

Original Research Article

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Estimation of Genetic Variability and Divergence for Fruit Yield and Yield Attributing Traits in Salad Cucumber (*Cucumis sativus* L.) in Southern Districts of Tamil Nadu

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ABSTRACT

Keywords

Cucumber, Genetic Advance, Heritability Genetic Divergence and Mahalanobis D2 Cluster composition

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Twenty four diverse genotypes of cucumber collected from different indigenous sources were planted in randomized complete block design, for three consecutive seasons during *Rabi* for the years 2016, 2017 and 2018 and were assessed on pooled analysis basis to know the nature and magnitude of variability and genetic divergence for different horticultural traits. The genotype KCS 7 gave maximum value for number of fruits per plant, yield per vine and yield per hectare. High phenotypic coefficient of variability (PCV), genotypic coefficient of variability (GCV) and heritability estimates coupled with high genetic gain were observed for node at which first female flower appeared, number of fruits per plant, yield per vine and yield per hectare indicated the existence of wide range of variations and offers better scope for improvement through selection. The genotypes were grouped into 7 clusters and the highest (35.48) inter cluster distance was recorded between cluster III and VII. The diverse genotypes characterized by maximum inter cluster distance will differ in phenotypic performance and therefore, selection of divergent parents should be based on these cluster distances to obtain favorable hybrids and transgressive segregants in cucumber.

Introduction

Cucumber (*Cucumis sativus* L.) is one of the most important cucurbitaceous vegetable crops grown extensively in tropical and sub-tropical parts of the country. It is considered

as 4th most important vegetable crop after tomato, cabbage and onion (Tatlioglu, 1993). Cucumber is a thermophilic and frost susceptible crop species, growing best at a temperature above 20°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 vitamin B and C, carbohydrates, Ca and P (Yawalkar, 1985). In spite of being native of Indian sub-continent and endowed with enormous variability and genetic divergence, salad cucumber remains underutilized in terms of its economic potential and unexploited from breeding point of view. So, there is a great need of screening cucumber germplasm to select elite genotypes with improved quality and higher yield for direct selection or using as a parent in hybridization programme. Planning and execution of breeding programme for improvement of quantitative attributes depends, to a great extent, upon magnitude of genetic variability. The genotypic and phenotypic coefficients of variability are helpful in exploring the nature of variability in the breeding populations, whereas estimates of heritability provides index of transmissibility of characters. Hence, on the basis of these traits, suitable selection strategy can be formulated for higher yield in salad cucumber. Information on genetic diversity is used to identify the promising diverse genotypes, which may be used in further breeding programme. Therefore, with this backdrop, the present study was undertaken for three consecutive years to estimate the extent of variability, heritability, coefficients of variation, genetic advance and genetic divergence in twenty four diverse genotypes of cucumber.

Materials and Methods

Experimental Site and Environment

The present investigation was carried out during Rabi, 2016, 2017 and 2018 at Agricultural College & Research Institute, Killikulam, Thoothukudi district, Tamil Nadu Agricultural University, Tamil Nadu. This location is at an elevation of 40 m (131.2 feet)

above mean sea level lying between the 8°46 N latitude and 77° 42 E longitudes. The mean annual rainfall of the farm is 736.7 mm which is being received in 40 rainy days. The maximum and minimum temperatures ranged from 39°C and 20°C to 22°C, respectively. The relative humidity during the period of crop growth ranged between 42% to 98.71%.

Experimental Material, Layout and Observations

The present investigation aimed with the study of genetic variability and divergence using twenty four germplasm lines collected from different sources *viz.*, Assam Agricultural University, Jorhat and Kerala Agricultural University, Vellayani and also through intensive surveys made at Thoothukudi, Virudhunagar, Tenkasi and Tirunelveli districts in places like Radhapuram, Sattur, Sivakasi, Kallipatti, Surandai, Mecheri, Vembakottai, Pavorchatram, Chinakollanpatti, Periyakollanpatti, Erukanpatti, Yelayirampannai, Aalampalayam, Thaiyalpatti, Tenkasi, Nanguneri, Kuruvikulam, Aalantha, Manathi, Villikury and Karungulam. The field experiment was conducted at Department of Horticulture at Agricultural College and Research Institute, Killikulam during *rabi* season for three consecutive years 2016, 2017 and 2018. A set of twenty four genotypes of cucumber were evaluated in Randomized Block Design (RBD) with three replications. In each replication, each genotype was grown in a single row of 6 m length with a spacing of 75 x 60 cm accommodating 10 plants in a replication for all the experiments. Standard cultural practices recommended in the Package of Practices for Vegetable Crops, were followed to ensure a healthy crop stand (Veeraragavathatham, 1998). Observations were recorded on five randomly selected plants in each replication for ten quantitative characters *viz.*, plant height (cm), number of

primary branches per vine, days to 50% flowering, node at which first female flower appeared, fruit length (cm), fruit circumference (cm), number of fruits per plant, fruit weight (g), yield per plant (kg) and yield per hectare (t). Colour of fruits was observed visually after harvesting with the help of colour chart of Royal Horticultural Society, London.

Statistical Analysis

The pooled data obtained for three consecutive years were subjected to analysis of variance as per procedure described by Gomez and Gomez (1983). The genotypic and phenotypic coefficients of variation were calculated as per formulae given by Burton and De-Vane (1953). Heritability and genetic advance were calculated according to Allard (1960) and genetic gain was estimated as per the method given by Johanson *et al.*, (1955). Multivariate analysis was done utilizing Mahalanobis D² statistics and genotypes were grouped into four different clusters following Tochers method as described by Rao (1952).

Results and Discussion

Variability studies

Analysis of Variance

Genetic variability is the basic need for a plant breeder to initiate any breeding programme. Genetic improvement can be brought about by manipulating the genetic makeup of the plant for desirable characters or to remove the undesirable genes which retard, or inhibit, certain pathways. Analysis of variance (Table 2) indicated significant differences among the genotypes for all the characters under study. These differences indicated the presence of variability in the available germplasm and offers opportunity for improvement in yield and quality traits of cucumber.

Mean Performance of Genotypes

Genetic variability is the basic need for a plant breeder to initiate any breeding programme. Among the horticultural traits, comparatively wide range was observed for morphological characters vine length (179.84-294.28 cm) and number of branches (2.33-6.42). Similarly, for days to first female flower (28.17-52.55) and node at which first female flower appeared (7.00-20.74), which determine the earliness of a variety (Table 3). Fruit length, circumference and weight are the major yield contributing traits, wide variations were observed with respect to these traits (17.23-23.88 cm, 9.27-14.83 cm, 135.99-199.02 g, respectively). Tremendous variations with respect to number of marketable fruits per plant (4.67–12.54), yield per vine (0.88-2.21kg) and yield per hectare (3.89 – 9.82t) were obtained. The genotype KCS 7 was found highest in yield (9.82t/ha) among all which was followed by four other genotypes namely KCS9, KCS8, KCS14 and KCS6. Wide variations with respect to various quantitative characters were also reported by Munshi *et al.*, (2007), Kumar *et al.*, (2008), Hanchinamani *et al.*, (2008) and Yogesh *et al.*, (2009) in cucumber. All the genotypes under study also showed wide variations for fruit colour (green, light green, dark green and white), which decides the consumer's preference. Majority of the genotypes including both the check cultivars had light green coloured fruits, which are in general preferred by consumers. Similar results have also been reported by Verma (2003) and Kumar (2006) for these characters.

Parameters of Variability

Coefficients of Variability

The estimates of phenotypic and genotypic coefficients of variability gave a clear picture of amount of variations presents in the available germplasm (Table 4). For all the

characters studied, phenotypic coefficients of variability were higher in magnitude than genotypic coefficients of variability, though difference was not much in all the cases. Thus, showing that these traits are not much influenced by environmental factors. Hence, selection based on phenotypic performance will be more reliable. Coefficients of variability varied in magnitude from character to character, indicating that there was a great diversity in the experimental material used. The genotypic coefficients of variability (GCV) were high for node at which first female flower appeared, number of fruits/plant, yield per vine and yield per hectare. This reflects greater genetic variability among the genotypes for these characters for making further improvement by selection. Whereas, moderate GCV were recorded for number of primary branches, plant height and days to first female flower production. For, circumference of fruit, length of fruit and fruit weight GCV were low. Similar results had also been reported by Yogesh *et al.*, (2009).

Heritability and Genetic gain

The estimates of heritability were found high for the characters viz. plant height, fruit weight, number of fruits per plant, yield per plant, yield per hectare wherein it was moderate for node at which first female flower appeared, circumference of fruit, days to first female flower production and length of fruit and low for number of primary branches (Table 4). Kumar *et al.*, (2008) reported high heritability estimates for fruit yield per plant and moderate heritability for node number bearing first female flower. Similarly, high heritability was reported by Sandeep Kumar *et al.*, (2013) and Yogesh *et al.*, (2009) for fruit weight at edible maturity and fruit yield per plant and moderate heritability was found for node number bearing first female flower. High heritability estimates for fruit weight and fruit yield per plant were also reported by Singh

(1997) and Munshi *et al.*, (2007). In the light of results obtained in the present studies, it is concluded that selection can be performed based on phenotypic performance for highly heritable characters viz. average fruit weight and yield per plant.

Genetic gain (expressed as per cent of population mean) was low to high in nature for different characters. It was found high for node at which first female flower appeared and number of fruits per plant. Moderate genetic gain was observed for yield per plant, yield per hectare, number of primary branches and plant height, whereas it was recorded low for days to first female flower production, circumference of fruit, weight of fruit and length of fruit. These findings are in line with Kumar *et al.*, (2008) and Yogesh *et al.*, (2009).

High heritability estimates coupled with high genetic gain were observed for plant height, node at which first female flower appeared, number of fruits per plant, yield per vine and yield per hectare which indicated that these characters are under additive gene effects and these characters are more reliable for effective selection (Panse, 1957). Similar results for fruit yield per plant have been reported by Singh (1997). High heritability coupled with moderate genetic gain was observed for days to first female flower appear, fruit length, fruit circumference and average fruit weight, indicated that these characters are under non-additive gene effects and selection for these characters will be less effective.

Such traits are more under the influence of environment and do not respond to selection. Similar results were also reported by Sandeep Kumar *et al.*, (2013), Kumar *et al.*, (2008) and Yogesh *et al.*, (2009).

Genetic Divergence Studies

Cluster composition after computing D^2

values for all the possible pairs, 24 genotypes were grouped into 7 clusters, which indicated a large genetic diversity (Table 5). Maximum number of genotypes was accommodated in clusters II (7) followed by cluster III with 6, cluster V and cluster VI with 3 genotypes, cluster I and cluster IV with 2 genotypes and cluster-VII with 1 genotype, respectively. The resultant seven clusters showed considerable genetic diversity. Genotypes from different geographical regions were grouped in the same cluster indicating no relationship between geographic distribution and genetic divergence, while genotypes collected from same location were grouped into different

clusters, showing great genetic diversity. Similar results were also obtained by Rao *et al.*, (2003), Khan (2006) and Kabir *et al.*, (2009). Intra-cluster distance revealed that, cluster VI showed maximum intra-cluster distance (14.75) followed by cluster II (14.62), cluster V (14.48), cluster III (12.96), cluster IV(7.80) and cluster I with minimum intra-cluster distance (3.09), respectively. Based on distance between clusters, i.e., inter-cluster distance, the maximum divergence was observed between cluster III and VII (35.48) followed by divergence between cluster VI and VII (33.27) and the lowest (10.35) was recorded between cluster I and VI.

Table.1 List of cucumber genotypes studied along with their sources

Accession No.	Place of collection
KCS 1	Radhapuram
KCS 2	Vellayani
KCS 3	Assam Agri University
KCS 4	Sattur
KCS 5	Radhapuram
KCS 6	Sivakasi
KCS 7	Kallipatti
KCS 8	Surandai
KCS 9	Mecheri
KCS 10	Vembakottai
KCS 11	Pavoorchatram
KCS 12	Chinakollanpatti
KCS 13	Periyakollanpatti
KCS 14	Erukanpatti
KCS 15	Yelayirampennai
KCS 16	Aalampalayam
KCS 17	Thaiyalpatti
KCS 18	Tenkasi
KCS 19	Nanguneri
KCS 20	Kuruvikulam
KCS 21	Aalantha
KCS 22	Manathi
KCS 23	Villikury
KCS 24	Karungulam

Table.2 Analysis of variance for different horticultural traits in cucumber

Variables	Degrees of freedom	Vine length (cm)	No. of primary branches	Days to first female flower production	Node at which first female flower appeared	Length of fruit (cm)	Circumference of fruit (cm)	No. of fruits/plant	Fruit weight (g)	Yield/vine (kg)	Yield (t/ha)
Year	2	1034.02	0.37	21.04	10.73	8.66	3.85	5.81	239.70	0.26	5.18
Replication with in year	6	39.92	0.01	0.85	0.23	0.07	0.09	0.05	5.63	0.00	0.03
Genotypes	23	11845.59	6.42	268.00	112.91	33.75	14.80	40.47	2188.89	1.11	21.86
Year:Genotypes	46	28.49	0.53	7.56	2.85	0.99	0.40	0.44	17.51	0.02	0.30
Pooled Error	138	32.60	0.01	0.95	0.12	0.33	0.09	0.06	18.24	0.00	0.04
Total	215										

Table.3 Mean performance of cucumber genotypes for different horticultural traits

Accessions	Plant Height	No. of primary branches	Days to first female flower production	Node at which first female flower appeared	Length of fruit (cm)	Circumference of fruit (cm)	No. of fruits/plant	Fruit weight (g)	Yield/vine (kg)	Yield (t/ha)
KCS 1	261.09	3.23	32.32	11.44	17.65	11.36	10.33	151.35	1.56	6.95
KCS 2	230.55	5.03	41.00	11.15	19.65	11.17	10.67	163.79	1.75	7.76
KCS 3	235.17	3.73	33.33	12.33	20.53	11.00	9.50	167.77	1.59	7.09
KCS 4	285.26	5.02	52.55	13.78	21.41	14.03	8.08	193.44	1.56	6.95
KCS 5	291.80	3.73	39.67	15.72	21.40	14.83	6.58	199.02	1.31	5.83
KCS 6	194.57	4.49	29.44	11.17	17.23	12.20	10.75	166.71	1.79	7.97
KCS 7	205.39	6.42	28.17	7.00	18.54	10.56	12.54	176.18	2.21	9.82
KCS 8	249.18	4.52	37.58	8.30	20.46	11.52	11.15	176.00	1.96	8.72

KCS 9	260.58	4.53	39.00	9.17	20.95	11.77	11.42	178.00	2.03	9.04
KCS 10	200.81	4.52	43.44	12.55	22.87	12.65	9.33	193.98	1.81	8.05
KCS 11	208.75	5.38	35.78	12.12	20.21	10.19	9.67	177.37	1.71	7.62
KCS 12	288.44	4.20	37.86	11.54	19.40	9.27	9.92	135.99	1.35	5.99
KCS 13	200.94	3.55	41.00	13.05	18.28	10.12	8.67	146.58	1.27	5.65
KCS 14	179.84	4.22	40.22	11.08	23.63	12.37	10.50	184.74	1.94	8.63
KCS 15	221.57	3.98	38.73	12.52	22.83	12.31	9.78	181.66	1.78	7.90
KCS 16	215.53	4.28	40.68	13.42	23.48	9.74	9.33	171.23	1.60	7.11
KCS 17	211.12	4.49	36.67	14.75	22.77	11.75	7.00	183.10	1.28	5.70
KCS 18	241.44	5.14	31.10	12.65	19.61	12.24	9.75	176.84	1.72	7.66
KCS 19	278.53	3.80	31.07	13.11	20.92	12.84	9.67	180.78	1.75	7.77
KCS 20	244.69	3.26	39.67	9.81	19.12	10.53	11.67	148.64	1.74	7.71
KCS 21	294.28	4.19	37.94	20.74	20.16	11.91	5.08	176.02	0.90	3.98
KCS 22	222.06	2.33	28.61	15.89	21.79	11.12	6.92	178.54	1.24	5.49
KCS 23	190.53	3.50	33.83	19.39	23.01	12.12	5.67	182.32	1.03	4.59
KCS 24	182.03	3.51	37.11	21.28	23.88	12.37	4.67	187.90	0.88	3.89
Mean	233.09	4.21	36.95	13.08	20.82	11.66	9.11	174.08	1.57	6.99
SE d	5.10	0.09	0.79	0.28	0.44	0.24	0.19	4.11	0.04	0.16
CD (p=0.05 %)	10.93	0.17	1.56	0.56	0.87	0.47	0.38	8.81	0.07	0.32
CV (%)	5.25	1.98	1.98	1.98	1.98	1.98	1.98	5.25	1.98	1.98

Table.4 Estimates of phenotypic and genotypic coefficients of variability, heritability and genetic advance as percent of mean for different horticultural traits

S.No	Parameters	Coefficients of variability (%)		Heritability (%)	Genetic advance (%)
		Phenotypic	Genotypic		
1.	Plant Height	15.60	15.55	99.28	31.91
2.	No. of primary branches	21.65	19.22	78.83	35.16
3.	Days to first female flower appear	15.18	14.56	91.98	28.77
4.	Node at which first female flower appeared	27.75	26.73	92.79	53.04
5.	Length of fruit(cm)	9.57	9.16	91.64	18.06
6.	Circumference of fruit(cm)	11.28	10.85	92.37	21.47
7.	No. of fruits/plant	23.53	23.15	96.79	46.92
8.	Fruit weight (g)	9.03	8.92	97.64	18.16
9.	Yield/vine (kg)	22.59	22.14	96.02	44.68
10.	Yield (t/ha)	22.59	22.13	96.01	44.67

Table.5 Clustering pattern and average intra and inter cluster distance (D₂) of 24 genotypes of cucumber

Cluster	I	II	III	IV	V	VI	VII
I	3.09	17.90	12.28	24.46	12.95	10.35	28.56
II		14.62	24.86	14.23	16.41	22.96	18.37
III			12.96	31.71	17.30	12.82	35.48
IV				7.80	21.30	29.38	10.97
V					14.48	16.58	25.46
VI						14.75	33.27
VII							0.00

Table.6 Distribution of 24 cucumber genotypes in different clusters

S.No	Name of the cluster	No. of genotypes	Name of genotypes
1	I	2	KCS 15 and KCS 16
2	II	7	KCS 1, KCS 2, KCS 3, KCS 4, KCS 5, KCS 8 and KCS 9
3	III	7	KCS 6, KCS 7, KCS 10, KCS 11, KCS 23 and KCS 24
4	IV	2	KCS 12 and KCS 19
5	V	3	KCS 13, KCS 18 and KCS 20
6	VI	3	KCS 14, KCS 17 and KCS 22
7	VII	1	KCS 21

Table.7 Cluster means for different characters among 24 genotypes of cucumber

Cluster	Vine length (cm)	Number of primary branches	Days to first female flowering	Node at which first female flower appear	Fruit length (cm)	Fruit circumference (cm)	Number of fruits per plant	Fruit weight (g)	Yield per vine (kg)	Yield (t/ha)
I	218.55	4.13	39.71	12.97	23.16	12.34	6.81	62.79	118.71	1.33
II	259.09	4.26	39.35	11.70	20.29	11.89	6.21	51.86	117.79	1.43
III	197.01	4.64	34.63	13.92	20.96	12.14	5.78	63.01	120.48	1.15
IV	283.49	4.00	34.47	12.33	20.16	11.10	6.54	61.92	107.42	1.15
V	229.03	3.98	37.26	11.84	19.00	11.18	5.97	57.68	105.30	1.19
VI	204.34	3.68	35.17	13.91	22.73	15.09	5.19	56.99	122.33	1.01
VII	294.28	4.19	37.94	20.74	20.16	10.53	8.00	50.15	118.69	0.90

Cluster means for crop improvement, inter-crossing among genotypes with outstanding mean performance was suggested by Roy and Sharma (1996). The cluster means of the various horticultural traits are presented in Table 4. Moreover, for getting the reliable conformity on the basis of cluster means, cluster-VII exhibited higher means for vine length (294.28) and number of fruits per plant (8.00). Cluster-I gave maximum mean values for fruit length(23.16) wherein cluster II recorded lowest node at which first female flower appear(11.70), the highest (20.74) being recorded in cluster VII. Cluster II also exerted superiority for yield per hectare (1.43). Cluster VI recorded maximum mean values for yield per vine (122.33). Cluster IV exerted minimum values for days to first female flowering (34.47) wherein cluster I registered maximum values (39.71) for the same character. Cluster VI exerted superiority for the characters fruit circumference (15.09) and yield per vine (122.33). Cluster III registered higher means for the important yield attributing characters viz., number of primary branches (4.64) and fruit weight (63.01). Cluster V did not possess superiority for any character.

The genotypes having wide genetic base and desirable characteristics can be involved in intra-specific crosses which would lead to transmission of good genetic gain for various putative traits including yield for practical utility. Hence, crossing between the genotypes of maximum two clusters (II and III) appeared to be most promising to combine the desirable characters. Earlier workers like Kushwah *et al.*, (2005) and Khan (2006) have also indicated the significance of genetic divergence. But, Mian and Bhal (1989) reported that parental clusters separated by medium D₂ values had significant positive heterosis. Thus, heterosis could also be exploited by crossing between genotypes belonging to clusters with moderate diversity

like genotypes of cluster IV and X, cluster VI & X and X & XI. They are likely to produce new recombinant with desired traits. Considering the magnitude of genetic distance and cluster means for different characters performance, the genotype KCS-21 of cluster VII could be selected for vine length wherein KCS-24 of cluster III could be selected for fruit length. The genotypes KCS-5 in cluster II and KCS-19 in cluster IV were promising for the characters fruit weight and fruit circumference, respectively. In cluster III, the genotype KCS-7 could be selected for number of primary branches, days to first female flowering, node at which first female flower appeared, number of fruits per plant, yield per vine and yield per hectare if used in hybridization programme.

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