-RESEARCH PAPER

## Studies on genetic divergence on cucumber (*Cucumber sativum* L.)

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Evaluation of 41 diverse genotypes of cucumber was carried out in a randomized block design. Among the 41 genotypes studied, Mahalanobis  $D^2$  analysis confined the presence of wide genetic diversity through the formation of seven clusters. The clustering pattern showed the lack of parallelism between geographic and genetic diversities. Among the clusters, intercrossing the genotypes in the cluster I, II, IV and V had high mean values for many characters studied is likely to result in an enlargement of spectrum of variability facilitating the selection for higher yield. The ranking  $D^2$  values revealed that tender fruit yield per vine, tender fruit girth, tender fruit weight and number of tender fruit per vine contributed high genetic divergence. Hence, these characters could respond favourably for phenotypic selection.

Key words : Cucumber, Genetic diversity, Intra and inter cluster

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## INTRODUCTION

Cucumber (Cucumis sativus L.) is an important vegetable and one of the most popular members of the Cucurbitaceae family (Lower and Edwards, 1986; Thoa, 1998). It is one of the oldest vegetable cultivated by man with historical records dating back 5,000 years (Wehner and Guner, 2004). The crop is the fourth most important vegetable after tomato, cabbage and onion in Asia (Tatlioglu, 1997), the second most important vegetable crop after tomato in Western Europe (Phu, 1997). Growers, buyers and processors all demand uniformity in plant type, fruit type, and maturity, so it is necessary that cultivars developed for sale to meet commercial standards. The scope of selection in the improvement of cucumber depends upon the genetic diversity available in the germplasm. Since, a considerable amount of variability exists in this crop, a germplasm collection is essential for any rational plant breeding programme. To formulate a sound and successful breeding programme, the importance of the study of genetic variability in the population and the pattern of correlation existing among the traits needs emphasis.

## Research Methodology

The present experiment was conducted at the

Department of Horticulture, Agriculture College and Research Institute, Madurai, Tamil Nadu. A total of 41 cucumber genotypes were collected from different district of Tamil Nadu. The experiment was laid out in a Randomized Block Design with two replications. Fourteen biometric observations were recorded on five randomly selected plants in each genotype per replication for all the characters (vine length, number of primary branches per vine, days to first male flowering, days to first female flowering, node number of first male flower production, node number of first female flower production, number of male flowers per vine, number of female flowers per vine, sex ratio, number of tender fruits per vine, tender fruit length, tender fruit girth, tender fruit weight and tender fruit yield per vine.

The genetic diversity existing between different populations with respect to a set of correlated variables were measured using Mahalanobis's statistics. The data were computerized and the  $D^2$  values were obtained. For determining the clusters, the criterion suggested by Tocher as quoted by Rao (1952) was followed. The average intra and inter-cluster distances were computed according to the method described by Singh and Chaudhary (1979). The relative contribution of each character to genetic divergence was determined according to the method described by Singh and Chaudhary (1979).

## **Research Findings and Analysis**

The experimental findings of the present study have been presented in the following sub heads:

#### D<sup>2</sup> analysis :

By the application of clustering technique, the 41 genotypes were grouped in to eight clusters. The constituent of the clusters with their source are presented in Table 1. Among the eight clusters, cluster V was the largest consisting of 21 genotypes followed by the cluster I which had 11 types. Cluster II, III and IV had two types in each and cluster VI, VII and VIII consisted of only one type in each.

Though the genotypes chosen for the present study were selected from different geographical sources, they got themselves grouped in many of the clusters. This may be due to the fact that the nature of selection forces operating under respective domestic conditions might have the difference in geographical barriers. Thus, both local and other genotypes were found scattered in different clusters and had different magnitude of distances among them. Based on a similar study in 36 genotypes of cluster beans, wide genetic variability in the material from the same geographic region was reported by Henry *et al.* (1986).

The clustering of genotypes from same geographical regions in one luster showed the presence of similar genetic architecture of the genotypes from the same region. However, high diversity was observed even among the locally available genotypes from Tamil Nadu, as evidenced by the scattering of them in different clusters with different genetic distances. The genotypes CS-39, CS-40 and CS-41 were grouped in one cluster (*i.e.*) cluster VII indicating that the particular genotypes are highly divergent from all the other genotypes grouped in different clusters. The individuality can be attributed to the superiority or inferiority of these particular genotypes in respect of different traits, as evidenced from the mean performance.

#### Intra and inter cluster distances :

The intra and inter-cluster  $D^2$  and D values among eight clusters are presented in Table 2. The statistical distances among the clusters based on  $D^2$  values are also represented diagrammatically (Fig. 1 and 2).  $D^2$  values corresponding to all possible combinations among 41 genotypes ranged from 77.89 to 11908.88. The intra-cluster generalized distance ranged from 8.83 in cluster II to 33.10 in cluster I. The highest intercluster divergence was recorded between the cluster VII and VIII (109.13) while cluster II and III were the closest (20.22). Based on the range of  $D^2$  values (<20- least divergence; 20.01 to 30 - moderately divergent; > 30.01 - highly divergent) the rating of the distance was assumed for interpretation of results.

The cluster I was highly divergent from all the clusters except the cluster II and III. The cluster II and III were moderately divergent from all the clusters except the cluster VII and VIII. The cluster IV was highly divergent from all the clusters except the cluster V and VI. The cluster V was highly divergent except cluster VI while the cluster VI and VII were highly divergent.

A perusal of the intra and inter-cluster average distance exhibited a parallel and similar divergence, although the clusters varied in their constitution. The cluster VII consisted a maximum of 16 genotypes recorded the intra-cluster distance which was parallel to the distance recorded by the other clusters having lesser number of genotypes. A similar trend existed in the inter-cluster distance also. Gupta and Singh (1968) explained the phenomenon of parallelism and similar intra and inter cluster distances.

The cluster V had the highest mean values for vine length, number of male flowers per vine, number of tender fruits per vine and tender fruit length. The cluster IV had the highest mean values for number of tender fruits, tender fruits yield per vine and low mean value for days to first male and female flowering, node number of male and female flower production and sex ratio while the cluster II had the highest

Table 1: Composition of cluster							
Cluster number	Number of genotypes	Name of the genotype					
Ι	11	CS-1, CS-2, CS-3, CS-4, CS-5, CS-5, CS-6, CS-7, CS-8, CS-9, CS-25, CS-26,					
II	2	CS-34, CS-36					
III	2	CS-22, CS-23					
IV	2	CS-16, CS-17					
v	21	CS-10(MW), CS-11(IC223117A), CS-12(IC203064), CS-13(IC203114) CS-14(IC203117),					
		CS-15(IC203113), CS-18, CS-19, CS-20, CS-21, CS-24, CS-27, CS-28, CS-29, CS-30, CS-31, CS-32.					
		CS-33, CS-35, CS-37, CS-38					
VI	1	CS-40(Cucumber cross)					
VII	1	CS-41(IC202028)					
VIII	1	CS-39					

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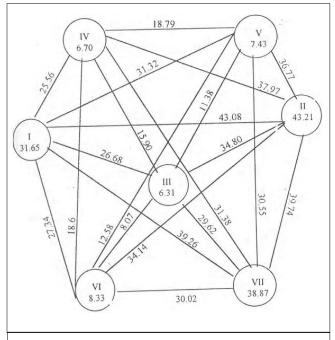


Fig. 1: Intra and inter cluster distances (D) among seven cluster

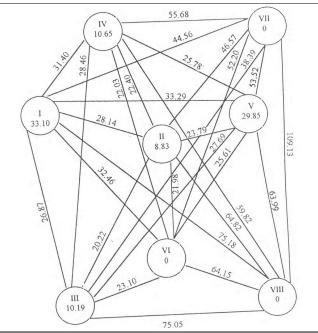


Fig. 2: Intra and inter cluster distances (D) among eight cluster in season II

Cluster	Ι	II	III	IV	V	VI	VII	VIII
I	1095.43	791.95	722.01	985.77	1108.41	1053.92	1985.85	5651.45
	(33.10)	(28.14)	(26.87)	(31.40)	(33.29)	(32.46)	(44.56)	(75.18)
П		77.89	408.97	501.55	565.88	482.98	2169.10	4201.58
		(8.83)	(20.22)	(22.40)	(23.79)	(21.98)	(46.57)	(64.82)
III			103.83	810.20	766.82	533.48	1473.39	5632.88
			(10.19)	(28.46)	(27.69)	(23.10)	(38.39)	(75.05)
IV				113.36	664.79	485.35	3100.29	3578.76
				(10.65)	(25.78)	(22.03)	(55.68)	(59.82)
V					891.26	656.09	2863.88	4095.29
					(29.85)	(25.61)	(53.52)	(63.99)
VI						0	2724.30	4114.88
							(52.20)	(64.15)
VII							0	11908.88
								(109.13)
VIII								0

mean values for tender fruit girth and weight of the fruit. The cluster I had the highest mean values for number of primary branches per vine and days to first male flowering.

The cluster VI had the lowest mean value for sex ratio and cluster III had highest mean value for tender fruit girth. The cluster I had highest means values for number of primary branches per vine. The present study indicated that the geographic diversity is not necessarily related to genetic divergence and the desirable diverse parents are available even within the genotypes of Tamil Nadu. Hence, these locally adapted diverse parents may be exploited more fruitfully for further breeding programme.

#### **Cluster mean values for characters :**

The cluster mean for the various characters are presented in Table 3. High ranges of mean value among the clusters were noticed for the characters *viz.*, vine length (313.71cm), number of male flowers per vine (175.75), tender fruit weight (164.61) and tender fruit yield per vine (1116.21g). the cluster VIII had the highest mean value for vine length (414.15cm),

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Cluster number	Ι	II	III	IV	V	VI	VII	VIII	Mean
Vine length	290.33	357.8	345.68	251.20	313.3	233.0	304.00	414.1	313.7
Number of primary branches	5.05	4.80	4.18	4.08	4.41	4.15	4.20	5.00	4.48
Days taken for first male flowering	31.44	27.88	29.56	22.71	28.32	29.20	36.86	21.59	28.44
Days taken for first female flowering	34.56	33.38	33.88	26.68	32.70	32.90	39.75	25.42	32.41
Node number of first male flower production	3.28	4.15	4.75	1.60	3.04	3.25	4.75	1.10	3.24
Node number of first female flower production	4.13	5.95	5.48	3.00	4.51	5.00	6.25	2.75	4.63
Number of male flowers per vine	182.68	227.0	190.75	195.00	176.0	109.00	100.50	255.0	175.75
Number of female flowers per vine	20.05	30.0	15.50	24.38	23.93	20.50	16.25	36.50	23.38
Sex ratio	9.35	7.58	12.35	7.99	7.65	5.31	6.20	7.01	7.93
Number of tender fruits per vine	7.29	8.25	6.38	8.00	7.46	6.25	5.50	12.25	7.67
Tender fruit length	14.84	17.08	16.80	15.03	16.00	16.50	12.75	21.25	16.28
Tender fruit girth	12.50	12.13	14.55	14.00	13.41	14.40	11.75	13.65	13.32
Tender fruit weight	148.02	159.5	161.88	158.1	168.7	197.85	112.65	210.0	164.61
Tender fruit yield per vine	1105.0	1009.6	949.5	1218.1	1146.	1010.0	440.2	2050	1116.2

number of male flowers per vine (255.00), number of female flowers per vine (36.50), number of tender fruits per vine (12.25), tender fruit length (21.25cm), tender fruit weight (210.05g) and tender fruit yield per vine (2050.50g) and lowest mean value for days to first male flowering (21.59days), days to first female flowering (25.42 days) and node number of first male flower production (1.10<sup>th</sup> node) and node number of the first female flower production (2.75<sup>th</sup> node). The cluster III had the highest mean value for tender fruit girth (14.55cm) and cluster I had the highest mean value for number of primary branches per vine (5.05). Cluster VI had the minimum mean value for narrow sex ratio (5.31:1).

# Relative contribution on the characters to genetic divergence :

The rating technique was adopted to rank the characters in the order of their contribution to the total genetic divergence. The contribution of each character towards the distances is furnished in Table 4. The tender fruit yield per vine contributed maximum to the genetic divergence (69.02%) followed by tender fruit weight (16.83%). Vine length, number of primary branches per vine and days to first female flowering contributed the least genetic divergence (0.01%). The contribution of the traits *viz.*, tender fruit length (0.73%), sex ratio (0.85%), number of male flowers per vine (1.22%), number of tender fruits per vine (1.22%), node number of first female flower production (1.46%), number of female flowers per vine(1.83%), tender fruit girth (2.07%) and days to first male flowering (3.41%) were low.

The use of  $D^2$  statistic is to estimate the relative contribution of various characters to the total genetic divergence. Murthy and Arunachalam (1966) suggested that in Mahalanobis's generalized distances ( $D^2$ ), the relative

Table	4: Relative contribution of each divergence in cucumber	characters	of genetic
Sr.	Source	No of	% of
No.		first rank	contribution
1.	Vine length	0	0.01
2.	Number of primary branches per vine	0	0.01
3.	Days to first male flowering	28	3.41
4.	Days to female flowering	0	0.01
5.	Node number of first male flower production	12	1.46
6.	Node number of first female flower production	11	1.34
7.	Number of male flowers per vine	10	1.22
8.	Number of female flowers per vine	15	1.83
9.	Sex ratio	7	0.85
10.	Number of tender fruits per vine	10	1.22
11.	Tender fruit length	6	0.73
12.	Tender fruit girth	17	2.07
13.	Tender fruit weight	138	16.83
14.	Tender fruit yield per vine	566	69.02

importance of the different characters in relation to their contribution to the total genetic divergence was given by their respective rank totals. They indicated that lesser the rank total of a character, higher was its contribution to the divergence and *vice versa*. This criterion was tested by Ram and Panwar (1970) and Vairavan *et al.* (1973). In this study, tender fruit yield per vine, girth of the tender fruit, weight of the tender fruit and number of tender fruits per vine and tender

fruit yield per vine and weight of the tender fruit contributed maximum towards genetic divergence. So these characters can be relied upon for further improvement by phenotypic selection. The genotypes in the cluster II *viz.*, CS-12, CS-13, CS-31 and CS-38 can be selected for crossing with the genotypes in the cluster I *viz.*, CS-1 to CS-9, CS-25 and CS-26 can be selected for crossing with the genotypes in the cluster II *(i.e.)* CS-34 and CS-36 due to their performance. Similarly, the genotypes in cluster I can be selected for crossing with the cluster VIII *i.e.* CS-39 to have better recombinants with higher tender fruit yield per vine, number of tender fruit per vine, length of the tender fruit and tender fruit weight.

#### **Conclusion:**

 $D^2$  analysis emphasized the exploitation of locally adapted diverse parents in the improvement of cucumber. Further, it revealed the relative contribution of economic traits *viz.*, tender fruits per vine, girth of the tender fruit, tender fruit weight and number of tender fruits per vine towards genetic divergence besides recording higher heritability for further heritability for further improvement by phenotypic selection. From the foregoing discussion it is suggested that the best genotypes namely CS-39, CS-21, CS-20, CS-16, CS-14, CS-12, CS-10, CS-5, CS-3 and CS-2 could be utilized for further improvement.

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