



ASSESSMENT OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR QUANTITATIVE TRAITS IN CHILLI (*CAPSICUM ANNUUM* L.)

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ABSTRACT

The present investigation was carried out during kharif 2012-13 at Horticultural Research Station, Lam, Guntur with 63 genotypes of chilli (*Capsicum annuum* L.) in a randomized block design with two replications to estimate the genetic variability, heritability and genetic advance for ten quantitative traits. Analysis of variance revealed significant differences among the genotypes for all the traits studied indicating the presence of sufficient variability in the studied material. 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 per cent fruit set, number of fruits per plant, fruit diameter, average dry fruit weight, number of seeds per fruit and yield per plant suggesting the existence of wide range of genetic variability in the germplasm 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 all the characters except days to 50 % flowering indicating the predominance of additive gene action making the simple selection more effective.

INTRODUCTION

Chilli (*Capsicum annuum* L.) a member of the *Solanaceae* family, originated from South and Central America. Chilli is an indispensable spice due to its pungency, taste, appealing colour and flavor and has its unique place in the diet as a vegetable cum spice crop (Gadaginmath, 1992). The alkaloid capsaicin present in placenta of the chilli fruit responsible for its pungency has diverse prophylactic and therapeutic uses in Allopathic and Ayurvedic medicine (Sumathy and Mathew, 1984) and can directly scavenge various free radicals (Bhattacharya *et al.*, 2010). Chilli is a good source of vitamin C (ascorbic acid) and is used in food and beverage industries (Bosland and Votava, 2000). It has also acquired a great importance because of the presence of 'oleoresin', which permits better distribution of color and flavor in foods. India is the largest producer, consumer and exporter of chilli in the world with an annual production of 1.30 million tonnes from 0.79 million ha with production share of 22.72%. (National Horticulture Board, 2012-13). Andhra Pradesh leads the country in its production, productivity and export followed by Karnataka, West Bengal, Madhya Pradesh and Orissa.

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).

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 63 chilli genotypes.

MATERIALS AND METHODS

The experiment was carried out with 63 genotypes (Table 1)

of chilli at Horticultural Research Station, Lam, Guntur, Andhra Pradesh, India. The site of the experiment at Lam is situated on 16.28° North latitude and 80.44° East longitude at an altitude of 31.5 m above mean sea level which falls under humid tropical climate. A total of 63 germplasm lines were raised in a Randomized Block Design with two replications. The nursery was raised during last week of July and the seedlings were transplanted at a spacing of 75 cm × 30 cm in a row of 4 m length (experimental unit) during first fortnight of September. Each row consisted of 12 plants, of which five competitive plants were selected at random for recording the observations on plant height (cm), number of primary branches per plant, days to 50 % flowering, fruit set per cent, number of fruits per plant, fruit diameter (cm), fruit length (cm), average dry fruit weight (g), number of seeds per fruit and dry fruit yield per plant (g). The crop was raised as per the recommended package of practices.

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) by using the following formulae.

$$PCV = (\sqrt{\sigma_p^2 \div \bar{X}})$$

$$GCV = (\sqrt{\sigma_g^2 \div \bar{X}})$$

Where,

PCV = Phenotypic Correlation Coefficient, GCV = Genotypic Correlation Coefficient

σ_g^2 = Genotypic variance = (Mean sum of squares due to genotypes – Error mean sum of squares) ÷ Replications

σ_p^2 = Phenotypic variance = $\sigma_g^2 + \sigma_e^2$

σ_e^2 = Environmental variance = (Error mean sum of squares) ÷ Replications

X = General mean

PCV and GCV were classified as suggested by Sivasubramanian and Menon (1973).

Less than 10% = Low

10-20% = Moderate

More than 20 % = High

Heritability in broad sense (h^2 (b)) was estimated as per the formulae suggested by Allard (1960).

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

The heritability (h^2 (b)) was categorised as suggested by Johnson *et al.* (1955).

0-30% = Low

31-60% = Medium

61% and above = High

Genetic advance (GA) was estimated as per formula given by Allard (1960)

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

Where,

K = Selection differential at 5 per cent selection intensity which

Table 1: List of chilli genotypes used in the experiment and their source

Treatment	Accession Number	Source
T ₁	G-3	HRS, Lam farm, Guntur
T ₂	G-4	HRS, Lam farm, Guntur
T ₃	G-5	HRS, Lam farm, Guntur
T ₄	LCA-206	HRS, Lam farm, Guntur
T ₅	LCA-235	HRS, Lam farm, Guntur
T ₆	LCA-305	HRS, Lam farm, Guntur
T ₇	LCA-315	HRS, Lam farm, Guntur
T ₈	LCA-353	HRS, Lam farm, Guntur
T ₉	LCA-357	HRS, Lam farm, Guntur
T ₁₀	LCA-424	HRS, Lam farm, Guntur
T ₁₁	LCA-436	HRS, Lam farm, Guntur
T ₁₂	LCA-620	HRS, Lam farm, Guntur
T ₁₃	LCA-625	HRS, Lam farm, Guntur
T ₁₄	LCA-702	HRS, Lam farm, Guntur
T ₁₅	LCA-703	HRS, Lam farm, Guntur
T ₁₆	LCA-704	HRS, Lam farm, Guntur
T ₁₇	LCA-705	HRS, Lam farm, Guntur
T ₁₈	LCA-706	HRS, Lam farm, Guntur
T ₁₉	LCA-707	HRS, Lam farm, Guntur
T ₂₀	LCA-708	HRS, Lam farm, Guntur
T ₂₁	LCA-709	HRS, Lam farm, Guntur
T ₂₂	LCA-710	HRS, Lam farm, Guntur
T ₂₃	LCA-711	HRS, Lam farm, Guntur
T ₂₄	LCA-712	HRS, Lam farm, Guntur
T ₂₅	LCA-713	HRS, Lam farm, Guntur
T ₂₆	LCA-714	HRS, Lam farm, Guntur
T ₂₇	LCA-715	HRS, Lam farm, Guntur
T ₂₈	LCA-716	HRS, Lam farm, Guntur
T ₂₉	LCA-718	HRS, Lam farm, Guntur
T ₃₀	LCA-720	HRS, Lam farm, Guntur
T ₃₁	LCA-722	HRS, Lam farm, Guntur
T ₃₂	LCA-724	HRS, Lam farm, Guntur
T ₃₃	LCA-726	HRS, Lam farm, Guntur
T ₃₄	LCA-728	HRS, Lam farm, Guntur
T ₃₅	LCA-730	HRS, Lam farm, Guntur
T ₃₆	LCA-732	HRS, Lam farm, Guntur
T ₃₇	LCA-734	HRS, Lam farm, Guntur
T ₃₈	LCA-736	HRS, Lam farm, Guntur
T ₃₉	LCA-738	HRS, Lam farm, Guntur
T ₄₀	LCA-740	HRS, Lam farm, Guntur
T ₄₁	LCA-742	HRS, Lam farm, Guntur
T ₄₂	LCA-744	HRS, Lam farm, Guntur
T ₄₃	LCA-746	HRS, Lam farm, Guntur
T ₄₄	LCA-748	HRS, Lam farm, Guntur
T ₄₅	LCA-750	HRS, Lam farm, Guntur
T ₄₆	LCA-752	HRS, Lam farm, Guntur
T ₄₇	LCA-754	HRS, Lam farm, Guntur
T ₄₈	LCA-756	HRS, Lam farm, Guntur
T ₄₉	LCA-758	HRS, Lam farm, Guntur
T ₅₀	LCA-760	HRS, Lam farm, Guntur
T ₅₁	LCA-762	HRS, Lam farm, Guntur
T ₅₂	CA-960	HRS, Lam farm, Guntur
T ₅₃	HC-28	HAU, Hisar
T ₅₄	KT-I	IARI, Katrain
T ₅₅	Aparna	HRS, Lam farm, Guntur
T ₅₆	Pandava	Local collection, Guntur
T ₅₇	Pant C-1	GBPUA&T, Pantnagar
T ₅₈	Phule Jyoti	MPKV, Rahuri
T ₅₉	Punjab Guccedar	PAU, Ludhiana
T ₆₀	Pusa Sadabahar	IARI, New Delhi
T ₆₁	Super-10	Local collection, Guntur
T ₆₂	Warangal Chapata	Local collection, Warangal
T ₆₃	LCA-334	HRS, Lam farm, Guntur

Table 2: Analysis of variance for quantitative characters in chilli (*Capsicum annum* L.)

S.No.	Character	Mean sum of squares		
		Replications	Genotypes	Error
1	Plant height (cm)	28.097	563.376**	43.543
2	Number of primary branches per plant	0.701	1.117**	0.219
3	Days to 50 per cent flowering	1.341	25.422**	3.954
4	Per cent fruit set	176.198*	501.725**	39.198
5	Number of fruits per plant	409.320	9125.453**	634.339
6	Fruit diameter (cm)	0.024**	0.276**	0.0007
7	Fruit length (cm)	0.956*	6.022**	0.234
8	Average dry fruit weight (g)	0.00002	0.369**	0.028
9	Number of seeds per fruit	1.28	580.326**	80.323
10	Yield per plant (g)	2143.226	3553.576**	541.662

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

Table 3: Estimates of mean, range, components of variance, heritability and genetic advance for yield and it's component characters in chilli (*Capsicum annum* L.)

Character	Mean	Range	GCV (%)	PCV (%)	h ² (b) (%)	GA @ 5%	GAM @ 5%
Plant height (cm)	87.17	49.95-127.75	18.49	19.98	85.65	30.73	35.25
No. of primary branches per plant	3.61	2.3-5.3	18.55	22.64	67.11	1.13	31.30
Days to 50 per cent flowering	31.42	24-42	10.42	12.19	73.08	5.77	18.36
Per cent fruit set	50.50	17-87	30.11	32.56	85.50	28.96	57.36
No. of fruits per plant	172.48	49.8-480	37.77	40.50	87.00	125.19	72.58
Fruit diameter (cm)	1.35	0.76-3.17	27.44	27.52	99.50	0.76	56.39
Fruit length (cm)	8.65	4.06-12.97	19.64	20.42	92.48	3.37	38.92
Average dry fruit weight (g)	1.09	0.5-3.35	37.77	40.75	85.92	0.78	72.11
No. of seeds per fruit	61.36	32.8-152.5	25.76	29.61	75.68	28.33	46.17
Yield per plant (g)	146.82	83.95-295.10	26.43	30.81	73.54	68.55	46.69

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 per cent of mean (GAM)

accounts to a constant value 2.06

σ_p = Phenotypic standard deviation

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

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

The genetic advance as per cent over mean was categorized as suggested by Johnson *et al.* (1955).

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

RESULTS AND DISCUSSION

Analysis of variance (Table 2) revealed significant differences among the genotypes for all the traits indicating presence of significant variability in the genotypes which can be exploited through selection. These findings are in line with earlier reports of Vani *et al.* (2007), Farhad *et al.* (2008), Singh and Singh, (2011), Krishnamurthy *et al.* (2013). The extent of variability with respect to 10 characters in different genotypes measured 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 3.

The mean performances of genotypes (Table 3) for different

traits indicated that the high range of variability was recorded for no. of fruits per plant (49.80 to 480 fruits per plant) followed by yield per plant (83.95 to 295.10 g), plant height (49.95-127.75 cm), no. of seeds per fruit (32.80-152.50), per cent fruit set (17-87 %) and days to 50 % flowering (24-42 days). Relatively low range of variability was observed in respect of average dry fruit weight (0.5-3.35 g), fruit diameter (0.76-3.17 cm), no. of primary branches per plant (2.3-5.3) and fruit length (4.06-12.97 cm) and these findings are in accordance with those of Munshi *et al.* (2010), Arunkumar *et al.* (2013).

The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters (Table 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 are supported by earlier observations of Munshi *et al.* (2010), Krishnamurthy *et al.* (2013), Sandeep *et al.* (2013). The estimates of PCV and GCV were high for per cent fruit set (32.56 and 30.11 %), no. of fruits per plant (40.50 and 37.77 %), fruit diameter (27.52 and 27.44 %), average dry fruit weight (40.75 and 37.77 %), no. of seeds per fruit (29.61 and 25.76 %) and yield per plant (30.81 and 26.43%) indicating the existence of wide range of genetic variability in the germplasm for these traits. This also indicates broad genetic base, less environmental influence and these traits are under the control of additive gene effects and hence, there is a good scope for further improvement of these characters through simple selection. These findings are in agreement with results of Krishna *et al.* (2007) for per cent fruit set, Farhad *et al.* (2008), Tembhrne *et al.* (2008),

Rajyalakshmi and Vijayapadma (2012) for no. of fruits per plant, Smitha and Basvaraja (2007), Suryakumari *et al.* (2010) for no. of seeds per fruit, Gupta *et al.* (2009), Singh *et al.* (2009) for fruit diameter, average dry fruit weight and Padhar and Zaveri (2010), Arup *et al.* (2011), Kumar *et al.* (2012), Sandeep *et al.* (2013) for yield per plant.

The estimates of PCV and GCV were moderate for plant height (19.98 and 18.49 %) and days to 50 % flowering (12.19 and 10.42%). Similar observations were earlier reported by Kumar *et al.* (2010), Nehru *et al.* (2012) for plant height and Bendale *et al.* (2006), Bharadwaj *et al.* (2007) for days to 50 % flowering. The estimates of PCV and GCV were high and moderate respectively for no. of primary branches per plant (22.64 and 18.55 %) and fruit length (20.42 and 19.64). These results are in conformity with findings of earlier works of Kumar *et al.* (2010), Munshi *et al.* (2010) for no. of primary branches per plant and Rajyalakshmi and Vijayapadma (2012) for fruit length.

High heritability coupled with high genetic advance as per cent of mean was observed for all the characters except for days to 50 % flowering indicating the predominance of additive gene action and hence direct phenotypic selection is useful with respect to these traits. These results are in line with results of earlier works of Arup *et al.* (2011), Kumar *et al.* (2012), Sandeep *et al.* (2013) for yield per plant, Rajyalakshmi and Vijayapadma (2012) for plant height, number of fruits per plant and fruit length, Munshi *et al.* (2010) for number of primary branches per plant, Gupta *et al.* (2009) for fruit diameter and average dry fruit weight, Krishna *et al.* (2007), Meena and Bahadur (2014) for per cent fruit set and Suryakumari *et al.* (2010) for number of seeds per fruit.

High heritability coupled with moderate genetic advance as per cent of mean was observed for days to 50 % flowering indicating the role of additive and non additive gene action and further improvement of this character would be easier through mass selection, progeny selection or any modified selection procedure aiming to exploit the additive gene effects rather than simple selection. As reported by Tembhurne *et al.* (2008), Suryakumari *et al.* (2010).

The findings indicate that there exists adequate genotypic variation in the genotypes for per cent fruit set, number of fruits per plant, fruit diameter, average dry fruit weight, number of seeds per fruit and 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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