population for plant height, fruit length, fruit diameter, number of fruits per plant, test weight and dry fruit yield per plant showing high values of PCV, GCV and high heritability coupled with high genetic advance as per cent of mean suggesting predominance of additive gene action and lower influence of environmental factors in the expression of these traits with possibility for improvement through selection.

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