



P-ISSN: 2349-8528

E-ISSN: 2321-4902

IJCS 2018; 6(2): 3593-3595

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Received: 25-01-2018

Accepted: 26-02-2018

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Genetic variability studies in F_2 segregating population of chilli (*Capsicum annuum* L.)

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Abstract

Genetic variability, heritability and genetic advance for nine yield and quality traits were studied in F_2 population obtained from the cross of K-1 x China type. The study indicated existence of considerable amount of genetic variability for all the characters studied. Higher GCV and PCV were recorded for characters like yield per plant, number of seeds per fruit, plant height and number of fruits per plant indicating higher magnitude of variability for these characters and high estimates of heritability with high genetic advance as percent of mean were recorded for yield per plant, number of fruits per plant, number of seeds per fruit, single dry fruit weight, plant height, capsaicin and number of branches per plant. These characters can be effectively improved through selection.

Keywords: *Capsicum annuum*, GCV, PCV, h^2 , GA, F_2 population

Introduction

Chilli (*Capsicum annuum* L.) is one of the important commercial crops of India. It is a widely cultivated vegetable cum spice crop and plays an important role as a constituent in many of the world food industries (Basland and Votava, 2000) [1]. It belongs to the family Solanaceae and It is native to Mexico, having a secondary centre of origin in Guatemala. It is also a valuable foreign exchange earner. Chillies are in different sizes, shapes and colours and have important qualities, the presence of biting pungency attributed to an alkaloid capsaicin. Chilli being an often cross pollinated vegetable (Murthy and Murthy, 1962) [4], exhibits wide variability for yield and its components under diverse conditions. Crop improvement mainly depends on the magnitude of genetic variability and the extent to which the desirable characters are inherited. F_2 generation obtained from selfing of F_1 hybrid provides all possible variations. So, selection with particular objectives in F_2 generation is very much effective and selfing of those selected genotypes generation after generation helps to develop inbred lines (similar to the parental lines of the exotic hybrids). While initiating our breeding programme we should also be aware of the fact that our selection for the desired traits may be under the influence of environment i.e. the variability in the population may be environmental instead of genetic consequently the selection may not gain positive results in next generation therefore we should have knowledge of existing genetic variability in order to develop high yielding varieties (Reddy *et al.* 2013) [6]. The studies on genetic variability are very important since the individual plant selection is solely dependent upon it. The mean and heritability estimates of the quantitative character are useful for predicting the progress from selection and an estimate based on single plant will be most reliable (Johnson *et al.*, 1955) [2]. Besides knowing the extent of genetic variability and heritability, it is essential to estimate genetic advance which may highly useful to conform. Estimation of coefficient of variation helps to assess the variability in the population.

Materials and methods

The experiment was carried out at the farmer field in virudhunagar district. Totally 250 F_2 chilli plants obtained from the cross K-1 x China type was evaluated for high yield and quality characters during the year 2016 – 2017. The F_2 progenies obtained by selfing from the F_1 hybrid. The F_2 generation of K-1 x China type cross combination was raised along with their parents. Observations were recorded on single plant wise for each of F_2 populations and ten plants in parents. Each plant in the cross was labelled for recording nine quantitative and qualitative characters, which includes plant height, number of branches per plant, number of fruits per plant, fruit length, single dry fruit weight, number of seeds per fruit, yield per plant, relative water content and capsaicin. Genotypic coefficient of variation (GCV), phenotypic

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coefficient of variation (PCV), heritability in broad sense (h^2) and genetic advance (GA) and genetic advance as percentage over mean were analyzed following the formula illustrated by Singh and Chaudhary (1997) [8].

Results and Discussion

Variability plays an important role in crop breeding material

Table 1: Range, mean, variability, heritability, genetic advance and genetic advance as per cent of mean in F₂ generation for cross K-1 x China type

Characters	Mean	Range	PCV (%)	GCV (%)	Heritability (%)	Genetic advance	GA as per cent of mean
Plant height	59.23	37.0 - 97.3	23.36	22.52	92.93	26.49	44.73
Number of branches per plant	6.12	4.0 - 9.0	18.82	16.65	78.23	1.86	30.33
Number of fruits per plant	133.56	75.0 - 213.0	22.65	22.39	97.68	60.87	45.58
Pod length	6.14	5.0 - 7.5	8.47	7.46	77.58	0.83	13.53
Single dry fruit weight	0.76	0.56 - 0.93	10.79	10.43	93.45	0.16	20.77
Number of seeds per fruit	66.61	34.0 - 109.0	29.70	29.13	96.18	39.20	58.84
Relative water content	73.94	67.50 - 79.51	3.82	3.78	98.30	5.71	7.73
Capsaicin	0.52	0.34 - 0.72	20.22	19.05	88.76	0.19	36.96
Dry fruit yield per plant	100.83	51.6 - 181.0	29.47	29.29	98.78	60.46	59.96

Results showed that the genotypic coefficient of variation was observed highest for yield per plant (29.29%) followed by number of seeds per fruit (29.13%), plant height (22.52%), number of fruits per plant (22.39%). while moderate in capsaicin (19.05%) followed by number of branches per plant (16.65%), single dry fruit weight (10.43%). whereas the lowest was found in pod length (7.46%) followed by relative water content (3.78%).

The highest phenotypic coefficient of variation was recorded for number of seeds per fruit (29.70%) followed by yield per plant (29.47%), plant height (23.36%), number of fruits per plant (22.65%) and capsaicin (20.22%). While moderate in number of branches per plant (18.82%) followed by single dry fruit weight (10.79%). Whereas the lowest was found in pod length (8.47%) followed by relative water content (3.82%). Higher GCV and PCV were recorded for characters like yield per plant, number of seeds per fruit, plant height and number of fruits per plant 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 Sharanappa and mogali (2014) [7], Ullah *et al.* (2015) [9] and Rai *et al.* (2016) [5].

Highest value of heritability was noticed in for yield per plant (98.78%) followed by relative water content (98.30%), number of fruits per plant (97.68%), number of seeds per fruit (96.18%), single dry fruit weight (93.45%), plant height (92.93%), capsaicin (88.76%), number of branches per plant (78.23%), pod length (77.58%). High heritability estimates indicated the presence of large number of fixable additive factors and hence these traits can be improved by direct selection.

Genetic advance as percent of mean was highest for yield per plant (59.96%) followed by number of seeds per fruit (58.84%), number of fruits per plant (45.58%), plant height (44.73%), capsaicin (36.96%), number of branches per plant (30.33%), single dry fruit weight (20.77%). while moderate in pod length (13.53%). Whereas, the lowest was found in relative water content (7.73%).

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

ensures the better chance of producing desirable crop plant. The results of range, mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2 g), genetic advance% (GA %) in F₂ population of cross K-1 x China type are shown in the table 1.

were recorded for yield per plant, number of fruits per plant, number of seeds per fruit, single dry fruit weight, plant height, capsaicin and number of branches per plant. These findings are similar to Mehta and Asati (2008) [3], Reddy *et al.* (2013) [6], Ullah *et al.* (2015) [9] and Rai *et al.* (2016) [5]. 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.

Conclusion

Genotypic coefficient of variation was observed highest for yield per plant followed by number of seeds per fruit, plant height, number of fruits per plant. The highest phenotypic coefficient of variation was recorded for number of seeds per fruit followed by yield per plant, plant height, number of fruits per plant and capsaicin. High heritability coupled with high genetic advance as percent of mean were recorded for yield per plant, number of fruits per plant, number of seeds per fruit, single dry fruit weight, plant height, capsaicin and number of branches per plant. It indicates the changes for wide range in cross K-1 x China type it will be very useful in selection of F₂ segregating population.

References

1. Bosland PW, Votava EJ. Peppers: vegetable and spice Capsicums. CABI Publishing, New York, 2000.
2. Johnson HW, Robinson HF, Comstock RE. Estimation of genetic and environmental variability in soybean. *Agron. J* 1955; 47:477-483.
3. Mehta N, Asati B. Genetic relationship of growth and development traits with fruit yield in tomato (*Lycopersicon esculentum* Mill.). *Karnataka J Agric. Sci.* 2008; 21(1):92-96.
4. Murthy NSR, Murthy BS. Natural cross pollination in chilli. *Andhra Agric. J* 1962; 9:161-165.
5. Rai AK, Vikram A, Pandav A. Genetic variability studies in tomato (*Solanum lycopersicum* L.) for yield and quality traits. *Intern. J Agril, Environ. Biotech.* 2016; 9(5):739-744.
6. Reddy BR, Reddy DS, Reddaiah K, Sunil N. Studies on genetic variability, heritability and genetic advance for yield and quality traits in tomato (*Solanum lycopersicum* L.). *Intern. J Curr. Microbiol. App. Sci.* 2013; 2(9):238-244.

7. Sharanappa KP, Mogali SC. Studies on genetic variability, heritability and genetic advance for yield and yield components in F₂ segregating population of tomato (*Solanum lycopersicon* L.). Karnataka J Agric. Sci. 2014; 27(4):524-525.
8. Singh PK, Choudhary RD. Biometrical methods In: Quantitative Genetic Analysis, Kalyani publishers, New Delhi, 1977, 178-185.
9. Ullah MZ, Hassan L, Shahid SB, Patwary AK. Variability and inter relationship studies in tomato (*Solanum lycopersicum* L.). J Bangladesh. Agri. 2015; 13(1).