

Genotypic variation for biochemical compounds in capsicum

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ABSTRACT

Studies were conducted on genetic variability of 103 chilli genotypes for major fruit qualitative characters, viz., total capsaicinoids, total carotenoids, red and yellow carotenoids. Total carotenoids content exhibited positive correlation with the fruit colour, while the total capsaicinoids exhibited negative and significant correlation with total carotenoids content. A wide range of variation was noticed in the contents of total capsaicinoids (0-1.67%), total carotenoids (8.6-357.9 ASTA), red carotenoids (0-0.27%) and yellow carotenoids (0-0.2%). These major fruit quality traits showed high values for GCV, PCV and heritability coupled with high GAM suggesting predominance of additive gene action and low influence of environmental factors in the expression, with possibility for improvement through selection.

Keywords: Capsaicinoids, carotenoids, genotypic coefficient of variance, genetic advance, phenotypic coefficient of variance.

INTRODUCTION

In recent years crop quality improvement is gaining more importance as quality produce improves human welfare and increased farm income. Thus, the improvement of quality characters in crop plants has great potential to alleviate problems related to poverty and malnutrition. Capsaicinoids and carotenoids are major chemical constituents of chilli fruits which add higher commercial value to the crop. The carotenoids contribute to fruit colour and act as dietary precursors of vitamin A, which plays an important role in the regulation of vision, growth and reproduction. Capsaicinoids are responsible for the nature of pungency, which has wide applications in the food, medicine and pharmaceutical. The availability of data on pungency and colour are important criteria for selection of genotypes from a genebank for use in crop improvement. A wide range of pungency values and varied colours are known to occur in the *Capsicum* spp. gene pool. However, data on pungency and carotenoids among the accessions in *Capsicum* genebanks are currently limited (Jarret *et al.*, 9).

The evaluation of natural and ancient genetic resources is the first step in genetic improvement because they potentially contain valuable alleles. To improve the quality characters, information on genetic variability is of great importance and is a pre-requisite for the effective screening of genotypes. It is essential to partition the overall variability into

its heritable and non-heritable components with the help of genetic parameters like genetic co-efficient of variation, heritability and genetic advance. However, there is a lack of comprehensive studies related to the diversity and other genetic parameters of interest for breeding of the nutritional value of *Capsicum* spp. With the major objective of assessing the variability in major biochemical compounds, i.e. colour (provitamin A bioactive compounds like total carotenoids, red and yellow fractions of carotenoids) and pungency (total capsaicinoids) an investigation was carried using a set of chilli germplasm accessions consisting 103 lines, which includes accessions which includes cultivated, semi-wild and wild accessions.

MATERIALS AND METHODS

The experiment was conducted at Indian Institute of Horticultural Research (IIHR), Bengaluru during 2009-10 to evaluate 103 germplasm accessions consisting of *C. annuum* (92), *C. frutescens* (2; EC631830 & EC631844), *C. chinense* (5; EC631815, EC631816, EC631817, EC631826 & EC631829), *C. baccatum* (2; PBC 80 & PBC 81), *C. chacoense* (1; EC631803) and one unknown species, maintained at IIHR, collected from different locations including AVRDC, Taiwan and LAM farm, Guntur. The plants were grown in field (eastern dry zone of Karnataka state, India, at 12°58' north latitude, 77°45' east longitude and at an altitude of 930 m above the mean sea level and average rainfall of this area is about 800 mm) and all standard cultivation practices recommended for the locality were practiced and the soil of the experimental site is red loamy. Fruit samples were harvested at full ripe stage and

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were dried in the oven at 60°C for 36 h, ground in an electronic grinder, and passed through a 0.5 mm sieve. Following biochemical constituents were measured. Total extractable colour of fruits measured in ASTA (American Spice Trade Association units) (Rosebrook *et al.*, 15). Total red (C_R ; capsanthin, capsorubin and capsanthin-5, 6-epoxide) and yellow (C_Y ; zeaxanthin, violaxanthin, antheraxanthin, β -cryptoxanthin, β -carotene and cucurbitaxanthin A) carotenoid isochromic fractions were estimated following protocol of spectrophotometric method (Hornero-Mendez and Minguez-Mosquera, 8). Total capsaicinoids content was determined using colorimetric method (Bajaj, 2). Capsaicinoids concentrations were converted to Scoville Heat Units (SHU) values by multiplying the pepper dry weight concentrations (%) by the coefficients of heat value, *i.e.*, 1,60,00,000 for capsaicin (Govindarajan *et al.*, 6; Zewdie and Bosland, 20).

Analysis of variance was carried out as per the procedure (Panse and Sukhatme, 13). Genotypic and phenotypic coefficients of variation were estimated based on estimate of genotypic and phenotypic variance (Burton and Devane, 4). Heritability in broad sense was

calculated as the ratio of genotypic variance to the phenotypic variance and expressed in percentages (Falconer, 5). The calculated heritability was classified into three groups and genetic advance as percent of mean for each character calculated (Johnson *et al.*, 10). The correlation coefficients among all possible character combinations at phenotypic (r_p) and genotypic (r_g) level were estimated (Al-Jibouri *et al.*, 1).

RESULTS AND DISCUSSION

The analysis of variance showed significant differences among the accessions for the characters studied, indicating the presence of wide variation (Fig. 1). Dendrogram was constructed to group the genotypes on the basis of biochemical traits by Wards method. The 103 genotypes were classified into two major clusters which further subdivided into sub-clusters (Table 1). The estimates of mean, range, genotypic variance (GV), phenotypic variance (PV), genotypic co-efficient of variance (GCV), phenotypic co-efficient of variance (PCV), heritability (h^2), genetic advance (GA) and genetic advance over mean (GAM) for different characters are presented in Table 2.

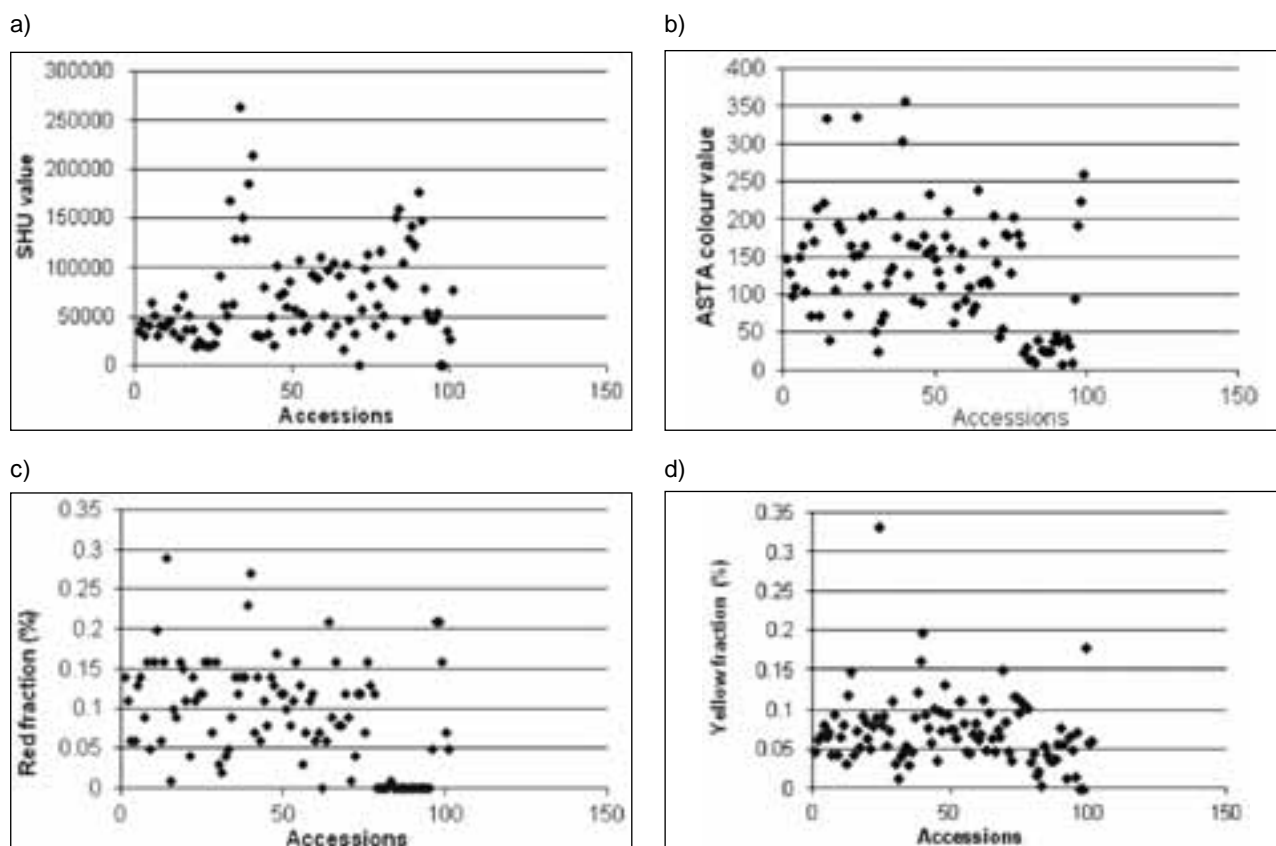


Fig. 1. Variability for a) pungency values (SHU), b) ASTA colour values (total carotenoids), c) Red fraction of carotenoids, d) Yellow fraction of carotenoids, among the chilli accessions.

Total capsaicinoids content of fruits ranged from zero SHU (0%) (*C. annuum*- Arka Mohini, PBC1022) to 2,64,000 SHU (1.27%) in EC631817 (*C. chinense*). The average total capsaicinoids content of the fruits was to the extent of 0.42%. Similar high variation in chilli accessions was reported (Balvir Kaur and Daljit Singh, 3; Thul *et al.*, 18). Highest capsaicinoids content was observed in EC631817 (*C. chinense*) (2,64,000 SHU), followed by EC631844 (*C. frutescens*) (214400) whereas, in other accessions, it did not appear to be correlated with specific species as reported earlier (Jarret *et al.*, 9; Zewdie and Bosland, 20). In the present study smaller sized fruits were associated with higher capsaicinoids content.

Total carotenoids ranged from 8.6 (LCA1081) to 357.9 ASTA (Byadagi Dabbi), the red carotenoids ranged from zero (all yellow cultivars) to 0.27 per cent (Byadagi Dabbi) with average of 0.09 per cent and

yellow carotenoids content ranged from zero (Arka Mohini) to 0.2 per cent (Byadagi Dabbi) with average of 0.07%. The total carotenoids content was highest in dark red lines (Byadagi Dabbi), followed by light red (EC631815). In all yellow pepper lines evaluated under study lower total carotenoids content was found (8.6-48.5 ASTA). Similar observations were made in yellow accessions that, the total carotenoids levels do not increase and remain low, whereas in red peppers during the process of ripening the levels of total carotenoids increases due to synthesis of capsanthin, capsorubin, β -cryptoxanthin and zeaxanthin (Ha *et al.*, 7). All the accessions with yellow coloured fruits did not contain red carotenoids content (Rodriguez-Burruezo *et al.*, 14) as the deletion of the candidate gene *Capsanthin capsorubin synthase (Ccs)* gene (Thorup *et al.*, 17) or structural changes in the gene such as mutation or deletion (Ha *et al.*, 7) prevents the synthesis of red

Table 1. List of genotypes in each clusters formed by Ward's method.

I	I.1	Light red to orange - yellow and mild pungent	<i>C. annuum</i> (HDC75, EC631798, HSHP154, ICPN11-7, Sringeri Local, CM334, LCA333, EC631787, EC631769, EC631774, LCA1083, LCA1084, CHIVAR9, LCA1068, LCA1075, LCA1082, CHIVAR 1).
		Red and less pungent	<i>C. annuum</i> (EC631773, LCA443, EC631777, EC631779, EC631782, EC631791, LCA1070, Arka Mohini, PBC1022, EC631768, LCA206, EC631786, Arka Suphal, LCA357, EC631793, Arka Abhir, EC631795, EC631790, EC631789, EC631792, GCVMV2), <i>C. baccatum</i> (PBC80 & PBC81), unknown species (Ornamental chilli).
	I.2	Deep red and less pungent	<i>C. annuum</i> (EC631784, Byadagi Dabbi, Byadagi Kaddi, EC631794, PC 7, CHI VAR5, EC631775, PC 2062, VN2 , EC631782, EG 132, EC631788, EC631796, EC631778, Kashi Anmol, MS1 (P), MS3 (P), EC631783, ACS 2001-01, EC631799, EC631780, ICPN11-2, MS2 (P), EC631776).
II	II.1	Pungent and orange-red	<i>C. annuum</i> (EC631785, LCA1071, LCA1069 , G4, EC631770, LCA334, PBC495, PBC569, Arka Lohit, Pant C-1, Perennial, PBC549, BCC1, JCA283, VC246, PMR14, EC631797, PC-56, CHI VAR 2), <i>C. chinense</i> (EC631815).
	II.2	Very Highly pungent and red	<i>C. frutescens</i> (EC631830 & EC631844), <i>C. chinense</i> (EC631817).
	III.3	Highly pungent and light red - yellow	<i>C. annuum</i> (LCA1077, LCA1080, LCA1072, LCA 1073, LCA1079, LCA1076, LCA1078, LCA1074, CHI-VAR4, CHIVAR8, PBC521), <i>C. chacoense</i> (EC631803), <i>C. chinense</i> (EC631816, EC631826 & EC631829).

Table 2. Estimate of mean range components of variance heritability and genetic advance for different characters in chilli.

Character	Mean	Range	GV	PV	GCV (%)	PCV (%)	h ² (%)	GA (%)	GAM (%)
Total capsaicinoids	0.431	0-1.67	0.088	0.086	68.49	68.7	99.4	61	141
Total carotenoids	0.165	0.012-0.468	0.0093	0.0094	58.47	58.5	99.9	20	121
Red fraction of carotenoids	0.092	0-0.27	0.0043	0.0044	70.82	70.9	99.8	13	139
Yellow fraction of carotenoids	0.073	0-0.2	0.0020	0.002	60.31	60.6	99	9	122

pigments capsanthin and capsorubin, respectively. Contrarily to what occurred with the red carotenoids, all the accessions including those with red coloured, contained yellow carotenoids and the accessions with higher total carotenoid contained higher yellow carotenoids, suggesting that enzymes like zeaxanthin epoxidase, β -ring carotene hydroxylase *etc.* required for yellow pigments production will be active in all the accessions including red fruited ones.

The degree of variability can be judged by the values of GCV & PCV. The respective PCV & GCV were high for total capsaicinoids (68.7 & 68.49), total carotenoids (58.5 & 58.47), red carotenoids (70.9 & 70.82) and yellow carotenoids (60.6 & 60.31). A close proximity in the PCV & GCV values (Table 2) was observed justifying that variability is due to genetic constitution and indicating lesser influence of environment in the expression of the biochemical traits studied. This suggests that selection based on phenotypic performance would be reliable in improvement of these traits in capsicum.

The heritability was very high for all the traits studied indicating lesser influence of environment in expression. The heritability along with genetic advance over mean is more useful than the heritability alone in predicting the effect of selection. The higher estimates of heritability coupled with higher genetic advance over mean for total capsaicinoids (99.4 & 141), total carotenoids (99.9 & 121), red carotenoids (99.8 & 139) and yellow carotenoids (99 & 122), indicates dominance of additive gene action and consequently higher genetic gain by selection. Similar results were reported for capsaicinoids, total carotenoids (Khurana *et al.*, 11; Sonia Sood *et al.*, 16; Yudhivir Singh *et al.*, 19), and red carotenoids (Rodriguez-Burruezo *et al.*, 14). Results are contrasting to low PCV, GCV, heritability and GAM reported for total capsaicinoids using 30 diverse genotypes (Munshi *et al.*, 12). However, these reports were based on lesser number of genotypes (<50), in contrast our experiment had 103

different genotypes with higher variability to capture accurate genetic components of variation.

The total capsaicinoids exhibited negative and significant correlation with total carotenoids content (-0.327), red fraction of total carotenoids (-0.347) and yellow fraction of total carotenoids (-0.197) at phenotypic level and with total carotenoids content (-0.327), red fraction of total carotenoids (-0.349) and yellow fraction of total carotenoids (-0.1984) at genotypic level (Table 3). Red fraction of total carotenoids exhibited positive and significant correlation with yellow fraction of total carotenoids at genotypic (0.5083) and at phenotypic (0.5) level. The high value of correlations between red and yellow carotenoids was observed, as both these carotenoids are produced through the same biosynthetic pathway and from same precursors (Thorup *et al.*, 17). However, the negative correlation between carotenoids and capsaicinoids suggests that some regulatory gene(s) may alter the expression of the other gene(s) involved in different pathways.

Finally our findings indicates that there exists adequate genotypic variation in the population for these major biochemical traits, *i.e.*, total capsaicinoids, total carotenoids, red and yellow carotenoids, showing high values for GCV, PCV and heritability coupled with high GAM suggesting predominance of additive gene action and lower influence of environmental factors in the expression of these traits with possibility for improvement through phenotypic selection. Several lines have been identified as potential sources of these bioactive biochemical compounds, for pungency from exotic accessions and local land races, which can be effectively used in breeding chilli and *Capsicum* cultivars with rich nutraceutical value for future nutritional security.

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Table 3. Phenotypic and genotypic correlations for fruit quality traits in chilli.

Trait	Correlation			
	Total capsaicinoids	Red fraction	Yellow fraction	Total carotenoids
Total capsaicinoids (P)	1.000	-0.347**	-0.197*	-0.327**
(G)		-0.349**	-0.198*	-0.328**
Red fraction (P)		1.000	0.502**	0.9156**
(G)			0.508**	0.917**
Yellow fraction (P)			1.000	0.8065**
(G)				0.809**
Total carotenoids				1.000

*,** Significant at 5, and 1% (P) = Phenotypic correlation and (G) = Genotypic correlation.

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