

Assessment of genetic divergence in Chilli (*Capsicum annuum* L.) genotypes

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Plant Gene and Trait, 2015, Vol.5, No.3 doi: 10.5376/pgt.2015.06.0003

Received: 09 Feb., 2015

Accepted: 17 Apr., 2015

Published: 29 Apr., 2015

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Preferred citation for this article:

Hasan et al., 2015, Assessment of genetic divergence in Chilli (*Capsicum annuum* L.) genotypes, Plant Gene and Trait, Vol.6, No.3 1-5 (doi: [10.5376/pgt.2015.06.0003](https://doi.org/10.5376/pgt.2015.06.0003))

Abstract Thirteen genotypes of chilli (*Capsicum annuum* L.) were investigated to understand the extent of genetic diversity through 6 yield attributing characters. Genetic diversity in chilli genotypes based on six characters was estimated using Mahalanobis's D^2 statistics. The genotypes were grouped into five different clusters by non-hierarchical clustering. The cluster I had the maximum number (5) of genotypes while cluster IV and V each contained only one genotype. The highest inter-cluster distance was observed between cluster I and IV (24.483) and the lowest inter-cluster distance was observed between the clusters II and V (11.633). The results indicated that fruits/plant (35.8%) contributed maximum to the total divergence followed by fruit length (21.6%) and yield/plant (21.1%). Cluster IV produced highest mean for fruit weight (4.48), fruits/plant (149.90) and yield/plant (676.03). Cluster V produced highest mean for fruit length (10.23), pedicel length (4.94) and fruit diameter (10.36). Cluster I and III produced maximum lowest mean for almost all characters. Therefore, genotypes belonging to the cluster IV and V may be used as potential parents for future hybridization programme to develop superior Chilli variety with desired traits.

Keywords Chilli; Genetic divergence; Cluster analysis; D^2 statistics.

Background

Chilli (*Capsicum annuum* L.) ($2n = 24$) is one of the most popular vegetables, originated from South and Central America (Bahurupe et al. 2013). It is the second most important solanaceous vegetable after tomato grown worldwide both as a spice or vegetable crop (Hasan et al. 2014). It genetically self-pollinated and chasmogamous crop whose flowers open only after pollination (Lemma 1998).

Chilli is used as spice, condiment, vegetable, culinary supplement, medicine and as ornamental plant (Berke and Shieh 2001). The pungent chemical principle of *Capsicum* is fruit specific capsaicin which is found useful in a wide range of pain problems, including post-mastectomy syndrome, urticaria, psoriasis, diabetic neuropathy, arthritis, pruritis, contact allergy, post-surgical neuromas etc (Palevitch and Craker 1995).

Chilli is an inevitable spice used in every Bangladeshi cuisine due to its pungency, taste, appealing colour and flavour. It is widely grown in various parts of Bangladesh mostly in Rabi season. A wide variability

in chilli fruit morphology, pungency, bearing habit and crop duration is found throughout Bangladesh (Farhad et al. 2010).

However, despite its high medicinal value and wider genetic variability, the average yield of chilli in Bangladesh is very low compared to other countries of the world. The average yield of chilli in Bangladesh was 1256.5 kg/ha in 2011 which is very low compared to some top chilli producing countries like India (1638.05 kg/ha), China (6162.80 kg/ha) and Thailand (2235.27 kg/ha) (FAOSTAT 2011). The major constraints in achieving high yield of this crop are lack of genetic variability and susceptibility to diseases and pests. Therefore, it is desirable to develop a new better adaptable and productive variety through systematic breeding programme.

Genetic diversity is the basic requirement for any successful breeding programme. Assessment of genetic diversity among germplasms is a prerequisite for plant breeders in choosing potential parental lines because of two reasons: i.e., (i) In the hybridization programme, genetically diverse parents likely to

produce high heterotic effect, and (ii) Genetically distant parents could produce a wide spectrum of variability in the segregating generation. Therefore, a clear characterization of germplasms is the first step to facilitate successful breeding efforts.

The degree of genetic divergence can be quantified using Mohalanobis's D^2 statistic of multivariate analysis which is recognized as a powerful tool for assessing the relative contribution of different characters to the total divergence in self-pollinated crops. (Golokia and Makne 1992; Natarajan et al. 1988; Das and Gupta 1984; Shidhu et al. 1989). Therefore, the present study was undertaken to assess the genetic diversity in 13 genotypes of chilli to identify suitable genotypes.

1 Result and Discussion

Analysis of variances for yield and yield contributing traits showed that the genotypes differed significantly for the traits (Table 1). This indicates that the materials were genotypically divergent. Based on PCA score I, II, and III obtaining from the principal component analysis which account for 91.4% toward to total variation, a three dimensional scattered diagram was developed. The positions of 13 genotypes in the generated scattered diagram were apparently distributed into five groups indicating a considerable genetic diversity (Figure 1). Similar grouping of the genotypes has also been observed by Tocher's Method (Table 2). The name and source of

origin of the genotypes studied here are presented in Table 6. The clustering pattern of different genotypes did not follow their geographical distribution and was fairly at random. This suggests that falling of materials of same origin into different clusters was an indication of broad genetic base of the genotypes belonging to the origin. Maximum numbers of genotypes were accommodated in cluster I containing 5 genotypes, followed by cluster II and cluster III containing 4 and 2 genotypes, respectively. Cluster IV and V each contained single genotype (Figure 1 & Table 2).

Table 1 Analysis of variance for various quantitative traits in chilli

Characters	Genotypes (df=12)	CV %
Fruit length (cm)	14.718**	4.356
Pedical length (cm)	0.817**	5.684
Fruit diameter (cm)	25.597**	5.028
No. of fruits/plant	5120.467**	6.417
Fruit weight (gm)	2.507**	10.506
Yield/plant (gm)	114479.397**	16.965

Note: ** p < 0.01

Table 2 Distribution of different chilli genotypes by tocher's clustering method

Cluster	No. of genotypes	Name of the genotypes
I	5	v1,v7,v11,v12,v13
II	4	v2 ,v5,v6,v10
III	2	v3,v8
IV	1	v4
V	1	v9

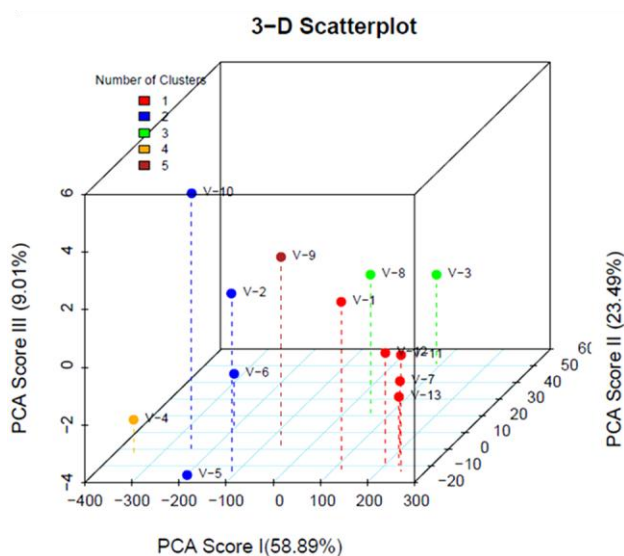


Figure 1 Three dimensional scattered diagram based on three PCA scores showing the distribution of different genotypes

The average intra and inter cluster distances are presented in Table 3. The inter-cluster distances were larger than the intra-cluster distances that indicated wider genetic diversity among the genotypes of different groups. Cluster II showed maximum intra-cluster distance (9.048) followed by cluster I (7.682) and cluster III (6.979). Cluster IV and V showed no intra-cluster distance because of having solitary genotype. The inter-cluster distances were calculated by averaging all possible D^2 values among all genotypes belonging to different clusters concerned. The maximum inter-cluster distance was observed between Cluster I and cluster IV (24.483) followed by cluster III and cluster IV (21.461), and cluster I and cluster II (20.501) (Table 3). Therefore, the genotypes falling in these clusters were genetically more divergent. Hybridization between the genotypes from

these clusters should generate greater number of useful segregants, maximum hybrid vigour and is expected to create high yielding chilli varieties. The minimum inter cluster D^2 value (11.633) was observed between cluster II and V indicating that genotypes of these two clusters were genetically close (Table 3).

Table 3 Average intra (bold) and inter cluster distance (D^2) for chilli genotypes

Cluster	I	II	III	IV	V
I	7.682	20.501	12.386	24.483	16.923
II		9.048	16.836	13.411	11.633
III			6.979	21.461	12.254
IV				0.000	17.707
V					0.000

The percentage contribution of different traits towards genetics divergence is presented in Figure 2. Among the six characters studied the highest contribution towards divergence was found for fruits/plant (35.8%). Similar result was obtained by Smitha and Basavaraja (2006). Moderate contribution was found for fruit length (21.6%) and yield/plant (21.1%). Remaining characters had very less contribution toward genetic diversity. The higher contribution towards genetic divergence was also recorded in fruits per plant and fruit length by Sreelathakumari and Rajamony (2004). The maximum contribution was found in yield per plant, fruit weight, number of fruits per plant, fruit length, fruit diameter and plant height towards divergence in chilli by Vani et al. (2007); Karad et al. (2002); Senapati et al. (2003); Varalakshmi and Babu (1991); Thul et al. (2009); Roy and Sarma (1996), respectively.

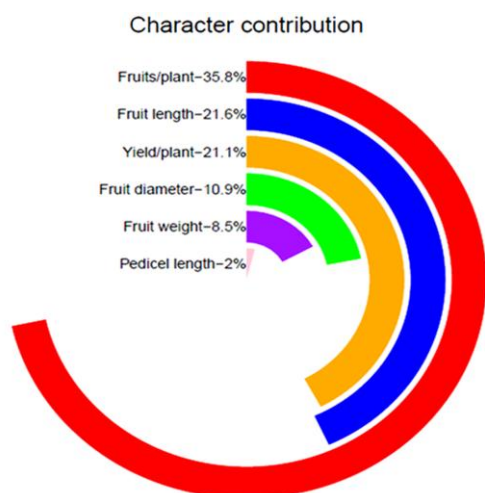


Figure 2 Contribution of individual characters towards divergence

Character wise mean were calculated for all the genotypes spread over five clusters (Table 4). Cluster IV showed highest mean value for fruit weight (4.48), fruits/plant (149.90) and yield/plant (676.03). Cluster V showed highest mean value for fruit length (10.23), pedicel length (4.94) and fruit diameter (10.36). Cluster I and III had the genotypes that showed lowest mean value for almost all the characters studied indicating selection of parental lines from this cluster for future hybrid chilli breeding programme will be ineffective. Cluster IV and V together contributed 100% towards divergence that means possession of all characters in respect of yield indicating presence of most promising genotypes in them can be extensively used for further breeding programmes to generate new high yield chilli lines.

Table 4 Cluster mean for various characters of chilli genotypes

Characters	I	II	III	IV	V
Fruit length (cm)	5.77	8.94	4.64	7.43	10.23*
Pedicel length (cm)	3.59	4.10	3.65	4.03	4.94*
Fruit diameter (cm)	9.75	7.87	6.29	3.95	10.36*
No. of fruits/plant	44.83	119.94	114.40	149.90*	104.47
Fruit weight (gm)	2.85	4.30	2.23	4.48*	3.71
Yield/plant (gm)	131.18	512.76	251.32	676.03*	389.43
Contribution (%)	00	00	00	50	50

Note: *= Highest mean value

Taking consideration the mean data of fruit length (cm), fruit/plant and yield/plant, as these three characters contribute most towards the divergence, it can be recommended that the genotypes Bogra Morich and Demon could be good parents for hybridization (Table 5).

Table 5 Finally selected chilli genotypes for important traits

Sl. No.	Selection traits	Genotypes	Cluster	Mean value
1	Fruit length (cm)	Demon	V	10.23
2	Fruits /plant	Bogra Morich	IV	149.90
3	Yield/plant (gm)	Bogra Morich	IV	676.03

2 Materials and Method

2.1 Plant materials

Thirteen chilli (*Capsicum annum* L.) genotypes (Table 6) were collected from national research institute and different part of the Bangladesh.

Table 6 List of chilli genotypes with their sources

Name of genotypes	Place/Source of collection	Code
Baromasi morich	Foysal nursery, Jahangirnagar University	V-1
BARI Morich-1	Bangladesh Agricultural Research Institute	V-2
Black Lady	Local seed market of Dhaka	V-3
Bogra morich	Shawom seed company (Dhaka)	V-4
Premium	Lal Teer (Gazipur)	V-5
Jhal Lomba Morich	Local seed market of Dhaka	V-6
Haitta Morich	Local seed market of Damrai	V-7
Jhal Morich	Alomgir seed company (Dhaka)	V-8
Demon	Lal Teer (Gazipur)	V-9
Baromashi Lomba Morich	Foysal nursery, Jahangirnagar University	V-10
Norsingdi -1	Local seed market of Norsingdi	V-11
Norsingdi -2	Local seed market of Norsingdi	V-12
Norsingdi -3	Local seed market of Norsingdi	V-13

2.2 Field experiment

The investigation was conducted during November 2013- April 2014 at Botanical Garden of Jahangirnagar University, Savar, Dhaka, Bangladesh. The experimental field was located inside the Botanical Garden of Jahangirnagar University at 23° 52' 27.76" north latitude, 90° 16' 5.16" east longitude. The experimental area was under the sub-tropical climatic zone and characterized by scanty rainfall, moderate humidity, moderate temperature and relatively short days during late Rabi season (January-March, 2014). The soil of the experimental field was sandy loam in texture and belongs to the 'Shallow Red Brown Terrace' under Madhupur tract with a pH of around 6.2-6.8 (Haider et al. 1991; Anonymous 1998). The field experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The plot was 3x2 feet maintaining a plant spacing of 1x1 feet. A distance of 1.5 feet in the form of drain was maintained between the block and between the plots within a block. Manures and fertilizers were applied as per recommended dose to raise good crop. Weeding was done as and when necessary to keep the crops free from weeds. Flood irrigation was given to the plants when necessary.

Data were collected from 5 randomly selected plants basis for fruit length (cm), pedicel length (cm), fruit diameter (cm), fruit weight (gm), number of fruit/plant, yield/plant (gm).

2.3 Statistical analysis

The mean data of five randomly selected plants were used for statistical analysis. Analysis of variance, cluster analysis based on Tocher's method using Squared Euclidean Distance (Kumar et al. 2009) was performed using the statistical software Indostat Version 8.5. The principal component analysis and genetic divergence was calculated according to Mahalanobis D^2 statistics (Mahalanobis 1936) using statistical programme R-3.1.1 and "Biotools" package.

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