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Estimation of genetic variability parameters for yield and yield components in chilli (*Capsicum annuum* L.)

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Abstract

The study was carried out during kharif 2014-15 at Horticultural Research Station, Lam, Guntur with 71 genotypes (54 F₁ hybrids, 15 parents and two commercial checks) of chilli in a randomized block design with three replications to estimate the genetic variability, heritability and genetic advance for twelve yield and yield attributing traits. Analysis of variance revealed the significant differences among the genotypes for all the traits studied indicating the presence of sufficient variability in the studied material. The phenotypic coefficient of variation (PCV) was slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the characters indicating the some degree of environment influence on their genetic expression. Numbers of fruits per plant and dry fruit yield per plant have registered high estimates of PCV and GCV, whereas no. of seeds per fruit recorded high PCV. High heritability coupled with high genetic advance as % of mean was observed for days to 50% flowering, no. of fruits per plant, fruit length, fruit diameter, average dry fruit weight, no. of seeds per fruit and dry fruit yield per plant. The characters viz. no. of fruits per plant, no. of seeds per fruit and dry fruit yield per plant exhibited high values of PCV, GCV and high heritability coupled with high genetic advance as % of mean suggesting that existence of wide range of genetic variability, broad genetic base, less environmental influence, predominance of additive gene action and selection for these traits based on phenotypic would be rewarding.

Keywords: Chilli, *Capsicum annuum*, variability, GCV, PCV, heritability, genetic advance

Introduction

Chilli (*Capsicum annuum* L.) is 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. India is the largest producer, consumer and exporter of chilli in the world with productivity of 1.9 metric t/ha (National Horticulture Board, 2014) [20]. Andhra Pradesh is the leading producer and exporter of the chilli with an annual production of 0.60 million tonnes from 0.13 million ha (NHB, 2014) followed by Telangana, Karnataka, West Bengal and Madhya Pradesh etc. In Andhra Pradesh, Guntur, Prakasam, Kurnool, Krishna, Kadapa and West Godavari are the major chilli growing districts.

Even though India ranks first in area and production of chilli, its productivity is very low as compared to other countries like Japan (3.6 t/ha) and Korea (2 t/ha), USA and Indonesia (Patil *et al.*, 2012) [22] due to many limiting factors mainly due to lack of superior genotypes or improved cultivars for use in breeding programmes to develop potential hybrids. So, there is a need to develop new varieties and hybrids with high productivity to meet demand. The critical assessment of nature and magnitude of variability in the germplasm stock is one of the important pre-requisite for formulating the effective breeding methods (Krishna *et al.* 2007) [14]. The crop improvement depends on the magnitude of genetic variability present in germplasm and the extent to which the desirable characters are heritable. Greater the variability in a population, there will be the greater chance for effective selection for desirable types (Vavilov, 1951) [33]. Genotypic and phenotypic coefficients of variation (GCV and PCV) are useful in detecting the amount of variability present in the available genotypes. Heritability and genetic advance helps in determining the influence of environment in expression of characters and the extent to which improvement is possible after selection (Robinson *et al.*, 1949) [25]. Higher the heritable variation, greater will be the possibility of fixing the characters by selection. High heritability is not enough to make efficient selection in segregating generations, unless the information is accompanied with substantial amount of genetic advance (Johnson *et al.*, 1955) [11]. The Genetic variability studies in chilli have also carried out by earlier workers viz. Janaki *et al.* (2015) [10] and Meena *et al.* (2016) [18]. 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 71 chilli genotypes comprising 54 F₁ hybrids, 15 parents and two commercial checks.

Materials and Methods

An experiment was conducted at Horticulture Research Station, Dr. Y. S. R. Horticultural University, Lam farm, Guntur. The experimental material and their characters used in this experiment were presented in Table 1. The experimental material comprised of nine lines (LCA 504, LCA 615, LCA 446, LCA 466, LCA 442, LCA 654, LCA 607, LCA 655 and LCA 355) and six testers (G4, LCA 678, LCA 453, LCA 703-2, LCA 705-2 and LCA 315). These parents were crossed in Line \times Tester fashion during *Kharif*, 2013-14 and developed 54 F₁ hybrids. The resulting 54 F₁ hybrids along with their 15 parents and two commercial checks (Tejaswini and Indam-5) were evaluated during *Kharif*, 2014-15 in a Randomized Block Design with three replications in two rows (one row of 4 m length) of each genotype at a spacing of 75 cm x 30 cm. The crop was raised as per the standard package of practices. The observations were recorded on five randomly selected plants for twelve characters *viz.*, plant height (cm), plant spread (cm), number of primary branches, days to 50% flowering, days to fruit maturity, number of fruits per plant, fruit length (cm), fruit diameter (cm), average dry fruit weight (g), dry fruit yield per plant (g), number of seeds per fruit and seed weight (g/1000 seed).

Analysis of variance was carried out as per the procedure given by Panse and Sukhatme (1985) [21]. The genotypic and phenotypic coefficients of variation were computed as per Burton and Devane (1953) [4] and categorized as per Sivasubrahmanian and Menon (1973) [28] while the heritability in broad sense and genetic advance were calculated as per Allard (1960) [1] and categorized as per Johnson *et al.* (1955) [11].

Results and Discussion

Analysis of variance (Table 2) revealed significant differences among the genotypes for all the traits indicating presence of wide range of variability in the genotypes which can be exploited through selection. These findings were in line with earlier reports of Krishnamurthy *et al.* (2013) [15] and Kannan *et al.* (2016) [12]. The extent of variability with respect to 12 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 % 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 (124.93-447.03 fruits per plant) followed by fruit yield per plant (151.93-328.53 g), no. of seeds per fruit (41.80-90.47), plant spread (70.93-106.70 cm), plant height (74.57-109.77 cm), days to fruit maturity (48.67-69.33 days) and days to 50 % flowering (22.67-38.00 days). Relatively low range of variability was observed in respect of average dry fruit weight (0.75-1.83 g), fruit diameter (0.98-2.08 cm), no. of primary branches per plant (3.03-5.23), 1000 seed weight (5.05-7.74 g) and fruit length (7.54-15.18 cm). Similar kinds of results were also reported in earlier findings of Munshi *et al.* (2010) [19], Arunkumar *et al.* (2013) [3].

The phenotypic coefficient of variation (PCV) was higher than the corresponding genotypic coefficient of variation (GCV) for all the characters (Table 3) indicating the effect of environment on their genetic expression (Meena *et al.*, 2016) [18] and which is obvious as PCV is the variability due to genotype and genotype \times environment interaction. However, the effect of environment on any trait is indicated by the

magnitude of the differences between the genotypic and phenotypic coefficients of variation as wide differences reflect the large environmental effect and narrow differences reveal the high genetic influence (Khatun *et al.*, 2015) [13]. In present study, the differences between PCV and GCV was found to be narrow for days to 50% flowering, plant height, plant spread, fruit length, fruit diameter and average dry fruit weight which suggesting that these traits were least affected by the environment and genetic factors were predominantly responsible for expression of those attributes and selection could be made effectively on the basis of phenotypic performance (Satish *et al.*, 2016) [27]. These results were in consonance with earlier observations of Sandeep *et al.* (2013) [26] and Janaki *et al.* (2015) [10].

Numbers of fruits per plant and dry fruit yield per plant have registered high estimates (>20%) of PCV and GCV, whereas no. of seeds per fruit recorded high PCV with 22.61% and indicating the existence of wide range of genetic variability, broad genetic base, less environmental influence. Hence, there is a good scope for further improvement of these characters through simple selection. These findings were in agreement with results of Farhad *et al.* (2008) [7], Kumar *et al.* (2012) [16] and Suryakumari *et al.* (2010) [30].

The estimates of PCV and GCV were moderate (10-20%) for no. of primary branches per plant, days to 50% flowering, fruit length, fruit diameter and average dry fruit weight. Whereas, plant height, plant spread, 1000 seed weight recorded moderate PCV and no. of seeds per fruit has observed moderate GCV which indicated that there is scope for further improvement of these characters through any modified selection procedure rather than simple selection. Similar results were noticed by Surya Kumari *et al.* (2010) for plant height; Uma Jyothi *et al.* (2011) [32] for plant spread; Sreelathakumary and Rajamony (2002) [29] for no. of primary branches per plant; Dutonde *et al.* (2006) [6] for days to 50 % flowering; Gupta *et al.* (2009) [8] for fruit diameter; Manju and Sreelathakumary (2002) [17, 29] for fruit length and Tembhurane *et al.* (2008) [31] for average dry fruit weight. Days to fruit maturity recorded the low estimates (<10%) of PCV and GCV, whereas plant height, plant spread and 1000 seed weight registered only low GCV and indicated that there is limited scope for improvement. These findings are in line with earlier reports of Patil *et al.* (2008) [23].

The genotypic coefficient of variation provides help to measure the genetic variability in a character, but it does not offer full scope to estimate the variation that is heritable or environmental. Hence, along with PCV and GCV estimates, the estimation of heritability and genetic advance becomes necessary. 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. The ratio of genotypic variance to total variance is known as heritability in broad sense (Hanson *et al.*, 1956) [9]. The characters with high heritability in broad sense indicated that large proportion of phenotypic variance was attributable to the genotypic variance and were less influenced by environment. Hence, selection can bring worthwhile improvement in those characters (Meena *et al.*, 2016) [18]. Genetic advance is still more useful estimate because heritability estimates may not provide clear predictability of the breeding value. Therefore, 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) [11].

High heritability (>60%) coupled with high genetic advance as % of mean (>20%) was observed for days to 50% flowering, no. of fruits per plant, fruit length, fruit diameter, average dry fruit weight, no. of seeds per fruit and dry fruit yield per plant indicating the predominance of additive gene action and hence direct phenotypic selection is useful with respect to these traits. These results were in line with results of earlier findings of Arup *et al.* (2011) [2] for days to 50% flowering; Rajyalakshmi and Vijayapadma (2012) [24] for number of fruits per plant and fruit length; Gupta *et al.* (2009) [8] for fruit diameter and average dry fruit weight; Suryakumari *et al.* (2010) [30] for number of seeds per fruit and Janaki *et al.* (2015) [10] for dry fruit yield per plant.

High heritability coupled with moderate genetic advance as % of mean was observed for plant height and plant spread, whereas moderate heritability coupled with moderate genetic advance as % of mean was registered for no. of primary branches per plant, days to fruit maturity and no. of seeds per fruit. These results indicating the role of additive and non additive gene action in the expression of these characters and further improvement of these characters would be easier through mass selection, progeny selection or any modified selection procedure aiming to exploit the additive gene effects rather than simple selection (Dhana Lakshmi, 2011) [5]. Similar results were also reported by Uma Jyothi *et al.* (2011) [32] and Meena *et al.* (2016) [18].

Conclusion

The present study can be concluded that significant differences were observed among the genotypes for all the traits indicating the presence of wide range of variability in the genotypes. The phenotypic coefficient of variation (PCV) was slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the characters indicating the some degree of environment influence on their genetic expression. The characters *viz.* no. of fruits per plant, no. of seeds per fruit and dry fruit yield per plant exhibited high values of PCV, GCV and high heritability coupled with high genetic advance as % of mean suggesting that existence of wide range of genetic variability, broad genetic base, less environmental influence, predominance of additive gene action and making the simple selection more effective for their further improvement.

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Table 1: Salient features of parents used in Line × Tester analysis of chilli

S. No	Parents	Features
Lines	1. LCA 504	Drought resistant, highly pungent
	2. LCA 615	High yielding line with parrot green fruits
	3. LCA 446	Bold pod, high colour and oleoresin
	4. LCA 466	Bold and long pod, high colour and oleoresin
	5. LCA 442	Bold and long pod, high colour and mild pungent
	6. LCA 654	Medium bold, shiny fruit surface, light green in colour
	7. LCA 607	Light green pod, profuse branching
	8. LCA 655	Dual purpose variety, bold light green pod
	9. LCA 355	High colour with wrinkled surface
Testers	1. G4	Dark green (olive green) fruits, virus resistant
	2. LCA 678	More primary branches, semi erect plant habit
	3. LCA 453	Bold pod, erect growth habit
	4. LCA 703-2	Virus resistant, dark green fruits
	5. LCA 705-2	More no. of fruits, shiny dry pod
	6. LCA 315	Virus resistant, fruits are long and dark green
Checks	1. Indam 5	IndoAmerican Hybrid Seeds (India) Pvt.Ltd. (IAHS)
	2. Tejaswini	Maharashtra Hybrid Seeds Co.Ltd. (MAHYCO)

Table 2: Analysis of variance for yield and its component characters in chilli (*Capsicum annum L.*)

S. No.	Characters	Mean Sum of Squares		
		Replications	Treatments	Error
1	Plant height (cm)	38.02	253.36**	23.13
2	Plant spread (cm)	54.44	191.81**	27.89
3	No. of primary branches per plant	0.15	0.71**	0.18
4	Days to 50 % flowering	2.80	39.65**	2.16
5	Days to fruit maturity (red)	14.89	60.69**	12.88
6	No. of fruits per plant	1207.15	11584.90**	1053.79
7	Fruit length (cm)	0.49	6.46**	0.45
8	Fruit diameter (cm)	0.00	0.14**	0.01
9	Dry fruit weight (g)	0.03	0.14**	0.01
10	Fruit yield (g/plant)	53.05	7882.51**	601.5
11	No. of seeds per fruit	260.34	539.22**	88.22
12	Seed weight (g/1000 seed)	0.67	1.35**	0.36

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

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

Character	Mean	Range	GCV (%)	PCV (%)	h ² (b)	h ² (b) %	GA @5%	GAM @ 5%
Plant height (cm)	91.37	74.57 - 109.77	9.59	10.94	0.77	76.83	15.82	17.31
Plant spread (cm)	88.41	70.93-106.70	8.36	10.27	0.66	66.20	12.39	14.01
No. of primary branches per plant	4.18	3.03-5.23	10.13	14.26	0.50	49.43	0.62	14.81
Days to 50 % flowering	30.10	22.67 - 38.00	11.75	12.72	0.85	85.25	6.73	22.35
Days to fruit maturity (red)	60.42	48.67 - 69.33	6.61	8.88	0.55	55.29	6.12	10.12
No. of fruits per plant	230.41	124.93-447.03	25.71	29.32	0.77	76.91	107.04	46.46
Fruit length (cm)	11.04	7.54 -15.18	12.82	14.18	0.82	81.63	2.64	23.89
Fruit diameter (cm)	1.42	0.98 - 2.08	14.35	16.03	0.80	80.00	0.38	26.49
Dry fruit weight (g)	1.25	0.75 - 1.83	16.58	18.65	0.80	80.00	0.38	30.36
Fruit yield (g/plant)	225.29	151.93 - 328.53	21.86	24.42	0.80	80.13	90.68	40.25
No. of seeds per fruit	68.32	41.80 - 90.47	17.95	22.61	0.63	63.01	20.05	29.35
Seed weight (g/1000 seed)	6.38	5.05 - 7.74	9.03	13	0.48	47.82	0.83	12.93

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 % of mean (GAM)

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