The Pharma Innovation

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Genetic divergence among chilli (*Capsicum annuum* L.) genotypes based on quantitative and qualitative traits

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Abstract
A study on genetic diversity was conducted with forty-eight chilli (*Capsicum annuum* L.) genotypes which were collected from different agro ecological regions of India. Fourteen quantitative characters were taken into consideration. Mahalanobis D^2 statistics was employed to study genetic divergence among 48 genotypes and they were grouped into thirteen clusters on the basis of relative magnitude of D^2 values using Euclidean method. Cluster I accommodated maximum number (30) of genotypes followed by cluster V (7) and cluster II, III, IV, VI, VII, VIII, IX, X, XI, XII, XIII (each one). The inter cluster distance D^2 values was highest between cluster II and IX (13956.99) followed by XIII and XI (10595.24) and cluster X and XI (10183.48). The intra cluster distance ranged from 0.00 (cluster II) to 691.01 (cluster I). The members of cluster I exhibited maximum divergence (intra cluster distance 691.01) followed by members of cluster V (474.76). The inter cluster distance were larger than the intra cluster distances indicating a wider genetic diversity between genotypes of cluster with respect to traits considered. Maximum inter-cluster distance indicates that genotypes falling in these clusters had wide diversity and can be used for hybridization programme to get better recombinants in the segregating generation.

Keywords: *Capsicum annuum,* Mahalanobis D^2, Euclidean method, genetic divergence

Introduction

Chilli (*Capsicum annuum* L.) 2n = 2x = 24 is a spice cum vegetable crop belonging to the family Solanaceae. It is an indispensable spice due to its pungency, taste, appealing colour and flavor and has its unique place in the diet as a vegetable cum spice crop. The primary centre of origin of chilli is said to be Mexico with secondary centre in Guatemala and Bulgaria (Salvador, 2002) [8]. The chilli was probably introduced by Portuguese into Southern parts of India and cultivation spread out throughout India by the end of 19th centuries.

India is the largest producer, consumer and exporter of chilli in the world. The area under chilli in India is 831 thousand hectares with a production of 1872 thousand million tonnes (Anonymous, 2017) [1]. In Jammu and Kashmir, it is grown over an area of 0.60 thousand hectares with an annual production of 0.40 thousand million tonnes (Anonymous, 2017) [1]. Due to long history of cultivation, selection and popularity of crops sufficient genetic variability has been generated. Rich variability in morphological traits in chilli occurs throughout India particularly in South peninsular region, North Eastern foot hills of Himalayas and Gangetic plains (Pradheep and Veeraragavathatham. 2006) [15]. Collection and maintainance of the genetic diversity in capsicum are important to avoid genetic erosion. Besides the identification of species, the characterization and evaluation of genotypes maintained in gene banks are of fundamental importance (Sudre *et al*., 2010). A wide variability in chilli fruit morphology, pungency, bearing habit and crop duration is found throughout India (Asati and Yadav, 2004) [2].

Genetic divergence existing in the population helps in selection of suitable parents for any crop breeding programme, leading to reduction in the number of crosses. Selection of parents depends on specific objective of the research programme and their performance. Various statistical analysis are available to select suitable parents. Mahalanobis D^2 statistics of multivariate analysis is recognized as a powerful tool in quantifying the degree of genetic divergence among the populations. The information on the nature and degree of genetic divergence is essential for the breeder to choose the right type of parents for purposeful hybridization in heterosis breeding (Farad *et al.,* 2010; Khodadabi *et al.,* 2011) [3, 8].

In order to benefit transgressive segregation, the knowledge of genetic distance between parents is necessary (Khodadabi et al., 2011) [8]. Therefore, the present study was undertaken to assess the genetic diversity in 48 genotypes of chilli and to identify suitable donors for a successful breeding programme in this crop.

Materials And Methods

Forty-eight chilli (*Capsicum annuum* L.) genotypes were collected in the experimental field at the Division of Vegetable Science and Molecular biology, ICAR- Central Institute of Temperate Horticulture Srinagar (CITH) during Kharif 2018. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The sowing was carried out on 5th April 2018. Seedlings were transplanted in the field on first June 2018 at a spacing of 60cm between row to row and 45cm between plant to plant. Ten plants of each genotype were transplanted in a randomized complete block design. The observations were recorded on five randomly selected plants of each genotype on plant height (cm), plant spread (cm), number of primary branches, days to 50% flowering, days taken to first fruit set, fruit diameter (cm), fruit length (cm), pedicel length (cm), number of fruits per plant, fruit weight (g), fruit yield per plant (g), number of seeds per fruit, average dry fruit weight (g), fruit yield per hectare (q). Mahanalobis D^2 statistics (Mahalanobis, 1936) [11] was used for assessing the genetic divergence. between the groups. The grouping of the population was done by using squared Euclidean distance (Kumar et al., 2009) [9].

The genotypes were grouped into different clusters by employing Tocher's method as outlined by Roa (1952) [17]. The average intra and inter cluster distances were calculated by the formula given by Singh and Chaudhary (1977) [20].

Results And Discussion

Genetic divergence existing in the population helps in the selection of suitable parents for utilization in chilli crop breeding programs. Inter-specific hybridization is possible, though it is not common. Identification and characterization of desirable parental combinations provide the basis for selection in the follow-up breeding process for exploitation of heterosis. Multivariate analysis utilizing the concept of statistical distance has been found to be a very powerful statistical tool in estimating diversity in biological populations. Ecological diversity has been regarded as a reasonable index of genetic diversity (Moll et al., 1962; Vavilov, 1926) [12]. The 48 chilli genotypes included in the present study had considerable diversity as observed by the magnitude of all possible D^2 values.

The computations from distance matrix gave non- hierarchical clustering among 48 chilli genotypes and they were grouped into thirteen clusters (Table 1). Cluster I was the largest one comprising of thirty chilli genotypes followed by cluster V (7) and cluster II, III, IV, VI, VII, VIII, IX, X, XI, XII, XIII (each one), indicating high degree of heterogeneity among the genotypes. This was supported by Yatung et al., 2014 [24] in a study of genetic diversity in 30 chilli genotypes and they were grouped into 6 clusters, Hasan et al., 2014 [4] studied 54 chilli genotypes which were fallen into seven clusters, Srinivas et al., 2013 [21] also conducted study on genetic diversity in 78 chilli genotypes and they were divided into nine clusters. Janaki et al., 2016 [6] in a genetic divergence study showed the clustering of 63 genotypes into 8 groups. Karad et al. (2002)

[7] reported 8 clusters with 40 chilli genotypes, Hasan et al. (2015) [5] observed 5 clusters with 13 chilli genotypes, Janaki et al. (2016) [6] observed 8 cluster with 63 genotypes, Pradhan et al. (2017) [14] reported 5 clusters with 12 genotypes, Pujar et al. (2017) [16] observed 5 clusters with 63 chilli genotypes, Nahak et al. (2018) reported 4 clusters with 11 chilli genotypes. The selection of genotypes for hybridization should be based on genetic divergence rather than geographical diversity.

Intra and inter cluster distances (D values) are shown in Table 2. The inter-cluster distances were larger than the intra-cluster distances. The intra and inter cluster distance represent the index of genetic diversity among clusters. Of the 13 clusters formed, the mean intra cluster D^2 distance values ranged from a minimum of 0.00 to a maximum of 691.01. The maximum intra cluster distance was found in cluster I (691.01) followed by cluster V (474.76). The high intra-cluster distance in cluster I indicates the presence of wide genetic diversity among the genotypes present within this cluster. The inter cluster distance D^2 values was highest between cluster II and IX (13956.99) followed by XIII and XI (10595.24), cluster X and XI (10183.48), III and XIII (9985.17), IV and XI (8747.08), V and XI (8618.95), VI and XI (8439.09) and VII and X (7875.24). The hybrids of distant genotypes are reported to yield better (Kumar et al., 2010) and thus crosses between the genotypes from cluster II and IX can be used in chilli breeding to achieve maximum heterosis and to obtain heterotic hybrids and desirable segregants. The selection of diverge genotypes from a cluster would produce a broad spectrum of variability for morphological and quality traits studied which may enable futher selection and improvement. Hasan et al., 2014 [4] Yatung et al., 2014 [24], Srinivas et al., 2013 [21], Janaki et al., 2016 [6], Singh and Singh (2010) [19], Farhad et al. (2010) [3], Hasan et al. (2015) [5] and Nahak et al. (2018) [13] also indicate the presence of a high genetic divergence among chilli genotypes in their respective experiments. The genotypes grouped into the same cluster presumably diverge very little from one another and crossing of genotypes belonging to the same cluster is not expected to yield desirable segregants. The intra and inter cluster distances are pictorially represented in Fig-2 and cluster dendrogram in Fig-3.

Difference in cluster mean existed for almost all the characters studied and are presented in Table 3. The perusal of data indicated considerable differences for all the characters among clusters. It is inferred from the cluster means that each cluster has its uniqueness that separated it from other cluster. Highest cluster mean plant height (94.07), fruit diameter (2.60), average dry fruit weight (2.83) were recorded in cluster XIII; Lowest cluster mean for plant spread (24.03) was observed in cluster VI; Highest cluster mean for number of primary branches (8.00) and lowest cluster mean for days to 50% flowering (52.00), days to first fruit set (54.00) was found in cluster VIII; Highest cluster mean for fruit length (13.80), pedicel length (4.07), number of fruits per plant (100.50), fruit yield per plant (750.10), fruit yield per hectare (277.60) was found in cluster XII; Highest cluster mean for average fruit weight(15.03), number of seeds per fruit (139.47) was found in cluster XI. The results indicated that selection of genotypes having high values for a particular trait can be made and they can be utilized in the hybridization programme for improvement of that particular character. The results were supported by Lahibib et al., 2013 [10]; Yatung et al., 2014 [24]; Hasan et al., 2014 [4]; Srinivas et al., 2013 [21] and Janaki et al., 2016 [6].

Table 1: Distribution of chilli (*Capsicum annuum* L.) genotypes into clusters based on D^2 Statistics

S. No	Cluster	No. of genotypes in the cluster	Name of genotypes
1	I	30	LSVT-Red-1, LSVT-Red-2, LSVT-Red-3, IC-561652, IC-561614, IC-561610, IC-561730, IC-572487, IC-561661, IC-561691, IC-561657, CITH-HP-16, CITH-HP-71/13, CITH-HP-111, Sel-917-111, CITH-HP-1154, IC-561631, IC-561627, Guccha Mirch-1, SK-SC-1161, Guccha Mirch-2, CITH-HP-17/13. ARCH-228, SKAU-084, G-4, CITH-HP-171/13, Sel-680/11, SKAU-089, CITH-HP-1154-1/13, SKAU-092,
2	II	1	Jawahar Mirch
3	III	1	Pusa Sadabahar
4	IV	1	SK-SC-1162
5	V	7	SKAU-096, IC-561665, IC-561731, Sel-839-2, CITH-HP-22, SKAU-O78, Kashmiri Long-1
6	VI	1	Goa-Sel-1
7	VII	1	IC-561618
8	VIII	1	IC-561635
9	IX	1	IC-561622
10	X	1	IC-561639
11	XI	1	VOBC-0289
12	XII	1	Kashi Anmol
13	XIII	1	Bhut Jolokia

Table 2: Average intra cluster (Diagonal) and inter cluster (above diagonal) distance values in chilli (*Capsicum-annuum* L.)

S.NO.	Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
1	I	691.01	1247.57	1277.22	1254.05	1732.38	1827.47	1226.35	1680.87	1709.60	3233.38	4852.50	1768.84	2382.21
2	II		0.00	207.56	2469.62	3956.07	566.63	752.15	198.90	374.68	996.75	8747.08	3268.26	1074.42
3	III			0.00	2465.39	3928.99	187.75	1012.13	.319.32	578.27	922.02	8618.95	3497.70	1588.40
4	IV				0.00	600.86	3533.17	3292.39	2721.43	3900.87	6124.09	2646.93	2989.97	4094.05
5	V					474.76	5013.67	4100.57	4482.26	5241.04	7875.24	1635.18	2710.77	5460.47
6	VI						0.00	1176.12	823.79	659.76	628.35	10183.48	4008.04	2095.67
7	VII							0.00	1222.00	370.90	1376.08	8439.09	1692.71	1565.35
8	VIII								0.00	631.25	1190.58	9431.70	4096.67	1372.78
9	IX									0.00	578.14	10595.24	2914.81	1477.33
10	X										0.00	13956.99	5324.37	1728.35
11	XI											0.00	5167.19	9985.17
12	XII												0.00	4397.12
13	XIII													0.00

Table 3: Cluster means for various characters in different clusters of chilli (*Capsicum annuum* L.)

| S. No	Cluster	Plant height (cm)	Plant spread (cm)	Number of primary branches	Days to 50% flowering	Days to first fruit set	Fruit diameter (cm)	Fruit length (cm)	Pedicel length(cm)	Number of fruits per plant	Fruit weight (g)	Fruit yield per plant (g)	No. of seeds per fruit	Average dry fruit weight (g)	Fruit yield per hectare (q)
1	I	63.40	47.91	4.94	65.08	61.75	1.19	9.47	3.54	42.97	6.24	261.05	82.83	1.58	96.50
2	II	58.67	54.00	5.00	73.57	69.83	1.20	4.57	3.23	35.20	4.33	152.27	58.20	1.00	26.10
3	III	49.03	34.27	4.93	63.00	65.00	1.20	4.57	3.20	43.13	4.80	207.00	52.00	1.00	76.50
4	IV	57.83	51.23	3.87	72.33	66.00	1.53	4.90	2.70	49.67	2.97	148.30	106.40	0.83	54.77
5	V	60.80	49.39	4.61	68.77	66.06	1.30	9.25	3.64	41.79	5.52	228.39	118.03	1.56	84.40
6	VI	42.27	24.03	3.60	74.00	71.20	1.10	7.33	3.43	45.47	4.27	192.47	42.03	0.90	71.03
7	VII	59.30	57.47	5.07	67.03	70.03	1.27	11.13	2.50	44.33	8.27	366.13	61.80	1.27	135.40
8	VIII	51.90	52.67	8.00	52.00	54.00	1.40	2.60	2.67	40.00	3.67	143.97	54.20	0.87	53.17
9	IX	63.57	55.70	5.93	61.00	65.00	0.80	8.07	3.50	52.33	5.40	283.23	47.87	1.27	104.63
10	X	56.97	33.50	5.67	68.00	65.03	1.20	7.43	3.67	31.20	7.00	219.03	22.93	0.77	80.93
11	XI	58.20	46.13	4.73	74.27	67.17	2.57	9.27	3.53	29.70	15.03	445.87	139.47	2.70	165.03
12	XII	66.20	63.87	5.73	66.00	72.07	1.20	13.80	4.07	100.50	7.47	750.10	96.93	1.87	277.60
13	XIII	94.07	48.17	6.23	80.00	73.67	2.60	6.70	3.03	10.17	6.00	68.43	52.00	2.83	25.23

Tocher Method
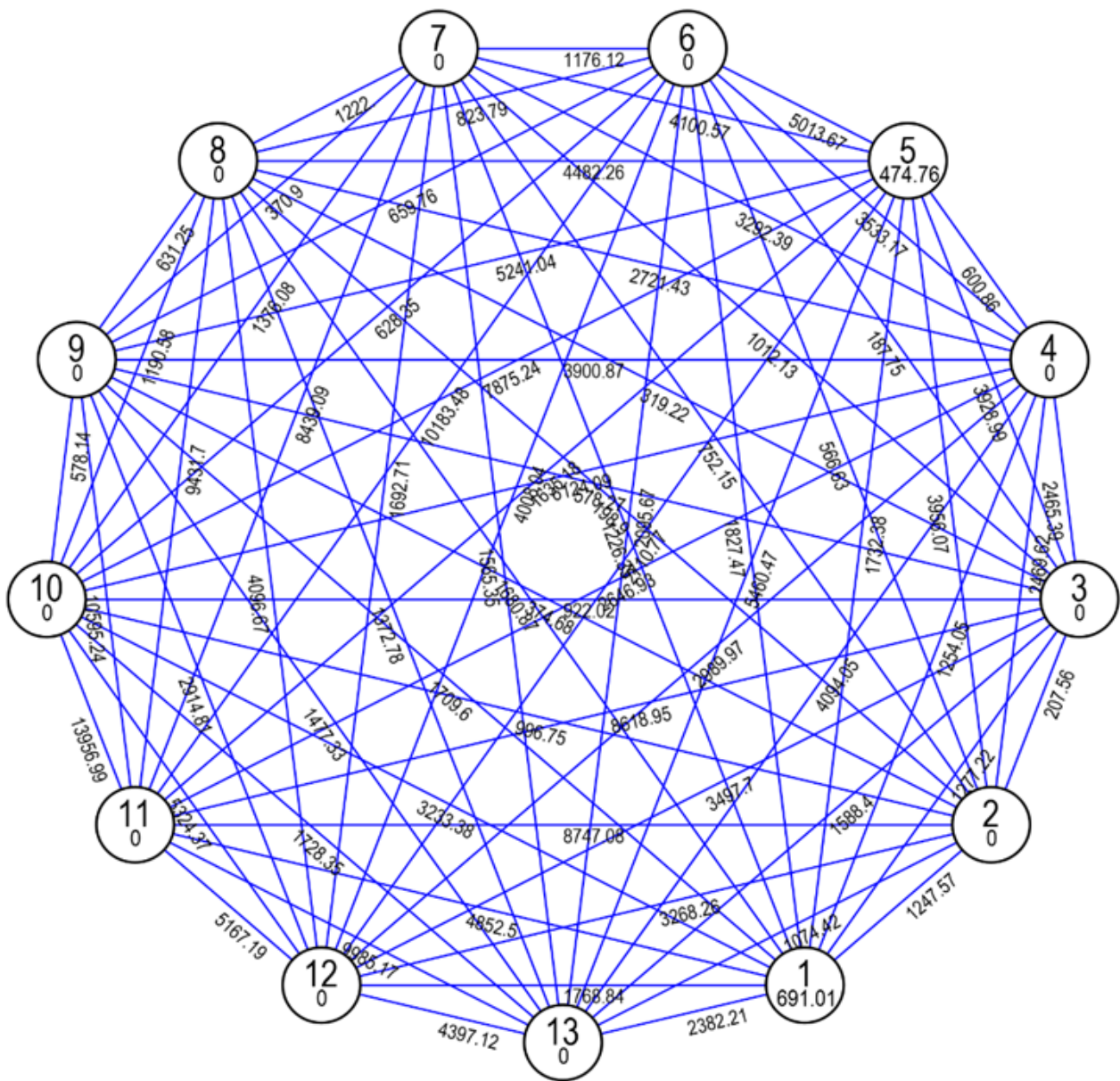
Fig 1: Mahalnobis Euclidean distance (not to scale)
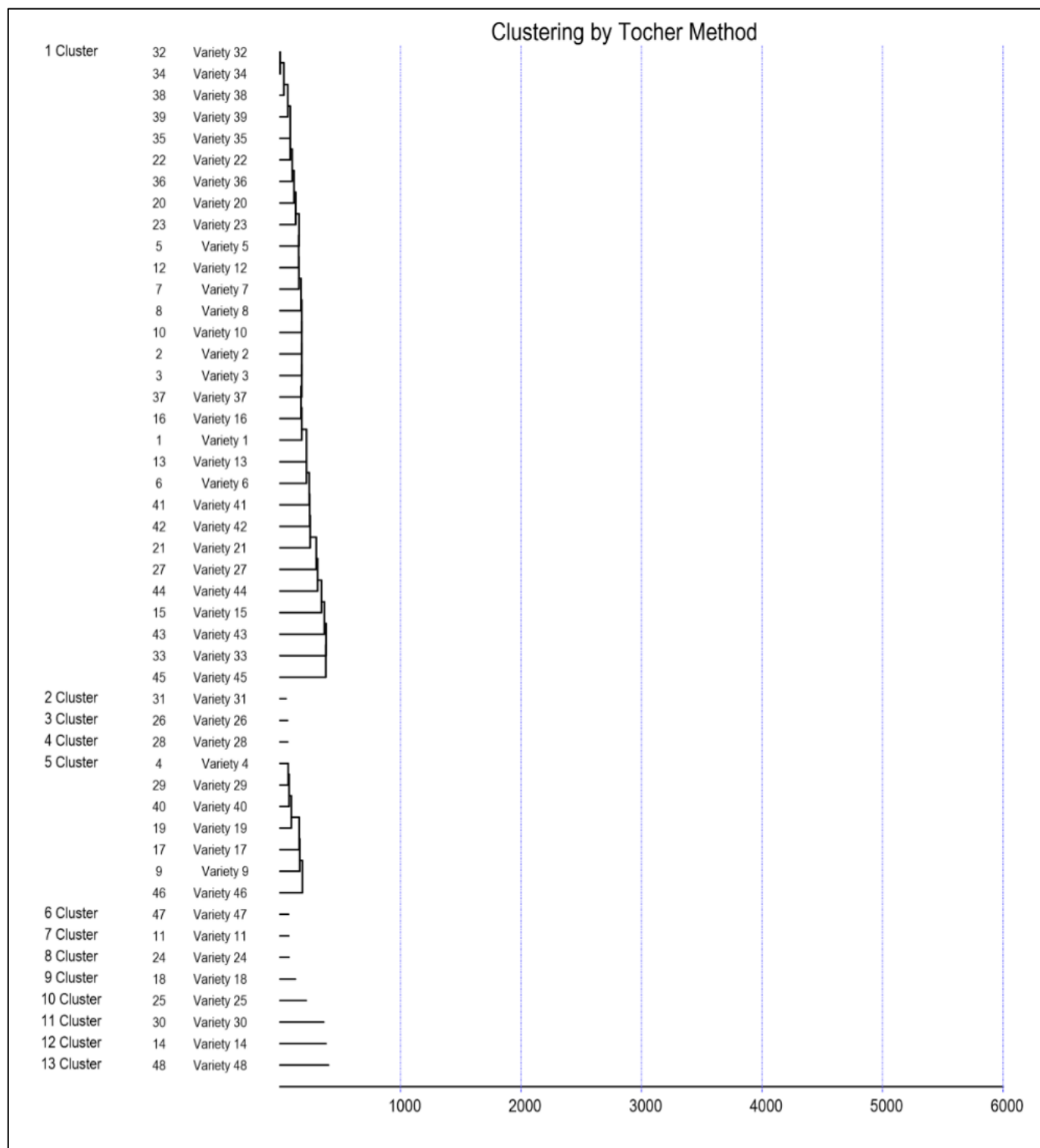
Fig 2: 1 = LSVT-Red-1; 2= LSVT-Red-2; 3 = LSVT-Red-3; 4= Kashmiri Long-1; 5 = IC-561652; 6= IC-561614; 7= IC-561610; 8 = IC-561730; 9 = IC-561665; 10= IC-572487; 11= IC-561618; 12= IC-561661; 13= IC-561691; 14= Kashi Anmol ; 15 = IC-561657; 16= CITH-HP-16; 17 = IC-561731; 18 = IC-561622; 19= Sel- 839-2; 20 = CITH-HP-111; 21= Sel- 917-111; 22= CITH-HP-1154; 23= IC-561631; 24= IC-561635; 25= IC-561639; 26 = Pusa Sadabahar; 27= IC-561627; 28 = SK-SC-1162; 29 = SKAU-078; 30= VOBC-0289; 31= Jawahar Mirch; 32= Guchha Mirch-1; 33 = SK-SC-1161; 34= Guchha Mirch-2; 35= CITH-HP-17/13; 36= ARCH-228; 37= SKAU-084; 38= G-4; 39= CITH-HP-171/13; 40= CITH-HP-22; 41= Sel-680/11; 42= CITH-HP-71/13; 43= SKAU-089; 44= CITH-HP-1154-1/13; 45= SKAU-092; 46= SKAU-096; 47= Goa –Sel-1; 48 = Bhut Jolokia.

Conclusion

The forty-eight genotypes of chilli (*Capsicum annuum* L.) under study were grouped into 13 clusters. D^2 cluster analysis revealed wide genetic distance (inter cluster) between the genotypes of cluster II and IX (13956.99) and the crossing between genotypes of these two clusters can be exploited for the development of heterotic hybrids in future breeding programmes. The clusters VIII, XI, XII and XIII were found superior for one or more characters. Therefore, a multiple crossing programme can be proposed involving genotypes from these clusters for the development of superior segregants in advanced generations with high yield potential combined with better quality in chilli.

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