

Variability and genetic divergence in paprika (*Capsicum annuum* L.)¹

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Abstract

Ninety four paprika (*Capsicum annuum*) accessions were evaluated for 17 characters for variability, heritability, genetic advance and genetic divergence at Lam, Guntur (Andhra Pradesh). Higher phenotypic and genotypic coefficient of variation (PCV and GCV) and heritability coupled with high genetic advance was observed for number of fruits plant⁻¹, fresh fruit yield plant⁻¹, dry fruit yield plant⁻¹, 100 seed weight, number of seeds fruit⁻¹ and capsanthin, capsaicin and oleoresin contents indicating the higher magnitude of variability for these traits and consequently more scope for their improvement through selection. Plant height, plant spread and fruit diameter exhibited moderate PCV and GCV estimates suggesting the possible role of environment in expression of these characters. Cluster analysis through Mahalanobis D² analysis classified the 94 genotypes into 10 clusters indicating considerable genetic diversity in the material studied.

Keywords: *Capsicum annuum*, genetic advance, genotypic coefficient of variation, heritability, paprika, phenotypic coefficient of variation.

There is need to develop a long term strategy for development of paprika (*Capsicum annuum* L.) in view of its increasing demand in the domestic and export sectors. Hence a genetic divergence study which is a basic requirement for effective selection, was undertaken along with an attempt to estimate genetic variability, heritability and genetic advance in the available germplasm of paprika at Andhra Pradesh Horticultural University, Horticultural Research Station, Lam, Guntur (Andhra Pradesh).

The material chosen for the investigation was a set of 94 paprika genotypes comprising of established varieties, advanced true breeding lines and local collections, collected and developed at Horticultural Research Station, Lam, Guntur. The experiment was laid out in a completely randomized block design with 94 paprika accessions as treatments during *kharif* 2005. Each treatment was randomly replicated thrice. Each treatment or a genotype in each replication was represented by a plot of four rows each of 5 m length. The crop

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Table 1. Genetic parameters in respect of quantitative traits in paprika germplasm

Character	Range		Geno- typic varia- tion σ^2_g	Pheno- typic varia- tion σ^2_v	Geno- typic coeffi- cient of variation (%)	Pheno- typic coefficient variation (%)	Broad sense heri- tability % (h ²)	Gene- tic ad- vance (%)	GA cent mean (%)
	Mean	Min. Max.							
Plant height (cm)	95.20	51.17(LCA445)	128.8(LCA449)	199.60	210.20	14.84	15.23	95.0	28.37 29.79
Plant spread (cm)	124.9	44.8(LCA442)	172.8(LCA433)	677.20	694.60	20.83	21.09	97.5	52.94 42.37
Days to 50% flowering	75	67(LCA424)	82(LCA403)	15.54	17.86	5.24	5.62	87.02	7.57 10.01
Days to maturity	110	98(LCA424)	132(LCA403)	81.63	85.11	8.20	8.37	95.91	18.22 16.34
Fruits plant ⁻¹	126	30(IC 413706)	255(LCA432)	1674.31	1712.15	32.46	32.82	97.80	83.36 66.13
Fruit length (cm)	8.61	3.97(LCA457)	13.17(LCA414)	3.96	4.40	22.69	24.37	86.68	3.74 43.50
Fruit girth (cm)	2.32	1.25(LCA404)	4.6(LCA448)	1.77	2.02	28.63	30.61	87.50	2.56 51.16
Fruit shape index	3.70	0.47(LCA457)	8.8(LCA427)	0.55	0.65	36.97	40.07	85.10	1.42 70.28
Fresh fruit wt plant ⁻¹ (g)	517.65	291.67(IC413706)	1195.5(LCA43)	33819	33892	35.53	35.56	99.80	378.42 73.10
Dry fruit wt plant ⁻¹ (g)	160.37	337.36(IC413706)	91.04(LCA427)	2412	2465	30.62	30.96	97.82	100.05 62.39
Recovery % of fresh to dry	31.84	23.0(LCA415)	46.3(LCA419)	25.06	27.66	15.73	16.52	90.60	9.82 30.83
Wt. of dry stalkless chilles (g)	124.55	289.33(IC413701)	66.83(LCA432)	1244.4	1271.40	28.32	28.63	97.90	71.89 57.72
Seeds fruit ⁻¹	71.52	21.0(LCA422)	188.33(LCA434)	894.13	915.13	41.81	42.30	97.71	60.89 85.13
100 seed wt. (g)	0.45	1.49(LCA422)	0.15(LCA434)	0.07	0.08	60.11	61.80	94.63	0.54 120.46
Oleoresin (%)	8.14	2.42(LCA436)	17.34(KTPL19)	8.93	9.00	36.71	36.86	99.20	6.13 75.32
Capsanthin (EOA)	33625	8235(MCA35)	88733(LCA424)	388379000	392060600	58.61	58.89	99.10	40406 120.20
Capsaicin (%)	0.18	0.1(Byadigi)	0.44(LCA454)	0.005	0.005	39.83	40.31	97.62	0.15 81.05

received timely management practices as per the package of practices and recommendations of the Andhra Pradesh Horticultural University. Five plants were randomly selected per accession and observations were recorded on plant height, plant spread, days to 50% flowering, days to maturity, number of fruits plant⁻¹, fruit length, fruit girth, fruit shape index, fresh fruit yield plant⁻¹, dry fruit plant⁻¹, weight of dry stalk-less chillies plant⁻¹, number of seeds fruit⁻¹, 100 seed weight and oleoresin, capsanthin and capsaicin contents. Analysis of variance in respect of various characters was done (Panse & Sukhatme 1967). Genetic variability for different characters was estimated as suggested by Singh & Choudary (1985). Heritability (broad sense) and genetic advance as percentage of mean were calculated as per Hanson *et al.* (1956) and Johnson *et al.* (1955), respectively. Assessment of genetic diversity in classifying the genotypes into different clusters was done by Mahalanobis D² analysis (1928).

The analysis of variance in the 94 paprika genotypes indicated highly significant differences among the genotypes for all the 17 quantitative and qualitative characters studied (Table 1). The genotype LCA 432 recorded the highest number of fruits plant⁻¹. The highest dry fruit yield plant⁻¹ was recorded in LCA 427. The highest capsanthin content was recorded in LCA 424 and highest oleoresin content in KTPL 19.

The phenotypic coefficient of variation (PCV) in general, was higher than genotypic coefficient of variation (GCV) for all the traits, but the differences were very narrow indicating low environmental influence on the expression and are suggestive of the heritable nature. Similar results were reported by Chatterjee (2006) in chilli. Higher PCV and GCV were observed for number of fruits plant⁻¹, fresh fruit yield, dry fruit yield, 100 seed weight, number of seeds fruit⁻¹ and capsanthin, capsaicin and oleoresin contents indicating the higher magnitude of variability for these traits and consequently more scope for their improvement through selection.

Plant height, spread and fruit diameter exhibited moderate PCV and GCV estimates suggesting the possible role of environment in influencing these characters. Similar results were reported by other workers also (Gogoi & Gautam 2002; Rathod *et al.* 2002; Wasule *et al.* 2004; Mishra *et al.* 2005). Days to 50% flowering and days to maturity recorded low PCV and GCV suggesting limited variability indicating need to generate more variability for wider spectrum of selection (Chatterjee 2006).

The effectiveness of the selection depends upon genetic advance of the character selected along with heritability. The study revealed high heritability coupled with high genetic advance for several biometric characters including yield plant⁻¹, fruits plant⁻¹, fruit weight, number of seeds fruit⁻¹, 100 seed weight and oleoresin, capsanthin and capsaicin contents indicating the effect of additive genes. These characters could be considered reliable for effective selection in paprika. High heritability and low genetic advance was observed for days to 50% flowering and days to maturity indicating that these characters are controlled by non-additive genes and improvement through selection for these characters will not be very much effective (Chatterjee 2006; Choudhary & Samadia 2004).

Based on D² values, the 94 genotypes were grouped into 10 clusters (Table 2) which indicated considerable genetic diversity in the material studied. The largest was cluster I which comprised of 24 genotypes. The cluster distances ranged from 15789.6 (between cluster II and cluster X) to 856.7 (between cluster 1 and cluster II) (Table 3) (Sreelathakumary & Rajamony 2004; Varalakshmi & Babu 1991).

On the basis of present study, yield plant⁻¹, fruits plant⁻¹, number of seeds fruit⁻¹, 100 seed weight and oleoresin, capsanthin and capsaicin contents were the most important quantitative and qualitative characters to be taken into consideration for effective selection in paprika. It is desirable to attempt crosses

Table 2. Clustering of 94 paprika genotypes based on Mahalanobis D² analysis

Cluster no.	No. of genotypes	Genotypes
Cluster I	24	Byadigi Dabbi, LCA406, LCA427, LCA429, LCA417, LCA464, LCA468, IC119530, MCA34, LCA477, MCA29, LCA469, MCA28, LCA420, LCA470, LCA478, LCA449, LCA465, MCA33, LCA457, LCA460, LCA461, PSR11853, IC413699
Cluster II	9	LCA-450, PSR 11674, LCA405, IC 413701, MCA35, LCA455, LCA428, LCA445, IC413716
Cluster III	9	LCA475, LCA454, LCA479, MCA32, LCA448, KTPL19, , IC92109, IC119300, IC119365
Cluster IV	14	LCA419, LCA484, LCA421, LCA435, LCA437, LCA438, LCA422, LCA416, LCA441, LCA442, LCA439, LCA443, LCA458, LCA425
Cluster V	4	LCA440, LCA447, LCA434, LCA467
Cluster VI	17	LCA402, LCA428, LCA413, CA960, LCA411, LCA453, LCA456, LCA459, LCA403, LCA401, LCA412, LCA423, LCA404, LCA409, LCA415, LCA407, LCA418
Cluster VII	3	LCA451, LCA462, LCA433
Cluster VIII	5	LCA414, LCA446, LCA426, LCA452, IC413702
Cluster IX	6	LCA-427, LCA-436, LCA-424, MCA-30, IC119444, LCA-408
Cluster X	3	LCA-431, LCA-432, LCA-466

Table 3. Nearest and the farthest cluster from each cluster based on D² values

Cluster no.	Nearest cluster	Farthest cluster
I	II (856.71)	X (13922.30)
II	I (856.71)	X (15789.59)
III	I (1014.42)	X (12331.22)
IV	I (1346.80)	X (10491.00)
V	I (1548.23)	X (12546.60)
VI	VII (1237.62)	X (8774.02)
VII	VI (1237.62)	X (6792.58)
VIII	VI (1414.63)	X (5421.30)
IX	VII (2007.69)	II (6647.19)
X	IX (3587.76)	I (13922.30)

between desirable genotypes belonging to different clusters with desirable genotypes for getting highly heterotic crosses.

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