Doi: HTTPS://DOI.ORG/10.23910/2/2023.0512

Divergence Studies in Chilli Genotypes (*Capsicum annuum* L.)

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Article History

Article ID: IJEP0512
Received on 04th January, 2023
Received in revised form on 04th February, 2023
Accepted in final form on 18th February, 2023

Abstract

A study on genetic diversity was conducted at Experimental Farm of Regional Horticultural Research and Training Station Dhaulakuan, District Sirmour (HP), Dr. YS Parmar University of Horticulture and Forestry, Nauni, Solan, Himachal Pradesh, India during *kharif* season, 2018 to assess the genetic diversity in 21 genotypes of chilli (*Capsicum annuum* L.) and to identify suitable donors for successful breeding programme in this crop.The twenty one (21) chilli genotypes were evaluated for seven horticultural traits viz., days to 50% flowering, days to first green fruit picking, fruit length (cm), fruit diameter (cm), number of fruits plant^{-1}, fruit weight at edible maturity (g), green fruits yield plant^{-1} (g). The experiment was laid out in RCBD with three replications at spacing of 45×45 cm^2. By estimating D^2 values in all possible combinations of the genotypes, the 21 genotypes of chilli were grouped into 6 clusters based on green fruit characters, revealing the genetic diversity among the parents. Cluster IV had maximum (6) andCluster I with only one genotype. Average intra-cluster distance was maximum in cluster VI (19.56). The inter cluster distance was recorded maximum between cluster I and VI (207.49). Therefore, hybridization between the genotypes from cluster I and VI (green) can be utilized for getting superior recombinants/ transgressive segregants in segregating generations of chilli.

Keywords: chilli, cluster mean, genetic divergence, intra-cluster distance

1. Introduction

Capsicum annuum L. commonly known as chilli or pepperis a dicyotyledonous flowering plant belonging to Solanaceae family (Knapp, 2002) and having chromosome number, 2n=2x=24 (Kim et al., 2014) is widely grown for its pungent fruits and has gained importance due to varied shape, size, colour and pungency (Tong and Bosland, 2003). The crop originated from South and Central America (Darsheen et al., 2007, Misra et al., 2011, Thakur et al., 2019). The origin of chilli is primarily Mexico with the secondary centers of origin being Guatemala and Bulgaria (Bosland and Votava, 2000). It is commercially grown for immature green and red ripe fruits and consumed both as vegetable (green chilli), and spice (dry chilli) (Perkins et al., 2002, Sun et al., 2014), condiment, sauce and pickles in tropical and sub tropical regions of the world (Hazra et al., 2011). The genus Capsicum consists of approximately 27 species including 22 of wild species and five domesticated species. Domesticated chilli species include *C. annuum*, *C. frutescens*, *C. baccatum*, *C. chinense*, and *C. pubescens* (Andrews, 1984, Arimboor et al., 2015, Padilha and Barbieri, 2016). The crop is often cross-pollinated and out crossing may occur upto 50% (Joshi et al., 2000). Based on its uses, chilli has been classified into bell group, pimento group, squash/cheese group, ancho group, Anaheim group (long green chile group), cayenne group, cuban group, jalapeno group, small hot group, cherry group and short wax group. Our study is confined to hot pepper only, consumed for taste in India. The fruits are rich source of Vitamin A (Marin et al., 2004) and is excellent source of β-carotene (Shetty et al., 2013), phytochemicals like carotenoids,flavonoids, ascorbic acid, phenolic compounds and capsaicinoids (pungent compound) possessing anticancerous properties (Pramanick and Srivastava, 2013). Capsaicinoids found in chilli fruit contains more capsaicin and dihydrocapsaicin which are responsible for about 90% of the spicy taste of chilli and is very important in the food industry (Lyu et al., 2019). The major chilli producing countries are India, China, Korea, Japan, Spain, Nigeria, Pakistan Indonesia, Mexico etc. Chilli is cultivated in an area of 20.69 lha with the production of 361.36 lMt for green fruits and 41.57 lMt over an area of 16.15 lha of dry peppers in the world (Anonymous, 2020). India is the leading producer, consumer and exporter of chilli in the world. In India, the states of Andhra Pradesh, Karnataka, Maharashtra, Orissa and Tamil Nadu account for more than 75% of the area and production of chilli.In India, chilli is grown in area of 366000 ha with the production of 3737000 mt and productivity of 10.21 mt ha^{-1} (Anonymouus, 2019). The crop has good export potential and huge domestic demand. In terms of export potential, the export of 45,369 Mt of chilli resulted in earning $41 million in 2019 (Anonymous, 2021).

Chilli production both globally and domestically is beset with many challenges such as low productivity of cultivars, climate change, improper management and utilization of genetic resources, lack of good quality seeds, increased susceptibility to major insect-pests and diseases and abiotic stresses are the major constraints which needs a serious concern.Chilli offers much scope of improvement in terms of yield and other quality traits through heterosis breeding (Chaudhary et al., 2013, Singh et al., 2012, Singh et al., 2014). Hence, reliable selection of productive genotypes is pre requisite for any crop improvement programmes.The knowledge of nature and degree of genetic divergence is useful in selecting the desirable parents for breeding programme. The genetically diverse parents are known to produce high heterotic effects (Tomooka, 1991) and consequently give desirable recombinants in the breeding material or wide spectrum of transgressive segregants in segregating generations.Thus, the present study was undertaken to assess the genetic diversity in 21 genotypes of chilli (*Capsicum annuum* L.) and to identify suitable donors for successful breeding programme in this crop. Mahalanobis D^2 statistic of multivariate analysis as a powerful tool in quantifying the degree of genetic divergence among the populations has been utilized in this study.

2. Materials and Methods

The divergence study for green fruited characters was carried out at the Experimental Farm of Regional Horticultural Research and Training Station Dhaulakuan, District Sirmour (HP), Dr. YS Parmar University of Horticulture and Forestry, Nauni-Solan, Himachal Pradesh, India which is at an elevation of 468 m above mean sea level under the sub-tropical low hills during *kharif* season, 2018. The experiment was laid out in a Randomized Complete Block Design (RCBD) with 21 genotypes (20 genotypes+1 check) and three replications at 45 cm×45cm row to row and plant to plant spacing. All the recommended cultural practices were adopted to raise the healthy crop. Data were recorded on days to 50% flowering, days to first green fruit picking, fruit length (cm), fruit diameter (cm), number of fruits plant^{-1}, fruit weight at edible maturity (g), green fruits yield plant^{-1} (g) from 5 randomly selected plants from each plot. Mean data of each character was subjected to Mahalanobis D^2 statistic analysis.

3. Results and Discussion

3.1. Composition of clusters of 21 genotypes of chilli

In the present investigation, all the 21 genotypes were grouped into six clusters based on Mahalanobis D^2 values (Table 1). The cluster IV was the longest with six genotypes (RACH-74, RACH-137, RACH-131, RACH-136, RACH-133, DKC-8) followed by cluster II with five genotypes (RACH-5, RACH-11, RACH-16, RACH-28, DKC-2363), cluster III with four genotypes (RACH-15, RACH-51, RACH-117, RACH-138), cluster V with three genotypes (RACH-112, RACH-114, RACH-135), cluster VI with two (RACH-121, RACH-132) and cluster I with only one genotype (RACH-1). Such grouping pattern where genotypes appear in the same cluster were due to their genetic homogeneity with each other. Similarly, most divergent genotypes remained alone in cluster. Group constellation of chilli genotypes through genetic divergence has also been reported by Farhad et al. (2010), Hasan et al. (2014), Yatung et al. (2014), Hasan et al. (2015), Vanitha and Jansirani (2017) and Pujar et al. (2017).

Table 1: Clustering pattern of genotypes based upon genetic divergence of green fruit yield

Clusters	No. of geno-types	Genotypes
Cluster I	1	RACH-1
Cluster II	5	RACH-5, RACH-11, RACH-16, RACH-28, DKC-2363
Cluster III	4	RACH-15, RACH-51, RACH-117, RACH-138
Cluster IV	6	RACH-74, RACH-137, RACH-131, RACH-136, RACH-133, DKC-8
Cluster V	3	RACH-112, RACH-114, RACH-135
Cluster VI	2	RACH-121, RACH-132

3.2. Intra and inter-cluster genetic distance (√D²)

Intra-cluster distance denotes genetic dissimilarity among the genotypes grouped in the same cluster whereas, inter-cluster distance indicates the genetic distance between the genotypes grouped in any two clusters. The perusal of data based on green fruit characters in Table 2 depicted that maximum intra-cluster distance (√D²) was found in cluster VI (19.56) followed by cluster IV (17.04), cluster III (12.29), cluster II (10.56) and cluster V (5.89). The intra-cluster (√D²) value in cluster I was zero as this cluster consisted of only single genotype. Maximum inter-cluster distance was found

Table 2: Intra (diagonal) and inter cluster √D² values in chilli genotypes based on green fruit yield

	Clus I	Clus II	Clus III	Clus IV	Clus V	Clus VI
Cluster I	0.00	47.89	91.26	120.79	160.01	207.49
Cluster II		10.56	43.41	74.29	114.30	161.63
Cluster III			12.29	34.60	74.69	121.01
Cluster IV				17.04	41.60	87.99
Cluster V					5.89	47.61
Cluster VI						19.56

Clus: Cluster

between cluster I and VI (207.49) whereas, minimum inter-cluster distance was observed between cluster III and IV (34.60). High intra-cluster distance indicated that genotypes included in these clusters were genetically heterogenous to a great extent whereas the clusters with 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. Similar results have also been reported by Farhad et al. (2010), Yatung et al. (2014), Hasan et al. (2015), Vanitha and Jansirani (2017).

3.3. Cluster means

Cluster means indicates average performance of all the genotypes included in a particular cluster for a particular character. High cluster mean for a particular character denotes high vigour possessed by the genotypes included in cluster for that character.

The data pertaining to cluster mean for green fruit traits presented in Table 3 indicated that cluster VI was found promising for earliness characters viz. days to 50% flowering (33.02 days) and days to first green fruit picking (65.00 days) whereas, cluster V was promising for fruit length (8.49 cm). Maximum mean for fruit diameter (1.09cm), number of fruits plant^{-1} (89.23), fruit weight at edible maturity (3.55 g) and green fruit yield plant^{-1} (262.47 g) were recorded in cluster VI. Hence, the genotypes grouped in the same cluster will prove ineffective in expressing the high heterotic hybrids, if the crossing is practiced within the same cluster. Variable cluster means for different plant growth and fruit yield characters have also been reported by Smitha and Basavaraja (2006), Farhadet al. (2010), Yatung et al. (2014), Hasan et al. (2014), Hasan et al. (2015), Pujar et al. (2017) and Vanitha and Jansirani (2017).

So, to have better hybrids, crosses must be attempted between the genotypes of clusters I and VI (green) as the cumbersome job of crossing has been reduced with the least number of genotypes constituting these clusters.

Table 3: Cluster mean for different green fruit characters among 21 genotypes of chilli

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
DTTF	78.000	59.67	45.46	48.98	43.43	33.02
DTGP	103.67	87.93	72.67	74.89	71.89	65.00
FL	6.13	7.46	8.05	7.36	8.49	7.85
FD	0.72	0.79	0.78	0.84	0.86	1.09
NOF	33.87	49.36	63.70	73.94	74.44	89.23
FWT	2.05	2.61	2.56	2.60	3.42	3.55
GFYP	71.52	109.84	145.10	177.89	218.98	262.47

DTTF: Days to 50% flowering; DTGP: Days to first green fruit picking; FL: Fruit length; FD: Fruit diameter; NOF: Number of fruits plant^{-1}, FWT: Fruit weight at edible maturity; GFYP: Green fruit yield plant^{-1}

4. Conclusion

More diverse the parents within a reasonable range, better are the chances of improving economic characters under consideration in the offspring. So, to have better hybrids, crosses must be attempted between the genotypes of clusters I and VIwhich performed superior in terms of yield and its contributing characters. Therefore, the cumbersome job of crossing has been reduced with the least number of genotypes constituting these clusters.

4. Acknowledgement

I emphatically express my heartiest thanks to the Major Advisor and worthy members of my Advisory committee for their sincere help, kind cooperation and impeccable guidance as and when required.

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