Original Research Article

Genetic Diversity for Fruit Quality Traits in EliteCapsicum(*Capsicum Annuum*) Germplasm Lines

ABSTRACT

The study aimedto assess the genetic diversity of twenty-two elite capsicum (*Capsicum annuum* L.) germplasm linesacross nine quanlitative traits. The researchwas conducted atthe research farm of ICAR-Indian Institute Horticultural Research, Hessaraghatta, Bengaluru, Karnataka, during 2014-2015 period. The experimental design employedwasa randomized complete block design with three replications. The quality parameters under studyincludedfruit length (cm), fruit width (cm), pericarp thickness (mm), placenta length (cm), placenta width (cm), total soluble solids (°Brix), fruit to seed ratio, seed number and total capsaicinoids (Scoville Heat Units). Based on the performance of the study, a cluster analysis of twenty-two chilli germplasm lines were grouped into three clusters. Cluster I had a maximum ofsixteengenotypes and clusters III had a minimum of onegenotype. The highest inter–cluster distance(60.521)was observed in between clusters I and II and the lowest (17.964) in between clusters I and III. Among the traits examined,fruit length and total capsaicinoidscontributed the most to the genetic divergence. Considering group cluster analysis, mean performance and variability,it is recommended to explore inter genotypic crosses between cluster I and cluster II, as well as cluster I and cluster III, for future hybridization programmesinchilli crop improvement.

Keywords: Genetic diversity; fruit quality; capsicum; germplasm; TSS; cluster analysis.

1. INTRODUCTION

Chillialso known as hot pepper, sweet pepper, paprika, pimiento, cayenne or bird eye pepper, is an economically important crop belonging to the botanical species *Capsicum annuum* within the Solanaceae family. Chilli is believed to have originated around 7000 B.C in Mexico and Central America [1]. Peppers are considered one of the earliest spices used by humans,with archaeological evidence dating back as far as 6000 years ago [2].Currently, there are five recognized cultivated species (*C. annuum*, *C. baccatum*, *C. chinense*, C. *frutescens* and *C. pubescens*) and there are at least 20-30 reported wild species,all of which are diploid with a chromosome count of 2n=2x=24.Most of these species are self-compatible and self-pollination predominatesamong thecultivated varieties. It was introduced to India in 1498 by Portuguese

traders,since its arrival,chilli has become an indispensable commodity in every Indian cuisine due to its pungency, spicy taste, appealing color and flavor. Today, India stands as the world's leading producer and exporter ofchilli,contributing42% of global chilli production. In India, chillicultivation covers an area of 8.82 thousand hectares,yielding a production of 18.36 lakh tons[3].

Genetic diversity and the relationships between various genotypes play a crucial role in enhancing crop quality. Morphological characteristics are often difficult since most of these characteristics are under the influence of environmental factors. However, genetic diversity estimation among plant genotypes allowsa more reliable differentiation of the genotypes. Analyzing genetic diversity proves valuable for selecting diverse parental combinations, reliable classifying accessions, and precisely identifyingvarieties. The characterization of germplasm is important for the conservation and effective utilization of plant genetic resources [4].The presence of genetic divergence within a population serves as a valuabletool for selecting suitable parents and utilization in any crop breeding programmes leading to reduction in the number of required crosses [5].The selection of parents depends on the specific objectives of the research programme and their performance. Various statistical analyses are available to aid in the selectionof suitable parents. Understanding the nature and extend of genetic divergence is essential for breederswhen selecting the most suitable parents for purposeful hybridization in heterosis breeding [6,7,8]. In order to benefit transgressive segregation, the knowledge of genetic distance between parents is essential[9,8].The Euclidean distance can be employed as a theoretical measure to estimate the genetic distance between parents, with the aim of maximizing transgressive segregation[10].It is important to note that ahigher genetic distance between parents leads to increased heterosis in the progeny [11]. In the present study, twenty-two chilligenotypes were collected from various regions and cultivated followinga standard package of practices at the research farm of ICAR-Indian Institute of Horticultural Research, Bengaluru. These genotypes were then analyzed for their genetic diversity based on fruit quality traits in elite capsicum germplasm lines.

2. MATERIALS AND METHODS

The experimental study was conducted at Research Farm of Vegetable crops Block number VIII of ICAR-Indian Institute of Horticultural Research, Bengaluru, Karnataka, during 2014-2015.The soil of the experimental site is red loamy,comes under zone-5 of region-3 among the agro-climatic zones of Karnataka state andis situated in the eastern dry zone at 12.58 ºN latitude and 77.45 ºE longitude at an altitude of 930 meters above mean sea level.The average rainfall in this region is800 mm, well-distributed over a period of five to six months from May to October, with peaks during September.The experimental study was laid out in randomized complete block design with three replications. The four weeks old seedlings oftwenty-two chilli germplasm lines (Table 1)were transplanted witha spacing of 60 cm x 20 cm. Recommended doses of fertilizersand standard cultivation practices were followed.Weeding and irrigation were given to the plants whennecessary.The fruits were harvested at fully matured red-ripe stage, oven-dried and powdered. Important quantitative characterssuch as fruit length (cm), fruit width (cm), pericarp thickness (mm), placenta length (cm), placenta width (cm), TSS (°Brix), fruit to seed ratio, seed number andtotal capsaicinoids (SHU) were recorded from the

randomly selected five plants of each plot andthe collectedmean data of two-season crops were subjectedto statistical analysis.Analysis of variance and cluster analysis were performed using the statistical software window stat and statistical package for agricultural research (SPAR) version 2.0 programme. The genetic divergence was calculated according to Mahalanobis D^2 statistic [12].

Table 1. *Capsicum* germplasm lines used in the study

Sl. No.	Accession No.	Capsicum species
1.	IHR 500	*Capsicum annuum*
2.	IHR 1485	*Capsicum annuum*
3.	IHR 2451	*Capsicum annuum*
4.	IHR 3014	*Capsicum annuum*
5.	IHR 324	*Capsicum baccatum*
6.	IHR 3241	*Capsicum baccatum*
7.	IHR 3315	*Capsicum annuum*
8.	IHR 3443	*Capsicum annuum*
9.	IHR 3447	*Capsicum annuum*
10.	IHR 3448	*Capsicum annuum*
11.	IHR 3449	*Capsicum annuum*
12.	IHR 3453	Derivative of *Capsicum chinense*
13.	IHR 3455	*Capsicum annuum*
14.	IHR 3476	*Capsicum annuum*
15.	IHR 4357	*Capsicum chinense*
16.	IHR 4500	*Capsicum chinense*
17.	IHR 4501	Natural cross between *Capsicum chinense*and*Capsicum frutescens*
18.	IHR 4502	*Capsicum chinense*
19.	IHR 4503	*Capsicum annuum*
20.	IHR 4506	*Capsicum annuum*
21.	IHR 4517	*Capsicum annuum*
22.	IHR 4550	*Capsicum chinense*

3. RESULTS AND DISCUSSION

3.1 Cluster analysis

The analysis of variance exhibited significant differences among the genotypes for all the traits under study which indicated a considerable amount of genetic variability and was subjected to further analysis.Thecomputation from the distance matrixwas given on-hierarchical clustering basedonMahalanobisD^2 values among twenty–two chilligenotypes and grouped them into three clusters (Table 2).It was explained that cluster I contained the highest number of genotypes (16), followed by Cluster II,which consistedof fivechilli genotypes. Cluster III was composed of a single genotype which is IHR 3443. This indicated that this genotype is different from other genotypes used in this study.

Table 2. Distribution of *Capsicum* germplasm lines into three different clusters in the study

Cluster No.	Number of germplasm lines	Germplasm lines
I	16	IHR 1485, IHR 2451, IHR 3014, IHR 3240, IHR 3241, IHR 3315, IHR 3447, IHR 3448, IHR 3449, IHR 3453, IHR 3455, IHR 3476, IHR 4502, IHR 4503, IHR 4506, IHR 4517,
II	5	IHR500, IHR 4357, IHR 4500, IHR 4501, IHR 4550
III	1	IHR 3443

Cluster analysis allowed a natural grouping of the genotypes, although groupings of different clusters indicate that there is no firm conclusion regarding the relation between genetic divergence and geographical distance in capsicum. Accordingly, different measurement techniques canbe appropriately used for genotype grouping [13,14]. Evaluation of genetic diversity can be useful for the selection of efficient genotypes and if such efforts result in reduction of diversity, the production of crop plants with higher uniformity may assure the supply of nutrients to under nourished population of the world. Consequently, it is suggested that choosing a parent for hybridization or in other crop improvement programmes need not necessarily be based on geographical distance. Some of the desirable genotypes identified by the study include: IHR 4506, IHR 1485, IIHR-3453, IHR 2451, IHR 4517, IHR 3448, IHR 3240, IHR4503, IHR 3455, IHR 3315, IHR3447, IHR3449, IHR 3014, IHR 3241, IHR 4502 in cluster I, IHR 4550, IHR 4357, IHR 4500, IHR4501, IHR 500, in cluster II, and IHR 3443 in cluster III.

Breeding and development of superior varieties requires prior quantitative assessment of genetic divergence in the available gene pool. The genetic distance was observed between clusters I and II (60.521). According to Mahalanobis D^2 statistics, the intra and inter-cluster distance (D^2) values are presented in Table 3. The inter-cluster distances were larger than the intra cluster distances. The inter-cluster distance was the maximum between clusters I and II (60.521), indicating wide genetic diversity between these two-cluster followed by the distance between cluster II and III

Table 3. The inter and intra cluster distances (D^2) of twenty- two *Capsicum*germplasm lines

Cluster	Cluster1	Cluster 2	Cluster 3
Cluster 1	**22.603**	60.521	17.964
Cluster 2		**27.697**	60.337
Cluster 3			**0.000**

Table 4. Percent contribution of 9 traits to total divergence in twenty-two *Capsicum* germplasms

Sl. No.	Characters	Number of times ranked first	Contribution %
1.	Fruit length (cm)	24	11.4286
2.	Fruit width (cm)	17	8.0952
3.	Pericarp thickness (mm)	0	0.0000
4.	Placenta length (cm)	1	0.4762
5.	Placenta width (cm)	10	4.7619
6.	TSS (^{o}Brix)	0	0.0000
7.	Fruit to seed ratio	0	0.0000
8.	Seed number	6	2.8571
9.	Total capsaicinoids(SHU)	44	20.9524

(60.337).Genotypes from these two clusters if they involve hybridization, may occur across a wide spectrum of segregating populations as genetic diversity is very distinct among the groups. The selection of divergent genotypes from clusters would produce a broad spectrum of variability for the morphological and quality traits studied, which may enable further selection and improvement. The minimum inter-cluster distance was observed between cluster I and cluster III (17.964), indicating that the genotypes of these clusters were genetically close to each other.According to Kumar et al.[15], the hybrid of genotypes with maximum distance resulted in high fruit quality and thus the cross between the genotypes from clusters I and II can be used in capsicum breeding to achieve maximum heterosis. The minimum distance was between the genotypes of clusters I and III (17.964), which can be used for backcrossing programmes. Similar to findings by Sundaram et al. [16]which reported that cluster analysis can prove useful for finding high quality capsicum genotypes. Further studies reported by Indira [17]; Roy &Sorma[18]; Mishra et al. [19] also indicate the presence of a high genetic divergence among capsicum genotypes in their respective experiments.Considering the main component of diversity, the total capsaicinoid content contributed 20.95% towards diversity analysis in the present study (Table 4).The D^2 statistic has been found as a tool to estimate genetic divergence and being a numerical estimate, it has added advantage over other criteria permitting precise comparison among all possible pairs of population in any group.

3.1.1 Performance of fruit quality characters in various clusters

The cluster mean values of nine different characters for three clusters are summarized in Table 5. Differences in cluster means existed for almost all the characters studied. The highest mean values for fruit width (cm), pericarp thickness (mm), placenta length(cm), placenta width(cm),total soluble solid (°Brix), fruit to seed ratio andtotal capsaicinoid (SHU)

were observed in cluster II,which means the genotypes in cluster II group have the genetic potential to contribute to better performance for maximization of chilli genotypes. Cluster III had the genotypes that showed the lowest mean value for almost all the characters studied, indicating that the selection of genotypes from these cluster for future chilli breeding programmes has no positive impact.

Table 5. Mean values of different fruit quality traits cluster-wise among twenty-two *Capsicum* germplasm lines

Sl. No.	Characters	I	II	III
1.	Fruit length (cm)	7.855	4.265	8.525
2.	Fruit width (cm)	1.435	1.835	0.800
3.	Pericarp thickness (mm)	2.180	2.840	1.575
4.	Placenta length (cm)	1.633	1.740	0.625
5.	Placenta width (cm)	1.500	1.875	0.725
6.	Total soluble solids (°Brix)	9.210	21.705	10.800
7.	Fruit to seed ratio	1.945	2.662	1.670
8.	Seed number	82.100	36.950	81.750
9.	Total capsaicinoids (SHU)	255.709	1758.07	279.225

Crop improvement is made by generating variability in desired traits, followed by selection. Continued success in crop improvement can only be realized when substantial variability is found and used in a population. Divergence between any two parents expresses the allelic difference between them[20]. The genotypes grouped into the same cluster presumably diverge very little from one another. Crossing of genotypes belonging to the same cluster is not expected to produce fruit character segregants. Consequently, a crossing programme should be conducted with putative parents belonging to different characters. Therefore, crosses between the members of cluster separated by inter-cluster distance are likely to be beneficial for further improvement.

4. CONCLUSIONS

A significant diversity in fruit quality traits was evident among the twenty-two studied Capsicum genotypes, which were sources from diverse eco-geographical regionswithin the countryand interestingly, there was no correlation between their genetic diversity and geographical origins. Total capsaicinoidscontent was the most significant primary contributor to genetic divergence, followed by fruit length, fruit width, placenta width and seed number. Additionally, it was revealed that genotypes belonging to clusters I and II exhibited promising economic traits, indicating theirsuitability for inclusion in effortsto genetically improve Capsicum varieties.

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