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## Assessment of genetic variability, heritability and genetic advance for quantitative, qualitative traits and ChLCV resistance in chilli (*Capsicum annum* L.)

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#### Abstract

An investigation was carried out during *kharif* 2017-18 at College of Horticulture, Venkataramannagudem with 53 genotypes of chilli (*Capsicum annum* L.) in a randomized block design with three replications to estimate the genetic variability, heritability and genetic advance for quantitative traits and chilli leaf curl virus resistance. 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 plant height, number of fruits per plant, fruit length, fruit width, fruit weight, number of seeds per fruit, red ripe fruit yield per plant, dry fruit yield per plant, capsaicin content, oleoresin content, ascorbic acid content, colour value, ChLCV disease incidence and disease severity 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 more effective. High heritability coupled with high genetic advance as per cent mean indicates existence of additive gene action which was observed in plant height, plant spread, number of primary branches per plant, days to 50 per cent flowering, number of fruits per plant, fruit length, fruit width, fruit weight, number of seeds per fruit, seed weight, fresh to dry recovery, capsaicin content, oleoresin content, ascorbic acid content, colour value, ChLCV disease incidence and disease severity. Hence, direct selection could be effective for desired genetic improvement for these traits.

**Keywords:** *Capsicum annum*, GCV, PCV, heritability, genetic advance

#### Introduction

Chilli (*Capsicum annum* L.) an important spice cum vegetable crop, is extensively cultivated in India both under rainfed and irrigated conditions. Chilli belongs to the genus *Capsicum* of family Solanaceae. It has originated in Mexico, Southern Peru and Bolivia. There are mainly five cultivated *Capsicum* spp. viz., *C. annum*, *C. baccatum*, *C. chinense*, *C. frutescens*, and *C. pubescens* of which *Capsicum annum* is the dominant species world over and could be broadly classified into non-pungent (sweet pepper) and pungent (chilli or hot pepper) based on their level of pungency (Bosland and Votava, 2000) [6]. In India, it is an important ingredient in daily cuisine and is a rich source of vitamin A, E, C and potassium. It is also a good source of oleoresin which has good export potential.

Pepper (chilli and sweet) market types prevalent in India can broadly be grouped into the following 4 categories: (i) fresh market (green, red, multi-color whole fruits), (ii) fresh processing (sauce, paste, canning, pickling), (iii) dried spice (whole fruits and powder), and (iv) industrial extracts (oleoresin, capsaicinoids and carotenoids). Besides conventional nutritional food uses, a number of versatile food (paprika oleoresin) and non-food (defense, spiritual, ethnobotanical) uses of chillies are known Meghavansi *et al.* (2010) [16]. Among the exported spices from India, export of dry chilli and its derived products stand first in terms of quantity and second in terms of total value after mints (menthol, menthol crystal and mint oils). Malaysia is the largest importer of Indian chilli (~30%), followed by other traditional importers like Bangladesh (~20%), Sri Lanka (~15%), USA (~9%) and UAE (~8%).

India is the largest producer, consumer and exporter of chilli with an annual production of 2.09 million tonnes from 0.84 million ha (National Horticulture Board, 2016-17) [18]. According to an estimate for 2016, in India, chillies (dry-red and fresh-green fruits) were cultivated in 797,029 ha with a total production of 1.3 million tonnes of dry fruits and 679,17 tonnes of

tonnes of fresh fruits. Average yield of dry chilli harvest was around 1.7 t/ha compared to that of 8.4 t/ha for green chilli (FAOSTAT, 2016) [8]. In India, the states of Andhra Pradesh, Telangana, Karnataka, Maharashtra, Orissa and Tamil Nadu account for more than 75% of the area and production of chilli.

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) [12]. Improvement in any crop is proportional to the magnitude of its genetic variability present in germplasm. Greater the variability in a population, greater the chance for effective selection for desirable types. 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, yield components and quality characters in 53 chilli genotypes.

### Materials and Methods

The experiment was carried out with 53 chilli genotypes (Table 1) at Collage of Horticulture, Venkataramannagudem, Dr. YSR Horticultural University, Andhra Pradesh, India during 2017 -2018 in a randomized block design with three replications. Each genotype was raised in 3.6 m × 1.8 m plot size with a spacing of 60 × 45 cm accommodating 24 plants per plot. The crop was grown with standard package of practices. Five competitive plants were selected at random for recording the observations on 20 characters *viz.*, plant height (cm), plant spread (cm<sup>2</sup>), number of primary branches per plant, days to 50 per cent flowering, days to 50 per cent ripening, number of fruits per plant, fruit length (cm), fruit width (cm), fruit weight (cm), number of seeds per fruit, seed weight (g/1000 seed), red ripe fruit yield per plant, dry fruit yield per plant, fresh to dry recovery (%), capsaicin content (%), oleoresin content (%), ascorbic acid content (mg/100g), colour (ASTA), ChLCV disease incidence (%) and disease severity (%). 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) [20]. Genotypic and phenotypic correlation coefficients of variability were estimated according to the Burton and Devane (1953) [7] 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

$\sigma_g^2$  = Genotypic variance = (Mean sum of squares due to genotypes – Error mean sum of squares) ÷ Replications  
 $\sigma_p^2$  = Phenotypic variance =  $\sigma_g^2 + \sigma_e^2$   
 $\sigma_e^2$  = Environmental variance = (Error mean sum of squares) ÷ Replications  
 X = General mean

PCV and GCV were classified as suggested by Sivasubramanian and Menon (1973) [27].

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) [1].

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

The heritability ( $h^2_{(b)}$ ) was categorized as suggested by Johnson *et al.* (1955) [11].

0-30% = Low

31-60% = Medium 61%

and above = High Genetic advance (GA) was estimated as per formula given by Allard (1960) [1]

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

Where,

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

$\sigma_p$  = Phenotypic standard deviation

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

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

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

Less than 10 % = Low

10-20 % = Moderate

More than 20 % = High

### Results and Discussion

In the present investigation, estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ( $h^2_{(b)}$ ) in broad sense and genetic advance as per cent of mean (GAM) were calculated for 53 genotypes.

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 Farhad *et al.* (2008) [9], Singh and Singh, (2011) [25], Krishnamurthy *et al.* (2013) [13]. The extent of variability with respect to 20 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 performance of genotypes for different traits indicated that the high range of variability was recorded for plant height (39.40 to 109.33 cm), plant spread (47.05 to

108.07 cm<sup>2</sup>), days to 50 per cent flowering (27.33 to 52.67), days to 50 per cent ripening (68.67 to 97.67), number of fruits per plant (11.44 to 798.67), number of seeds per fruit (24.40 to 153.62), red ripe fruit yield per plant (238.89 to 1028.44 g), dry fruit yield per plant (64.67 to 312.49 g), ascorbic acid content (22.22 to 198.88 mg/100g), colour value (36.60 to 280.87 ASTA), ChLCV disease incidence (6.14 to 90.00 per cent) and disease severity (0.66 to 86.00 per cent). Relatively low range of variability was observed in respect of number of primary branches per plant (2.20 to 5.33), fruit length (2.15 to 14.48 cm), fruit width (2.09 to 22.42 cm), fruit weight (0.52 to 72.47 g), seed weight (3.38 to 10.07g), fresh to dry recovery (19.86 to 36.33 per cent), capsaicin content (0.03 to 1.84 per cent) and oleoresin content (6.80 to 17.75 per cent) and these findings are in accordance with those of Munshi *et al.* (2010) [17] and Arunkumar *et al.* (2013) [2]. The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters (Table 3) 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) [17], Krishnamurthy *et al.* (2013) [13] and Sandeep *et al.* (2013) [23]. The estimates of PCV and GCV were high for plant height (22.76 to 20.98 per cent), number of fruits per plant (62.31 to 58.68 per cent), fruit length (32.94 to 32.64 per cent), fruit width (72.11 to 71.80 per cent), fruit weight (187.64 to 187.53 per cent), number of seeds per fruit (33.64 to 33.17 per cent), red ripe fruit yield per plant (32.12 to 24.63 per cent), dry fruit yield per plant (35.16 to 25.27 per cent), capsaicin content (80.64 to 80.49 per cent), oleoresin content (21.58 to 21.23 per cent), ascorbic acid content (50.60 to 50.36 per cent), colour value (45.90 to 45.62 per cent), ChLCV disease incidence (21.85 to 21.07 per cent) and disease severity (31.31 to 30.80 per cent) 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 Farhad *et al.* (2008) [9] and Rajyalakshmi and Vijayapadma (2012) [21] for number of fruits per plant, Smitha and Basvaraja (2007) [28], Suryakumari *et al.* (2010) [29] for number of seeds per fruit, Gupta *et al.* (2009) [10], Singh *et al.* (2009) [26] for fruit diameter, average dry fruit weight and Padhar and Zaveri (2010) [19], Arup *et al.* (2011) [3], Kumar *et al.* (2012) [14], Sandeep *et al.* (2013) [23] for yield per plant.

The estimates of PCV and GCV were moderate for, plant spread (18.31 to 16.09 per cent), number of primary branches per plant (17.88 to 14.49 per cent), days to 50 per cent flowering (14.28 to 12.62 per cent), seed weight (19.71 to 19.47 per cent) and fresh to dry recovery (12.65 to 12.50 per cent). Similar observations were earlier reported by Bendale *et al.* (2006) [4] and Bharadwaj *et al.* (2007) [5] for days to 50 per cent flowering. The estimates of PCV and GCV were low for days to 50 per cent ripening (8.66 to 6.50 per cent). High heritability coupled with high genetic advance as per cent of mean was observed for plant height (84.90 per cent, 39.82), plant spread (77.30 per cent, 29.13), number of primary branches per plant (65.70 per cent, 24.20), days to 50 per cent flowering (78.20 per cent, 23.00), number of fruits per plant (88.70 per cent, 113.83), fruit length (98.20 per cent, 66.63), fruit width (99.10 per cent, 147.28), fruit weight (100.00 per cent, 386.07), number of seeds per fruit (97.20 per cent, 67.36), seed weight (97.60 per cent, 67.36), fresh to dry recovery (97.60 per cent, 25.44), capsaicin content (99.60 per cent, 165.48), oleoresin content (96.70 per cent, 43.00), ascorbic acid content (99.00 per cent, 103.23), colour value (98.80 per cent, 93.41), ChLCV disease incidence (93.00 per cent, 41.87) and disease severity (96.70 per cent, 62.40). These results are in line with results of earlier works of Rajyalakshmi and Vijayapadma (2012) [21] for plant height, number of fruits per plant and fruit length, Munshi *et al.* (2010) [17] for number of primary branches per plant, Gupta *et al.* (2009) [10] for fruit diameter and average dry fruit weight, Krishna *et al.* (2007) [12], Meena and Bahadur (2014) [15] for per cent fruit set and Suryakumari *et al.* (2010) [29] for number of seeds per fruit.

High heritability coupled with moderate genetic advance as per cent of mean was observed for days to 50 per cent ripening (56.30 per cent, 10.04) was observed for this trait indicating the preponderance of non-additive gene action and further improvement of this character would be possible through heterosis breeding rather than simple selection. These results are in agreement with Kumar *et al.* (2012) [14] and Rosmaina *et al.* (2016) [22].

Moderate heritability coupled with high genetic advance as per cent of mean was observed for red ripe fruit yield per plant (58.88 per cent, 38.90) and dry fruit yield per plant (51.70 per cent, 37.41) reveals the operation of additive gene action and moderate heritability may be due to high environmental effects and suggesting for the improvement of yield traits through selection as well as their exploitation through combination breeding. Similar results were reported by Gupta *et al.* (2009) [10], Suryakumari *et al.* (2010) [29] and Sharma *et al.* (2010) [24].

**Table 1:** Germplasm accessions of chilli (*Capsicum annum L.*)

Treatments	Accession number or Varieties	Source
T <sub>1</sub>	IHR 1485	Indian Institute of Horticultural Research, Bengaluru
T <sub>2</sub>	IHR 1732	IIHR, Bengaluru
T <sub>3</sub>	IHR 2452	IIHR, Bengaluru
T <sub>4</sub>	IHR 2596	IIHR, Bengaluru
T <sub>5</sub>	IHR 2900	IIHR, Bengaluru
T <sub>6</sub>	IHR 3014	IIHR, Bengaluru
T <sub>7</sub>	IHR 3024	IIHR, Bengaluru
T <sub>8</sub>	IHR 3310	IIHR, Bengaluru
T <sub>9</sub>	IHR 3315	IIHR, Bengaluru
T <sub>10</sub>	IHR 3443	IIHR, Bengaluru
T <sub>11</sub>	IHR 3447	IIHR, Bengaluru
T <sub>12</sub>	IHR 3448	IIHR, Bengaluru
T <sub>13</sub>	IHR 3449	IIHR, Bengaluru

T <sub>14</sub>	IHR 3455	IIHR, Bengaluru
T <sub>15</sub>	IHR 3478	IIHR, Bengaluru
T <sub>16</sub>	IHR 3517	IIHR, Bengaluru
T <sub>17</sub>	IHR 3587	IIHR, Bengaluru
T <sub>18</sub>	IHR 3915	IIHR, Bengaluru
T <sub>19</sub>	IHR 4597	IIHR, Bengaluru
T <sub>20</sub>	IHR 4595	IIHR, Bengaluru
T <sub>21</sub>	IHR 4598	IIHR, Bengaluru
T <sub>22</sub>	IHR 4600	IIHR, Bengaluru
T <sub>23</sub>	IHR 4601	IIHR, Bengaluru
T <sub>24</sub>	IHR 4602	IIHR, Bengaluru
T <sub>25</sub>	IHR 4603	IIHR, Bengaluru
T <sub>26</sub>	IHR 4604	IIHR, Bengaluru
T <sub>27</sub>	IHR 4605	IIHR, Bengaluru
T <sub>28</sub>	IHR 4606	IIHR, Bengaluru
T <sub>29</sub>	IHR 4607	IIHR, Bengaluru
T <sub>30</sub>	IHR 4608	IIHR, Bengaluru
T <sub>31</sub>	IHR 4609	IIHR, Bengaluru
T <sub>32</sub>	IHR 4610	IIHR, Bengaluru
T <sub>33</sub>	IHR 4611	IIHR, Bengaluru
T <sub>34</sub>	IHR 4612	IIHR, Bengaluru
T <sub>35</sub>	IHR 4031	IIHR, Bengaluru
T <sub>36</sub>	IHR 4516	IIHR, Bengaluru
T <sub>37</sub>	IHR 4592	IIHR, Bengaluru
T <sub>38</sub>	IHR 4593	IIHR, Bengaluru
T <sub>39</sub>	IHR 4594	IIHR, Bengaluru
T <sub>40</sub>	G3	Horticultural Research Station, Lam, Guntur
T <sub>41</sub>	G4	HRS, Lam farm, Guntur
T <sub>42</sub>	G5	HRS, Lam farm, Guntur
T <sub>43</sub>	LCA 206	HRS, Lam farm, Guntur
T <sub>44</sub>	LCA 235	HRS, Lam farm, Guntur
T <sub>45</sub>	LCA 305	HRS, Lam farm, Guntur
T <sub>46</sub>	LCA 334	HRS, Lam farm, Guntur
T <sub>47</sub>	LCA 353	HRS, Lam farm, Guntur
T <sub>48</sub>	LCA 620	HRS, Lam farm, Guntur
T <sub>49</sub>	LCA 625	HRS, Lam farm, Guntur
T <sub>50</sub>	LCA 960	HRS, Lam farm, Guntur
T <sub>51</sub>	BhutJolokia	Tura, Meghalaya
T <sub>52</sub>	Meghalaya Local	Tura, Meghalaya
T <sub>53</sub>	CaliforniaWonder	Namdhari Seed Company

**Table 2:** Analysis of variance for yield, yield attributes, quality traits and ChLCV disease incidence in chilli

S. No	Character	Mean sum of Squares		
		Replications	Treatments	Error
1.	Plant height (cm)	28.54	601.62 **	33.62
2.	Plant spread (cm <sup>2</sup> )	43.86	336.19 **	30.03
3.	Number of primary branches per plant	0.34	0.87 **	0.12
4.	Days to 50 per cent flowering	11.84	74.03 **	6.29
5.	Days to 50 per cent ripening	31.13	104.82 **	21.56
6.	Number of fruits per plant	1830.81	41832.40 **	1706.66
7.	Fruit length (cm)	0.030	21.18 **	0.128
8.	Fruit width (cm)	0.26	34.01 **	0.09
9.	Fruit weight	0.22	423.80 **	0.17
10.	Number of seeds per fruit	32.36	2023.27 **	19.28
11.	Seed weight (g/1000 seed)	0.03	4.19 **	0.03
12.	Red ripe fruit yield (g/plant)	10125.08	72208.23 **	13671.31
13.	Dry fruit yield (g/plant)	1144.87	6320.75 **	1502.76
14.	Fresh to dry recovery (%)	0.58	37.53 **	0.30
15.	Capsaicin content (%)	0.00	0.18 **	0.00
16.	Oleoresin content (%)	0.35	16.83 **	0.18
17.	Ascorbic acid content (mg/100g)	49.88	6718.75 **	21.65
18.	Colour value (ASTA units)	29.57	6589.61 **	26.99
19.	ChLCV disease incidence (%)	29.24	965.32 **	23.45
20.	Disease severity (%)	10.49	847.14 **	9.38

\* Significant at 5 % level \*\* Significant at 1 % level

**Table 3:** Genetic parameters for yield, yield attributes, quality characters and ChLCV disease incidence in chilli

S. No	Character	General Mean	Range		Variance		PCV (%)	GCV (%)	h <sup>2</sup> (%)	G A	GAM
			Minimum	Maximum	P	G					
1.	Plant height(cm)	65.60	39.40	109.33	222.96	189.34	22.76	20.98	84.90	26.12	39.82
2.	Plant spread (cm <sup>2</sup> )	62.79	47.05	108.07	132.09	102.05	18.31	16.09	77.30	18.29	29.13
3.	Number of primary branches	3.44	2.20	5.33	0.38	0.25	17.88	14.49	65.70	0.83	24.20
4.	Days to 50% flowering	37.64	27.33	52.67	28.88	22.58	14.28	12.62	78.20	8.66	23.00
5.	Days to 50% ripening	81.07	68.67	97.67	49.32	27.75	8.66	6.50	56.30	8.14	10.04
6.	No of fruits/plant	197.09	11.44	798.67	15081.91	13375.25	62.31	58.68	88.70	224.36	113.83
7.	Fruit length(cm)	8.12	2.15	14.48	7.15	7.02	32.94	32.64	98.20	5.41	66.63
8.	Fruit width(cm)	4.68	2.09	22.42	11.40	11.31	72.11	71.80	99.10	6.90	147.28
9.	Fruit weight (g)	6.34	0.52	72.47	141.38	141.21	187.64	187.53	100.00	24.46	386.07
10.	Number of seeds per fruit	77.92	24.40	153.62	687.28	668.00	33.64	33.17	97.20	52.49	67.36
11.	Seed weight (g/1000 seed)	6.05	3.38	10.07	1.42	1.39	19.71	19.47	97.60	2.40	39.62
12.	Red ripe yield (g/plant)	567.19	238.89	1028.44	33183.62	19512.31	32.12	24.63	58.88	220.66	38.90
13.	Dry fruit yield (g/plant)	158.60	64.67	312.49	3108.76	1606.00	35.16	25.27	51.70	59.34	37.41
14.	Fresh to dry recovery (%)	28.19	9.86	36.33	12.71	12.41	12.65	12.50	97.60	7.17	25.44
15.	Capsaicin content (%)	0.31	0.03	1.83	0.06	0.06	80.64	80.49	99.60	0.51	165.48
16.	Oleoresin content (%)	11.10	6.80	17.75	5.74	5.55	21.58	21.23	96.70	4.77	43.00
17.	Ascorbic content (mg/100g)	93.83	22.22	198.88	2254.02	2232.37	50.60	50.36	99.00	96.86	103.23
18.	Colour value (ASTA)	102.52	36.60	280.87	2214.54	2187.54	45.90	45.62	98.80	95.76	93.41
19.	ChLCV disease incidence (%)	84.08	6.14	90.00	337.41	313.96	21.85	21.07	93.00	35.21	41.87
20.	Disease severity (%)	54.26	0.66	86.00	288.64	279.25	31.31	30.80	96.70	33.86	62.40

GCV-genotypic coefficients of variation, PCV-phenotypic coefficients of variation, h<sup>2</sup>-heritability, GAM (%) -genetic advance mean percentage

### Conclusion

The findings indicate that high PCV, GCV, heritability and GAM were observed for characters like plant height, number of fruits per plant, fruit length, fruit width, fruit weight, number of seeds per fruit, capsaicin content, oleoresin content, ascorbic acid content, colour value and ChLCV disease incidence suggesting predominance of additive gene action and lower influence of environmental factors in the expression of these traits with possibility for improvement through selection. These characters were governed by additive genes where selection will be rewarding for improvement of such traits.

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