*Indian J. Genet.*, **67**(1): 97-98 (2007)

Short Communication

# Evaluation of chilli (*Capsicum* spp.) germplasm for extractable colour and pungency

**D. Prasath[1], V. Ponnuswami and V. Muralidharan**

Horticulture College and Research Institute, Tamil Nadu Agricultural Univeristy, Coimbatore 641 003

(Received: March 2006; Revised: September 2006; Accepted: October 2006)

Chilli (*Capsicum annuum* L.) has its unique place in the world diet in its ripe dried form (as a spice) as well as green fruits (as vegetable). It is one of the major spice crops in India with different varieties and quality attributes [1] and is used as an essential condiment in foods for its pungency and red colour [2]. Chilli colourant, which imparts appealing colour, aesthetic flavour and aroma, has many end uses in various food, pharmaceutical and cosmetic preparations. The indiscriminate use of synthetic colours for the food colouring has several harmful effects. This has resulted in huge demand for chilli and paprika oleoresin with high colourant and mild pungency as natural colour. In the present investigation 27 accessions of chilli (*Capsicum* spp.) (26 belonging to *C. annuum* and one to *C. baccatum*) obtained from different eco-geographical regions were analysed for different quality traits. The experiment was conducted in randomized block design with two replications during 2003-2004.

The colour value chilli of pod was estimated as per the standard procedure [2] and expressed in ASTA units. The capsaicin content in dry fruit was estimated by adopting the procedure given by [3] and expressed in per cent. Observations on plant height, fruits per plant, fruit weight and yield per plant were recorded on five randomly selected plants of each replication. The data were analyzed according to [4]. The traits (interval data) recorded were standardized using the STAND programme of the NTSYSpc [5]. From the standardized values Euclidean distances were computed for all pair wise combinations of genotypes using SIMINT programme of the NTSYSpc. The average taxonomic distances for different genotypes were also computed for all the pair wise genotype combinations. The best fitting similarity/dissimilarity matrices identified for different data sets were further subjected to cluster analysis by neighbour joining method as suggested by [6] using NJOIN programme of NTSYSpc. Clustering was performed to provide useful additional information and to show interrelationships among entries.

Analysis of variance of treatments (Table 1) was found significantly superior for all the characters indicating that there is much variability to take up further studies involving these accessions. Mean, standard errors, range of variation and coefficients of variation estimated for each trait in all entries are reported in Table 2. Total extractable colour ranges from 32.82 to 208.56 ASTA units with a mean value of 117.05 ASTA units. The Acc. 22 exhibited the maximum extractable colour followed by Acc. 25 (tomato chilli) followed by Acc 23 (bydagi kaddi). Extreme capsaicin levels are 0.10 and 1.26 %, showing a mean value of 0.36 %. Six genotypes exhibited high capsaicin per cent (>1) and low capsaicin value was seen for 3 genotypes (< 0.20). The same extent of variability for capsaicin and extractable colour were also reported by earlier workers. Plant height and fruits per plant were more variable ranging from 53.10 to 112.85 cm and 4.15 to 257.50, respectively. Similarly, range for fruit weight was from 1.5 to 26.24 (g/fruit). The six genotypes (Acc. 18, 19, 22, 23, 25 and 27) possessed individual fruit weight of more than 10 g. Thirteen accessions gave higher yield than arithmetic mean (324.01±104.47 g/plant). The maximum yield per plant was noticed for Acc. 27 (797.10) followed by Acc. 16 (684.55) and Acc. 22 (530.05) etc. Similar observation were made earlier in respect of yield and quality characters. The accessions 22 and 23 were found to be with high extractable colour and low pungency, as the colour values and pungency were more than 190 ASTA units and less

**Table 1.** Analysis of variance (ANOVA) for six characters of *Capsicum* accessions

| Source of variation | Degrees of freedom | Characters MS value | | | | | |
|---|---|---|---|---|---|---|---|
| | | Total extractable colour | Capsaicin (%) | Plant height (cm) | Number of fruits per plant | Fruit weight (g) | Yield per plant (g) |
| Replication | 1 | 99.472 | 0.014 | 3.016** | 117.555 | 0.849 | 2548.789 |
| Germplasm | 26 | 3643.780** | 0.329* | 1085.164** | 1127.494** | 33.478** | 123157.073** |
| Error | 26 | 64.947 | 0.055 | 37.890 | 37.584 | 0.809 | 8223.636 |

*Significant at p = 0.01 and p = 0.05 probability levels relspectively

[1]Present address: Indian Institute of Spices Research, Research Centre, Appangala, Madikeri 571 201

**Table 2.** Mean values, Standard Error (SE), ranges, coefficients of variation observed in 27 *Capsicum* germplasm

| Genotypes/ characters | Cultivar/eco-geographical region | Total extractable colour (ASTA units) | Capsaicin (%) | Plant height (cm) | Fruits per plant | Fruit weight (g) | Yield per plant (g) |
|---|---|---|---|---|---|---|---|
| Acc. 1 | BD-I, Karnataka | 115.66 | 0.79 | 62.30 | 38.40 | 5.24 | 197.50 |
| Acc. 2 | BD-2, Karnataka | 125.82 | 0.31 | 72.00 | 20.35 | 3.86 | 77.62 |
| Acc. 3 | BD-3, Karnataka | 99.07 | 0.43 | 61.30 | 8.50 | 5.38 | 42.89 |
| Ace. 4 | BD-4, Karnataka | 121.50 | 0.78 | 62.35 | 20.00 | 7.46 | 149.22 |
| Acc. 5 | S 1, Tamil Nadu | 118.98 | 1.13 | 75.02 | 51.20 | 5.72 | 303.43 |
| Acc. 6 | Tomato Chilli, Andhra Pradesh | 182.66 | 0.92 | 57.00 | 11.45 | 9.36 | 100.19 |
| Acc. 7 | BD-15, Karnataka | 100.32 | 0.22 | 56.00 | 41.20 | 6.66 | 290.60 |
| Acc. 8 | BD-17, Karnataka | 129.84 | 0.83 | 63.35 | 26.85 | 8.24 | 220.45 |
| Acc. 9 | BD-18, Karnataka | 119.08 | 0.45 | 65.70 | 18.10 | 8.63 | 163.04 |
| Acc. 10 | BD-19, Karnataka | 105.00 | 0.81 | 72.10 | 4.15 | 3.32 | 15.51 |
| Acc. 11 | Arka Lohit, Karnataka | 115.32 | 0.94 | 112.85 | 91.00 | 4.47 | 416.38 |
| Acc. 12 | Arka Abir, Karnataka | 196.39 | 0.42 | 87.85 | 60.50 | 5.43 | 325.85 |
| Acc. 13 | Co 4, Tamil Nadu | 98.62 | 0.60 | 71.40 | 60.50 | 7.63 | 510.92 |
| Acc. 14 | K 2, Tamil Nadu | 74.19 | 1.05 | 68.85 | 113.50 | 3.60 | 408.25 |
| Acc. 15 | HOE 1888, unknown | 47.58 | 1.26 | 87.35 | 257.50 | 2.17 | 550.45 |
| Acc. 16 | PBC 81, *C. baccatum*, unknown | 32.82 | 0.20 | 91.00 | 76.25 | 9.10 | 684.55 |
| Acc. 17 | CC 4, Tamil Nadu | 74.70 | 1.16 | 68.85 | 133.50 | 1.59 | 210.10 |
| Acc. 18 | Kt PI 19, Himachal Pradesh | 110.15 | 0.63 | 64.65 | 8.10 | 16.77 | 133.35 |
| Acc. 19 | Simla Parika, Himachal Pradesh | 106.52 | 0.86 | 77.75 | 35.50 | 10.88 | 390.55 |
| Acc. 20 | BD-14, Karnataka | 60.95 | 1.15 | 66.75 | 140.55 | 3.78 | 528.75 |
| Acc. 21 | MDU Y, unknown | 137.88 | 0.42 | 54.75 | 43.35 | 8.83 | 386.00 |
| Acc. 22 | MDU R, unknown | 208.56 | 0.12 | 70.50 | 27.50 | 19.84 | 530.05 |
| Acc. 23 | Bydagi-Kaddi, Karnataka | 191.00 | 0.10 | 61.60 | 45.00 | 11.86 | 524.55 |
| Acc. 24 | Bydagi-dabbi, Karnataka | 165.93 | 0.74 | 65.60 | 41.85 | 8.37 | 367.45 |
| Acc. 25 | Tomato chilli-1, Andhra Pradesh | 203.73 | 0.84 | 53.10 | 12.05 | 26.24 | 268.55 |
| Acc. 26 | Kt PI 18, Himachal Pradesh | 136.18 | 1.03 | 53.55 | 20.10 | 7.64 | 155.35 |
| Acc. 27 | Kt PI 19-1, Himachal Pradesh | 131.98 | 0.91 | 74.75 | 28.50 | 14.03 | 797.10 |
| | Mean | 117.05 | 0.69 | 69.57 | 52.95 | 8.37 | 324.01 |
| | SEd | 3.56 | 0.036 | 12.09 | 13.73 | 1.24 | 104.47 |
| | Minimum | 32.82 | 0.10 | 53.10 | 4.15 | 1.59 | 15.51 |
| | Maximum | 208.56 | 1.26 | 112.85 | 257.50 | 26.24 | 797.10 |
| | CV (%) | 3.04 | 5.26 | 17.38 | 25.91 | 14.77 | 32.64 |

than 0.15 % respectively. The available and potential phenotypic variability described above may be interesting for potential users of the *Capsicum* germplasm in relation to the prospect of producing new genotypes with high extractable colour and mild pungency traits. All the high colour low pungent accessions with good yield have been processed in different programmes to develop high yielding varieties with extractable colour value. On the other hand the high colour accessions with average yield may be utilized as donor parent to isolate desirable recombinants.

The Euclidian distance values (d), which reflected divergence for quantitative traits among genotypes, ranged from 0.397 to 2.530. Highest 'd' value was observed between genotypes Acc. 15 and Acc. 25 and least 'd' value was noticed between genotypes Acc. 1 and Acc. 4. The close similarity between Acc. 1 and Ace 4 may be explained by commonness in their ancestry. Cluster analysis revealed two distinct groups involving 16 and 11 accessions. The genotypes included in a cluster have exhibited less variation with in themselves where as genotypes of one main cluster had a wide variation between individuals of another cluster. The determinants such as gene frequencies, mutation, introgressive hybridization, random genetic drift, preferential selection pressure, and distantly exchange of germplasm by the people, microclimates and erratic changes in the environment conditions are likely to be predominant factors responsible for infusing such a high degree of genetic divergence and heterogeneity.

The present study revealed that there is large genetic diversity for colour and pungency between the germplasm collected from different parts of India. The accessions 22 and 23 had high colour and low pungency and are potential parents to breed high yielding accessions with extractable colour.

## References


1. **Anu A., Babu K. N. and Peter K. V.** 2002. Evaluation of paprika genotypes in Kerala. Indian J. Plant Genet. Resour., **15**: 93-99.
2. **Woodbury E. J.** 1997. Extractable colour of capsicum and oleoresin paprika, J.A.O.A.C., **60**: 1-4.
3. **Sadasivam S. and Manickam A.** 1992. Biochemical methods for agril sciences, Wiley Eastern Ltd., Madras.
4. **Panse V. G. and Sukhatme P. V.** 1961. Statistical Methods for Agricultural Workers. Indian Council of Agricultural Research, New Delhi.
5. **Rohlf F. J.** 1998. Numerical taxonomy and multivariate analysis system, Version 2.02 i.100. North Country Road, Setanket, New York.
6. **Saitou N. and Nei M.** 1987. The neighbour-joining method: a new method for reconstructing phylogenetic trees. Mol. Biol. Evol., **4**: 406-425.