Research Article

GENETIC DIVERGENCE STUDIES IN BELL PEPPER (*Capsicum annuum* L. var. Grossum) UNDER MID HILL CONDITIONS OF SOLAN DISTRICT OF HIMACHAL PRADESH

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Abstract: Bell pepper (*Capsicum annuum* L. var. grossum), a member of family Solanaceae, is commonly known as sweet pepper or capsicum. Genetic divergence plays a key role in analyzing the general distance among the genotypes selected as parents. The assessment of genetic divergence helps in identification of breeding lines with broad spectrum of genetic variability thus providing better scope to isolate superior recombinants. The present investigations were carried out at the Experimental Farm of Department of Vegetable Science, Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan HP. The experiment was laid out in a Randomized Complete Block Design (RCBD) with twenty-five genotypes in three replications. The results concluded that for the traits, where selection is not effective, genetic divergence can play an important role on further partitioning of variability. The results grouped twenty-five genotypes into four clusters. The hybridization between genotypes of cluster II and cluster III can be utilized for getting superior recombinants or transgressive segregants in segregating population because these clusters were found most divergent.

Keywords: Bell pepper, Genetic divergence, transgressive segregants

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Introduction

Bell pepper, commonly known as 'Shimla Mirch' is one of the most popular and highly remunerative fresh vegetable grown worldwide due to its combination of colour, flavour, and nutritional value. It occupies a pride of place among the vegetables in Indian cuisine due to its delicate taste and pleasant flavour coupled with rich ascorbic acid, minerals and vitamins. In India, it was first introduced by the Britishers in Nineteenth century in Shimla hills [1] therefore, known as 'Shimla Mirch'. It is now widely cultivated in Himachal Pradesh, Jammu and Kashmir, hills of Uttar Pradesh, Andhra Pradesh and Nilgiris during summer months and as an autumn crop in Karnataka, Tamil Nadu, Maharashtra, Bihar, West Bengal and Madhya Pradesh. In India, bell pepper is cultivated over an area of about 46,000 ha with a production of 288,000 MT [2]. In Himachal Pradesh, bell pepper is grown as an off-season crop during the summer and rainy seasons and is economically important to small and marginal farmers. There are a very few varieties available for cultivation in bell pepper in the public sector which has led to near genetic uniformity among these cultivars. Few old introductions like California Wonder are still recommended for commercial cultivation. Now a day's farmers are largely dependent on the private sector for the supply of seed. Genetic restructuring of the bell pepper germplasm in public sector is the need of the hour. Genetic divergence plays a key role in analyzing the general distance among the genotypes selected as parents. Within a certain limit, hybridization of more divergent parents is expected to enhance the level of heterosis and generate wide range of variability in segregating generations. The assessment of genetic divergence helps in identification of breeding lines with broad spectrum of genetic variability thus providing better scope to isolate superior recombinants. D^2 statistic developed by Mahalanobis (1936) is effective tool to measure genetic divergence among genotypes in any crop plant.

Materials and Methods

The present investigations were carried out at the Experimental Farm of Department of Vegetable Science, Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan HP during Kharif, 2017. The experimental site of the Department of Vegetable Science is located at Nauni, about 13 km from Solan, at an altitude of 1276 m above mean sea level lying between latitude 30°52' 30" North and longitude 77° 11' 30" East. It falls in sub-humid, sub temperate and mid-hill zone of Himachal Pradesh. The experiment was laid out in a Randomized Complete Block Design (RCBD) with twenty-five genotypes in three replications. Sixteen seedlings of each entry were transplanted on April 21, 2017 at a spacing of 60 × 45 cm in a plot size of 2.4 m × 1.80 m in each replication. Data were recorded on five randomly taken plants from each plot/treatment and the average was worked out to record the mean value in each replication for all the characters under study. The observations were recorded for various horticultural and yield traits *viz*., Days to first picking, Number of branches per plant, Plant height (cm), Fruit shape, Fruit colour, No. of lobes per fruit, Fruit length (cm), Fruit breadth (cm), Fruit Weight (g), Pericarp Thickness (mm), No. of fruits per plant, Fruit yield /plant (g), No. of seeds / fruit, Thousand seed weight (g), Total Soluble Solids (o B) and Ascorbic acid content (mg/100 g), Phytopthora fruit rot incidence, Phytopthora leaf blight incidence.

Results and Discussion

In genetic studies the study of genetic divergence is used to differentiate well defined population and to choose suitable parents for obtaining heterotic hybrids and cross combinations that are likely to provide better recombinants with desired agronomic values in later generations. The theoretical background of Mahalanobis D^2 statistics or generalized distance among group constellation has been critically discussed in a series of communications [3,4]. The D^2 statistics was found to be an effective tool among the various techniques available for genetics differentiation among population [5-7]. Estimating genetic diversity and determining the relationships between germplasm collections helps to ensure that germplasm is efficiently collected and managed.

In the present investigation twenty-five genotypes were grouped in to three clusters based on Mahalanobis D^2 values. The cluster I contained thirteen genotypes, cluster II contained five genotypes and cluster III contained seven genotypes. Group constellation of bell pepper genotypes through genetic divergence has also been reported by earlier workers like Sudre *et al.* (2006), Buttow *et al.* (2010), Farhad *et al.* (2010), Ghazizadeh *et al.* (2010), Monteiro *et al.* (2010), Zadeh *et al.* (2010), Misra *et al.* (2011), Maga *et al.* (2012) and Occhiuto *et al.* (2014) [8-17].

Table-1 *Bell pepper genotypes along with sources of collection*

SN	Genotype	Source
1	Palam Bell	IARI Regional Station, Katrain (Kullu Valley)
2	Yolo Wonder	IARI Regional Station, Katrain (Kullu Valley)
3	Arka Basant	IARI Regional Station, Katrain (Kullu Valley)
4	Nishat	IARI Regional Station, Katrain (Kullu Valley)
5	Harit Red Fruit	IARI Regional Station, Katrain (Kullu Valley)
6	HC-201 PL-3	IARI Regional Station, Katrain (Kullu Valley)
7	CW-308	IARI Regional Station, Katrain (Kullu Valley)
8	RY.PL-1	IARI Regional Station, Katrain (Kullu Valley)
9	PT.12.3	IARI Regional Station, Katrain (Kullu Valley)
10	KC-10	IARI Regional Station, Katrain (Kullu Valley)
11	KC-11	IARI Regional Station, Katrain (Kullu Valley)
12	KC-12	IARI Regional Station, Katrain (Kullu Valley)
13	IIVR CW	IIVR, Varanasi, UP
14	Nirmal Karol	Village Karol, P.O – Kandaghat
15	Dyarag Selection	Village Dyarag, P.O – Juanji, Solan
16	Deothi Selection	Village Deothi, P.O – Solan
17	Kadar Selection	Village Kadar, P.O – Kandaghat
18	Ghalai Selection	Village Ghalai, P.O – Kandaghat
19	Tikker Selection	Village Tikker, P.O – Solan
20	YW.PL-4	Department of Vegetable Science, UHF, Nauni
21	UHFBP-3	Department of Vegetable Science, UHF, Nauni
22	UHFBP-5	Department of Vegetable Science, UHF, Nauni
23	UHFBP-6	Department of Vegetable Science, UHF, Nauni
24	CW.PL-2	Department of Vegetable Science, UHF, Nauni
25	Solan Bharpur*	Department of Vegetable Science, UHF, Nauni

Solan Bharpur = check variety

Table-2 *Clustering pattern of twenty-five genotypes on the basis of genetic divergence*

Cluster	Number of genotypes	Genotypes
I	13	Harit Red Fruit, HC-201-PL-3, PT.12.3, KC-12, Nirmal Karol, Dyarag Selection, Deothi Selection, Ghalai Selection, Tikker Selection, UHFBP-3, UHFBP-5, UHFBP-6, Solan Bharpur
II	5	Yolo Wonder, CW-308, IIVR CW, YW.PL-4, CW.PL-2
III	7	Palam Bell, Arka Basant, Nishat PL-2, RY.PL-1, KC-10, KC-11, Kadar Selection

Table-3 *Average intra (Diagonal) and inter- cluster (Lower half diagonal) distance (D^2)*

Clusters	I	II	III
I	2.895		
II	3.84	3.147	
III	3.008	4.351	3.961

Table-4 *Cluster means for different trait in twenty-five genotypes of bell pepper*

Characters	I	II	III
Days to first picking	70.62	71	73
Number of branches per plant	2.86	3.28	2.76
Plant height (cm)	72.05	70.08	81.2
Number of lobes per fruit	2.96	3.65	3.14
Fruit length (cm)	7.22	8.19	6.93
Fruit breadth (cm)	5.38	5.45	5.58
Fruit weight (g)	57.16	81.51	54.49
Pericarp thickness (mm)	4.79	5.17	5.01
Number of fruits per plant	13.6	10.47	12.07
Fruit yield per plant (g)	769.13	853.64	627.91
Number of seeds per fruit	197.34	229.31	192.11
Thousand seed weight (g)	6.45	6.85	8
Total soluble solids (⁰B)	5.56	6.12	5.74
Ascorbic acid (mg/ 100g)	127.21	146.51	135.4

Average inter-cluster and intra-cluster distance (D^2) values are presented in Table II. The diagonal figures in the table represent the intra-cluster distance. The intra-cluster distance varied from 2.895 (cluster I) to 3.961 (cluster III). The inter cluster distance was maximum to the tune of 4.351 between cluster II and III followed by cluster I and II (3.840) and cluster I and III (3.008). The minimum inter cluster distance was observed for cluster I and III (3.008). The cluster with higher inter cluster distances indicated that the genotypes included in those clusters had high genetic variation and hybridization between genotypes of these cluster may result heterotic progenies because of convergence of diverse genes scattered in parents .A wide range of inter cluster genetic distance among the different cluster of bell pepper genotypes have also been reported by Sudre *et al.* (2006), Buttow *et al.* (2010), Farhad *et al.* (2010), Ghazizadeh *et al.* (2010), Monteiro *et al.* (2010), Zadeh *et al.* (2010), Misra *et al.* (2011), Maga *et al.* (2012) and Occhiuto *et al.* (2014). Furthermore, for getting the reliable conformity on the basis of cluster means, it was calculated for various horticulture traits and had been represented in Table IV. Minimum days to first picking were observed in cluster I (70.62) followed by cluster II (71.00) and cluster III (73.00). Cluster II exhibited maximum mean value for number of primary branches (3.28) followed by cluster I (2.86) and cluster III (2.76). Cluster III recorded maximum plant height (81.20 cm) followed by cluster I (72.05 cm) and cluster II (70.08 cm). Number of lobes per fruit were maximum in cluster II (3.65) followed by cluster III (3.14) and cluster I (2.96). Maximum fruit length was exhibited by cluster II (8.19 cm) followed by cluster I (7.22 cm) and cluster III (6.93 cm), while maximum fruit breadth was recorded in cluster III (5.58 cm) followed by cluster II (5.45 cm) and cluster I (5.38 cm). Fruit weight was maximum in cluster II (81.51 g) followed by cluster I (57.16 g) and cluster III (54.49 g). For pericarp thickness, cluster II (5.17 mm) exhibited maximum value followed by cluster III (5.01 mm) and cluster I (4.79 mm). Maximum number of fruits per plant was observed in cluster I (13.60) followed by cluster III (12.07) and cluster II (10.47). Fruit yield per plant was recorded maximum in the cluster II (853.64 g) followed by cluster I (769.13 g) and cluster III (627.91 g). Cluster II exhibited maximum number of seeds per fruit (229.31) followed by cluster I (197.34) and cluster III (192.11). Whereas maximum thousand seed weight was observed in cluster III (8.00 g) followed by cluster II (6.85 g) and cluster I (6.45 g). Highest total soluble solid was recorded in cluster II (6.12 0B) followed by cluster III (5.74 0B) and cluster I (5.56 0B). The highest ascorbic acid content was recorded in cluster II (146.51 mg/ 100g) followed by cluster III (135.40 mg/ 100g) and cluster I (127.21 mg/ 100g). Similar results were also recorded by earlier workers like Sudre *et al.* (2006), Buttow *et al.* (2010), Farhad *et al.* (2010), Ghazizadeh *et al.* (2010), Monteiro *et al.* (2010), Zadeh *et al.* (2010), Misra *et al.* (2011), Maga *et al.* (2012) and Occhiuto *et al.* (2014). For those traits, where selection is not responsive and non-additive gene action plays a major role in the expression, hybridization between diverse parents on the basis of their cluster mean performance is advocated to get superior hybrids in F1 or transgressive segregants in subsequent generations. In the present studies, on the basis of genetic divergence, twenty five genotypes were grouped in to three clusters. Maximum number of genotypes were accommodated in cluster I. Average intracluster distance was maximum in cluster III (3.961) and minimum in cluster I (2.895). The inter cluster distance was recorded maximum to the tune of 4.351 between cluster II and III, indicating that hybridization between the genotypes from cluster II and III can be utilized for getting superior recombinants/transgressive segregants in segregating generations of bell pepper. Furthermore, cluster means of the various characters indicated that among the three clusters, cluster II was found superior for important traits *viz*., fruit length (cm), fruit weight (g), pericarp thickness (mm), number of seeds per fruit, number of lobes per fruit, fruit yield per plant (g), number of branches, total soluble solids (0B) and ascorbic acid content (mg/100 g). Cluster III was found superior for the traits like days to first picking, plant height (cm) and thousand seed weight (g). Cluster I was found superior for number of fruits per plant.

Application of research: Study of genetic divergence is used to differentiate well defined population

Research Category: Genetic divergence

Author Contributions: All authors equally contributed

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Conflict of Interest: None declared

Study area / Sample Collection: Experimental Farm of Department of Vegetable Science, Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan HP during Kharif, 2017
Cultivar/ / Variety name: *Capsicum annuum* L. var. Grossum

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.
Ethical Committee Approval Number: Nil

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