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Estimation of variability parameters for growth, yield and yield traits in chilli (*Capsicum annuum* L.)

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Abstract

The present investigation was conducted to estimate variability parameters in forty diverse chilli (*Capsicum annuum* L.) genotypes for growth, yield, and yield traits at the College of Horticulture, Sri Konda Laxman Telangana State Horticultural University, Rajendranagar, Hyderabad, India during Kharif 2018. The experiment was laid out in a Randomized Block Design with three replications. Observations were recorded on twenty quantitative characters. The analysis of variance revealed highly significant differences among genotypes for all characters studied, indicating substantial genetic variability. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all traits, with narrow differences suggesting minimal environmental influence. High PCV and GCV (>20%) were recorded for plant height (23.59%, 23.00%), number of primary branches per plant (23.99%, 23.41%), number of flowers per axil (25.06%, 23.52%), average fruit weight (54.69%, 53.32%), fruit length (37.61%, 37.53%), fruit diameter (41.86%, 41.03%), fruit yield per plant (44.54%, 44.40%), fruit yield per plot (44.35%, 44.07%), oleoresin content (23.47%, 23.38%), capsaicin content (39.21%, 39.14%), and chlorophyll content (28.37%, 28.01%), indicating wider genetic variability. High heritability coupled with high genetic advance as percent of mean was observed for plant height (95.0%, 46.18%), number of primary branches per plant (95.2%, 47.05%), average fruit weight (95.0%, 107.08%), fruit length (99.6%, 77.16%), fruit diameter (96.1%, 82.86%), fruit yield per plant (99.4%, 91.17%), fruit yield per plot (98.7%, 90.22%), ascorbic acid content (99.6%, 40.97%), oleoresin content (99.2%, 47.97%), capsanthin content (99.5%, 29.72%), capsaicin content (99.6%, 80.47%), and chlorophyll content (97.5%, 56.96%), indicating predominance of additive gene action. The study concludes that characters exhibiting high heritability with high genetic advance can be improved through direct selection.

Keywords: Chilli, *Capsicum annuum* L., genetic variability, genotypic coefficient of variation, phenotypic coefficient of variation, heritability, genetic advance

Introduction

Chilli (*Capsicum annuum* L.) is one of the most important commercial spice crops belonging to the family Solanaceae, widely cultivated throughout India for its pungent fruits that are used as vegetables, spices, condiments, pickles, and in pharmaceutical industries. India is the world's largest producer, consumer, and exporter of chilli. The crop exhibits ample variability in morphological characters throughout India, particularly in the south peninsular region, North Eastern foot hills of Himalayas, and Gangetic plains (Pradheep and Veeraragavatham, 2006) [13]. The evaluation of germplasm is immensely important in genetic improvement of the crop for achieving higher yields and productivity (Munshi *et al.*, 2000) [11].

The magnitude of variability and its genetic components are the most important aspects of breeding material. Hence, the basic understanding of genetic variability is a prerequisite for the planning of breeding programmes. Variability helps to choose the potential genotype, since it indicates the extent of recombination for implementing effective selection. Genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) are measured to study the variability (Burton and De Vane, 1953) [2]. Heritability estimates give a measure of transmission of characters from one generation to another, thus giving an idea of heritable portion of variability and enabling the plant breeder in isolating the elite genotype (Lush, 1949; Hanson *et*

al., 1956) [9, 6]. Heritability coupled with genetic advance is an important selection parameter. Johnson *et al.* (1955) [8] reported that heritability along with genetic gain is more useful than heritability alone in predicting the resultant effect for selecting the best individuals. The present investigation was undertaken to estimate variability parameters for growth, yield and yield traits in diverse chilli germplasm.

Materials and Methods

Experimental Site and Climate

The field experiment was conducted on red soil with coarse texture at the P.G research block, Sri Konda Laxman Telangana State Horticultural University, College of Horticulture, Rajendranagar, Hyderabad during Kharif 2018. The site of the experiment is situated in semi arid tropical zone at an altitude of 542.6 m above mean sea level. Geographically, it lies at latitude of 17°19' N and a longitude of 78°23' E.

Experimental Material

The experimental material comprising of 40 chilli genotypes, homozygous accessions obtained from NBPGR Regional Station, Rajendranagar, Hyderabad and one local variety collected from Warangal district of Telangana state and few released varieties from RARS, Lam, Guntur, Andhra Pradesh were systematically evaluated for 20 quantitative traits (Table 1).

Experimental Design

The experiment was laid out in a Randomized Block Design with 40 chilli accessions as treatments during Kharif, 2018-19. Each treatment was randomly replicated thrice. Six weeks old healthy seedlings were transplanted in the main field. Each germplasm line was grown in a plot of 1.8 m × 3.15 m (5.67 Sq. meters), 8 plants per row with spacing of 60×60 cm per replication.

Table 1: List of 40 chilli genotypes used in the study

Tr. No.	Genotype	Source	Tr. No.	Genotype	Source
T ₁	SR 6514	NBPGR, Hyderabad	T ₂₁	EC 378688	NBPGR, Hyderabad
T ₂	IC 528454	NBPGR, Hyderabad	T ₂₂	EC 391083	NBPGR, Hyderabad
T ₃	IC 255896	NBPGR, Hyderabad	T ₂₃	EC 402109	NBPGR, Hyderabad
T ₄	AAT 2	NBPGR, Hyderabad	T ₂₄	EC 399567	NBPGR, Hyderabad
T ₅	NIC 23923	NBPGR, Hyderabad	T ₂₅	PSR 13976	NBPGR, Hyderabad
T ₆	PSR 7075	NBPGR, Hyderabad	T ₂₆	NIC 19969	NBPGR, Hyderabad
T ₇	IC 572469	NBPGR, Hyderabad	T ₂₇	ST 13837	NBPGR, Hyderabad
T ₈	SD 5335	NBPGR, Hyderabad	T ₂₈	NIC 19967	NBPGR, Hyderabad
T ₉	ST 13874	NBPGR, Hyderabad	T ₂₉	PBC 80	NBPGR, Hyderabad
T ₁₀	IC 214966	NBPGR, Hyderabad	T ₃₀	EC 399572	NBPGR, Hyderabad
T ₁₁	PSR 13944	NBPGR, Hyderabad	T ₃₁	SR 3429	NBPGR, Hyderabad
T ₁₂	PSR 7074	NBPGR, Hyderabad	T ₃₂	EC 399575	NBPGR, Hyderabad
T ₁₃	EC 402101	NBPGR, Hyderabad	T ₃₃	EC 401105	NBPGR, Hyderabad
T ₁₄	PSR 13968	NBPGR, Hyderabad	T ₃₄	ST 13875	NBPGR, Hyderabad
T ₁₅	SRS 13578	NBPGR, Hyderabad	T ₃₅	Warangal Chapata	Warangal, Telangana
T ₁₆	EC 391087	NBPGR, Hyderabad	T ₃₆	Hirkani	PDKV, Akola
T ₁₇	AVPP 9813	AVRDC, Taiwan	T ₃₇	Sindhur (C)	RARS, Lam, Guntur
T ₁₈	IC 572480	NBPGR, Hyderabad	T ₃₈	LCA 620 (C)	RARS, Lam, Guntur
T ₁₉	EC 399565	NBPGR, Hyderabad	T ₃₉	LCA 625 (C)	RARS, Lam, Guntur
T ₂₀	EC 399574	NBPGR, Hyderabad	T ₄₀	LCA-334 (C)	RARS, Lam, Guntur

C = Check variety

Estimation of Genetic Variability Parameters

Phenotypic and genotypic components of variance were estimated using the formula given by Cochran and Cox (1957) [4]. Genotypic variance (σ^2_g) = [MSS due to genotypes - MSS due to error] / r. Phenotypic variance (σ^2_p) = Genotypic variance (σ^2_g) + Error variance (σ^2_e). Both phenotypic and genotypic coefficients of variability were estimated using the formula of Burton and De Vane (1953) [2]. PCV and GCV were classified as per Sivasubramanian and Menon (1973) [17] as: Low (<10%), Moderate (10-20%), and High (>20%).

Broad sense heritability (h^2_{bs}) was estimated as the ratio of genotypic variance to phenotypic variance expressed in percentage (Lush, 1949; Hanson *et al.*, 1956) [9, 6]. Heritability was categorized as per Johnson *et al.* (1955) [8]: Low (<30%), Moderate (30-60%), and High (>60%). Genetic advance was estimated using the formula $GA = h^2_{bs} \times \sigma_p \times K$, where K is the standard selection differential at 5% intensity (2.06). Genetic advance as percent of mean was classified as: Low (<10%), Moderate (10-20%), and High (>20%).

Results and Discussion

Analysis of Variance

The analysis of variance in 40 chilli genotypes indicated highly significant differences among the genotypes for all the 20 quantitative characters studied (Table 2), indicating the existence of adequate genetic variability among the genotypes. This was in accordance with the reports of Sarma and Roy (1995) [15]. The significant variation among genotypes suggests ample scope for selection of superior genotypes for yield improvement in chilli breeding programmes.

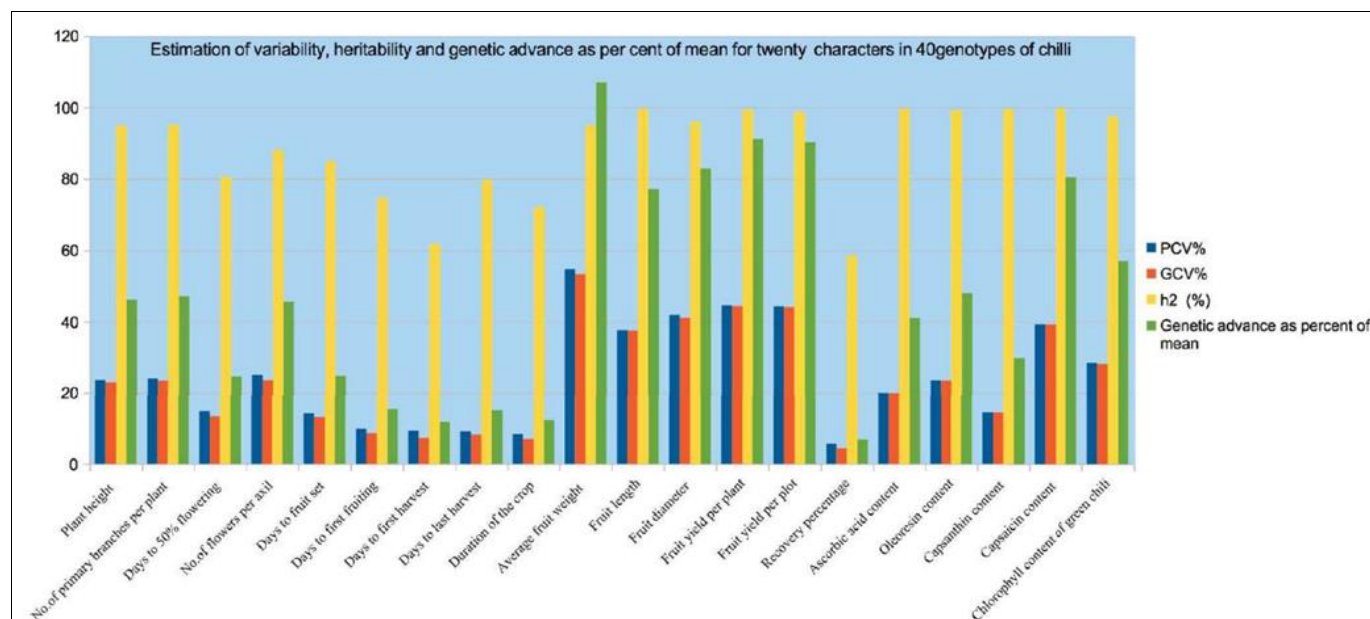
Estimates of Variability, Heritability and Genetic Advance

The estimates of variability parameters including range, mean, phenotypic variance, genotypic variance, PCV, GCV, heritability, genetic advance and genetic advance as percent of mean for twenty characters are presented in Table 2. The PCV was higher than GCV for all characters, indicating that all characters interacted with environment to some degree. However, the narrow differences between PCV and GCV values for most characters suggest that environmental influence was minimal and the traits were predominantly under genetic control.

Table 2: Estimates of variability, heritability and genetic advance for 20 characters in 40 chilli genotypes

S. No.	Characters	Min	Max	Mean	σ^2_p	σ^2_g	PCV%	GCV%	h^2	GA	GAM%
1	Plant height (cm)	36.84	86.30	56.82	179.69	170.75	23.59	23.00	95.0	26.24	46.18
2	No. of primary branches/plant	2.67	8.18	4.87	1.37	1.30	23.99	23.41	95.2	2.29	47.05
3	Days to 50% flowering	39.67	73.33	57.26	72.06	58.15	14.83	13.32	80.7	14.11	24.65
4	No. of flowers per axil	1.00	2.83	1.54	0.15	0.13	25.06	23.52	88.1	0.70	45.49
5	Days to fruit set	43.00	77.00	61.38	76.01	64.53	14.20	13.09	84.9	15.25	24.84
6	Days to first fruiting	71.00	104.67	88.44	77.33	57.74	9.94	8.59	74.7	13.53	15.30
7	Days to first harvest	81.00	115.00	100.30	86.50	53.53	9.27	7.29	61.9	11.86	11.82
8	Days to last harvest	122.67	170.67	142.06	169.80	135.25	9.17	8.19	79.7	21.38	15.05
9	Duration of the crop	149.00	212.67	182.32	227.02	163.77	8.26	7.02	72.1	22.39	12.28
10	Average fruit weight (g)	0.44	17.11	6.12	11.20	10.65	54.69	53.32	95.0	6.55	107.08
11	Fruit length (cm)	3.08	19.14	8.82	11.26	11.22	37.61	37.53	99.6	6.88	77.16
12	Fruit diameter (cm)	0.26	3.28	1.28	0.29	0.27	41.86	41.03	96.1	1.06	82.86
13	Fruit yield per plant (kg)	0.053	0.690	0.302	0.02	0.02	44.54	44.40	99.4	0.28	91.17
14	Fruit yield per plot (kg)	0.863	11.00	4.836	4.60	4.54	44.35	44.07	98.7	4.36	90.22
15	Recovery percentage (%)	32.00	40.33	36.06	4.20	2.45	5.69	4.34	58.4	2.47	6.84
16	Ascorbic acid (mg/100g)	61.45	150.13	111.25	494.02	491.81	19.98	19.94	99.6	45.58	40.97
17	Oleoresin content (%)	5.79	14.73	9.08	4.55	4.51	23.47	23.38	99.2	4.36	47.97
18	Capsanthin (ASTA units)	126.65	276.59	219.76	1015.96	1010.63	14.50	14.47	99.5	65.32	29.72
19	Capsaicin content (%)	0.15	0.82	0.45	0.03	0.03	39.21	39.14	99.6	0.36	80.47
20	Chlorophyll content (%)	0.00	2.37	1.88	0.29	0.278	28.37	28.01	97.5	1.07	56.96

σ^2_p = Phenotypic variance, σ^2_g = Genotypic variance, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, h^2 = Heritability (broad sense), GA = Genetic advance, GAM = Genetic advance as percent of mean

**Fig 1:** Estimation of variability, heritability and genetic advance as percent of mean for twenty characters in 40 chilli genotypes

High PCV and GCV values (>20%) were recorded for plant height (23.59%, 23.00%), number of primary branches per plant (23.99%, 23.41%), number of flowers per axil (25.06%, 23.52%), average fruit weight (54.69%, 53.32%), fruit length (37.61%, 37.53%), fruit diameter (41.86%, 41.03%), fruit yield per plant (44.54%, 44.40%), fruit yield per plot (44.35%, 44.07%), oleoresin content (23.47%, 23.38%), capsaicin content (39.21%, 39.14%), and chlorophyll content (28.37%, 28.01%), indicating the existence of wider genetic variability for these traits and the potential for improvement through selection. Similar findings were reported by Sharma *et al.* (2010) [16], Suryakumari *et al.* (2010) [18], Datta and Das (2013) [5], and Amit *et al.* (2014) [1] in chilli.

Moderate PCV and GCV values (10-20%) were observed for days to 50% flowering (14.83%, 13.32%), days to fruit set (14.20%, 13.09%), ascorbic acid content (19.98%, 19.94%), and capsanthin content (14.50%, 14.47%). Low PCV and GCV

values (<10%) were recorded for days to first fruiting, days to first harvest, days to last harvest, duration of crop, and recovery percentage, indicating narrow range of genetic variability for these traits.

High heritability estimates (>60%) were observed for all the characters except recovery percentage (58.4%), which showed moderate heritability. Very high heritability (>95%) was recorded for plant height (95.0%), number of primary branches per plant (95.2%), average fruit weight (95.0%), fruit length (99.6%), fruit diameter (96.1%), fruit yield per plant (99.4%), fruit yield per plot (98.7%), ascorbic acid content (99.6%), oleoresin content (99.2%), capsanthin content (99.5%), capsaicin content (99.6%), and chlorophyll content (97.5%). These findings are in agreement with the reports of Chattopadhyay *et al.* (2011) [3], Priyanka and Naidu (2015) [14], and Udachappa *et al.* (2017) [19].

High heritability coupled with high genetic advance as percent

of mean (>20%) was observed for plant height, number of primary branches per plant, number of flowers per axil, days to 50% flowering, days to fruit set, average fruit weight, fruit length, fruit diameter, fruit yield per plant, fruit yield per plot, ascorbic acid content, oleoresin content, capsanthin content, capsaicin content, and chlorophyll content, indicating the predominance of additive gene action in the expression of these traits and suggesting that these characters could be improved through direct selection. Similar findings were reported by Sharma *et al.* (2010) [16], Suryakumari *et al.* (2010) [18], Datta and Das (2013) [5], Amit *et al.* (2014) [1], Priyanka and Naidu (2015) [14], and Mallikarjun *et al.* (2003) [10].

Moderate heritability coupled with moderate genetic advance as percent of mean was observed for days to first fruiting (74.7%, 15.30%), days to first harvest (61.9%, 11.82%), days to last harvest (79.7%, 15.05%), and duration of crop (72.1%, 12.28%), indicating the role of both additive and non-additive gene action in the expression of these traits. Recovery percentage showed moderate heritability (58.4%) with low genetic advance as percent of mean (6.84%), indicating the predominance of non-additive gene action and environmental influence on this trait.

Conclusion

The present investigation on estimation of variability parameters in forty diverse chilli genotypes revealed the existence of substantial genetic variability for all the twenty characters studied. The phenotypic coefficient of variation was consistently higher than genotypic coefficient of variation for all characters; however, the narrow differences suggest that environmental influence was minimal. High PCV and GCV recorded for plant height, number of primary branches per plant, number of flowers per axil, average fruit weight, fruit length, fruit diameter, fruit yield per plant, fruit yield per plot, oleoresin content, capsaicin content, and chlorophyll content indicate the presence of wider genetic variability. High heritability coupled with high genetic advance as percent of mean observed for these characters indicates the predominance of additive gene action, suggesting that simple selection based on phenotypic performance would be effective for genetic improvement. Hence, breeders are recommended to adopt mass selection, pure line selection, or pedigree method of breeding for improving these traits in chilli.

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