

*Short Communication*

## Genetic diversity in parthenocarpic cucumber (*Cucumis sativus* L.) for yield and quality traits under protected cultivation

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Cucumber (*Cucumis sativus* L.) is one of the most important cucurbitaceous vegetable crops grown extensively in tropical and subtropical parts of the country. Cucumber is thermophilic and required optimum temperature range between 18 °C and 24 °C. It is grown for its tender fruits, which are consumed either raw as salad, cooked as vegetable or as pickling cucumber in its immature stage. It is a rich source of carbohydrates, Ca, P and vitamin C. The appreciable yield deficit between potential and realized crop yield indicated an urgent need to develop superior hybrids having desirable yield and quality attributes. Diverse parents are expected to produce high yielding hybrids through manifestation of heterosis, increase the probability to obtain transgressive segregants in F<sub>2</sub> and in subsequent generations. Moreover, evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm. Considering the importance of cucumber and keeping in view the facts, the present study has been undertaken to estimate the genetic divergence through Mahalanobis D<sup>2</sup> analysis in twenty-three genotypes of parthenocarpic cucumber.

The present investigation was conducted at the Polyhouse Complex, Department of Horticulture (Vegetable and Floriculture), Bihar Agricultural College, Bhagalpur, during spring-summer months of 2021. Experimental material consists 23 genotypes of parthenocarpic cucumber including 1 check (KPCH-1) and the experiment was laid out in Randomized Block Design with three replications on raised beds. The seeds were raised in pro trays to get healthy and uniform seedlings and 30 days old healthy seedlings were transplanted in double row planting (50 cm × 50 cm) system in naturally ventilated polyhouse. The observations were recorded from five randomly selected

plants in each replication for seventeen characters viz., days to first flower, node to first flower, number of flowers per node, inter-nodal length (cm), number of nodes per vine, days to first picking, span of harvest (days), average fruit weight (g), fruit length (cm), fruit diameter (cm), thickness of flesh (cm), number of fruits per vine, yield per vine (kg), vine length (cm) at last harvest, TSS (<sup>0</sup>Brix), ascorbic acid (mg/100 g), shelf life (days). Genetic divergence was estimated using Mahalanobis D<sup>2</sup> (1928) and the population were grouped in clusters as per Rao (1952).

The analysis of variance revealed highly significant differences among the genotypes for all the characters studied, indicating the existence of wide genetic divergence among them. Information on genetic diversity was also used to identify promising diverse genotypes, which may further be used in breeding programme. On the basis of performance of various traits, the clustering pattern of 23 diverse genotypes of parthenocarpic cucumber has been presented in Table-1. Based on D<sup>2</sup> analysis, twenty-three genotypes were grouped into seven clusters (Fig.1). Cluster 1 contains maximum 12 genotypes followed by cluster 2 which contain 6 genotypes while rest of clusters was found to be monogenotypic. Wide range of diversity was also reported by Sharma and Sharma (2006), Gaekwad et al. (2011), Sharma et al. (2018), Kumar et al. (2018), Thakre (2019) and Kumawat et al. (2020) in cucumber.

Average intra and inter cluster distance are presented in Table-2. Average intra cluster distance varied from 0.00 to 74.87. Intra cluster distance was highest in cluster 1 (74.87) followed by cluster 2 (61.73). The inter. cluster distance varied from 409.19 to 90.18. It was highest among cluster 3 and cluster 7 (409.19) and it was minimum (90.18) between cluster 3 and cluster 5. The cluster means of 23 genotypes (Table 3) showed that the mean values of cluster varied in magnitude for all the seventeen characters. Cluster 2 better performed in term of days to first flower (28.12) and maximum value

**Table 1:** Grouping of 23 genotypes of parthenocarpic cucumber into clusters

Cluster No.	No. of genotypes	Genotypes
1	12	Variety 3- BRPCU-3 Variety 5- BRPCU-6 Variety 23- KPCH-1 (Check) Variety 17- BRPCU-3×BRPCU-7 Variety 21- BRPCU-6×BRPCU-7 Variety 13- BRPCU-2×BRPCU-7 Variety 8- BRPCU-1×BRPCU-2 Variety 22- BRPCU-6×BRPCU-8 Variety 11- BRPCU-2×BRPCU-3 Variety 14- BRPCU-2×BRPCU-8 Variety 1- BRPCU-1 Variety 2- BRPCU-2
2	6	Variety 4- BRPCU-5 Variety 6- BRPCU-7 Variety 10- BRPCU-1×BRPCU-8 Variety 16- BRPCU-3×BRPCU-6 Variety 12- BRPCU-2×BRPCU-5 Variety 20- BRPCU-5×BRPCU-8
3	1	Variety 7- BRPCU-8
4	1	Variety 18- BRPCU-3×BRPCU-8
5	1	Variety 9- BRPCU-1×BRPCU-7
6	1	Variety 19- BRPCU-5×BRPCU-7
7	1	Variety 15- BRPCU-3×BRPCU-5

for number of flowers per node (1.99), number of nodes per vine (33.43), number of fruits per vine (29.74), span of harvesting (55.81 days) and yield per vine (3.81 kg). Cluster 4 better performed in term of days to first picking (40.73) and maximum value for node to first flower (4.80), average fruit weight (140.47 g), fruit

diameter (3.90 cm) and thickness of flesh (1.30 cm).

Contribution of different attributes toward genetic diversity are presented in Table-4. The highest contribution toward genetic diversity was shown by ascorbic acid (25.69%) followed by yield per vine (20.95%), vine length (15.81%), total soluble solid (12.25 %), internode length (6.32%), thickness of flesh (4.74%), number of node per vine (3.16%), span of harvesting (3.16%), number of fruits per vine (2.77

**Table 4:** Contribution of different attributes toward genetic diversity

Characters	Times ranked first	Contribution %
Days to first flower	0	0.00
Node to first flower	2	0.79
Number of flowers per node	5	1.98
Days to first picking	0	0.00
Average fruit weight (g)	1	0.40
Fruit length (cm)	2	0.79
Fruit diameter (cm)	0	0.00
Thickness of flesh (cm)	12	4.74
Total soluble solid (°Brix)	31	12.25
Ascorbic acid (mg/100 g)	65	25.69
Shelf life (days)	3	1.19
Number of nodes per vine	8	3.16
Vine length (m)	40	15.81
Inter-nodal length (cm)	16	6.32
Number of fruits per vine	7	2.77
Span of harvest (days)	8	3.16
Yield per vine (kg)	53	20.95

**Table 2:** Average intra and inter cluster distance in parthenocarpic cucumber

Cluster	1	2	3	4	5	6	7
1	74.87						
2	181.34	61.73					
3	104.23	300.13	0				
4	154.79	212.33	109.69	0			
5	127.18	333.03	90.18	102.27	0		
6	308.35	247.86	287.33	102.88	229.02	0	
7	369.43	178.76	409.19	216.26	373.05	102.31	0

**Table 3:** Cluster means for twenty-three genotypes of parthenocarpic cucumber

Characters	1	2	3	4	5	6	7
Days to first flower	30.41	28.12	30.80	28.53	31.80	32.40	29.87
Node to first flower	4.10	4.23	4.47	4.80	3.80	4.13	3.60
Number of flowers per node	1.53	1.99	1.20	1.53	1.33	1.53	1.73
Days to first picking	44.24	41.64	44.60	40.73	46.80	46.27	44.67
Average fruit weight (g)	127.42	128.21	120.17	140.47	125.23	126.83	133.63
Fruit length (cm)	16.14	17.90	15.87	16.40	17.43	19.27	16.30
Fruit diameter (cm)	3.49	3.29	3.53	3.90	3.82	3.50	3.27
Thickness of flesh (cm)	1.15	1.08	1.19	1.30	1.27	1.10	1.04
Total soluble solid (°Brix)	3.10	3.46	3.30	3.43	2.57	3.58	3.17
Ascorbic acid (mg/100 g)	2.31	2.37	2.65	3.04	2.89	3.16	3.26
Shelf life (days)	5.57	5.43	6.20	4.93	5.07	4.27	5.80
Number of nodes per vine	28.13	33.43	22.20	28.27	26.33	28.80	32.47
Vine length (m)	2.85	2.82	2.39	2.91	2.81	3.06	2.67
Inter-nodal length (cm)	10.54	8.58	11.78	10.61	11.23	10.78	8.44
Number of fruits per vine	27.89	29.74	26.00	27.73	26.40	27.87	28.40
Span of harvest (days)	52.22	55.81	50.53	54.47	49.47	50.13	53.20
Yield per vine (kg)	3.55	3.81	3.26	3.53	3.33	3.55	3.70

%), numbers of flowers per node (1.98%), indicating the major role of these characters in building up diversity and differentiating of inter cluster level. Similar results were also reported by Sharma and Sharma (2006), Hasan et al. (2015) and Ahirwar et al. (2017) in cucumber.

Maximum inter cluster distance was observed between cluster 3 and cluster 7 (409.19). Maximum inter cluster distance between cluster 3 and 7 indicated that the genotypes falling in these clusters were genetically more divergent and genotypes included in these clusters can be used as a parent for hybridization programme to get higher heterotic hybrids from the segregating population.

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