



ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2023; 12(7): 1532-1538
© 2023 TPI

www.thepharmajournal.com

Received: 08-05-2023

Accepted: 21-06-2023

Shuchismita Patra

G. B. Pant University of
Agriculture and Technology,
Pantnagar, Uttarakhand, India

DK Singh

G. B. Pant University of
Agriculture and Technology,
Pantnagar, Uttarakhand, India

Shashank Shekhar Singh

SMS Horticulture KVK Nawada,
Bihar, India

Malani Negi

G. B. Pant University of
Agriculture and Technology,
Pantnagar, Uttarakhand, India

Assessment of genetic diversity of parthenocarpic cucumber (*Cucumis sativus* L.) genotypes under polyhouse condition

Shuchismita Patra, DK Singh, Shashank Shekhar Singh and Malani Negi

Abstract

The present investigation was carried out at the Vegetable Research Centre, G.B. Pant University of Agriculture and Technology, Pantnagar, during February-May, 2023 with total twenty-three genotypes of Parthenocarpic cucumber including two check varieties Pant Parthenocarpic Cucumber 3 and Pusa Parthenocarpic Cucumber 6 under randomized block design to study genetic variability and diversity. According to statistical analysis of data, the result revealed significant differences among parthenocarpic cucumber genotypes observed for sixteen growth and yield related characters. High PCV and GCV were recorded for main vine length (m), number of nodes per vine, days to first male flower, node number at which first male flower appears, node number at which first female flower appears, fruit yield per plant (kg), fruit yield per hectare (q). The difference between PCV and GCV was less which indicates these traits are less influenced by the environment. High value of heritability was reported for days to first male flower followed by main vine length(m), number of nodes per vine, node at which first male flower appears, node at which first female flower appears, fruit yield per plant (kg), fruit yield per hectare(q), days from flower initiation to harvest, internodal length(cm), number of pickings, fruit weight (g), fruit length(cm), number of fruits per plant, days to first fruit harvest, days to first female flower and fruit diameter (cm). High genetic advance as percentage of mean was obtained for the characters under study. The inter cluster D^2 values of the six clusters revealed that highest inter cluster generalized distance was observed between cluster IV and V indicating that the genotypes in these clusters can be used as parents in hybridization programme to develop high heterotic hybrids. It was observed that fruit yield per plant (kg) contributed maximum towards divergence followed by fruit yield per hectare (q) and fruit weight (g). Five genotypes namely Aviva, PPCUC 13, PPCUC 6, Safran Plus and PPCCU 7 were superior for fruit yield per plant (kg) and these genotypes may be considered as promising ones for the improvement of parthenocarpic cucumber in breeding programme.

Keywords: Parthenocarpic cucumber, genotypes, variability, genetic diversity

1. Introduction

Cucumber (*Cucumis sativus* L., $2n=2x=14$), in the family Cucurbitaceae, is believed to be originated in India (Harlan, 1975) [8] and Parthenocarpic Cucumber is one of the most valuable types of cucumber which is widely grown for its seedless edible fruit. Parthenocarpy has long been known to occur within the species of *Cucumis sativus* L. (Sturtevant, 1890) [36]. Parthenocarpy is regarded as the ability to develop fruits without pollination. Fruits with developing seeds inhibit the growth of later fruits, however, to a lesser extent if fruits are grown parthenocarpically (Denna, 1973) [6]. The inheritance of parthenocarpy in cucumber is governed by an incomplete dominant gene (P). Parthenocarpic cucumbers are advantageous because of increased numbers of pistillate flowers, thus greater opportunities for higher fruit set and per unit production. It can produce fruits with smoother skin, seedless nature, thin skin, lush green appearance, tender texture and used for raw snacking. Cultivation of parthenocarpic cucumber under the protected environment having partial/fully environment control has been undertaken during last three decades in our country and very little work has been done for developing varieties for the protected environment.

Therefore, suitable breeding strategy should be formulated for the improvement of parthenocarpic cucumber based on the magnitude of parameters of variability as the success of any breeding programme depends on this. Hence the present study has been undertaken to estimate the extent of variability, heritability and genetic divergence in twenty-three genotypes of parthenocarpic cucumber.

Corresponding Author:

Shuchismita Patra

G. B. Pant University of
Agriculture and Technology,
Pantnagar, Uttarakhand, India

Cucumber being a cross pollinated crop with numerous seeds per fruit and practically no inbreeding depression with very few commercial hybrids, offers a great opportunity for exploitation of heterosis. Genetic divergence among the population is necessary for the selection of parents in hybridization programme to produce heterotic effects. Thus, to determine the extent of genetic diversity, Mahalanobis D^2 statistic has been widely used in the material irrespective of the number of populations. Keeping above points in view, twenty three genotypes were evaluated for the study of genetic divergence in parthenocarpic cucumber.

2. Materials and Methods

The present investigation was conducted in February - May, 2023 at Vegetable Research Centre, Department of Vegetable Science in G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand at the foot hills of Himalayan region (Shivalik hills) under humid subtropical climate zone in narrow belt called Tarai. Geographically, Vegetable Research Centre is situated at the latitude of 29.5°N, longitude 79.3°E and at an altitude of 243.84 meters above the mean sea level. The materials for study had twenty-three genotypes of Parthenocarpic cucumber such as Pant Parthenocarpic Cucumber 2 (PPCUC 2), Pant Parthenocarpic Cucumber 3 (PPCUC 3), PPCUC 4, PPCUC 5, PPCUC 6, PPCUC7, PPCUC 9, PPCUC 10, PPCUC 11, PPCUC 12, PPCUC 13, PPCUC 14, Punjab Kheera 1, Pusa Parthenocarpic Cucumber 6, X1, Zaara, Safran Plus, Aviva, Infinity, Lucro, Gurka, Mini Cucumber and Multifruit Parthenocarpic Cucumber. The studied genotypes were statistically placed out in the field using Randomized Block Design (RBD) together with three replications.

The planting spacing was 90 cm×60cm. After the emergence of seedlings, only one healthy plant per hill was retained. The standard cultural practices as recommended in the package of practices for vegetable crops, were followed to ensure a healthy crop stand. The observations were recorded from five randomly selected plants in each replication for all characters following viz., main vine length(m), internodal length(cm), number of nodes per vine, days to first female flower, days to first male flower, node at which first male flower appears, node at which first female flower appears, days to flower initiation to harvest, days to first fruit harvest, average fruit length (cm), average fruit diameter (cm), individual fruit weight (g), number of fruits per vine, number of pickings, fruit yield per plant(kg), total fruit yield per hectare (q) and fruit morphological characters-fruit skin colour, fruit shape at base of peduncle, fruit spininess. Statistical analysis such as analysis of variance for individual traits was done as per Panse and Sukhatme (1967) [23], Components of variance, heritability, genetic advance and genetic divergence were estimated as per Burton and Devane (1953) [4], Allard (1960) [3], Johnson *et al.*, (1955) [10], Mahalanobis (1936) [17] and Singh and Chaudhary (1977) [33].

3. Results and Discussion

3.1 Mean performance of genotypes

In the current investigation, twenty-three diverse genotype of cucumber were studied in terms of yield and yield attribute traits. The high and significant differences among the genotypes were observed for all the characters indicating presence of sufficient amount of variability for all the characters studied. Thus, it specified the sufficient variability

in the resources studied, which could be utilized in further breeding programme.

Mean performance of parthenocarpic cucumber genotypes with respect to fruit yield and its component characters have been presented in Table 2. The wide variation observed in respect to main vine length(m) was from 0.93 m to 2.97 m. in the genotypes Gurka and Pant Parthenocarpic Cucumber -2 respectively, inter nodal length (cm) ranged from 6.40 to 9.13 cm in Infinity and Pant parthenocarpic Cucumber 2 respectively. The number of nodes per vine maximum and minimum for Punjab Kheera 1 (35.89) and Gurka (17.25) respectively. The genotypes Aviva was earliest to open first female flower (42.66) whereas, PPCUC 13 took maximum number of days (52.00) for female flower opening. Among all the genotypes X1, Aviva and Safran Plus had no male flower that means they had totally female flower (as in case of gynocious type) in all nodes. The lowest node number at which first female flower appears was observed in PPCUC 12 (2.40), whereas Zaara (5.86) showed the highest node position. The lowest node number was observed in genotypes X1, Aviva and Safran Plus (0.00) as these genotypes had no male flower, whereas the highest node position was observed in PPCUC 4 and Zaara (2.60). Days from flower initiation to harvest ranged 10.53 to 19.54 in Punjab Kheera 1 and PPCUC 4 respectively. The mean of days to first fruit harvest ranged from 52.60 to 71.39 where Aviva took minimum number of days (52.60) to first fruit harvest. Fruit length was minimum in PPCUC 4 (13.79 cm) and maximum fruit length was recorded in PPCUC 13 (22.97 cm). Maximum fruit diameter was recorded in PPCUC 6 (4.46 cm). Least fruit weight was observed in the check variety Pusa Parthenocarpic Cucumber 6 (102.36 g) and PPCUC 13 (216.74 g) recorded highest fruit weight. The genotype Aviva recorded significantly superior genotype for a greater number of fruits per vine (27.80). Minimum number of pickings were recorded in PPCUC 10 (6.78), while genotype Aviva recorded maximum number of pickings (10.43). Among all, lowest yield per plant was recorded in Punjab Kheera 1 (2.01 kg) whereas, Aviva (5.79 kg) reported highest yield per plant (kg).

Out of twenty-three genotypes, five genotypes namely Aviva (1068.92 q), PPCUC-13 (880.47 q), PPCUC 6(880.23 q), Safran Plus (852.13 q) and PPCUC 7(848.22 q) were superior for fruit yield per hectare(q) and these genotypes may be recommended for large scale farming for commercial cultivation and can be used in Parthenocarpic cucumber breeding programme. Similar findings were reported by Kumar *et al.* (2018) [13], Nagagami *et al.* (2019) [22], Karthick *et al.* (2019) [11], Mehta and Sharma (2020) [20], Dhillon and Singh (2021) [7], Kaur and Sharma (2022) [12] and Singh *et al.* (2022) [31].

3.2 Genetic variability, heritability and genetic advance

The phenotypic variances for sixteen characters under study were higher than the genotypic variances (Deepa *et al.*, 2018; Karthick *et al.*, 2019) [5, 11]. This possibly will be due to the non-genetic or environmental influence which played vital role in the pointer of these characters. It is an efficient tool to identify the nature of variability in the group of diverse population. High (>20%) phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for main vine length (34.43 and 33.86) number of nodes per vine (22.91 and 22.22), days to first male flower

(40.05 and 39.65), node number at which first male flower appears (49.49 and 47.81), node number at which first female flower appears (22.75 and 21.82), fruit yield per plant (27.34 and 25.49), fruit yield per hectare (27.62 and 25.40). Moderate (10-20%) PCV and GCV recorded for internodal length (cm), days from flower initiation to harvest, fruit length (cm), fruit weight (g), number of fruits per plant. Number of pickings has recorded moderate PCV (10.81) and low GCV (9.46). The characters showing high PCV and GCV can be improved through different breeding methods. Karthick *et al.* (2019) [11] reported high PCV and GCV for number of nodes bearing first male flower, primary branches, number of female flower, number of male flower, fruits per plant, weight of the fruit, length of the fruit and yield per plant. Results were in accordance with earlier findings of Pushpalatha *et al.* (2016) [25], Shah *et al.* (2017) [28], Deepa *et al.* (2018) [5] and Ahirwar and Singh (2018) [2].

Heritability provide us the characters which are all inherited from parents to off springs. Highest value of heritability was reported for days to first male flower (98.00%) followed by main vine length (96.70%), number of nodes per vine (94.10%), node at which first male flower appears (93.30%), node at which first female flower appears (92.00%), fruit yield per plant (87.00%), fruit yield per hectare (84.50%), days from flower initiation to harvest (83.60%), internodal length (78.80%), number of pickings (76.70%), fruit weight (73.80%), fruit length (69.30%), number of fruits per plant (66.60%), days to first fruit harvest (57.20%), days to first female flower (32.90%) and fruit diameter (29.70%). Highest genetic advance as percent of mean was observed in case of node number at which first male flower appears (95.12) followed by days to first male flower (80.86) Similar results are from Ahirwar and Singh (2018) [2], Kumar *et al.*, (2018) [13], Mehta and Sharma (2020) [20], Dhillon and Singh (2021) [7], Singh *et al.* (2022) [31]. High genetic advance as percent of mean obtained for the characters under study presented in Table 3 indicates that these characters are governed by additive genes and selection will be worthwhile for exploiting these characters and their improvement.

3.3 D² analysis

Information about genetic diversity will help to select the promising diverse genotypes, which may be utilized in future breeding programme. Mahalanobis D² statistic is an exclusive tool for classifying genetically diverse parents based on quantitative traits (Mahalanobis, 1936; Rao, 1952) [17, 26]. In this study, six clusters were formed among which cluster I comprise eight genotypes which is highest number of genotypes followed by cluster II and cluster III had five genotypes, cluster IV had three genotypes whereas, cluster V and cluster VI had one genotype (Table 4).

From the present data, it is evident that main vine length was highest in cluster II (2.30 m) and lowest in cluster I (1.19 m). The cluster I had the lowest internodal length (6.82 cm) whereas, cluster VI had the highest internodal length (8.86 cm). The cluster V has the highest number of nodes per vine (35.89) whereas, cluster I has the lowest number of nodes per vine (19.70). The number of days to first female flower was least in cluster IV (44.44 days) followed by cluster I (45.00 days), whereas cluster II had the highest number of days to first female flower (49.53 days). The cluster IV had the least number of days to first male flower (0.00 days) as there was no male flower in the genotypes and it was followed by

cluster VI (45.00 days), whereas cluster V has the highest number of days to first male flower (47.00 days). The cluster I has the lowest number of nodes at which first female flower appears (2.96) followed by cluster IV (3.04) whereas, cluster VI has the highest node number at which first female flower appears (5.86).

Similarly, cluster IV has the lowest node number at which first male flower appears (0.00) as there was no male flower, whereas cluster VI had the highest node number at which first male flower appears (2.60). The number of days from flower initiation to harvest was minimum in cluster V (10.53 days) and maximum in cluster VI (17.98 days). The days to first fruit harvest was recorded lowest in cluster V (57.52 days) and highest in cluster II (69.62 days). Fruit length was recorded highest in cluster III (18.84 cm) and lowest in cluster V (15.49 cm). Average fruit diameter was recorded highest in cluster III (3.99 cm) and lowest in cluster V (3.82 cm). Similarly, cluster III had maximum fruit weight (199.31 g) and cluster V had minimum fruit weight (129.78 g). Cluster IV had maximum number of fruits per plant (25.08), whereas, cluster II (19.89) had minimum number of fruits per plant. The genotypes of cluster V had maximum number of pickings (9.52) whereas, genotypes of the cluster I had minimum number of pickings (8.17). The fruit yield per plant was highest in cluster IV (4.86 kg) and lowest in cluster V (2.01 kg). Fruit yield per hectare (q) was highest in cluster IV (898.81 q) and lowest in cluster V (370.52 q).

The mean intra and inter cluster D² values among the six clusters are given in the Table 6. The intra cluster D² values ranged from 0.00 (Cluster V and VI) to 75.48 (Cluster III). The cluster III had the maximum intra cluster D² value (75.48) followed by Cluster V (70.12). The inter cluster D² values of the six clusters revealed that highest inter cluster generalized distance (493.66) was between cluster IV and V followed by cluster II and IV (374.61), while the lowest (110.72) was between cluster I and cluster II. Cluster IV followed by the cluster V is the most diverse from all other clusters. Thus high degree of genetic diversity and thus may be utilized under inter varietal hybridization program (transgressive breeding) for getting high yielding recombinants. Similar results showed by Ahirwar *et al.* (2017) [1], Pal *et al.* (2017) [22], Shah *et al.* (2017) [29], Kumar *et al.* (2018) [14], Sharma *et al.* (2018) [30], Kumar *et al.* (2020) [15], Suma *et al.* (2021) [35].

The percent contribution of each character towards divergence is presented in Table 7. It was observed that fruit yield per plant contributed maximum (15.63%) towards divergence followed by fruit yield per hectare (13.54%), fruit weight (12.32%), number of fruits per plant (6.85%), number of nodes to male flower (6.68%), number of nodes per vine (5.93%), main vine length (5.66%), number of pickings (5.65%), number of nodes to female flower (5.41%), fruit diameter (5.40%), days to first male flower (4.02%), days to first female flower (4.00%), days from flower initiation to harvest (2.77%), fruit length (2.17%), internodal length (2.00%) and days to first fruit harvest (2.00%). Thus, the study suggested scope for improvement in the characters were rewarding. Similar results were reported in Mahohar and Murthy (2011) [19], Punitha *et al.* (2012) [24], Hasan *et al.* (2015) [9], Ahirwar *et al.* (2017) [1], Kumawat *et al.* (2020) [16]. This indicates that selection of genotypes for these traits may be effective for future utilization in breeding programme for yield improvement.

Table 1: Analysis of variance for different characters of genotypes for fruit yield and fruit related attributes

Sl. No.	Source	Mean Squares		
		Replication	Treatment	Error
Degrees of freedom		2	22	44
1	Main vine length(m)	0.0070	0.968**	0.008
2	Internodal length(cm)	0.0230	2.626**	0.229
3	Number of nodes per vine	0.0070	105.634**	2.299
4	Days to first female flower	21.4220	24.344*	10.69
5	Days to first male flower	20.9590	320.875**	6.654
6	Node at which first female flower appears	0.0850	6.067**	0.043
7	Node at which first male flower appears	0.0270	0.775**	0.008
8	Days to flower initiation to harvest	2.0850	17.517**	1.046
9	Days to first fruit harvest	17.8390	77.766**	19.593
10	Fruit length(cm)	1.1850	16.046**	2.066
11	Fruit diameter(cm)	0.0640	0.092*	0.04
12	Fruit weight(g)	116.0630	2381.223**	251.982
13	Number of fruit per plant	1.1460	20.501**	2.917
14	Number of pickings	0.5090	2.287**	0.21
15	Fruit yield per plant(kg)	0.0880	2.68**	0.128
16	Fruit yield per hectare(q)	2780.4580	91708.654**	5266.177

** - Significant at 1% level of probability, * - Significant at 5% level of probability

Table 2: Mean performance of different genotypes for fruit yield and yield related traits

Sl. No.	Genotypes	MVL	IL	NNPV	DFFF	DFMF	NNFF	NNMF	DFIH	DFFH	FL	FD	FW	NFPP	NP	FYPP	FYPH
1	PPCUC 2	2.97	9.13	33.19	51.00	49.33	3.27	2.40	15.71	71.39	16.83	3.90	159.62	21.23	8.43	3.39	625.53
2	PPCUC 3(C)	2.92	8.40	34.00	50.33	49.00	3.87	1.42	15.07	70.64	19.69	3.79	196.40	21.63	9.09	4.45	822.68
3	PPCUC 4	2.68	8.20	32.94	49.67	45.67	3.33	2.60	19.54	70.17	13.79	3.82	145.27	21.40	9.20	3.12	575.20
4	PPCUC 5	1.82	6.78	28.03	50.00	46.00	3.30	2.03	14.43	70.08	14.58	3.91	138.95	18.83	7.66	2.62	482.08
5	PPCUC 6	1.53	6.82	22.73	46.67	44.33	2.93	1.58	14.15	63.07	14.30	4.46	185.83	25.56	10.36	4.76	880.23
6	PPCUC 7	2.51	7.55	32.46	47.33	44.33	4.67	2.17	16.47	64.24	17.20	3.97	203.40	22.57	8.51	4.59	848.22
7	PPCUC 9	1.88	7.08	27.29	47.67	47.33	2.93	1.47	19.20	69.04	14.43	3.91	160.86	17.40	8.89	2.81	518.57
8	PPCUC 10	1.43	6.52	21.86	47.00	47.67	3.07	1.55	15.25	66.84	14.78	4.04	151.09	19.47	6.78	2.94	542.55
9	PPCUC 11	2.19	8.62	26.00	46.33	44.67	3.07	1.28	17.50	66.91	20.04	4.00	194.16	22.37	9.63	4.35	802.70
10	PPCUC 12	1.57	7.31	21.73	45.33	44.00	2.40	1.34	17.71	70.03	15.37	3.64	148.44	21.63	8.77	3.21	593.47
11	PPCUC 13	1.94	8.30	24.89	52.00	47.33	3.47	1.70	14.66	65.80	22.97	3.74	216.74	22.04	8.70	4.77	880.47
12	PPCUC 14	2.15	8.75	26.61	49.33	46.33	4.13	1.73	16.35	67.40	20.07	3.94	176.75	20.57	9.42	3.64	673.35
13	Punjab Kheera 1	2.08	7.51	35.89	49.00	47.00	3.07	1.17	10.53	57.52	15.49	3.82	129.78	15.37	9.52	2.01	370.52
14	PPC6 (C)	1.11	6.55	19.52	48.00	44.67	2.87	1.30	12.39	59.53	14.86	3.98	102.36	20.13	7.64	2.08	385.67
15	X1	1.24	6.89	21.36	45.00	0.00	3.13	0.00	15.85	65.87	16.18	3.76	185.31	22.60	8.94	4.19	775.37
16	Zaara	1.69	8.86	22.31	45.33	45.00	5.86	2.60	17.98	64.10	15.63	3.93	149.12	21.27	9.39	3.18	587.25
17	Safran Plus	1.56	8.45	21.73	45.67	0.00	3.20	0.00	15.23	63.15	17.04	3.87	185.61	24.83	8.75	4.61	852.13
18	Aviva	1.97	8.66	24.86	42.66	0.00	2.80	0.00	10.82	52.60	18.43	4.21	206.60	27.80	10.43	5.79	1068.92
19	Infinity	1.09	6.40	19.84	43.67	46.33	2.67	1.23	13.34	55.82	15.44	3.71	165.07	24.07	8.35	3.97	732.12
20	Lucro	1.23	8.03	17.58	45.33	46.00	3.33	1.99	17.67	61.58	17.33	3.77	145.28	21.50	8.47	3.13	578.05
21	Gurka	0.93	6.45	17.25	42.67	45.00	3.60	1.67	17.68	65.43	14.31	3.85	139.13	19.97	7.41	2.79	515.48
22	Mini Cucumber	1.14	6.60	21.00	45.33	49.00	2.90	2.32	17.37	65.17	16.90	3.89	154.47	21.85	9.27	3.38	626.25
23	Multifruit P. Cucumber	1.06	6.66	18.84	42.67	47.00	2.87	2.11	14.97	67.72	16.09	3.89	152.09	22.57	8.63	3.44	635.40
	Mean	1.77	7.59	24.87	46.87	40.26	3.34	1.55	15.65	64.96	16.60	3.91	164.88	21.59	8.79	3.62	668.36
	C.V.	6.24	6.07	5.55	6.41	5.65	6.45	12.81	6.52	5.87	8.66	5.09	9.63	7.91	5.22	9.87	10.86
	S.E.	0.06	0.27	0.80	1.74	1.31	0.12	0.12	0.59	2.20	0.83	0.12	9.17	0.99	0.27	0.21	41.90
	C.D. 5%	0.18	0.76	2.27	4.95	3.74	0.35	0.33	1.68	6.27	2.37	0.33	26.12	2.81	0.76	0.59	119.42
	C.D. 1%	0.24	1.01	3.03	6.61	5.00	0.47	0.44	2.24	8.38	3.16	0.44	34.90	3.76	1.01	0.79	159.52
	Range Lowest	0.93	6.40	17.25	42.67	0.00	2.40	0.00	10.53	52.60	13.79	3.64	102.36	15.37	6.78	2.01	370.52
	Range Highest	2.97	9.13	35.89	52.00	49.33	5.86	2.60	19.54	71.39	22.97	4.46	216.74	27.80	10.43	5.79	1068.92

MVL- main vine length(m), IL- internodal length(cm), NNPV- number of nodes per vine, DFFF- days to first female flower, DFMF- days to first male flower, NNFF- nodes number at which first female flower appears, NNMf- nodes number at which first male flower appears, DFIH- days from flower initiation to harvest, DFFH- days to first fruit harvest, FL- fruit length (cm), FD- fruit diameter (cm), FW- fruit weight (g), NFPP- number of fruits per plant, NP- number of pickings, FYPP- fruit yield per plant (kg).

Check varieties: PPCUC 3- Pant Parthenocarpic Cucumber 3, PPC 6- Pusa Parthenocarpic Cucumber 6

Table 3: Estimates of phenotypic (PCV) and genotypic (GCV) coefficients of variation, heritability and genetic advance in percent of mean among different characters

SL. No.	Genotype	Coefficient of Variance		h ² (Broad Sense)	Genetic Advance	Gen. Adv. as percent of Mean
		GCV (%)	PCV (%)			
1	Main vine length(m)	33.86	34.43	96.70	1.21	68.58
2	Internodal length(cm)	11.70	13.18	78.80	1.62	21.39
3	Number of nodes per vine	22.22	22.91	94.10	11.05	44.42
4	Days to first female flower	4.49	7.83	32.90	2.49	5.31
5	Days to first male flower	39.65	40.05	98.00	32.56	80.86
6	Node at which first female flower appears	21.82	22.75	92.00	1.44	43.10
7	Node at which first male flower appears	47.81	49.49	93.30	1.48	95.12
8	Days to flower initiation to harvest	14.73	16.10	83.60	4.34	27.74
9	Days to first fruit harvest	6.78	8.96	57.20	6.86	10.55
10	Fruit length(cm)	13.01	15.63	69.30	3.70	22.30
11	Fruit diameter(cm)	3.31	6.07	29.70	0.15	3.71
12	Fruit weight(g)	16.16	18.81	73.80	47.14	28.59
13	Number of fruit per plant	11.17	13.69	66.60	4.05	18.77
14	Number of pickings	9.46	10.81	76.70	1.50	17.07
15	Fruit yield per plant(kg)	25.49	27.34	87.00	1.77	48.97
16	Fruit yield per hectare(q)	25.40	27.62	84.50	92.54	48.11

Table 4: Distribution of different genotypes into different clusters by Tocher's method

Cluster Group	No. of Genotypes	List of Genotypes
Cluster I	8	Mini Cucumber, Multifruit Parthenocarpic Cucumber, Lucro, PPCUC 12, Gurka, Infinity, PPCUC 10 & Pusa Parthenocarpic Cucumber 6 (C)
Cluster II	5	PPCUC 5, PPCUC 9, PPCUC 4, Pant Parthenocarpic Cucumber 2 & PPCUC 14
Cluster III	5	PPCUC 11, PPCUC 13, Pant Parthenocarpic Cucumber 3(C), PPCUC 7 & PPCUC 6
Cluster IV	3	X1, Safran Plus & Aviva
Cluster V	1	Punjab Kheera 1
Cluster VI	1	Zaara

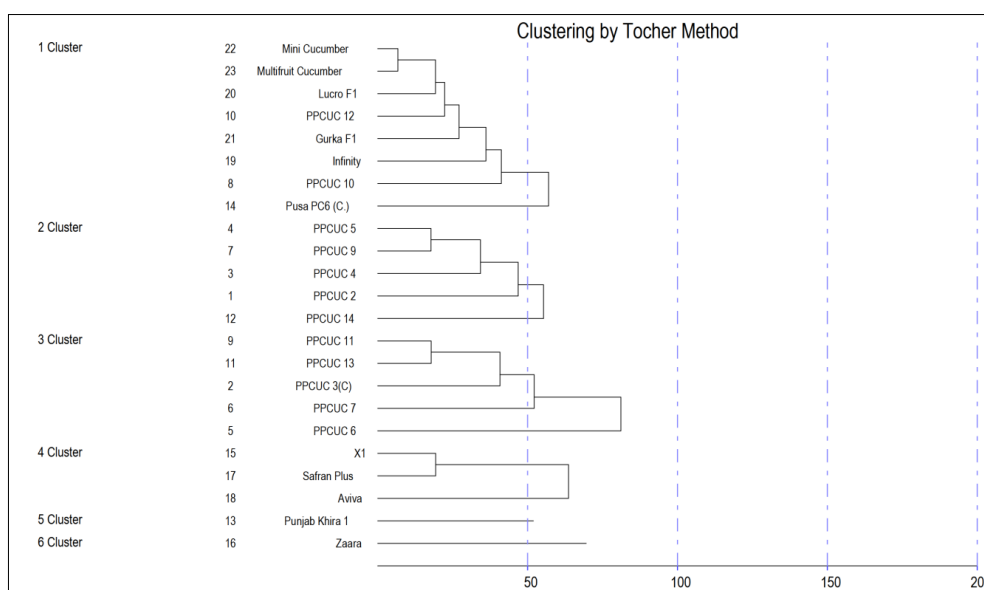


Fig 1: Dendrogram showing relationship among different genotypes in six clusters based on Mahalanobis D² values

Table 5: Mean values of six clusters for yield and yield related traits by Tocher's method

Characters	MVL	IL	NNPV	DFFF	DFMF	NNFF	NNMF	DFIH	DFFH	FL	FD	FW	NFPP	NP	FYPP	FYPH
Cluster I	1.19	6.82	19.70	45.00	46.21	2.96	1.69	15.80	64.02	15.63	3.85	144.74	21.40	8.17	3.12	576.12
Cluster II	2.30	7.99	29.61	49.53	46.93	3.39	2.05	17.05	69.62	15.94	3.90	156.29	19.89	8.72	3.12	574.95
Cluster III	2.22	7.94	28.02	48.53	45.93	3.60	1.63	15.57	66.13	18.84	3.99	199.31	22.83	9.26	4.58	846.86
Cluster IV	1.59	8.00	22.65	44.44	0.00	3.04	0.00	13.97	60.54	17.22	3.95	192.51	25.08	9.38	4.86	898.81
Cluster V	2.08	7.51	35.89	49.00	47.00	3.07	1.17	10.53	57.52	15.49	3.82	129.78	15.37	9.52	2.01	370.52
Cluster VI	1.69	8.86	22.31	45.33	45.00	5.86	2.60	17.98	64.10	15.63	3.93	149.12	21.27	9.39	3.18	587.25

MVL- main vine length(m), IL- internodal length(cm), NNPV- number of nodes per vine, DFFF- days to first female flower, DFMF- days to first male flower, NNFF- nodes number at which first female flower appears, NNMF- nodes number at which first male flower appears, DFIH- days from flower initiation to harvest, DFFH- days to first fruit harvest, FL- fruit length (cm), FD- fruit diameter (cm), FW- fruit weight (g), NFPP- number of fruits per plant, NP- number of pickings, FYPP- fruit yield per plant (kg), FYPH- fruit yield per hectare (q)

Table 6: Average intra and inter cluster D² values among six clusters of different genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster IV
Cluster I	44.69	110.72	137.39	329.54	190.02	119.51
Cluster II		58.45	119.41	374.61	120.60	153.81
Cluster III			75.48	248.17	252.77	133.80
Cluster IV				70.12	493.66	319.12
Cluster V					0.00	337.34
Cluster VI						0.00

Table 7: Relative contributions of characters studied towards genetic divergence

SL. No.	Source	Contribution (%)	Times ranked 1st
1	Main vine length(m)	5.66	14
2	Internodal length(cm)	2.00	5
3	Number of nodes per vine	5.93	15
4	Days to first female flower	4.00	10
5	Days to first male flower	4.02	10
6	Node at which first female flower appears	5.41	14
7	Node at which first male flower appears	6.68	17
8	Days to flower initiation to harvest	2.77	7
9	Days to first fruit harvest	2.00	5
10	Fruit length(cm)	2.14	5
11	Fruit diameter(cm)	5.40	14
12	Fruit weight(g)	12.32	31
13	Number of fruit per plant	6.85	17
14	Number of pickings	5.65	14
15	Fruit yield per plant(kg)	15.63	39
16	Fruit yield per hectare(q)	13.54	34

4. Conclusion

It was concluded that there was a wide range of variance between the genotypes for all the characters based on the overall results of the current analysis, suggesting that there was considerable scope for improving parthenocarpic cucumber cultivars through selection. High heritability combined with high genetic advance as percent mean for the traits can be effectively improved by selection. In present analysis, there was a maximum gap between cluster IV and V. More focus should be therefore given to cluster IV and V in the selection of inbreds for cross breeding in hybridization programme and the character fruit yield per plant (kg) which has highest contribution towards divergence.

5. Acknowledgement

The authors are thankful to Department of Vegetable Science, Govind Ballabh Pant University of Agriculture and technology, Pantnagar, Uttarakhand, India for undertaking the investigation properly. The authors are highly grateful to the department for providing necessary facilities for the experiment.

6. References

- Ahirwar CS, Singh DK, Kushwaha ML. Assessment of genetic divergence in cucumber (*Cucumis sativus* L.) germplasm through clustering and principal component analysis, J Pharmacogn. Phytochem. 2017;6(5):804-807.
- Ahirwar CS, Singh DK. Assessment of Genetic Variability in Cucumber (*Cucumis sativus* L.), Int. J Curr. Microbiol. App. Sci. 2018;7(03):813-822.
- Allard RW. Principles of plant breeding, John Wiley and Sons, Inc. New York and London; c1960. p. 485.
- Burton GW, Devane EM. Estimating heritability in tall festuca from replicated clonal material. Agron. J. 1953;45:478-481.
- Deepa SK, Hadimani HP, Hanchinamani CN, Shet R, Koulgi S, Ashok. Estimation of genetic variability in cucumber (*Cucumis sativus* L.). Int. J Chem. Stud. 2018;6(6):115-118.
- Denna DW. Effect of genetic parthenocarpy and gynoecious flowering habit on fruit production and growth of cucumber, *Cucumis sativus* L. JJ Am. Soc. Hortic. Sci. 1973;98:602-604.
- Dhillon NS, Singh G. Genetic variability studies in parthenocarpic cucumber. J Pharm. Innov. 2021;11(3):2142-2147.
- Harlan JR. Crops and Man. American Society of Agronomy: Crop Science Society of America, Madison, USA; c1975. p. 284.
- Hasan R, Hossain MK, Alam N, Bashar A, Islam S Tarafder MJA. Genetic Divergence In Commercial Cucumber (*Cucumis Sativus* L.) Genotypes Bangladesh J Bot. 2015;44(2):201-207.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. Agron. J. 1955;47:314-318.
- Karthick K, Arumugam T, Rajasree V, Ganesan KN, Karthikeyan M. Evaluation and assessment of genetic variability of cucumber (*Cucumis sativus* L.) genotypes. J Pharm. Innov. 2019;8(11):156-160.
- Kaur M, Sharma P. Performance of parthenocarpic cucumber (*Cucumis sativus* L.) genotypes for yield and quality characters under protected environment. Himachal J Agri. Res. 2022;48(2):220-224.
- Kumar P, Khapte PS, Saxena A, Kumar P. Evaluation of gynoecious cucumber (*Cucumis sativus* L.) hybrids for early-summer greenhouse production in western Indian arid plains. Indian J Agric. Sci. 2018;89(3):545-550.
- Kumar PJ, Syed S, Reddy PSS, Lakshmi LM, Reddy DS. Genetic Divergence Studies in Cucumber (*Cucumis sativus* L.) Genotypes for Yield and Quality. Int. J Curr. Microbiol. App. Sci. 2018;7(12):2633-2643.

15. Kumar R, Munshi AD, Behera TK, Jat GS, Choudhary H, Singh M, *et al.* Genetic diversity of cucumber (*Cucumis sativus* L.) accessions differing in quantitative traits and microsatellite marker. *Indian Journal of Agricultural Sciences*. 2020;90(11):2161.
16. Kumawat OP, Kumar U, Singh SK, Mauryal S, Sinha BM. Studies on Genetic Divergence for Yield and Quality Traits in Cucumber (*Cucumis sativus* L.). *Curr. J Appl. Sci.* 2020;39(12):136-143.
17. Mahalanobis PC. On the generalized distance in statistics. *Proc. Nat. Acad. Sci., India*. 1936;2:49-55.
18. Manisha Singh AK, Pal AK. Studies on correlation and path-coefficient analysis for yield and its contributing characters in Cucumber (*Cucumis sativus* L.). *Pharma Innov.* 2021;10(10):551-556.
19. Manohar SH, Murthy HN. Estimation of phenotypic divergence and powdery mildew resistance in a collection of cucumber (*Cucumis sativus* L.). *Afr. J Biotechnol.* 2011;10(11):1978-1987.
20. Mehta P, Sharma P. Genetic Evaluation for Fruit Yield and Related Traits in Parthenocarpic Cucumber. *Int. J Curr. Microbiol. App. Sci.* 2020;9(10):1388-1404.
21. Nagamani GV, Kumar JSA, Reddy TBM, Rajesh AM, Amarananjundeswara H, Reddy RLR, *et al.* Performance of Different Parthenocarpic Cucumber (*Cucumis sativus* L.) Hybrids for Yield and Yield Attributing Traits under Shade Net House. *Int. J Curr. Microbiol. App. Sci.* 2019;8:978-982.
22. Pal S, Sharma HR, Rai AK, Bhardwaj RK, Das A. Estimation of genetic divergence for yield and quality traits in cucumber (*Cucumis sativus* L.). *Green Farming*. 2017;8(2):296-300.
23. Panse VG, Sukhatme PV. *Statistical methods for agricultural workers*. 4th Edn. ICAR, New Delhi; c1985. p. 252-254.
24. Punitha A, Bharathi A, Devi DS. Studies on genetic divergence in cucumber (*Cucumis sativus* L.). *Asian J Biol. Sci.* 2012;7(2):169-173.
25. Pushpalatha N, Anjanappa M, Devappa V, Pitchaimuthu M. Genetic Variability and Heritability for Growth and Yield in Cucumber (*Cucumis sativus* L.), *J Hort. Sci.* 2016;11(1):123-127.
26. Rao CR. *Advanced statistical methods in biometrical research*, Ed. II. John Willey and Sons. New York; c1952. p. 357-363.
27. Robinson HF. Quantitative genetics in relation to breeding on centennial of Mendelism. In: *Indian Journal of Genetics and Plant Breeding*. Indian Soc. Genet. Plant Breed. 1966;26(2):171-187.
28. Shah KN, Rana DK, Singh V. Estimation of genetic variability for quantitative and qualitative traits in cucumber (*Cucumis sativus* L.) Under subtropical conditions of Garhwal Himalaya. *Plant Arch.* 2017;17(1):28-32.
29. Shah KN, Rana DK, Singh V. Studies on Genetic Divergence in Cucumber (*Cucumis sativus* L.) under Subtropical Conditions of Garhwal Himalaya. *Int. J Adv. Sci. Res. Manag.* 2017;I(Special Issue):39-42.
30. Sharma S, Kumar R, Sharma HR, Sharma A, Gautam N. Divergence Studies for Different Horticultural Traits in Cucumber (*Cucumis sativus* L.). *Int. J Curr. Microbiol. App. Sci.* 2018;7(02):1733-1741.
31. Singh DK, Bisht YS, Singh NK, Singh D, Singh SS. Studies of genetic variability in parthenocarpic cucumber (*Cucumis sativus* L.). *Pharma Inno.* 2022;11(8):2205-2209.
32. Singh Y, Safiullah Verma A, Sharma S, Sekhon BS. Genetic Evaluation of Cucumber [*Cucumis sativus* L.] Genotypes for Yield and its Contributing Traits under Mid-Hill Conditions of Himachal Pradesh, India. *Environment & Ecology*. 2017;35(4E):3621-3626.
33. Singh RK, Chaudhary BD. *Biometrical methods in quantitative genetic analysis*. Kalyani Publishers, New Delhi; c1977. p. 281.
34. Sturtevant EL. Seedless fruits. *Mem. Torrey Bot. Club*. 1890;1:141-185.
35. Suma A, Elsy CR, John KJ, Pradeepkumar T, Francis R, Joseph J, *et al.* Genetic Diversity in Indian Landraces of Cucumber (*Cucumis sativus* L.) Based on Morpho-Horticultural Trait. *Indian J Plant Genet. Resour.* 2021;34(3):411-423.