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Estimation of genetic diversity in local collections of cucumber (*Cucumis sativus* L.) Genotypes based on productivity traits

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Abstract

A field experiment was undertaken during the year 2017-2018 in *kharif* season at Kittur Rani Channamma College of Horticulture, Arabhavi to study the extent of genetic diversity existing in local cucumber collections. The experiment was laid out in randomized block designs with two replications. A total of 21 local collection of cucumber genotypes were used in the present study. Mahalanobis D^2 analysis indicated considerable diversity and 21 genotypes were grouped into six different clusters. The cluster II showed maximum (2242.20) intra cluster distance. Inter cluster distance revealed the maximum divergence between clusters IV and cluster III ($D^2 = 32489.21$) followed by cluster III and cluster II ($D^2 = 24315.24$). Among all the 19 productivity traits studied, flesh thickness, fruit diameter, fruit length and average fruit weight contributed greatly towards divergence. These traits may give more importance in selecting the genotypes the genotype KRCCH-CC-17 in cluster V recorded highest cluster mean. This genotype can be used as a base material for future breeding programme.

Keywords: estimation, genetic diversity, Cucumis sativus, productivity traits

Introduction

Cucumber (Cucumis sativus L.) is one of the most popular vegetable of family cucurbitaceae with chromosome number of 2n=14. It is an ideal summer vegetable crop chiefly grown for its edible tender fruits, preferred as salad ingredient, pickles and desert fruit and as a cooked vegetable. Cucumber has got cooling effect, so in the eastern countries; fruits are often used as cooling vegetable. It is ideal for people suffering from jaundice and allied diseases and also very much useful in preventing constipation. Seeds contain oil, which is helpful for brain development and body smoothness. Hence, it is being used in Ayurvedic preparations ^[1]. Cucumber is a highly cross pollinated crop and usually monoecious in nature preferring warm weather and bright light for its better growth and development. However, it can be grown in both summer and rainy season, but it cannot tolerate cold injury. Being primary centre of origin, India has accumulated wide range of variability in this crop. In spite of large number of varieties available in India, only few are promising. This fact draws the attention of plant breeder for its improvement. To formulate a sound and successful breeding programme, the importance of genetic variability in the population needs emphasis. To make an improvement in any crop species, the breeder is constantly engaged in effective choice of desirable parents of high genetic variation so that individuals with desirable character combination can be selected. Genetically diverse parents are likely to produce high genetic diversity effects and desirable traits tool in quantifying the degree of divergence among the biological populations.

Material and Methods

The present study was carried out at Kittur Rani Channamma, College of Horticuluture, Arabhavi during *Kharif* season in 2017-18 with 21 local collections of cucumber genotypes. The genotypes were assessed in a field experiment under a Randomized Block Design with two replications. Cultural practices including need based plant protection measures were followed as per the recommendations. The data were recorded on five randomly selected plants from each genotype for 19 traits. Observations were recorded on vine length (cm), number of leaves per vine, number of branches per vine, number of nodes per vine, node at first male flowering, days to first male flowering, days to first

female flowering, days to 50 percent flowering, number of male flowers, number of female flowers, sex ratio, days to first fruit harvest, number of fruits per vine, fruit yield per vine (kg), average fruit weight (g), fruit length (cm), fruit diameter (cm) and flesh thickness (cm). Mahalonobis (1936) ^[2] D² statistics was used for assessing the genetic divergence between 21 cucumber genotypes. A generalized distance (D²)

was calculated for each pair of genotypes. The D^2 values were obtained as the sum of squares of difference between two pairs of corresponding uncorrected values of any two genotypes ^[3]. Using all D^2 values, the genotypes were grouped into clusters using Tocher's method as described by ^[3]. The intra and inter-cluster distances were calculated by the formula given by ^[4].

Cluster number	No. of genotypes	s Genotype name					
Cluster I	7	KRCCH-CC-10, KRCCH-CC-18, Arabhavi local, KRCCH-CC-5, KRCCH-CC-2, KRCCH-CC- 19, KRCCH-CC-20.					
Cluster II	8	KRCCH-CC-9, KRCCH-CC-11, KRCCH-CC-12, KRCCH-CC-14, KRCCH-CC-7, KRCCH-CC-3, KRCCH-CC-1, KRCCH-CC-8.					
Cluster III	3	KRCCH-CC-4, KRCCH-CC- 6, KRCCH-CC- 16.					
Cluster IV	1	KRCCH-CC-13					
Cluster V	1	KRCCH-CC-17					
Cluster VI	1	KRCCH-CC-15					

Table 2: Percent contribution of different characters towards divergence in cucumber genotypes

Sl. No Characters		Times ranked 1 st	Percent Contribution		
1	Flesh thickness (cm)	153	72.86		
2	Fruit diameter (cm)	36	17.14		
3	Fruit length (cm)	16	7.62		
4	Average fruit weight (g)	3	1.43		
5	Number of female flowers	1	0.48		
6	Number of leaves per vine	1	0.48		
7	Vine length (cm)	-	0		
8	Number of branches per vine	-	0		
9	Number of nodes per vine	-	0		
10	Node at first male flowering	-	0		
11	Node at first female flowering	-	0		
12	Days to first male flowering	-	0		
13	Days to first female flowering	-	0		
14	Days to 50% flowering	-	0		
15	Number of male flowers	-	0		
16	Sex ratio	-	0		
17	Days to first fruit harvest	-	0		
18	Number of fruits per vine	-	0		
19	Fruit yield per vine (kg)	-	0		

Table 3: Cluster means for 19 traits from D² analysis and their rankings

Sl. No	Character	Ranking	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
1	Vina langth (am)		146.79	160.76	146.02	168.50	125.75	154.40
1	Vine length (cm)	R	4	2	5	1	6	3
2	Number of leaves per vine		55.93	77.56	63.17	58.00	50.50	79.00
2	Number of leaves per vine	R	5	2	3	4	6	1
3	Number of branches per vine		2.34	3.01	1.43	3.30	4.73	4.43
3	Number of branches per vine	R	5	4	6	3	1	2
4	Number of nodes non vine		12.78	11.56	13.75	10.50	11.00	10.25
4	Number of nodes per vine	R	2	3	1	5	4	6
5	Node at first male flowering		2.85	3.06	1.72	3.45	1.40	1.50
3	Node at first male flowering	R	4	5	3	6	1	2
6	Node at first female flowering		5.22	4.90	5.42	5.00	4.75	3.65
0	Node at first female flowering	R	5	3	6	4	2	1
7	Days to first male flowering		37.32	34.69	39.83	39.25	30.50	38.25
/	Days to first male nowering	R	3	2	6	5	1	4
8	Days to first female flowering		43.21	41.14	44.95	42.75	42.25	44.25
0	Days to first female nowening	R	4	1	6	3	2	5
9	Days to 50 percent flowering		53.48	51.94	56.04	52.50	58.63	49.00
9	Days to 50 percent nowening	R	4	2	5	3	6	1
10	Number of male flowers		65.89	77.59	72.30	58.85	59.90	65.85
10	Number of male nowers	R	3	1	2	6	5	4
11	Number of female flowers		8.22	7.50	9.77	7.65	12.50	9.80
11	Number of remaie nowers	R	4	6	3	5	1	2
12	Sex ratio		8.31	11.34	8.50	7.80	4.90	6.85
12	Sex ratio	R	3	1	2	4	6	5

13	Days to first fruit harvest		53.34	53.32	53.92	60.00	48.00	51.75
15 Days to first fruit flatvest		R	4	3	5	6	1	2
Sl. No	Character	Ranking	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
14 Nu	Number of family and since		5.46	4.13	5.67	6.63	9.63	8.38
	Number of fruits per vine	R	5	6	4	3	1	2
15	Empity isld non vine (1.2)		1.10	1.11	1.33	2.10	1.28	2.50
15	Fruit yield per vine (kg)	R	6	5	3	2	4	1
16	A		173.77	189.29	229.45	265.75	225.05	276.05
10	Average fruit weight (g)	R	6	5	3	2	4	1
17			12.34	19.53	18.52	21.65	26.20	23.45
17	Fruit length (cm)	R	6	5	4	3	1	2
10			5.48	6.49	5.62	5.35	7.75	4.50
18	Fruit diameter (cm)	R	4	2	3	5	1	6
10	Flesh thickness (mm)		2.01	2.09	1.78	2.20	2.30	1.90
19		R	4	3	6	2	1	5
		Overall score	88	61	76	72	54	55
		R	6	3	5	4	1	2

Table 4: Average intra and inter cluster distances for 21 cucumber genotypes.

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	1854.13	6238.10	8770.80	11648.81	3629.47	10634.65
Cluster II		2242.20	24315.24	3876.82	10340.96	8166.18
Cluster III			2166.64	32489.21	6415.99	23310.39
Cluster IV				0.00	12048.24	3080.32
Cluster V					0.00	6128.77
Cluster VI						0.00

• Diagonal values indicate intra cluster distance

• Above diagonal values indicate inter cluster dista

Result and Discussion

The analysis of variance has revealed highly significant differences between genotypes in respect of all characters, suggesting considerable divergence between them. 21 genotypes were grouped into six clusters by treating estimated D^2 values as the squares of generalized distances. Cluster II was the largest cluster comprising of eight genotypes, followed by cluster I, which is having seven genotypes. Cluster III consisted of three genotypes, whereas, cluster IV, V and VI were solitary clusters with single genotype (Table 1).

The selection and choice of parents mainly depends on contribution of characters towards divergence. In the present study (Table 2), Flesh thickness contributed maximum (72.86%) to the total diversity followed by fruit diameter (17.14%), fruit length (7.62%), average fruit weight (1.43%), number of female flowers (0.48%) and number of leaves (0.48%). The remaining all other traits did not contributed to the total diversity ^[5-9].

All genotypes spread over six clusters and means were scored across the clusters for all the 19 characters. The highest cluster mean was given the first rank and next clusters possessing next best means were given second, third, and so on up to sixth rank for all the traits except node at first male flower, node at first female flower, days to first male flowering, days to first female flowering, days to 50 per cent flowering and days to first fruit harvest, where lowest values were given first rank and highest values was last rank. Accordingly, cluster V with overall score of 54 across 19 characters secured first rank followed by clusters VI, II, IV, III and I indicating presence of most promising genotypes in them and can be extensively used for further breeding programme to generate new material.

Average intra and inter cluster distance for 21 cucumber genotypes were presented in the table 4. Cluster II, which contains eight genotypes exhibited maximum intra cluster distance ($D^2 = 2242.20$) followed by Cluster III ($D^2 = 2166.64$) and Cluster I ($D^2 = 1854.13$). Cluster IV, V and VI exhibited zero distance as they possess single genotype. Intercluster distances depict that cluster IV and cluster III had maximum divergence ($D^2 = 32489.21$) among them, followed by cluster III and cluster II ($D^2 = 24315.24$). The least intercluster distance was observed between cluster IV and cluster VI ($D^2 = 3080.32$). 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.

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