Genetic Divergence and Gene Source Studies in Cucumber (*Cucumis sativus* L.)

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Since there is an appreciable deficit between realized and potential crop yields in cucumber, so there is a strong need to develop hybrids having desirable horticultural traits. This necessitated the identification of suitable divergent parents to get high heterotic effect in terms of yield and quality. Thus, divergence analysis was carried out in 26 genotypes of cucumber. All the character under study showed a wide range of values except days to first picking and fruit circumference. Phenotypic variability was high for node at which first female flower appears, sex ratio, yield per plant, number of fruits and vine length. The genotypes could be grouped into 5 clusters. Cluster nos. I, II, III, IV and V contained 11, 3, 5, 2 and 5 genotypes, respectively which are independent of geographical distribution. The genotypes in cluster I had maximum intra-cluster distance closely followed by cluster nos. V and II. Inter-cluster distance was maximum between the clusters I and II followed by clusters II and III suggesting wide diversity between the groups.. Highest yield per plant was recorded in cluster no. IV followed by cluster no. III. Cluster nos. I and III may be employed for improvement programme in cucumber. Market Long was best gene source for yield, no. of fruits and TSS.

Key words: ***Cucumis sativus*, D^2 analysis, Cluster, Gene source**

Nature has endowed India with many precious gifts, wherein lies its immense potential for the vegetable sector. In the last three decades, India has witnessed a sea change in the scenario of vegetable production with the increasing popularity of hybrids in commercial cultivation. Cucumber (*Cucumis sativus* L.), a member of family Cucurbitaceae is one of the most important cucurbits grown in India for its tender fruits as summer vegetable and one of the oldest vegetable crop but little work has been done in hybridization programme. Thus, there is need to develop hybrids suitable for cultivation with high yield per unit area and quality. This necessitated the identification of suitable divergent parents to get high heterotic effect in terms of yield and quality.

To make an improvement in any crop species, the breeder is constantly engaged in effective choice of desireable parents of high genetic variation so that individuals with desirable character combination can be selected. Genetically diverse parents are likely to produce high heterotic effects and desirable segregants. Multivariate analysis by means of Mahalanobis's D^2 statistics is a powerful tool in quantifying the degree of divergence among the biological populations.

Divergence analysis in cucumber was employed by Prasad *et al.* (1993), Susic *et al.* (2000), Prasad *et al.* (2001) and Rao *et al.* (2003) in India and abroad. Thus, the present investigations are first attempt on divergence analysis in cucumber in Himachal Pradesh with the objective of ascertaining the nature and magnitude of genetic divergence present among twenty six genotypes of cucumber for further utilization in hybridization.

Materials and Methods

The present investigations on genetic divergence in cucumber (*Cucumis sativus* L.) were carried out on 26 genotypes at Nauni, Solan, Himachal Pradesh during *kharif*, 2005 at an altitude of 1270 m above mean sea level lying between latitude 30°52' North and longitude 77°11' East. It falls under the mid hill zone of Himachal Pradesh. The experiment was laid out in a Randomized Block Design with 3 replications. Direct sowing was done in the pits at a spacing of 1 x 1 m. Initially, 2-3 seed per pit were sown but only one healthy seedling per pit was retained. The standard cultural practices were followed for healthy crop.

The observations were recorded on ten randomly selected competitive plants from each treatment for the characters viz. days to first female flower appearance, node at which first female flower appears, sex ratio, days to first picking, harvest duration (days), yield per plant (g), number of fruits per plant, fruit weight (g), fruit length (cm), fruit circumference (cm), rind thickness (mm), flesh to seed cavity ratio, total soluble solids (°B), thousand

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seed weight (g), number of primary branches per plant and vine length (m).

For computing various statistical parameters like mean and standard deviation, the method suggested by Panse and Sukhatme (1985) was followed. Genetic divergence was determined using Mahalanobis D^2 statistics (Mahalanobis, 1936). Group constellation was formulated after computation of D^2 values by the method by Rao (1952)

Results and Discussion

It is axiomatic that for successful breeding programme, sufficient diversity should be present in the germplasm. The greater diversity of germplasm that a breeder handles, the better are the chances for selecting better genotypes (Vavilov, 1951). Now, F_1 hybrids are gaining momentum with high pace all over the world. Therefore, there is a strong need to isolate or to develop breeding lines which have high yielding potential, desirable horticultural traits and better quality. Selection of parents is the foundation stone of any hybridization programme. In context of this fact, the present investigations were undertaken to select horticulturally superior parent and to elicit information on divergence and clustering pattern in cucumber. The results obtained have been discussed below under the following sub-heads:

1. General Performance of the Genotypes

All the character under study showed a wide range of values except days to first picking and fruit circumference (Table 1). Phenotypic variability as revealed by coefficient of variation (%) was high for node at which first female flower appears, sex ratio, yield per plant, no. of fruits and vine length (also substantiated by wider range values) and moderate for harvest duration, fruit weight and fruit length. While, rest of the characters were of low variability. Coefficient of variation varied from 0.08% for fruit circumference to 53.45% for vine length. Coefficient of variation (%) was highest for vine length (53.45%) followed by sex ratio, node at which first female flower appears and yield per plant. Coefficient of variation depicted that differences among the genotypes were existing. The characters that exhibited high phenotypic variability had a wider range. Similar results on high phenotypic variability of vine length were reported by Solanki and Seth (1980) and Rastogi and Arya Deep (1990). Joshi *et al.* (1981) also observed a wide range of phenotypic variability in consonance with the present findings.

Phenotypic performance would be a good index for selection in cucumber for the characters like node at which first female flower appears, sex ratio, harvest duration, yield per plant, no. of fruits, fruit weight, fruit length and vine length as reported by Joshi *et al.* (1981).

2. Divergence Studies

Grouping pattern of genotypes under study into different clusters is given in Table 2. On the basis of D^2 analysis, the genotypes could be grouped into 5 clusters. Cluster no. I contained 11 genotypes *viz.* Henzil, SMR-58, Boston Pickling, Kakri, Sweet Delight, EC 381602, CHC-1, National, Yomaki, Hermaphrodite-61 and Poinsette which are of different geographical origin. Cluster no. II contained 3 genotypes namely LC-2, LC-7 and LC-12 which are of same geographical area i.e. these were collected from Hamirpur district of Himachal Pradesh. Cluster no. III contained 5 genotypes *viz.* Fazilka Coll.

Table 1. Range, mean, standard deviation and coefficient of variation of various characters in cucumber

Character	Range	Mean	Standard deviation	Coefficient of variation (%)
Days to first female flower appearance	38.27–59.73	47.28	6.29	13.30
Node number of first female flower	2.33–16.93	5.48	2.72	49.64
Sex ratio	1.00–22.79	11.30	5.97	52.83
Day to first picking	49.80–73.47	58.98	5.99	10.16
Harvest duration (days)	6.53–21.07	14.38	4.11	28.58
Yield (g)	392.00–2201.00	1081.13	484.77	44.84
No. of fruits	1.60–8.13	4.42	1.62	36.65
Fruit weight (g)	207.33–440.33	293.59	70.43	23.99
Fruit length (cm)	8.96–32.65	18.42	4.41	23.94
Fruit circumference (mm)	13.91–19.44	17.16	1.35	0.08
Rind thickness (mm)	0.86–1.88	1.40	0.30	21.43
Flesh to seed cavity ratio	0.17–0.42	0.24	0.06	0.25
TSS (°B)	1.97–3.47	2.26	0.40	14.87
1000–seed weight (g)	14.88–36.07	24.10	4.60	19.09
No. of primary branches per plant	2.00–4.50	3.47	0.53	15.27
Vine length (cm)	39.50–604.17	204.89	109.51	53.27

Table 2. Grouping pattern of different genotypes based on D^2 analysis

Cluster No.	No. of genotype	Genotype
I	11	Henzil, SMR-58, Boston Pickling, Kakri, Sweet Delight, EC 381602, CHC-1, National, Yomaki, Hermaphrodite-61, Poinsette
II	3	LC-2, LC-7, LC-12
III	5	Fazilka Coll. 94, CHC-2, Market-76, Market More-76, Market Long
IV	2	Khira-75, Khira-90
V	5	Sel. 75-2-10, Sel. 20-3-2-1, Shogain 1-48, Long Green, EC 381606

94, CHC-2, Market-76, Market More-76 and Market Long. There were only 2 genotypes namely Khira-75 and Khira-90 in cluster no. IV. Both these genotypes are from Solan (H.P.). Cluster no. V contained 5 genotypes viz. Sel. 75-2-10, Sel. 20-3-2-1, Shogain 1-48, Long Green and EC 381606 which are also from different geographical areas.

Genotypes from different locations/ countries are accommodated in the same cluster (Table 2). This indicates their close affinity. On the other hand, genotypes from same location/ country were distributed into different clusters indicating the geographical diversity may not necessarily be related to genetic diversity. These findings were in general agreement with Prasad *et al.* (1993), Prasad *et al.* (2001) and Rao *et al.*(2003) in cucumber.

Table 3 indicated inter and intra-cluster distances between the 5 clusters. Intra-cluster distance ranged from 0.761 (cluster no. IV) to 2.826 (cluster no. I). The genotypes in cluster I had maximum distance closely followed by cluster nos. V and II. As for as inter-cluster distance is concerned, maximum distance was observed between the clusters I and II followed by clusters II and III suggesting wide diversity between the groups. The crosses made between the genotypes from the above clusters may give transgressive segregants. On the other hand, minimum distance (3.380) was recorded between clusters I and V indicating minimal diversity between these clusters.

On the basis of inter- and intra-cluster distance, cluster nos. I, II and III may be considered as most diverse and can be utilized for hybridization when selecting genotypes for breeding purposes.

Besides high genetic divergence, the performance of genotypes for characters with maximum contribution towards genetic divergence should also be given due consideration. Mean performance of the clusters with respect to different character (Table 4) indicated that

Table 3. Inter- and intra-cluster distances between the clusters

Cluster	I	II	III	IV	V
I	**2.826**				
II	7.035	**2.520**			
III	3.445	6.807	**2.311**		
IV	4.740	5.301	4.217	**0.761**	
V	3.380	5.804	3.513	4.414	**2.773**

Bold figures are the intracusters distances

Table 4. Mean performance of the clusters with respect to different characters

Character	Cluster					Percent contribution towards diversity
	1	2	3	4	5	
Days to first female flower appearance	42.85	58.87	47.65	55.33	46.48	38.18
Node number of first female flower	4.27	11.49	4.89	5.53	5.12	14.19
Sex ratio	9.17	22.36	9.14	13.97	10.44	13.64
Day to first picking	55.12	70.11	59.67	65.50	57.49	8.91
Harvest duration (days)	16.51	11.11	18.24	7.70	10.48	6.08
Yield (g)	1020.82	495.44	1641.87	1756.00	734.53	5.04
No. of fruits	4.84	1.82	6.28	4.40	3.19	4.32
Fruit weight (g)	258.61	357.11	307.67	404.83	273.87	3.22
Fruit length (cm)	15.96	18.55	20.61	18.48	21.55	2.21
Fruit circumference (mm)	17.15	18.91	16.70	18.79	15.94	1.37
Rind thickness (mm)	1.15	1.69	1.54	1.37	1.64	1.21
Flesh to seed cavity ratio	0.26	0.20	0.24	0.22	0.22	0.76
TSS (°B)	2.47	2.67	3.05	2.60	2.88	0.53
1000-seed weight (g)	22.57	29.80	24.03	22.28	24.86	0.19
No. of primary branches per plant	3.17	3.50	3.97	3.58	3.57	0.11
Vine length (cm)	163.89	457.00	189.43	178.42	169.87	0.05

Table 5. Gene sources for some important characters in cucumber genotypes under study

Sr. No.	Character	Potential	Genotype
1	Days to first female flower appearance	38.27 days	Hermaphrodite-61
2	Node number of first female flower	2.33	Hermaphrodite-61
3	Sex ratio	1.00	Hermaphrodite-61
4	Day to first picking	49.80 days	SMR-58
5	Harvest duration (days)	21.07 days	Fazilka Coll. 94
6	Yield (g)	2201.00 g	Market Long
7	No. of fruits	8.13	Market Long
8	Rind thickness (mm)	1.88 mm	Fazilka Coll. 94
9	TSS (°B)	3.47	Market Long

minimum number of days to first female flower appearance and lowest node of first female flower exhibited by cluster no I. However, minimum sex ratio was recorded in cluster no III closely followed by cluster no I. Cluster no. I also recorded minimum days to first picking. Cluster no. II recorded maximum days to first female flower appearance, highest node of first female flower, highest sex ratio and maximum days to fruit picking. Longest harvest duration was found in cluster no. III followed by cluster I. However, highest yield per plant was recorded in cluster no. IV followed by cluster no. III. Cluster II recorded lowest yield per plant which might be due to the fact that it took maximum no. of days to first female flower appearance, bore female flower on higher nodes and exhibited high sex ratio. No. of fruits per plant were highest in case of cluster no. III. Fruit weight was highest in cluster no. IV which might be a reason for highest yield per plant in this cluster.

Cluster no. V had longest fruits while cluster no. II showed highest fruit circumference and thickest fruit rind. Flesh to seed cavity ratio and TSS were highest in cluster no. I and III, respectively. Maximum thousand seed weight and no. of primary branches were observed in cluster II and III, respectively. Vine length was minimum in cluster no. I and maximum in cluster no. II. Comparison of cluster means for all the sixteen characters indicated that different characters showed considerable differences between the clusters.

Relative contribution of different characters towards genetic divergence in the cucumber germplasm (Table 4) indicated that first 9 characters explained more than 95 % variation in cucumber germplasm under study. Days to first female flower appearance gave maximum contribution (38.18%) followed by node of first female flower (14.19%) and sex ratio (13.64%). Considering the cluster distances and cluster means, cluster nos. I and III may be employed for improvement programme in cucumber.

3. Gene Source Studies

Gene sources for some important character are given in Table 5. It is evident from the data in the Table that gene source for minimum days to first female flower, node of first female flower appearance and sex ratio was Hermaphrodite-61. Gene source for minimum days to first picking was SMR-58. Fazilka Coll. 94 was found best gene source in the germplasm for longest harvest duration and thickest fruit rind. Thick fruit rind is important for fruit fly resistance breeding. Gene source with high potential in terms of yield per plant, no. of fruits and TSS was Market Long. These gene sources can be employed according to the need of improvement programme.

In the light of present findings, it may be concluded that on the basis of the cluster distances and cluster means, cluster nos. I and III may be employed for improvement programme in cucumber. Gene source Hermaphrodite-61 was found best for earliness and Market Long for yield and quality.

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