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## Genetic variability, heritability and genetic advance for quantitative traits in paprika (*Capsicum annuum* L.)

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**Abstract**

The present investigation was carried out during kharif 2016-17 at Horticultural Research Station, Lam, and Guntur with 44 genotypes of paprika (*Capsicum annuum* L.) in a randomized block design with two replications to estimate the genetic variability, heritability and genetic advance for thirteen 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 number of fruits per plant, fruit diameter, number of seeds per fruit, weight of seeds per fruit, 1000 seed weight and dry fruit 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 plant height, plant spread, number of primary branches per plant and days to 50% flowering indicating the predominance of additive gene action making the simple selection more effective.

**Keywords:** *Capsicum annuum*, GCV, PCV, Heritability, Genetic advance

**Introduction**

Paprika (*Capsicum annuum* L.  $2n = 24$ ) is one of the most important commercial vegetable as well as spice crops grown all over the world. The genus *Capsicum* belongs to family Solanaceae comprises of about 20 to 30 species of the new world tropics and subtropics and native to tropical areas of the Western Hemisphere, including Mexico, Central America, South America, and West Indies. Paprika, a form of chilli is mainly valued for its high colour, low or no pungency and oleoresins. In chilli, three major products viz., paprika, oleoresins and dried chilli (both in whole and powder form) are traded in the world market. The pungent principle of paprika is capsaicin, an acid amide of Vanillylamine. They are widely used in curry powder, paste, pickles, sauces and ketchups for its characteristic pungency, color and aroma (Shiva *et al.*, 2006) [31].

Globally, chilli and paprika (dry) are grown on a total area of 1.94 million hectares with global production of 3.35 million tonnes. The global productivity of chilli and paprika (dry) is 1.73 metric tonnes/ha (Kumari *et al.*, 2014) [16], and the value of the total chilli and paprika is estimated at 3.42 million USD. India is the world's leading producer occupying an area of 0.83 million hectares with a production of 1.8 million tonnes and productivity of 2MT/ha (NHB, 2016) [24].

Chilli besides imparting pungency and red colour to dishes, is also rich source of vitamin C, A and E and assists in good digestion. The vitamin C content (150-200 mg/100g) of chilli is the highest among all the vegetables. It has also acquired a great importance because of the presence of 'oleoresin', which permits better distribution of color and flavor in foods. There is considerable demand for paprika powder in the western countries. There is a great demand for the natural colour from paprika fruits and is used in processed foods in place of synthetic colours. The demand for paprika oleoresin as a coloring agent has increased in international market especially in Europe and USA due to ban on artificial coloring substances (Joshi *et al.*, 1995) [12].

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.

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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) [15]. 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) [38]. 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) [11].

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 44 chilli genotypes.

### Materials and Methods

The experiment was carried out with 44 genotypes (Table 1) of paprika at Horticultural Research Station, Lam, Guntur, and 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 44 germplasm lines were raised in a Randomized Block Design with two replications. The nursery was raised during first week of August 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), Plant spread (cm), number of primary branches per plant, days to 50% flowering, day to maturity, number of fruits per plant, fruit length (cm), fruit diameter (cm), fruit pedicel length (cm), number of seeds per fruit, weight of seeds per fruit (g), 1000 seed weight (g) 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) [26]. Genotypic and Phenotypic correlation coefficients of variability were estimated according to the Burton and Devane (1953) [7] by using the following formulae.

$$\text{Genotypic variance (V}_g \text{ or } \sigma^2_g) = \frac{\text{Genotype MSS-Error MSS}}{r}$$

$$\text{Environmental variance (V}_e \text{ or } \sigma^2_e) = \frac{\text{Error MSS}}{r}$$

Where,

r = number of replications

Phenotypic variance (V<sub>p</sub> or σ<sup>2</sup><sub>p</sub>) = V<sub>g</sub> + V<sub>e</sub>

$$\text{PCV} = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

$$\text{GCV} = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

Where,

σ<sub>g</sub><sup>2</sup> = Genotypic variance

σ<sub>e</sub><sup>2</sup> = Environment variance

σ<sub>p</sub><sup>2</sup> = Phenotypic variance

X = General mean

PCV and GCV were classified as shown below (Sivasubramanian and Menon 1973) [33].

Less than 10% = Low

10-20% = Moderate

More than 20% = High

Heritability in broad sense was estimated as per the formulae suggested by Allard (1960) [2].

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

Where,

h<sup>2</sup>(b) = Heritability estimates in broad sense

σ<sub>g</sub><sup>2</sup> = Genotypic variance

σ<sub>p</sub><sup>2</sup> = Phenotypic variance

The heritability (h<sup>2</sup>(b)) was categorised as suggested by Johnson *et al.* (1955) [11].

0-30% = Low

31-60% = Medium

61% and above = High

This was estimated as per formula proposed by Allard (1960) [2].

$$\text{GA} = Kx \sigma_p \times h^2(b)$$

Where,

K = Selection differential at 5 per cent selection intensity which accounts to a constant value 2.06

h<sup>2</sup>(b) = Heritability in broad sense

σ<sub>p</sub> = Phenotypic standard deviation

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

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

Where,

GA = genetic advance

X̄ = general mean of the character

The genetic advance as per cent over mean was categorized as mentioned below (Johnson *et al.*, 1955) [11].

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 results are in conformity with earlier reports of Nandadevi and Hosmani (2003) [23], Vani *et al.* (2007) [37], Farhad *et al.* (2008) [8], Patil *et al.* (2008), Jyothi *et al.* (2008) [13], Tembhumne *et al.* (2008) [36], Gupta *et al.* (2009) [9], Kumari *et al.* (2010) [18], Berhanu *et al.* (2011) [6], Arup *et al.* (2011) [4], Kumar *et al.* (2012) [17] and Lakshmi and Padma (2012) [19], Tasso *et al.* (2014) [35], Pandit and Ahikary (2014) [25], Vijaya *et al.* (2014) [38], Janaki *et al.* (2015) [10], and Leeladhar *et al.* (2016) [20]. The extent of variability with respect to 13 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 dry fruit yield per plant (82.00 -220.00g), number of fruits per plant (90.50-214.20), number of seeds per fruit (37.30-154), plant spread (57.40-176cm), plant height (54.80-119cm), days to maturity (87-163.50), days to 50 per cent flowering (41.50-65.50). Relatively low range of variability observed for weight of seeds per fruit 90.215-0.355g), number of primary branches per plant (2.30-4.20), fruit pedicel length (2.15-4.55cm), fruit diameter (2.55-9.70cm), fruit length (5.70-16.80cm) and 1000 seed weight (2.21-18.10 g).

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. The estimates of PCV and GCV were high for number of fruits per plant (21.84 and 20.90%), fruit diameter (26.58 and 25.55%), number of seeds per fruit (36.45 and 33.95%), weight of seeds per fruit (46 and 44.14%), 1000 seed weight (50.14 and 48%) and dry fruit yield per plant 27.48 and 25.43%) 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 Pandit and Adhikary (2014) [25], Vijaya *et al.* (2014) [38], Janaki *et al.* (2015a) [15], Satish *et al.* (2016) [29] for number of fruits per plant, fruit diameter and number of seeds per fruit, dry fruit yield per plant and Shirshat *et al.* (2007) [30], Vani *et al.* (2007) [37], Singh *et al.* (2009) and Ashish *et al.* (2015) [5] for weight of seeds per fruit and Smitha and Basvaraja (2006) [34], Amit *et al.* (2014) [3] and Ajith and Manju (2015) [1] for 1000 seed weight.

The estimates of PCV and GCV were moderate for plant spread (16.32 and 12.40%), days to maturity (16.51 and 14.28%) and fruit pedicel length (17.93 and 14.79%). Similar observations were earlier reported by Kumar *et al.* (2012) [16], Kranthi *et al.* (2016) [14] for plant spread and Sarkar *et al.* (2009), Sandeep *et al.* (2008) [28], Sharma *et al.* (2010), Pandit

and Adhikary (2014) [25], Priyanka and Madhvi (2016) for fruit pedicel length.

The estimates of PCV and GCV were high and moderate respectively for fruit length (20.20 and 18.71%). These results are in conformity with findings of earlier works of Janaki *et al.* (2015a) [15], and Meena *et al.* (2016) [22].

High heritability coupled with high genetic advance as per cent of mean was observed for all the characters except for plant height, plant spread, number of primary branches per plant and 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 Sandeep *et al.* (2008) [28] for days to maturity and Mahantesh *et al.* (2013) [21], Amit *et al.* (2014), Vijaya *et al.* (2014) [38], Janaki *et al.* (2015a) [15], Satish *et al.* (2016) [29], Kranthi *et al.* (2016) [14] for number of fruits per plant and Mahantesh *et al.* (2013) [21], Amit *et al.* (2014) [3], Vijaya *et al.* (2014) [38], Rosamaina *et al.* (2016) [27] for fruit length and Mahantesh *et al.* (2013) [21], Amit *et al.* (2014) [3], Janaki *et al.* (2015a) [15], Satish *et al.* (2016) [29] for fruit diameter and Mahantesh *et al.* (2013) [21], Amit *et al.* (2014) [3], Vijaya *et al.* (2014) [38], Janaki *et al.* (2015a) [15], Satish *et al.* (2016) [29], for number of fruits per plant and Shirshat *et al.* (2007) [30], Vani *et al.* (2007) [37], Singh *et al.* (2009) and Ashish *et al.* (2015) [5] for weight of seeds per fruit and Smitha and Basvaraja (2006a) [34], Amit *et al.* (2014) [3] and Ajith and Manju (2015) 2014 [1] for 1000 seed weight and Pandit and Adhikary (2014) [25], Vijaya *et al.* (2014) [38], Janaki *et al.* (2015) [15], Satish *et al.* (2016) [29] for dry fruit yield per plant.

High heritability coupled with moderate genetic advance as per cent of mean was observed for plant height, plant spread, number of primary branches per plant and 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 Tembhumne *et al.* (2008) [36] for plant height and Sandeep *et al.* (2008) [28] and Kranthi *et al.* (2016) [14] for number of primary branches per plant and Mahantesh *et al.* (2013) [21] for days to 50 percent flowering.

The findings indicate that there exists adequate genotypic variation in the genotypes for number of fruits per plant, fruit diameter, number of seeds per fruit, weight of seeds per fruit, 1000 seed weight 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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**Table 1:** Source of the paprika genotypes (*Capsicum annum L.*)

Treatment	Accession Number	Treatment	Accession Number	Source
T <sub>1</sub>	LCA 445	T <sub>23</sub>	LCA 465	HRS, Lam farm, Guntur
T <sub>2</sub>	LCA 447	T <sub>24</sub>	LCA 475	HRS, Lam farm, Guntur
T <sub>3</sub>	LCA 439	T <sub>25</sub>	LCA 488	HRS, Lam farm, Guntur
T <sub>4</sub>	LCA 442	T <sub>26</sub>	LCA 499	HRS, Lam farm, Guntur
T <sub>5</sub>	LCA 430	T <sub>27</sub>	LCA 506	HRS, Lam farm, Guntur
T <sub>6</sub>	LCA 457	T <sub>28</sub>	LCA 503	HRS, Lam farm, Guntur
T <sub>7</sub>	LCA 443	T <sub>29</sub>	LCA 490	HRS, Lam farm, Guntur
T <sub>8</sub>	LCA 437	T <sub>30</sub>	LCA 501	HRS, Lam farm, Guntur
T <sub>9</sub>	LCA 453	T <sub>31</sub>	LCA 504	HRS, Lam farm, Guntur
T <sub>10</sub>	LCA 450	T <sub>32</sub>	LCA 510	HRS, Lam farm, Guntur
T <sub>11</sub>	LCA 441	T <sub>33</sub>	LCA 510	HRS, Lam farm, Guntur
T <sub>12</sub>	LCA 425	T <sub>34</sub>	LCA 511	HRS, Lam farm, Guntur
T <sub>13</sub>	LCA 440	T <sub>35</sub>	LCA 512	HRS, Lam farm, Guntur
T <sub>14</sub>	LCA 446	T <sub>36</sub>	LCA 513	HRS, Lam farm, Guntur
T <sub>15</sub>	LCA 470	T <sub>37</sub>	Warangal chappatta single patti	HRS, Lam farm, Guntur
T <sub>16</sub>	LCA 436	T <sub>38</sub>	Warangal chappatta double patti	HRS, Lam farm, Guntur
T <sub>17</sub>	LCA 466	T <sub>39</sub>	Byadagi kaddi	HRS, Lam farm, Guntur
T <sub>18</sub>	LCA 472	T <sub>40</sub>	Byadagi dabbi	HRS, Lam farm, Guntur
T <sub>19</sub>	LCA 476	T <sub>41</sub>	Kt-1	HRS, Lam farm, Guntur
T <sub>20</sub>	LCA 480	T <sub>42</sub>	Jangareddy gudem local	HRS, Lam farm, Guntur
T <sub>21</sub>	LCA 482	T <sub>43</sub>	LCA 436	HRS, Lam farm, Guntur
T <sub>22</sub>	LCA 498	T <sub>44</sub>	LCA 424	HRS, Lam farm, Guntur

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

S.No.	Character	Mean sum of squares		
		Replications	Genotypes	Error
1	Plant height (cm)	0.1641	257.1176**	122.3585
2	Plant spread (cm)	12.4501	698.0582**	187.3496
3	Number of primary branches per plant	0.0223	0.1720**	0.0495
4	Days to 50 per cent flowering	0.4091	52.4641**	12.5951
5	Days to maturity	405.9204	840.9797**	121.3391
6	Number of fruits per plant	78.0956	2217.2776**	97.2712
7	Fruit length (cm)	2.1018	10.3219**	0.7897
8	Fruit diameter (cm)	0.1392	2.9213**	0.1155
9	Fruit pedicel length (cm)	0.2005	0.6842**	0.1300
10	Number of seeds per fruit	192.6368	1204.1255**	85.2880
11	Weight of seeds per fruit (g)	0.0018	0.0978**	0.0040
12	1000 seed weight (g)	1.7388	16.8606**	0.7356
13	Dry fruit yield per plant (g)	0.1023	2316.4702**	178.9162

\*: Significant at 5 per cent level;

\*\*: Significant at 1 per cent level

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

S.No.	Character	Mean	Range	V <sub>g</sub>	V <sub>p</sub>	GCV (%)	PCV (%)	h <sup>2</sup> (b) (%)	GA @ 5%	GAM @ 5%
1	PH	88.95	54.80- 119	67.38	189.74	9.23	15.48	35.51	10.08	11.33
2	PS	128.89	57.40-176	255.35	442.70	12.40	16.32	57.68	25	19.40
3	NPBP	3.57	2.30-4.20	0.06	0.11	6.92	9.30	55.31	0.38	10.60
4	DFF	59.97	41.50-65.50	19.93	32.53	7.44	9.51	61.28	7.20	12
5	DM	132.87	87-163.50	359.82	481.16	14.28	16.51	74.78	33.79	25.43
6	NFP	155.75	90.50-214.20	1060.00	1157.27	20.90	21.84	91.59	64.19	41.21
7	FL	11.67	5.70-16.80	4.77	5.56	18.71	20.20	85.79	4.17	35.69
8	FD	4.63	2.55-9.70	1.40	1.52	25.55	26.58	92.39	2.35	50.60
9	FPL	3.55	2.15-4.55	0.28	0.41	14.79	17.93	68.07	0.89	25.14
10	NSF	69.66	37.30-154	559.42	644.71	33.95	36.45	86.77	45.39	65.15
11	WSF	0.490	0.21-1.35	0.05	0.05	44.14	46	92.06	0.43	87.24
12	1000 SW	5.91	2.21-18.10	8.06	8.80	48.00	50.14	91.64	5.60	94.65
13	DFYP	128.55	82-220	1068.78	1247.69	25.43	27.48	85.66	62.33	48.48

Note :

PH – Plant height (cm), PS-Plant spread (cm), NPBP – Number of primary branches per plant, DFF – Days to 50 per cent flowering, DM –Days to maturity, NFP – Number of fruits per plant, FL – Fruit length (cm), FD – Fruit diameter (cm), FPL- Fruit pedicel length (cm), NSF – Number of seeds per fruit, WSP- Weight of seeds per fruit (g), 1000 SW- 1000 Seed weight (g), DFYP – Dry fruit yield per plant (g).

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