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Genetic Diversity Studies in Green Chilli (*Capsicum annum* L.) for Growth, Yield and Quality Parameters

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The present investigation was carried out at College of Horticulture, Bagalkot during *Kharif*2019-2020. Thirty eight chilli genotypes were evaluated for assessing genetic divergence for exploitation in breeding programme aimed at improving yield potential by using MahalanobisD^2 statistics. The genotypes showed significant variation for most of the traits like number of primary branches, number of secondary branches, number of fruits per, capsaicin content, fruit color and green fruit yield per plant indicating sufficient genetic variability and scope for better crop improvement. Genetic diversity analysis, based on D^2values grouped into eight clusters with highest inter cluster distance of 14.39 between cluster V and VI. Based on D^2values, the test genotypes were grouped into eight clusters and among them, cluster I was the largest with 18 genotypes, followed by Cluster II with 8 genotypes, Clusters VI and IV had 4 genotypes, whereas clusters III, V, VI and VIII had solitary genotypes. Intra cluster distance was found highest in Cluster VIII and V (23.54), followed by followed by clusters IV and V (D^2= 22.79), clusters III and VIII (D^2= 20.89), clusters II and IV (D^2= 20.40), clusters IV and VI(D^2= 20.16), cluster I and cluster V (D^2= 20.09), clusters III and IV (D^2= 19.29), cluster I and cluster VIII (D^2= 18.36), clusters V and VII (D^2= 18.15), clusters VI and VIII (D^2= 18.12), clusters IV and VII (D^2= 17.35), clusters I and VII (D^2= 17.21), clusters VI and VII(D^2= 17.07), clusters II and VI (D^2= 16.95), clusters II and VII (D^2= 16.94). The lowest inter- cluster distance between clusters III and V was observed (D^2= 7.76).Presence of significant difference for number of fruits per plant, test weight among the genotypes provides an opportunity to identify suitable genotypes through breeding programmes.

Introduction

Chilli is a major vegetable cum spice crop, which belongs to the family Solanceae having chromosome no. 2n=24. The genus capsicum consists of 30 species among which five are under cultivation namely *Capsicum annuum, C. frutescens, C. chinense*, C. *pubescens*and *C.baccatum*.

India is considered as principal producer, consumer and exporter of chilli covering an area of 7.33 lakh ha which accounts 42.81 % in the world area. In India the major chilli producing states are Andhra Pradesh, Telangana, Madhya Pradesh, Karnataka and West Bengal with a percent of 35, 17, 12, 11 and 6 respectively.

Chilli is a source of various products are used throughout the world in different forms like as vegetable, spice, cosmetic industry, paints, insecticidal sprays, ayurvedic and allopathic medicine. The important characteristic feature of chilli is pungency which is due to the presence of a crystalline acrid volatile alkaloid known as capsaicin (8-methyl-N-vanillyl-6-enamide). These are used as soothing effects on digestive system, cold, sour throat acts as an heart stimulant which reduces heart attacks. Chilli peppers especially hotter varieties such as cayenne and habanero used as a remedy for painful joints and also to stop bleeding. Chilli can be used in non -conventional way as defensive sprays which consist of capsicum oleoresin.

The coloring agents, capsanthin or capsorubin, used in the feed of laying hens to colour the egg yolk and the skin of broilers apart from pharmaceutical and cosmetic industries (Tepic *et al.*, 2008). Chilli fruit contains a vast variety of antioxidant vitamins especially vitamin A and C, capsaicin, which determine the great variability of the fruits smell, flavour, taste and consequently consumer preference (Bhattacharya *et al.*, 2010). The chilli crop is mainly cultivated in sub-tropical and tropical countries like Africa, Japan, India, Mexico, USA and Turkey. The Capsicum genus mostly originated in arid regions of the Andes Mountains (Peru and Bolivia) and then migrated to tropical regions of the America. It consists of five different domesticated species of Capsicum, each being domesticated in a different geographic region of North, Central or South America (Walsh and Hoot, 2001). While its, primary center of the species *Capsicum annuum* is known to be Mexico and the secondary centers in Guatemala and Bulgaria (Salvador, 2002). In 17th Century, Portuguese introduced it into India.

The diversity present in crop genetic resources provide an assurance for future genetics progress and insurance against unforeseen threat to agricultural production. Assessment of genetic diversity in a set of genotypes or a population is required for choosing divergent genotypes as parents in various crossing programmes for breeding applications. Thus, genetic diversity analysis is of utmost importance in breeding not only for yield improvement but also for enhanced resistance to pest, disease and improved fruit quality.

Materials and Methods

The experiment on genetic diversity in green chilli genotypes (*Capsicum annumm* L.) was conducted at department of biotechnology and crop improvement, College of Horticulture, Bagalkot (Karnataka) during *Kharif* 2019-20 which is situated in northern dry zone of Karnataka between the 16^0 46’ North latitude and 74^0 59’ East longitude with an altitude of 533.0 meters above mean sea level.

The experiment was laid out in Randomized block design. A total of thirty eight genotypes were used in study. Observations on various traits was recorded on five randomly selected

plants from each genotype *viz.*, number of primary branches, number of secondary branches, number of fruits per, capsaicin content, fruit color, days to first flowering, plant height and green fruit yield per plant. Along with analysis of variance, genetic divergence was estimated was estimated using Mahalanobis D^2statistics (1936) and clustering was done according to Tocher's method as described by Rao (1952).

Results and Discussion

The analysis of variance (ANOVA) for fourteen characters are given in Table 1 revealed that, there was a high significant (both at P = 0.05 and P = 0.01) differences in the genotypes studied in chilli (Table 1) indicating high genetic variability and scope for improvement.

Based on D^2values, the test genotypes were grouped into 8 clusters and among them, Cluster I was the largest with 18 genotypes, followed by Cluster II with 8 genotypes, Clusters VI and IV had 4 genotypes, whereas clusters III, V, VI and VIII had genotypes.

Table.1 Analysis of variance (mean sum of squares) for growth, yield and quality parameters in chilli collections

Sl. No.	Source of variation/Characters	Replications	Treatments (Genotypes)	Error
	Degrees of freedom	**1**	**37**	**37**
I. Growth parameters				
1.	Plant height at 30 DAT (cm)	90.86	56.92**	24.79
2.	Plant height at 60 DAT (cm)	157.47	150.30**	50.53
3.	Plant height at 90 DAT (cm)	333.3	147.38**	66.45
4.	Plant height at 120 DAT (cm)	443.53	153.47**	53.80
5.	Primary branches	0.002	0.62**	0.03
6.	Secondary branches	0.000	1.98**	0.764
II. Earliness parameters				
1.	Days to first flowering	162.70	25.76*	11.64
III. Yield parameters				
1.	Number of fruits/plant	0.538	897.27**	31.24
2.	Fruit length (cm)	6.276	17.75**	0.905
3.	Fruit diameter (mm)	11.87	7.95**	1.36
4.	Test weight (g)	0.038	1.02**	0.096
5.	Green fruit yield / plant (g)	1154.4	4477.01**	741.44
IV. Quality parameters				
1.	Capsaicin (SHU)	0.002	0.16**	0.00
2.	Fruit color (ASTA)	1.135	1371.41**	12.07

Similar findings were observed by previous workers Vavilov (1926) and Moll *et al.*, 1962 indicating scope for choice of parents to create new variability through hybridization or recombination programme. Intra cluster distance was found highest in Cluster VIII and V (23.54), followed by clusters IV and V (D^2= 22.79), clusters III and VIII (D^2= 20.89), clusters II and IV (D^2= 20.40), clusters IV and VI(D^2= 20.16), cluster I and cluster V (D^2= 20.09), clusters III and IV (D^2= 19.29), cluster I and cluster VIII (D^2= 18.36), clusters V and VII (D^2= 18.15), clusters VI and VIII (D^2= 18.12), clusters IV and VII (D^2= 17.35), clusters I and VII (D^2= 17.21), clusters VI and VII(D^2= 17.07), clusters II and VI (D^2= 16.95), clusters II and VII (D^2= 16.94). The lowest inter- cluster distance between clusters III and V was observed (D^2= 7.76).Similar findings were reported by the Mishra *et al.*, (2004), Kumari *et al.*, (2010), and Lahbib *et al.*, (2012), Kumari *et al.*, (2018) and Hasan *et al.*, (2014).

The cluster means in respect to 12 characters and overall character wise averages across the 8 clusters are presented in Table 4. These results are in accordance with the findings of Kumari *et al.*, (2018), Nagaraju *et al.*,(2018) and Lahbib (2013).

Table.2 Clustering pattern of 38 genotypes of chilli based on D^2 analysis

Sl. No	Cluster no	No of genotypes	Genotypes name
1	I	18	ST-17, ST - 22, ST-5, ST-21, ST- 16 , ST-8, ST-25, ST-17 ,ST-3 , ST-18 , ST-9 , ST -6 , ST-13 , ST-14 , ST-23, AH , ST- 20, ST-4
2	II	8	ST-24, ST-1, ST-2 , ST-10, ST-19 , ST-15 , ST-11 , ST -12
3	III	1	PSB SEL-1 UC
4	IV	4	KCA19-3-PSB-3, AM, KCA -33 (A)-USF , KCA-19-1-PC-1
5	V	1	PSB EC
6	VI	4	PS , KCA - 33(B) - ULF , GPM-33 , PSB –DC
7	VII	1	GPM-40
8	VIII	1	Byadagidabbi

Table.3 Average intra cluster distances among clusters for 38 chilli genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII
I	**9.3**	14.61	15.04	14.99	20.09	20.6	17.21	18.36
II		**9.45**	13.53	20.4	15.68	16.95	16.94	15.72
III			**0.00**	19.29	7.76	13.44	14.23	20.89
IV				**9.29**	22.79	20.16	17.35	18.12
V					**0.00**	11.79	18.15	23.54
VI						**14.39**	17.07	20.21
VII							**0.00**	12.54
VIII								**0.00**

GV- Genotypic variance
PV- Phenotypic variance
GCV- Genotypic co-efficient of variation
PCV- Phenotypic co-efficient of variation
h^2bs– Heritability in broad sense
GA- Genetic advance
GAM- Genetic advance as % over mean

Table.4 Cluster means of 12 traits from D^2 analysis for 38 chilli genotypes

Sl. No	Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VII
1	PHat30	41.71	38.67	36.20	32.08	33.95	34.70	34.20	32.20
2	PHat60	83.02	78.21	81.30	68.78	75.40	66.25	79.80	62.70
3	PHat90	89.23	82.46	87.01	72.53	79.80	71.58	85.93	74.05
4	PHat120	93.03	86.14	91.25	75.96	82.70	75.68	88.20	80.60
5	NPB	2.34	3.24	2.90	2.00	3.35	3.10	2.00	2.30
6	NSB	4.50	5.59	5.00	4.15	6.50	6.14	3.40	3.40
7	DFF	39.57	41.77	42.50	38.63	41.60	43.19	37.80	39.00
8	NFF	39.31	35.49	56.75	76.54	79.15	82.53	45.25	32.65
9	FL	14.66	13.60	8.04	11.23	7.72	7.78	8.84	13.36
10	FD	11.30	11.56	9.28	9.87	9.81	10.93	16.94	16.37
11	TW	3.98	4.74	3.44	5.06	3.39	4.66	4.71	6.06
12	GYL	193.16	164.69	134.55	239.89	148.30	217.16	152.35	168.80

It could be concluded that the 38 chilli genotypes used in the present study differed significantly for most of the characters studied indicating appropriate genetic material with good amount of variability.. In the view of these cluster means indicate that it is desirable to select the ecotypes for the further breeding programme will be helpful. From this it is clear that the ecotypes used in present study are of diverse in nature, hence they may be used in the hybridization or recombination programme.

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