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Genetic diversity analysis of indigenous and exotic chilli genotypes

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ABSTRACT

Genetic diversity analysis of 64 chilli accessions of Indian and exotic origins was performed using 14 qualitative and quantitative traits. Variation was not observed for mature fruit colour, corolla colour and number of anthers. Based on 11 polymorphic traits, the analysis allowed grouping of the accessions into 9 clusters. Using the polymorphic traits, all but one pair of accessions, *viz*. Selection 40 and ELS 82 were differentiated from each other. Euclidean's inter-cluster distances varied from 12.68 between clusters 5 and 6 to 90.77 between clusters 4 and 5. Intra-cluster distance was maximum in cluster 1 (21.18) and minimum in cluster 5 (6.99). cluster 2 was represented by only one genotype 'Faslima'. Based on the diversity analysis, parental lines were identified for their utilization in hybrids development and genetic improvement of chilli.

Key words: Capsicum, genetic diversity, morphological descriptors.

INTRODUCTION

Chilli (*Capsicum* sp.), also known as hot pepper, belongs to the family Solanaceae and has a chromosome number 2n = 2x = 24. Chilli is indigenous to South America and was first introduced in India from Brazil by Portuguese towards the end of 15th century (Krishna De, 8). Chilli is an often cross-pollinated crop and, therefore, exhibits wide variability for different qualitative and quantitative traits (Tanksley, 12). There are five cultivated species of chilli including *Capsicum annuum* L, *C. frutescens*, *C. chinense*, *C. pubescens* and *C. baccatum* (Smith and Heiser Jr, 11). India is considered to be the secondary centre of diversity of chilli (IBPGR, 7), especially of *C. annuum*, the most important cultivated species. North-Eastern states are home to the genetic variability for *C. chinense* to which Naga King, one of the world's hottest chilli also belongs. Over the years, chilli has become an important commercial crop of India. India is currently the leading producer, consumer and exporter of chilli in the world. Total area under the crop is estimated to be 792 thousand hectare with the production of 1,260 thousand tonnes of dry chilli during 2011-2012 (Anon, 1). Although chilli is cultivated almost throughout the country, Andhra Pradesh alone accounts for 25% of the total area and 40-50% of the total national production. In the world trade, India contributes about 25% of the total global chilli exports (Anon, 2).

Genetic resources are the most valuable and essential basic raw material to meet the current and future needs for genetic improvement of any crop. Characterization of the germplasm is important for its identification and registration with the competent authority for plant variety protection. The uniqueness of a variety is established by tests for distinctiveness, uniformity, and stability (DUS) for which the International Union for the Protection of New Varieties of Plants has provided guidelines in the case of most economically useful plant species (UPOV, 13). Characterization of the germplasm is also important from the point of view of its utilization in crop breeding programmes. The present investigation was, therefore, undertaken to characterize the available germplasm of cultivated chilli, assess genetic diversity using qualitative and quantitative traits and identify genotypes for hybrid development and genetic enhancement of the crop.

MATERIALS AND METHODS

The experiment was conducted at Vegetable Research Farm of the Punjab Agricultural University, Ludhiana, India during the crop season 2011-2012. The plant material comprised of 64 chilli germplasm of which 49 accessions belong to the indigenous sources and the remaining 15 to the exotic sources (Table 1). Except 'Naga King', 'Tabasco' and 'Punjab Longi', all accessions belong to the cultivated species, *Capsicum annuum* L. 'Naga King' is believed to be a naturally occurring hybrid between *C. chinense* and *C. frutescens* and 'Tabasco' belongs to *C. frutescens*. Phylogeny of 'Punjab Longi' is not clear but resembles that of *C. frutescens*. For diversity analysis, the germplasm was screened for 14 descriptors. These included growth habit, stem colour, leaf colour, leaf size, corolla colour, number of anthers, anther colour, fruit position, fruit length, fruit tip, fruit colour, fruit shape, seediness and pungency. Growth habit, stem colour, leaf colour, leaf size, corolla colour,

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Table 1. List of chilli accessions used for diversity analysis.

Genotype	Source
Selection-11, Selection-15, Selection-40, Selection-8E, Selection-40-1, Selection-20-1, S-217621, PAU Selection Long, ELS-82, PG-1-1, SAS-39, PC-7-1, Acc-34-1, Punjab Surkh, Punjab Gucchedar, Selection-7-1, MS 12, Acc-33-1, C-31-1, S-2530, Acc-06-01, Acc-06-02, Dev Long, LLS	PAU, Ludhiana
VR-338, Perennial, EC-532386, Long thick USA, PC-1, Chilli Shining, Yellow Bird Dark, VR-36, Tabasco, EC-532390, Pubescent	USA
JCA-283, JCA-288, DCL-524, PC-2062, Acc-2-1, PC-6, Acc-34, ATG	AICRP, India
PP91-7195-1, PP-9852-173, PP-0237-7508, CCA-4261	AVRDC, Taiwan
VS-5, Kashi Anmol, VS-5	IIVR, Varanasi
PLS-3, PLS-2, PLS-5	Moga, Punjab
Pepsi-17-2, Pepsi-8-1	Pepsi Foods, India
SHHP-404, SHHP-4884	SKUAST, Srinagar
Local Line Ropar	Ropar, Punjab
Punjab Longi	Amritsar, Punjab
Faslima	Rajasthan, India
NSS-2	Namdhari Seeds, India
Utkal Yellow	Bhubaneswar, Odisha
Naga King	Nagaland, India
Mehma Sarja	Bathinda, Punjab

anther colour, fruit position, fruit tip, fruit colour and fruit shape were scored visually. Number of anthers was counted from five flowers per plant. Fruit length was measured with the help of scale. Seediness was scored by counting seeds from five red ripe fruits per plant; and pungency was assessed by organoleptic test. Clustering was done by UPGMA using SHAN module of Windostat version 8.6.

RESULTS AND DISCUSSION

Among 14 qualitative and quantitative traits scored, variation was not observed for mature fruit colour, corolla colour and number of anthers. These traits were, therefore, not considered for genetic diversity analysis. Earlier, Fonseca *et al.* (5) also reported that variation was not observed for corolla color, corolla shape, calyx pigmentation, days to fructification, duration of fructification and seed color. Bozokalfa *et al*. (4) studied patterns of phenotypic variation in a germplasm collection of chilli from Turkey and reported that all lines had green stem. Yumnam *et al*. (14) reported variation for fruit colour as the green colour shades. However, variation was reported for corolla colour and plant growth habit by Bozokalfa *et al*. (4); fruit shape by Fonseca *et al*. (5) and Yumnam *et al*. (14); leaf size by Yumnam *et al*. (14); pungency, fruit tip and leaf colour by Bozokalfa *et al*. (4); and fruit position by Fonseca *et al*. (5).

In the given set of collections, intermediate type of growth habit was found to be the most frequent (45.35%). This was closely followed by erect growth habit (43.75) and only few genotypes (4.6%) showed prostrate type of growth habit. Among the characters analyzed, pungency, fruit length, fruit shape and seediness are commercially important. With regard to pungency level, the germplasm was classified into three groups. These included mildly pungent (32.8%), pungent (64.1%) and highly pungent (3.1%). However, none was found to be non-pungent. Other than 'Naga King', the world known hot pepper, 'Punjab Longi' was regarded as highly pungent. Data regarding fruit length showed wide variation among the genotypes. Mean values for fruit length ranged from 1.46 cm in 'Punjab Longi' to 16.23 cm in 'Faslima'. Of the total germplasm analyzed, 2.6% have fruit length ≤ 1.0 cm, 15.8% between 1.1 and 2.0 cm, 39.5% between 2.1 and 4.0 cm, 39.5% between 4.1 and 8.0 cm and 12.6% have fruit length more than 8.0 cm. A wide variation among the test genotypes was also observed for seediness. Number of seeds per fruit ranged from 46.0 in 'EC 532386' to 273.0 in 'MS-12'. Other genotypes with higher seed content included 'ACC-34-1' (269.0) and 'ACC-34' (205.0). The detailed genotypic data are not presented here.

Based on similarity co-efficient values, genetic relationship among the test genotypes were presented

in the form of dendrogram (Fig. 1). The UPGMA cluster analysis showed that the 64 genotypes were divided into two main clusters at similarity coefficient of 0.85. The first major cluster consisted of 45 genotypes and the second cluster consisted of 19 genotypes. The major cluster was further divided into two sub-groups at similarity coefficient of 0.62. The first sub-group of major cluster consisted of 26 genotypes, while the second sub-group consisted of 19 genotypes. The smaller cluster was further divided into two sub-groups at similarity coefficient of 0.44. The first sub-group consisted of seven, while second sub-group consisted of twelve genotypes. 'Punjab Longi' and 'Naga King' were clustered together in one group. Both the lines belong to high pungency group. The sixty four genotypes were finally divided into nine clusters. However, there were three clusters (1, 2 and 3) in the smaller group and six clusters (4 to 9) in the major group. Using 11 morphological descriptors, it was possible to distinguish 62 of the 64 genotypes evaluated. However, the available set of descriptors could not distinguish 'Sel 40' from 'ELS 82' (Fig. 1). There is need to evaluate these genotypes for additional descriptors to differentiate them from each other.

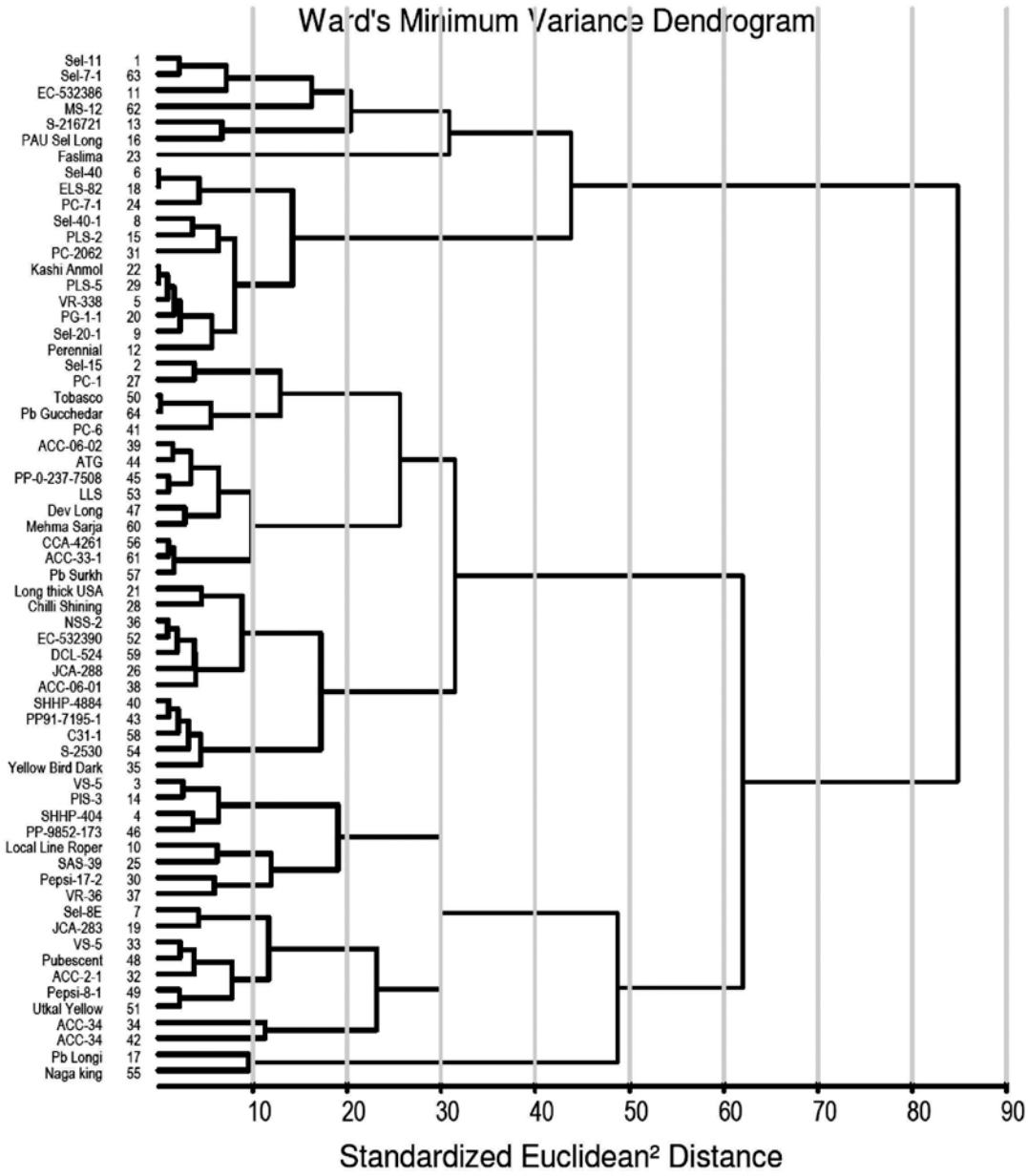

Fig. 1. Dendrogram depicting classification of 64 chilli genotypes based on 11 morphological descriptors.

Euclidean's inter- and intra-cluster distance matrices of 64 chilli genotypes based on 11 morphological descriptors are presented in Fig. 2 where each circle is represented by a cluster number. Numerical within the circle represent intra-cluster distance, whereas figures on the connecting lines denote the inter-cluster distances. The inter-cluster distance varied from 12.68 between Clusters 5 and 6 to 90.77 between Clusters 2 and 9. This indicated comparatively low to high level of genetic divergence between any two accessions of chilli. The genotypes, therefore, contained neither totally similar nor totally dissimilar accessions. The maximum intra-cluster distance matrix was observed in Cluster 1 (21.18) followed by Clusters 9 (19.15) and 8 (16.66). Cluster 5 exhibited the minimum intra-cluster variation (6.99). The Cluster 2 was represented by only one genotype 'Faslima'. Clustering patter of 64 chilli genotypes based on the Euclidean's analysis is given in Table 2.

The diversity analysis revealed that grouping of the genotypes was not based on their geographic distribution indicating that the geographic origins may not be true index for sampling genetic diversity in chilli. This is contrary to the earlier report of Loaiza Figueroa *et al.* (9) who found correlations of genetic differentiation with geographic isolation in chilli accessions from Mexico. Baral and Bosland (3) analyzed genetic diversity in *C. annuum* var. *annuum* landraces from Nepal and *C. annuum* var. *annuum* landraces from the centre of diversity, Mexico. All accessions from Nepal grouped into one cluster at a similarity index value of 0.80; whereas, accessions from Mexico grouped into 8 clusters at the same similarity level indicating greater genetic diversity in the accessions. This could be attributed to the fact that chilli has originated in Mexico and wide genetic diversity is still represented by different ecological regions of the country, whereas, in other geographic regions of the world only the improved genetic materials were introduced.

Based on the diversity analysis, genotypes clubbed in Cluster 9 (Punjab Longi and Naga King) and nuclear male sterile line MS 12 (Cluster 1), with inter-cluster distance of 44.99, were found to be the most divergent. Similarly, the cytoplasmic male sterile lines PP-0237-7508 and CCA 4261 represented in Cluster 5; PP-91-7195-1 in Cluster 6; and PP 9852-17 in Cluster 7 were found to be the most divergent from Faslima represented in Cluster 2; and Selection-8E, JCA 283, VS 2, Pubescent, Acc 2-1, Pepsi 8-1, Utkal Yellow, Acc 34 and Acc 34-1 represented in Cluster 9. Since heterosis has direct correlation with diversity between the parental lines (Geleta *et al.*, 6; Reif *et al.*, 10), crosses between the identified parental lines are likely to produce heterotic hybrids. For estimation of gene effects, mapping of useful genes and breeding

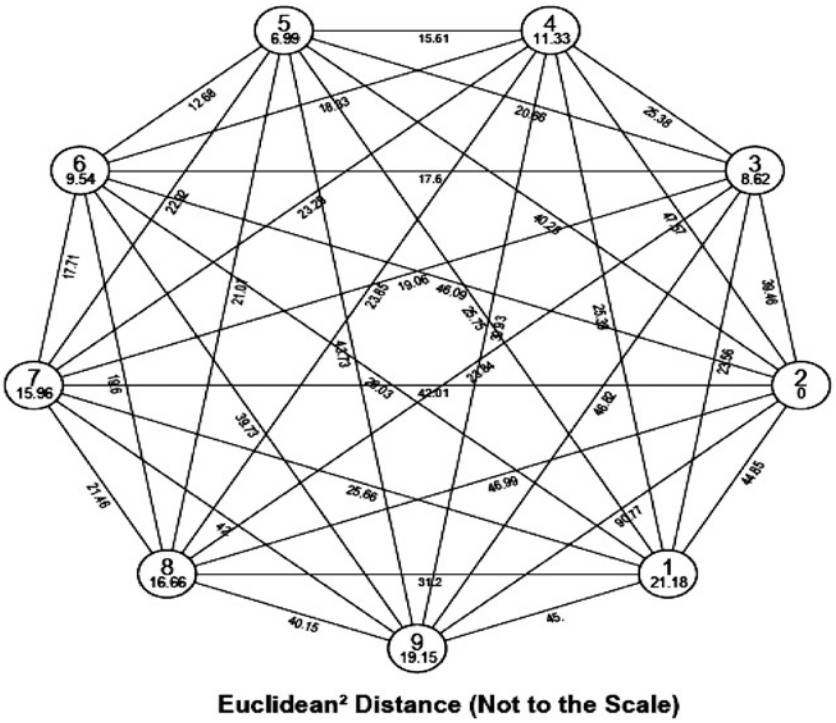

Fig. 2. Euclidean inter- and intra-cluster distance matrix of 64 chilli genotypes based on 11 morphological descriptors.

Table 2. Clustering pattern of 64 chilli genotype on the basis of Euclidean's analysis.

Cluster No.	No. of genotype(s)	Name of accession(s)
Cluster-1	6	Selection-11, Selection-7-1, EC-522386, MS-12, S217621, PAU Selection Long
Cluster-2	1	Faslima
Cluster-3	12	Selection-40, ELS-82, PC-7-1, Selection-40-1, PLS-2, PC-2062, Kashi Anmol, PLS-5, VR-338, PG1-1, Selection-20-1, Perennial
Cluster-4	5	Selection-15, PC-1, Tobasco, Punjab Gucchedar, PC-6
Cluster-5	9	ACC-06-02, ATG, PP-0-237-7508, LLS, Dev Long, Mehma Sarja, CCA-4261, ACC-33-1, Punjab Surkh
Cluster-6	12	Long Thick USA, Chilli Shining, NSS-2, EC-532390, DCL-524, JCA-288, ACC-06-01, SHHP-4884, PP-91-7195-1, C31-1, S-2530, Yellow Bird Dark
Cluster-7	8	VS-5, PLS-3, SHHP-404, PP-9852-173, Local Line Ropar, SAS-39, Pepsi-17-2, VR-36
Cluster-8	9	Selection-8E, JCA-283, VS-2, Pubescent, ACC-2-1, Pepsi-8-1, Utkal Yellow, ACC-34, ACC-34-1
Cluster-9	2	Punjab Longi, Naga King

of superior performing crop cultivars, parental lines from Clusters 2 and 9, with maximum inter-cluster distance, can be involved.

Our results vindicated that India is an important source of genetic variability of cultivated chilli. The relevance of morphological descriptors in genetic diversity analysis in chilli has been emphasized. This is evident from the fact that by using 11 polymorphic traits, the clustering analysis differentiated all 64 chilli genotypes from each other, except Selection 40 and ELS 82.

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