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Short Communication

Studies on parameters of genetic variability for yield and its attributing traits in chilli (*Capsicum annuum* L.)

Versha Kumari*, Jitendra Singh, Sunidhi Mishra, and D Sharma

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Chilli is an important vegetable as well as spice crop of India. Being an important commercial crop, it finds diverse utilities as a spice, condiment, culinary supplement, medicine, vegetable and ornamental plant. The important states growing chilli are Andhra Pradesh, Orissa, Maharashtra, West Bengal, Karnataka, Rajasthan and Tamil Nadu. Chilli has two important commercial qualities, red colour due to pigment capsanthin and biting pungency attributed by capsaicin. Importance of genetic variability in any breeding material is a pre-requisite as it provides not only a basis for selection but also some valuable information regarding selection of diverse parents for use in hybridization programme. The plant breeder has to identify the sources of favourable genes, incorporate them in breeding populations and aim for isolation of productive genotypes and cultivars. Thus, improvement in any crop is based on the extent of genetic variation and the degree of improvement depends upon the magnitude of available beneficial genetic variability. Knowledge of variability present in the population due to genetic and non-genetic factors facilitates to develop an appropriate and systematic breeding programme as it provides information about the expected response of various characters towards selection. The effect of environment on expression of various characters is often pronounced enough to affect the yield in a particular direction. Thus, it is quite inevitable to determine the distinct effect of various genetic and environmental factors on the expression of a yield attributing trait. Therefore, present investigation was undertaken to estimate genetic variability, heritability and genetic advance for important yield component characters in chilli.

Department of Vegetable Science, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh
*Corresponding author, Email: vershakumari2502@gmail.com

The present experiment was conducted at the research farm of Indira Gandhi Krishi Viswavidayalaya (IGKV), Raipur during *rabi* season of 2016-17 to evaluate the performance of sixteen genotypes of chilli for various yield and its component traits under field condition with three replications of each genotype. The mean of five plants was used for statistical analysis. Observations were recorded for various plant and fruit characters and study was made for the presence of genetic variability through estimation of genetic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), heritability, genetic advance and genetic advance as percentage of mean, where Genotypic and phenotypic coefficient of variation was calculated by using the following formula proposed by Burton (1952).The estimates of PCV and GCV were classified as low (< 10 %), moderate (10-20%) and high (> 20 %). Heritability in broad sense (h^2 bs) defined as the proportion of the genotypic variance to the total variance (phenotypic) was calculated as per the formula suggested by Burton and De Vane. Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. The magnitude of genetic advance as percent of mean was categorized as high (more than 20%), moderate (20-10%) and low (less than10%).

The phenotypic and genotypic coefficient of variance, heritability, genetic advance and genetic advance as percentage of mean was calculated for all the seventeen characters as given in Table 1. The result obtained showed that phenotypic coefficient of variance was in general higher than the genotypic coefficient of variance for all the characters. It is due to presence of substantial influence of environmental factors besides the genetic variation for expression of these traits. High magnitude of GCV and PCV (*i. e.* >20 per cent) were observed for dry weight of fruits, dry matter % of fruits, fresh weight of fruits, number of primary branches, fruit girth, fruit

yield per hectare and fruit yield per plant (Table 1). The low magnitude of GCV and PCV (<10 per cent) was observed for days to first picking and number of pickings in present study. The above findings indicate that the characters with high magnitude of GCV and PCV can be utilized for improvement as the population possesses considerable variability for these characters. These findings are in accordance with the findings by Sahu et al. (2016) for fruit yield per plot and fruit yield/ha. Amit et al. (2014) for fruit weight and dry yield, Patel et al. (2014) for fresh weight of fruits, Chattopadhyay et al. (2011) for green fruit weight, green fruit girth, weight of dry fruit and Singh et al. (2009) for number of primary branches per plant and average fresh and dry weight of green fruits.

Estimate of broad sense heritability (in per cent) was recorded highest for the character fruit girth (99.19), followed by dry weight of fruits (93.44), dry matter % of fruits (91.80), fruit length (91.04), fresh weight of fruits (90.99), number of primary branches (90.90), plant height (89.01), number of seeds per fruit (86.97), days to 50 % flowering (82 .92), fruit yield per plant (82.19), days to first picking (81.11), fruit yield per ha (78.74) and stem girth (78.72) . Low heritability (%) estimates were observed in number of fruits per plant (46.07) and number of pickings (24.00). Presence of high heritability indicated that these characters are less influenced by environmental fluctuations and governed by the additive gene effects that are substantially contributing towards the expression of these traits. However, rest of the traits seems to be governed by non-additive gene effects. The present findings on heritability are in accordance with findings reported by the various workers *viz* Jogi et al. (2015) for total number of fruits per plant fruit length, fruit width, stalk length and fruit weight, Amit et al. (2014) for number of fruits per plant, green fruit yield per plant, dry yield per plant number of seeds per plant and plant height, Datta and Jana (2010) for fruit length, fruit girth, fruit weight, fruit yield per plant. Similar results were also reported by Bhagyalakshmi, et al. (1990), and Das and Maurya (2004).

Highest estimates of genetic advance as percentage of mean were obtained for characters namely dry weight of fruits (130.15) followed by dry matter % of fruits (85.83), fresh weight of fruits (73.63), number of primary branches (72.19), fruit girth (64.20) and fruit yield per ha (41.63). The high value of genetic advance for these traits showed that these characters are governed by additive genes and selection will be rewarding for the further improvement of such traits. The moderate genetic advance was observed in fruit yield per plant (39.21 per cent), number of seeds per fruit (36.78), fruit length (35.06), plant height (32.34) and days to 50 % flowering (25.81). The presence of moderate genetic advance suggests that both the additive and non-additive variance is operating in these traits. However, the low genetic advance as per cent of mean was observed for the characters such as days to first flowering (22.32), number of fruits per plant (20.80), stem girth (19.66), stalk length (18.74), days to first picking (7.49), and number of pickings (6.33). This indicates the presence of non-additive gene effects. The above finding indicates that the characters with high and moderate heritability and genetic advance can be considered for direct selection for improvement. High heritability coupled with high genetic advance was observed for dry weight of fruits, dry matter % of fruits, fresh weight of fruits,

Table 1: Estimates of genetic parameters of variation for fruit yield and its attributing traits in chilli.

S. No.	Parameters	Mean	Range		Coefficient of Variation (%)		Heritability (H^2b) %	Genetic Advance	Genetic Advance as % of mean
			Minimum	Maximum	Genotypic	Phenotypic			
1	Days to first flowering	47.29	35.00	58.67	13.42	16.629	65.15	10.56	22.32
2	Days to 50 % flowering	59.65	43.67	69.00	13.76	15.108	82.92	15.39	25.81
3	Plant height (cm)	55.01	33.37	66.50	16.64	17.639	89.01	17.79	32.34
4	Number of primary branches	6.49	2.93	11.73	36.76	38.553	90.90	4.68	72.19
5	Stem girth (cm)	4.11	3.41	4.88	10.76	12.124	78.72	0.81	19.66
6	Days to first picking	99.48	91.00	103.00	4.04	4.484	81.11	7.45	7.49
7	Fruit length (cm)	8.99	7.11	13.84	17.84	18.693	91.04	3.15	35.06
8	Fruit girth (cm)	3.84	3.04	7.93	31.29	31.421	99.19	2.46	64.20
9	Stalk length (cm)	3.73	3.05	4.42	11.10	13.546	67.09	0.70	18.72
10	Number of seeds per fruit	64.38	33.67	84.20	19.15	20.53	86.97	23.68	36.78
11	Number of fruits per plant	118.00	79.40	157.67	14.88	21.918	46.07	24.54	20.80
12	Fresh weight of fruits (gm)	26.07	13.83	48.33	37.47	39.284	90.99	19.20	73.63
13	Dry weight of fruits (gm)	3.76	1.27	8.83	65.36	67.611	93.44	4.90	130.15
14	Number of pickings	5.04	4.33	5.67	6.27	12.803	24.00	0.32	6.33
15	Dry matter % of fruits	14.18	5.77	27.43	43.49	45.391	91.80	12.17	85.83
16	Fruit yield per plant (gm)	301.98	177.78	414.99	20.99	23.155	82.19	118.40	39.21
17	Fruit yield per ha (q)	95.40	54.41	132.75	22.78	25.667	78.74	39.72	41.63

number of primary branches, fruit girth and fruit yield per ha indicating that most likely the heritability is due to additive gene effects and selection may be effective. Similar results were also reported by Kumar et al. (2012), Singh et al. (2009), Manju and Sreelathakumary (2002), and Munshi and Behera (2000).

The high estimates of heritability recorded for most of the economic traits indicate that these characters are governed by additive gene effect and are less influenced by environment and hence, selection for these characters, if found positively associated with yield will be beneficial in improvement of chilli, whereas hybridization or heterosis breeding may be exploited for improvement of the characters with low genetic advance. In the present investigation, high heritability coupled with high genetic advance was recorded for the traits *viz.* dry weight of fruits, dry matter % of fruits, fresh weight of fruits, number of primary branches, fruit girth and fruit yield per ha. Thus, it can be concluded that these characters may respond effectively to phenotypic selection since it will result in accumulation of more desirable genotypes leading to improvement of these characters.

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