

Original Research Article

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Genetic Variability, Heritability and Genetic Advance in Chilli (*Capsicum annum* L.) Genotypes

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ABSTRACT

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The field experiment was conducted at Horticulture Complex, JNKVV, and Jabalpur (M.P.) during the year 2015-16 with 18 genotypes of chilli (*Capsicum annum* L.) in a Randomized Complete Block Design with three replications to estimate the genetic variability and heritability and genetic advance for thirteen quantitative traits. Analysis of variance revealed highly significant difference among the genotypes for all the characters studied. The PCV was higher than the GCV for all the traits. High magnitude of PCV and GCV were observed for number of fruit plant⁻¹ followed by average fruit weight, fruit yield plant⁻¹, while it was low for number of branches plant⁻¹. High heritability coupled with high genetic advance as percentage of mean were observed for average fruit weight, number of fruit plant⁻¹ suggested that the predominance of additive gene action indicating better scope for improvement of these traits by an effective selection programme.

Introduction

Chilli (*Capsicum annum* L.) is one of the most important vegetables as well as spice and cash crop of India. Chilli is a member of the Solanaceae family, originated from South and Central America. Chilli is very rich source of vitamin A and C. Green fruit of chilli is one of the richest sources of anti-oxidant. The pungency is due to alkaloid capsaicin. The genus *Capsicum* consists of approximately 22 wild and 5 cultivated species, which includes *C. annum*, *C. baccatum*, *C. chinense*, *C. frutescens* and *C. pubescens*. Chilli has been classified under often cross pollinated crops and the extent of natural out crossing has also reported up to 66.4 per cent (Singh *et al.*, 1994). A wide range of variability in chilli is available which provide a great scope for improving fruit yield

through a systemic and planned selection programme. Burton (1953) suggested that genetic variability along with heritability should be considered for assessing the maximum and accurate effect of selection. The knowledge of nature and magnitude of genetic variability in the population is of immense value for planning of efficient breeding programme to improve the yield potential of the genotype. Heritability is the portion of phenotypic variation which is transmitted from parent to progeny. High 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. Keeping in view of the above facts the present investigation was under taken with view to study the genetic variability, heritability and genetic advance for yield and yield component characters in chilli genotypes. The present study was, therefore aimed to study variability, heritability and genetic advance among 18 genotypes of chilli.

Materials and Methods

The experiment was conducted with eighteen genotypes of chilli at Horticulture complex, Maharajpur, Department of Horticulture, J.N.K.V.V. Jabalpur (M.P.) during Rabi season of 2015- 2016. The experiment was laid out in Randomized Complete Block Design (RCBD) with 18 genotypes (16 genotypes + 2 checks) and three replications. The nursery was raised during first week of September and the seedlings were transplanted at a spacing of 60 cm × 50 cm in a row during last week of October. Each row consisted of 8 plants, of which five competitive plants were selected at random for recording the observations on plant height at 150 DAT, no. of primary branches / plant, days to 1st flowering, days to 50% flowering, days to 1st picking, fruiting span, number of fruit per plant, fruit length (cm), fruit width (cm), average fruit weight (g), fruit yield /plant (g), fruit yield /plot (kg), fruit yield /ha (q). Genotypic and phenotypic coefficients of variations (GCV and PCV) heritability, genetic advance over mean were estimated by statistical analysis.

The data were statistically analyzed for computation of genetic coefficients of variation using appropriate statistical analysis. Analysis of variance was carried out as per the procedure given by Panse and Sukhatme (1985). Genotypic and phenotypic correlation coefficients of variability were estimated according to the Burton and Devane (1953).

Heritability in broad sense was estimated as per the formula given by Allard (1960). The expected genetic advance was calculated by using formula as suggested by Johnson *et al.*, (1955).

Results and Discussion

Analysis of variance revealed significant difference among the genotypes for all the traits indicating the presence of sufficient genetic variability in the germplasm and considerable scope for their improvement.

These results are similar with the findings of Singh *et al.*, (2013), Yatung *et al.*, (2014), Pandit and Ahikary (2014), Janaki *et al.*, (2015) and Patel *et al.*, (2015) also found sufficient variations for these traits. The result of analysis of variance is presented in table 1. The results obtained in terms of mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) along with the amount of heritability (h), expected genetic advance and genetic advance as per cent of mean (GAM) are presented in table 2. A wide range of variability was exhibited by most of the traits under study (Table 2). High range of variability recorded for fruit yield plant⁻¹ followed by days to first picking, fruiting span, number of fruit plant⁻¹, fruit yield ha⁻¹, plant height at 90,120, 150 DAT.

The present findings are in accordance with the earlier findings of Singh *et al.*, (2013), Janaki *et al.*, (2015). The phenotypic coefficient of variation (PCV) were of higher in magnitude than that of genotypic coefficient of variation (GCV) for all the characters showing that the environment had an important role in influencing the expression of the characters. The findings are in close harmony with the findings of Jyothi *et al.*, (2011), Singh *et al.*, (2013). The presence of high (PCV) for characters viz., number of fruit plant⁻¹, average fruit weight,

fruit yield plot⁻¹, fruit yield ha⁻¹, fruit yield plant⁻¹. Similar result was also reported by Sreelathakumari and Rajamony (2004), Patel *et al.*, (2015).

Presence of moderate (PCV) was reported for characters viz., plant height, fruit length, fruiting span, days to first picking. The

findings are in accordance with the findings of Diwakar *et al.*, (2012). Low PCV was exhibited for characters like number of branches plant⁻¹, days to 50% flowering, fruit width, days to first flowering. These results are quite similar to Manju and Sreelathakumari (2002), Tembhurne *et al.*, (2008) and Wilson and Philip (2009).

Table.1 Analysis of variance for different characters in chilli

Character	Mean sum of squares Replications (df = 2)	Genotypes (df = 17)	Error (df = 34)
Plant height at 150 DAT	7.200	224.093**	6.199
No. of primary branches /plant	14.851	1.551**	0.217
Days to 1 st flowering	156.351	23.155**	6.293
Days to 50% flowering	6.685	69.992**	14.253
Days to 1 st picking	4.462	158.763**	8.090
Fruiting span	4.462	158.763**	8.090
Number of fruit per plant	36.250	460.709**	33.794
Fruit length (cm)	0.925	8.618**	0.755
Fruit width (cm)	0.099	0.015**	0.003
Average fruit weight (g)	0.369	8.156**	0.398
Fruit yield/ plant (g)	4376.907	5595.351**	363.927
Fruit yield/ plot (kg)	5.810	6.561**	0.322
Fruit yield / ha (q)	865.935	711.119**	21.076

*: Significant at 5 % level; **: Significant at 1 % level

Table.2 Estimates of genetic parameters of variations for various characters in chilli

Characters		Grand Mean	Range		Variation (%)		h ² (b) (%)	GA	GAM
			Min.	Max.	PCV	GCV			
Plant height (cm)	30DAT	31.59	20.25	37.22	12.73	11.53	81.94	6.79	21.49
	60DAT	48.26	35.37	60.53	13.22	12.38	87.72	11.53	23.89
	90DAT	52.73	41.42	65.63	14.73	14.30	94.22	15.08	28.59
	120DAT	57.14	47.71	73.43	13.77	13.42	94.95	15.39	26.93
	150DAT	59.75	46.86	74.21	15.25	14.64	92.14	16.85	28.20
No. of primary branches / plant		18.14	16.87	19.60	4.48	3.68	67.18	1.13	6.21
Days to 1 st flowering		35.65	32.00	42.00	9.68	6.65	47.17	3.35	9.41
Days to 50% flowering		59.24	53.33	67.00	9.67	7.28	56.59	6.68	11.28
Days to 1 st picking		67.98	62.00	83.67	11.23	10.42	86.13	13.55	19.93
Fruiting span		74.02	58.33	80.00	10.32	9.57	86.13	13.55	18.30
Number of fruit per plant		42.20	22.00	67.00	31.44	28.26	80.80	22.09	52.34
Fruit length (cm)		12.72	7.34	15.12	14.44	12.72	77.64	2.94	23.10
Fruit width (cm)		0.99	0.87	1.16	8.66	6.56	57.42	0.10	10.28
Average fruit weight (g)		5.73	3.70	10.97	30.15	28.06	86.65	3.08	53.78
Fruit yield /plant (g)		228.35	166.67	315.00	20.10	18.29	82.73	78.25	34.27
Fruit yield /plot (kg)		7.41	5.30	10.06	20.92	19.46	86.57	2.76	37.30
Fruit yield /ha (q)		77.14	55.17	104.69	20.54	19.66	91.61	29.90	38.76

Where: GCV - genotypic coefficient of variation, PCV - phenotypic coefficient of variation, h² (b) - heritability in broad sense, GA - genetic advance and GAM - genetic advance as percent of mean

High heritability coupled with high genetic advance as percentage of mean were observed for number of fruit plant⁻¹, fruit yield plant⁻¹ (g), fruit yield ha⁻¹ (q) suggested that the preponderance of additive genes. The results were in consonance with Varkey *et al.*, (2005), Vani *et al.*, (2007) and Tembhrune *et al.*, (2008) for number of fruit plant⁻¹, Jyothi *et al.*, (2011) for number of fruit plant⁻¹, Shirshat *et al.*, (2007) for fruit yield ha⁻¹, fruit yield plant⁻¹. Higher estimates of heritability of the above characters might be due to additive gene effect. So, these characters could be considered as reliable selection indices and selection on the basis of these characters might be rewarding.

Low heritability coupled with low genetic advance as percentage of mean was observed for days to first flowering. This indicates the influence of non-additive gene action and considerable influence of environment on the expression of these traits. These traits could be exploited through manifestation of dominance and epistatic components through heterosis breeding. Hence, the breeder should adopt suitable breeding methodology to utilize both additive and non-additive gene effects simultaneously, since varietal and hybrid development will go a long way in the breeding programmes (Verma *et al.*, 2014).

From the above discussion it may be concluded that there was a wide variability among the different genotypes for most of the characters studied. So, these genotypes may be utilized for future breeding programme. Traits identified for high heritability coupled with high genetic gain like number of fruit plant⁻¹ may be considered well in selection for improvement of the crop.

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