

## Genetic Diversity Studies in Chilli (*Capsicum annuum* L.) Genotypes under Tarai condition of Uttarakhand

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**ABSTRACT:** For a breeding plan to be successful eventually and to make the most use of available germplasm resources, it is necessary to have an awareness of genetic diversity among cultivars of any crop. Hence studies on genetic diversity were conducted with 52 chilli (*Capsicum annuum* L.) genotypes at the G.B Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India during spring summer season 2023. Mahalanobis D<sup>2</sup> analysis was used to categorise genotypes based on the sum of squares of differences in mean values across contexts for all seventeen characteristics. Based on genetic distance, these genotypes were grouped into seven clusters. Cluster II had the maximum genotypes (16) followed by cluster I with 10 genotypes, cluster III and IV with 5 genotypes, cluster VI with 4 genotypes and cluster V and VII each had one genotype, Maximum intracluster distance was within cluster VI (34048.65), followed by clusters IV (21666.81), I (20433.92), III (18472.89), and II (16093.58) while minimum intracluster distance (0) was observed in cluster V and VII. With the inter cluster distance of 847929.00, cluster IV and cluster VII possessed highest intercluster distance. To achieve high quality segregates, a hybridisation method involving the genotypes from diverse clusters might be selected.

**Keywords:** Chilli, Genotypes, Genetic diversity, Clusters, Hybridisation.

### INTRODUCTION

Chilli (*Capsicum annuum* L.) is a valuable and lucrative spice and vegetable crop in India, cultivated across diverse agro-climatic zones, including tropical, sub-tropical, and temperate regions (Hazra *et al.*, 2011). Chilli, also known as hot pepper, was introduced into India from Brazil during 1584 by the Portuguese (Thamburaj and Singh 2003). According to Bosland (1996), fresh peppers are regarded as superior providers of flavonoids, carotenoids, and vitamins C and K. Capsaicinoids are the main phytochemicals found in hot pepper. Capsaicin, also known as capscutin (C<sub>18</sub>H<sub>27</sub>NO<sub>3</sub>), is the main component of the pericarp of chilli fruit (Suzuki *et al.*, 1984).

The chilli genotypes of the tarai region of Uttarakhand are highly divergent and serve as a source of genetic variability for chilli breeding. Farmers choose chilli genotypes based on agronomic and horticultural qualities that are significant to them (e.g., fruit size, fruit weight, pungency level, colour), and because of natural selection, they are admirably adapted to the regional environment. Genetic divergence in the chilli population accelerates the selection of acceptable parents for use in breeding

programmes, resulting in fewer crosses (Guerra *et al.*, 1999).

A genetic diversity evaluation is necessary to identify the source of genes for specific traits in accessible germplasm. Our goal is to uncover advantageous allele genes and genomic area variation that can aid in crop modification (Saidaiyah *et al.*, 2019) emphasised the need of analysing genetic variation among genotypes in breeding for effective genotype selection. This project aimed to examine genetic variety and choose appropriate genotypes for future hybridization programmes.

Cluster analysis categorises data into groups based on their similarity, with maximum similarity indicating belonging to the same group and minimal similarity otherwise. Clustering identifies distribution patterns and correlations among data properties. Mahalanobis D<sup>2</sup> analysis was used to categorise genotypes based on the sum of squares of differences in mean values across contexts for all seventeen characteristics. Tocher (Rao, 1952) introduced a method that classified 52 genotypes into seven clusters, with some genotypes having extreme values being separated.

### MATERIAL AND METHODS

Field experiment was carried out to assess the diversity among 52 diverse chilli genotypes during

spring-summer 2023 at Vegetable research centre (VRC), GBPUAT, Pantnagar, Uttarakhand. The location is at 29° 05' North latitude, 79° 03' East longitude, and 243.4 metres above mean sea level. It is located in the Shivalik hills and the *Tarai* region, north of the Indo-Gangetic plains. Uttarakhand falls under agro-climatic zone I, also known as the humid Western Himalaya. Pantnagar is located in the southern region of Uttarakhand. The area has a humid subtropical climate with wide temperature variations. In the proposed study, the experiment samples were comprised of 50 genotypes and two checks (Pant Chilli -1 and Kashi Anmol) were sown in Augmented-II design with five blocks of length 3m during spring season, 2023. Each genotype was sown in 2 rows by following the spacing of 50 × 50 centimetres. Raised bed of 15 cm above the ground level was prepared for all genotypes and channel of 25-30 cm thus formed around was used for irrigation and drainage. The bed size was 1m length and 20m length for sowing of seed. The bed was prepared on 3<sup>rd</sup> Feb 2023. Seedlings were transplanted. Seventeen observation were recorded namely plant height (cm), number of primary branches, days to 50 % flowering, leaves per plant, fruit weight per plant (g), fruit length (cm), stalk length (cm), number of seed per fruit, 100 seed weight (g), weight of seed per fruit (g), dry weight (g), ascorbic acid (mg/100g), TSS (°Brix), Oleoresin (ASTA), Number of fruit per plant and green fruit yield (q/ha). The intra and inter- cluster distances were calculated as per the formula given by Singh and Choudhary (1977).

## RESULT AND DISCUSSION

The analysis of variance for different quantitative traits for fifty-two chilli genotypes were highly significant difference among the genotypes for most of the observations recorded. Based on the D<sup>2</sup> Mahalanobis analysis (Table 1), 52 genotypes were broadly grouped into seven clusters with variable number of genotypes revealing the presence of considerable amount genetic diversity in the genotypes. Among the seven clusters, Cluster II had the maximum genotypes (16) followed by cluster I with 10 genotypes, cluster III and IV with 5 genotypes, cluster VI with 4 genotypes and cluster V and VII each had one genotype. Intercluster distance refers to the distance between entities from different clusters, whereas intracluster distance refers to the

distance between entities within the same cluster. Starting from the lowest value (0.000) in cluster V and VII, intracluster distance is the maximum (34048.65) in cluster VI. Intracluster distance of cluster II (16093.58) was found to be least next to cluster III (18472.89), cluster I (20433.92), cluster IV (21666.81). With the inter cluster distance of 847929.00, cluster IV and cluster VII possessed highest inter cluster distance followed by cluster IV and cluster V (578962.60). Cluster II and cluster IV also possessed higher inter cluster distance of (562108.70). Lowest inter cluster distance was reported between cluster II and cluster V (35809.15). Comparable results were also obtained by Farhad *et al.* (2008); Kumar and Tata (2010); Srinivas *et al.* (2013); Yattung *et al.* (2014); Zehera *et al.* (2015); Gayathri *et al.* (2022); Srinivas *et al.* (2021).

From Table 2, the nearest intercluster distance was found to be between cluster II and cluster V (35809.15) followed by (40113.31) between cluster II and cluster III, (45013.15) between cluster II and cluster VII. The farthest distance was reported 847929.00 between cluster IV and cluster VII, followed by 578962.60 between cluster IV and cluster V. From the statistical data in Table 2, it is noticed that, cluster I is nearest to cluster III with having a distance of 20433.92 and having a greater distance from cluster VII (256764.70). Similarly cluster II is much closer to cluster V having a distance of 16093.58 and having a greater distance from cluster V (270250.30). Cluster III is nearer to cluster II having a distance of 18472.89 and much distance from cluster IV (368373.20). As far as cluster IV is concerned the highest distance was found with cluster VII (21666.81) whereas the nearest cluster was found cluster VI (90987.41). Similarly in case of cluster V, the nearest cluster was noticed cluster II (35809.15) and farthest distance from cluster IV (578962.60). In case of cluster VI the nearest cluster was cluster I (34048.65) and farthest cluster was cluster VII (478864.90). Cluster VII was closest to cluster II at a distance of (45013.15) and farthest from cluster IV (847929.00). Similar findings were reported by Srivastava *et al.* (2016); Abhinaya *et al.* (2016). Choosing parents with high genetic variety is crucial for successful breeding, since it increases the likelihood of producing desired recombinants in progeny.

**Table 1: Clustering pattern of fifty-two chilli genotypes using Tocher's method.**

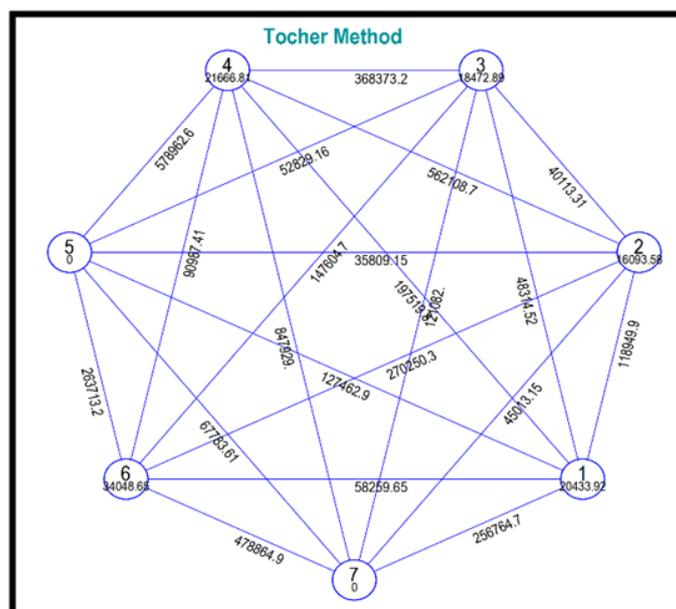
Cluster Group	No. of Genotypes	List of Genotypes
1 Cluster	10	Pant chilli-1, Kashi Anmol, PCHI/LCV/2022-7, PCHI/2021-10, PCHI/2022-11, PCHIH/2021-8, PCHIH/2020-5, PCHI/2022-1, PCHIH/2020-8 and PCHI/LCV/2022-3
2 Cluster	26	PCHI/2022-1, PCHI/2021-13, PCHIH/2022-3, PCHIH/2020-2, PCHIH/2020-9, PCHIH/2020-1, PCHI/2020-9, PCHIH/2022-6, PCHIH/2020-6, PCHIH/2020-3, PCHIH/2021-5, PCHIH/2020-11, PCHIH/2021-6, PCHIH/2022-2, PCHIH/2021-11, PCHI/2021-4, PCHI/2021-9, PCHIH/2020-4, PCHIH/2021-2, PCHIH/2021-3, PCHIH/2020-3, PCHIH/2022-7, PCHIH/2022-4, PCHI/2021-6, PCHI/2022-10 and PCHIH/2020-10
3 Cluster	5	PCHI/LCV/2021-9, PCHIH/2022-5, PCHIH/20217, PCHIH/2021-7 and PCHI/LCV/2022-4
4 Cluster	5	PCHI/2022-8, PCHI/2022-2, PCHI/LCV/2022-1, PCHI/LCV/2022-9 and PCHI/2022-4
5 Cluster	1	PCHI/LCV/2022-5
6 Cluster	4	PCHI/2022-7, PCHI/2022-5, PCHI/2021-11 and PCHIH/2021-4
7 Cluster	1	PCHI/2020-2

**Table 2: Average intra and inter cluster distance D2 for different traits of chilli genotypes.**

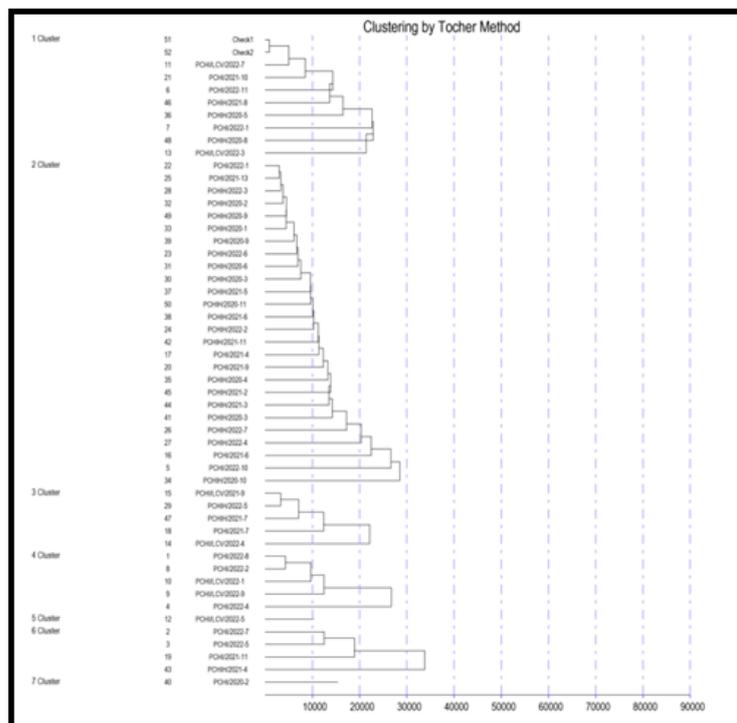
Cluster Distances							
	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Cluster 1	20433.92	118949.90	48314.52	197519.80	127462.90	58259.65	256764.70
Cluster 2		16093.58	40113.31	562108.70	35809.15	270250.30	45013.15
Cluster 3			18472.89	368373.20	52829.16	147604.70	121082.00
Cluster 4				21666.81	578962.60	90987.41	847929.00
Cluster 5					0.00	263713.20	67783.61
Cluster 6						34048.65	478864.90
Cluster 7							0.00

**Table 3: Mean values of different traits in seven clusters of Chilli.**

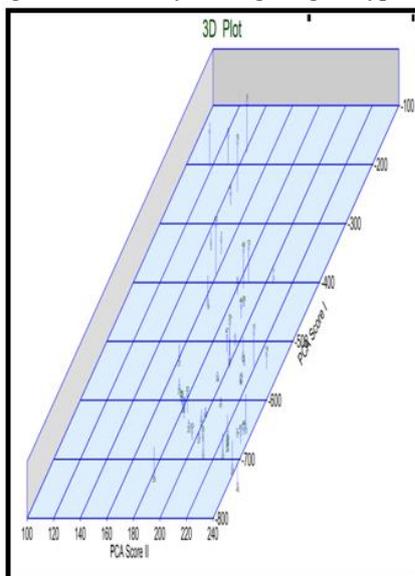
Sr. No.	Character	Clusters						
		I	II	III	IV	V	VI	VII
1.	Plant height (cm)	60.27	58.64	86.83	59.07	57.02	58.53	33.54
2.	Number of primary branches	7.58	7.85	7.58	7.34	7.91	8.69	7.22
3.	Days to 50% flowering	59.78	55	57.27	57.42	71.78	59.03	53.78
4.	Leaves per plant	122.77	126.78	167.72	133.32	115.11	122.89	124.55
5.	Fruit weight per plant (g)	107.27	84.34	102.91	76.03	243.57	162.73	60.05
6.	Fruit length (cm)	7.83	9.95	12.03	10.68	8.93	8.65	9.23
7.	Stalk Length (cm)	2.23	2.32	2.34	1.97	1.55	1.93	1.8
8.	Number of seed per fruit	55.42	50.58	56.25	59.62	64.53	49.12	50.53
9.	100 seed weight(g)	0.46	0.43	0.49	0.51	0.52	0.47	0.39
10.	Weight of seed per fruit	0.23	0.23	0.15	0.31	0.31	0.29	0.14
11.	Dry weight (g)	26.73	38.64	28.83	11.93	10.45	26.06	19.1
12.	Ascorbic acid (mg/100g)	136.76	104.52	124.36	176.5	130.2	119.44	139.22
13.	TSS (°Brix)	7.38	6.85	8.4	7.07	9.91	5.96	4.32
14.	Oleoresin (ASTA)	47.37	43.38	40.64	47.05	48.88	48.12	53.57
15.	Average fruit weight(g)	1.77	2.62	2.12	1.57	2.11	2.04	1.98
16.	No. of fruit per plant	146.51	132.22	142	96.88	156.78	102.89	189.43
17.	Green fruit yield (q/ha)	101.02	132.49	117.88	59.48	132.32	83.51	150.03



**Fig. 1.** Distance between inter and intra cluster distances in chilli genotypes.



**Fig. 2.** Dendrogram showing the genetic diversity among 52 genotypes of chilli using Tocher's method.



**Fig. 3.** 3-Dimensional plot showing clustering pattern for divergence of chilli genotype.

## CONCLUSIONS

Understanding genetic divergence is crucial for selecting varied parents and producing successful hybrids. Developing high-yielding, region-specific cultivars is crucial for addressing local issues and promoting wider adoption. In the present investigation, there was a maximum distance between cluster IV and cluster VII. The hybridisation between these clusters can be used to identify superior recombinants or transgressive segregates in segregating populations, as these clusters are the most diverse.

## FUTURE SCOPE

The promising Genotypes identified in this study can be exploited commercially to increase Chilli quality and yield.

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**Conflict of Interest.** None.

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