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Short Communication

Studies on genetic divergence for yield and quality traits in chilli (*Capsicum annuum* L.)

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ABSTRACT

A study was conducted to assess the genetic divergence of twenty-five chilli genotypes for fifteen parameters by adopting Mahalanobis D^2 statistics using Tocher's method. The genotypes were grouped into six clusters irrespective of their geographical divergence, indicating wide diversity among them. Cluster II was the largest with nine genotypes followed by Cluster I with eight genotypes, cluster III with four genotypes, cluster IV with two genotypes, and Clusters V and VI had only one genotype each. The maximum inter-cluster distance was observed between clusters V and VI followed by clusters IV and V and clusters III and IV. This indicates that hybridization between the genotypes belonging to clusters V and VI will be more rewarding for getting superior progenies in terms of yield and quality.

Keywords: Chilli, clusters, D^2 analysis, genetic divergence

INTRODUCTION

Capsicum annuum L. commonly known as chilli or hot pepper is a member of the family Solanaceae. It has a diploid genome with 12 pairs of chromosomes and is a partially self-pollinating crop (Allard, 1960). Because of its extensive out crossing in the field ranging from 7 to 90%, it is considered as a facultative cross-pollinating species (Singh et al., 1994, Joshi et al., 2000).

India holds the leading position in the production, consumption and export of chilli. In India, Andhra Pradesh, Telangana, Karnataka, Orissa, West Bengal, Maharashtra and Tamil Nadu are the leading chilli producing states. In India, green and dry chilli has an extensive annual production of 3851,000 MT in 364,000 ha acreage and 1702,000 MT in 683,000 ha, respectively (National Horticulture Board, 2020).

Due to the crop's long history of cultivation and selection within the Indian subcontinent, there is now enough genetic variation in the crop in terms of characteristics such as fruit shape, fruit weight, pungency, flower colour, plant height, and maturity that can be potentially be used for breeding purposes.

Table 1 : List of genotypes used along with their sources

Genotype	Source	Genotype	Source
LCC-1	Village Kyard, Solan (HP)	LCC-14	Village Jukhala, Bilaspur (HP)
LCC-2	Village Rouri, Solan (HP)	LCC-15	Village Namhol, Bilaspur (HP)
LCC-3	Village Hurang, Solan (HP)	LCC-16	Village Khadli, Solan (HP)
LCC-4	Village Nauti, Solan (HP)	LCC-17	Village Ruham, Solan (HP)
LCC-5	Village Badoh, Solan (HP)	LCC-18	Village Kando, Sirmaur (HP)
LCC-6	Village Rilli Kalan, Solan (HP)	LCC-19	Village Shilla, Sirmaur (HP)
LCC-7	Village Badounighat, Solan (HP)	LCC-20	Village Kamrou, Sirmaur (HP)
LCC-8	Village Bhaguri, Solan (HP)	LCC-21	Village Gangtoli, Sirmaur (HP)
LCC-9	Village Rampur, Solan (HP)	LCC-22	Gojatala, Sambalpur, Orissa
LCC-10	Village Salana, Sirmour (HP)	LCC-23	Jhankarpada, Sambalpur, Orissa
LCC-11	Village Kadyuth, Sirmour (HP)	LCC-24	Village Phallahi, Solan (HP)
LCC-12	Village Neri kotli, Sirmour (HP)	DKC-8	UHF, Nauni, Solan (HP)
LCC-13	Village Ser- Jagas, Sirmour (HP)		

Table 2 : Clustering pattern of 25 genotypes based on genetic divergence

Clusters	No. of genotypes	Genotype
I	8	LCC-1, LCC-2, LCC-4, LCC-12, LCC-14, LCC-18, LCC-20, LCC-23
II	9	LCC-3, LCC-6, LCC-7, LCC-19, LCC-11, LCC-13, LCC-15, LCC-16, LCC-24
III	4	LCC-8, LCC-19, LCC-21, LCC-22
IV	2	LCC-5, LCC-17
V	1	LCC-10
VI	1	DKC-8

(Verma et al., 2022) For the desired genetic improvement of any crop species, genetic diversity plays a crucial role in all types of cross-breeding programmes, as a crossing between genetically divergent parents leads to a large number of desirable segregants.

The present investigation was carried out using 25 diverse genotypes (Table 1) in randomized complete block design with three replications during the *kharif* season of 2019 at the Research Farm, Department of Vegetable Science, Dr Y.S. Parmar University of Horticulture and Forestry, Solan, Himachal Pradesh, under open conditions at a spacing of 45 cm × 45 cm. Standard cultural practices were followed to ensure a healthy crop stand.

The experimental site was located at 30°86' N and 76°17' E with an elevation of 1270 m above mean sea level. The mean temperature during the cropping season varied from 13.5 to 25.8ºC, while, the relative humidity varied from 44 to 79%. The observations pertaining to mature green fruit traits were recorded on five randomly selected plants and another five plants were tagged for recording red ripe fruit traits in each genotype of each replication. The data was subjected to multivariate analysis of genetic divergence using Mahalanobis D^2 statistic. The grouping of entries was done by Tocher's method (Rao, 1952).

The results from the analysis of variance for fifteen parameters indicated significantly high differences among twenty-five genotypes of chilli under study. These 25 genotypes were grouped into six clusters (Table 2) based on Mahalanobis D^2 values. Cluster II was the largest with nine genotypes followed by Cluster I with eight, cluster III with four and Cluster IV with two genotypes, respectively. Whereas, clusters V and VI had only one genotype each. Genotypes from the same geographical origin were placed in different clusters, indicating wide diversity among them. This may be due to the frequent exchange of germplasm between the different geographical regions. Group constellation of chilli genotypes through genetic divergence has also been reported by Vanitha & Jansirani (2017) and Singh et al. (2023).

It is evident from Table 3 that maximum intra-cluster distance ($\sqrt{D^2}$) was found in cluster III (268.24) followed by cluster II (216.67), cluster I (191.89) and cluster IV (75.90). The intra-cluster ($\sqrt{D^2}$) values in clusters V and VI were zero because these clusters consist of a single genotype. High intra-cluster distance in clusters indicated that genotypes included in these clusters were genetically heterogeneous to a great extent. The maximum inter-cluster distance was found between clusters V and VI (1184.92), whereas, the minimum inter-cluster distance was observed between clusters I and V (313.48). The clusters with

Table 3 : Intra (diagonal) and inter-cluster $\sqrt{D^2}$ values among 25 chilli genotypes

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	191.89	450.91	341.18	392.14	313.48	547.72
Cluster II		216.67	780.18	393.35	691.45	687.55
Cluster III			268.24	795.49	451.02	507.72
Cluster IV				75.90	799.53	608.38
Cluster V					0.00	1184.92
Cluster VI						0.00

Table 4 : Cluster means for 15 different characters among 25 genotypes of chilli

Character	Cluster means					
	I	II	III	IV	V	VI
Days to 50% flowering	51.00	47.00	61.42	51.83	54.00	60.00
Days to maturity (mature green stage)	77.79	74.37	89.25	79.17	82.67	87.67
Days to maturity (red ripe stage)	106.13	103.15	118.50	112.50	107.67	110.00
Plant height (cm)	77.54	78.90	78.95	77.85	62.04	65.56
Fruit length (cm)	9.32	9.32	8.86	9.70	9.19	6.07
Fruit diameter (cm)	0.94	0.92	0.86	0.95	0.82	0.83
Number of fruits plant^{-1}	60.61	90.49	54.14	66.80	40.47	88.53
Average fruit weight (g)	3.34	3.46	2.73	4.84	3.53	2.91
Green fruit yield plant^{-1} (g)	195.51	305.60	140.96	324.78	142.58	193.60
Ripe fruit yield plant^{-1} (g)	168.60	279.93	108.94	291.20	115.76	183.10
Dry fruit yield plant^{-1} (g)	37.77	58.46	18.10	56.46	19.24	35.65
Dry yield as % of fresh ripe (%)	20.11	20.89	14.41	18.27	17.78	19.06
Ascorbic acid (mg/100 g)	50.33	59.36	88.33	38.71	33.26	104.90
Oleoresin content (%)	10.57	9.22	11.48	8.63	5.17	16.18
Capsaicin content (%)	0.33	0.18	0.36	0.36	0.19	0.49

higher inter-cluster distances indicated that the genotypes included in those clusters had high genetic variation and hybridization between genotypes of these clusters may result in higher heterotic progenies because of convergence of diverse genes in the F_1 which were scattered in the parents.

A wide range of inter-cluster genetic distance among the different clusters of chilli genotypes has also been reported by Yatung et al. (2014) and Vanitha & Jansirani (2017).

The data pertaining to cluster means for different traits has been presented in Table 4. Inquisition of the data exemplified that cluster II was found promising for days to 50% flowering (47.00 days), days to maturity (mature green stage) (74.37 days), days to maturity (red ripe stage) (103.15 days), number of fruits plant^{-1} (90.49), dry fruit yield plant^{-1} (58.46 g) and dry yield as % of fresh ripe (20.89%) whereas, the cluster III was found promising for plant height (78.95 cm). Maximum cluster means for fruit length (9.70 cm), fruit diameter (0.95 cm), average fruit weight (4.84 g), green fruit yield plant^{-1} (324.78 g) and ripe fruit yield plant^{-1} (291.20 g), was recorded in cluster IV, whereas, cluster VI recorded maximum mean for ascorbic acid (104.90 mg/100g), oleoresin content (16.18%) and capsaicin content (0.49%).

The relative contribution of different characters depicted that average fruit weight contributed a maximum (33%) towards genetic divergence followed by ascorbic acid (29%), capsaicin content (27.67%), number of fruits plant^{-1} (4.67%) and oleoresin content (2.67%). Days to 50 % flowering, days to maturity (red ripe stage), days to maturity (mature green stage), plant height, dry fruit yield plant^{-1} and dry yield as % of fresh ripe exhibited relatively lower contribution to divergence *i.e.* 1%, 0.67%, 0.33%, 0.33%, 0.33% and 0.33%, respectively. However, fruit length, fruit diameter, green fruit yield plant^{-1} and ripe fruit yield plant^{-1} exhibited no contribution to total genetic distance.

In this way, assessment of the contribution of different characters indicated that average fruit weight, ascorbic acid, capsaicin content, number of fruits plant^{-1} and oleoresin content had a maximum contribution to genetic distance as these traits appeared maximum times first rank *viz*., 99, 87, 83, 14 and 8, respectively (Table 5) and therefore, these traits should be explored well while studying genetic divergence in chilli. The high contribution of average fruit weight, ascorbic acid and number of fruits plant^{-1} to total genetic divergence has also been reported by Pujar et al. (2017), whereas Janaki et al. (2016) purported high contribution of

Table 5 : Contribution of different traits to total divergence in chilli

Character	Times ranked 1st	Contribution (%)
Days to 50 % flowering	3	1.00
Days to maturity (mature green stage)	1	0.33
Days to maturity (red ripe stage)	2	0.67
Plant height (cm)	1	0.33
Fruit length (cm)	0	0.00
Fruit diameter (cm)	0	0.00
Number of fruits plant^{-1}	14	4.67
Average fruit weight (g)	99	33.00
Green fruit yield plant^{-1} (g)	0	0.00
Ripe fruit yield plant^{-1} (g)	0	0.00
Dry fruit yield plant^{-1} (g)	1	0.33
Dry yield as % of fresh ripe (%)	1	0.33
Ascorbic acid (mg/100g)	87	29.00
Oleoresin content (%)	8	2.67
Capsaicin content (%)	83	27.67

ascorbic acid and capsaicin content to total genetic divergence.

The highest inter-cluster distance between cluster V (LCC-10) and cluster VI (DKC-8) was accompanied by higher cluster mean values for ascorbic acid, oleoresin content and capsaicin content in cluster VI, the second highest inter-cluster distance between cluster IV (LCC-5 and LCC-17) and cluster V (LCC-10) accompanied with higher cluster mean values for fruit length, fruit diameter, average fruit weight, green fruit yield plant^{-1} and ripe fruit yield plant^{-1} in cluster IV lead to conclude that the crosses involving LCC-10 × DKC-8, LCC-5 × LCC-10, LCC-17 × LCC-10 could be expected to give heterotic hybrids for most of the yield and quality traits.

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