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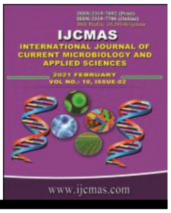

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Estimation of Genetic Divergence for Fruit Yield and Quality Traits in Cucumber (*Cucumis sativus* L.)

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ABSTRACT

Keywords

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Genetic diversity in commercial cucumber genotypes was estimated based on 10 characters. Twenty four cucumber genotypes were grouped into eleven different clusters. The highest inter-cluster distance (83.10) was observed between clusters VI and X whereas lowest inter-cluster distance (19.14) was observed between the clusters II and VII. Cluster X showed highest mean for number of primary branches, node at which first female flower appear, number of fruits per plant, yield per vine and yield per hectare, cluster VIII produced highest mean for fruit circumference and fruit weight, cluster IV registered highest mean for fruit length whereas cluster III recorded highest mean for vine length and earliness for days to first female flowering. Cluster II and III contributed 51.75 and 40.26%, respectively towards divergence.

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, 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. Information on genetic diversity is used to identify the promising diverse genotypes, which may be used in further breeding programme. Therefore, keeping in view the importance of above facts in mind, the present study has been undertaken to estimate the extent of genetic divergence in twenty four diverse genotypes of cucumber.

Materials and Methods

Experimental site: The present investigations were carried out at Department of Horticulture, Agricultural College & Research Institute, Killikulam in the state of Tamil Nadu, India during Rabi season of 2017. The campus and its farm is geographically located in 8°46 N latitude and 77°42 E longitude and at an altitude of 40 m above MSL. The mean annual rainfall of the farm is 736.7 mm which is being received in 40 rainy days.

Experimental material, layout and observations

The experimental material consisted of diverse group of 24 genotypes of cucumber (Table 1) collected from different regions of Tamil Nadu having tremendous genetic diversity of cucumber. The experiment was laid out in randomized block design with three replications of each genotype. Basal application of FYM 40 t/ha and 35 kg of N/ha at 30 days after sowing was done. Azospirillum and Phosphobacteria 2 kg/ha and Pseudomonoas 2.5 kg/ha along with FYM 50 kg and neem cake @ 100 kg were also applied before last ploughing. Seeds were directly sown in the field in the month of December, 2017. Three to four seeds per basin were sown at a spacing of 75 x 60 cm accommodating 10 plants in each replication. After the emergence of seedlings, only one healthy seedling per hill was retained. Standard cultural practices recommended in the Package of Practices for Vegetable Crops, were followed to ensure a healthy crop stand (Anonymous, 2009). The observations were recorded on 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)from five randomly selected plants in each replication for all characters.

Statistical analysis: The data were subjected to Multivariate analysis as per procedure described by Mahalanobis D2 statistics and genotypes were grouped into four different clusters following Tochers method as described by Rao (1952).

Results and Discussion

Cluster composition after computing D2 values for all the possible pairs, 24 genotypes were grouped into 11 clusters, which indicated a large genetic diversity (Table 2 and 3). Maximum number of genotypes were accommodated in clusters-I (5) followed by cluster-VIII with 3, cluster-II, cluster-III, cluster-IV, cluster-V, cluster-VI and cluster-VII with 2 genotypes, cluster-X and cluster-XI with 1 genotype, respectively. The resultant eleven 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 VIII showed maximum intra-cluster distance (26.88) followed by cluster IX (24.95), cluster VII (24.20) and cluster II with minimum intra-cluster distance (13.99), respectively. Based on distance between clusters, i.e., inter-cluster distance, the maximum divergence was observed between cluster VI and X (83.10) followed by cluster X and XI (69.85), cluster II and VI (66.81) and lowest (19.14) was recorded between cluster II and VII (Figure 1).

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-III exhibited higher means for vine length (256.08). Cluster-IV gave maximum mean values for fruit length(22.49) wherein cluster VI recorded highest node at which first female flower appear(20.33), the lowest (7.00) being recorded in cluster X. Cluster VI also recorded minimum mean values for yield per vine(0.98). Cluster XI exerted minimum values for days to first female flowering (26.66) wherein cluster VIII registered maximum values (46.33) for the same character. Cluster VIII exerted superiority for the characters fruit circumference (13.49) and fruit weight (196.33). Cluster X registered higher means for the important yield attributing characters *viz.*, number of primary branches (6.66), number of fruits per plant (12.38) and therefore for yield per vine (2.18) and yield per hectare (9.67). Cluster-I, Cluster-II, Cluster-V, Cluster-VII and Cluster-X did not possess superiority for any character.

Table.1 Cucumber accessions

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

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	17.96	20.53	19.33	31.14	20.88	53.56	21.16	31.86	27.50	39.52	39.44
II		13.99	23.54	42.94	25.80	66.81	19.14	38.43	34.76	30.11	52.39
III			14.87	30.23	22.31	51.81	25.09	30.50	29.42	36.64	38.58
IV				16.15	29.04	30.47	41.28	29.88	27.74	58.15	24.32
V					17.41	52.24	27.44	33.39	26.13	36.42	40.79
VI						21.53	64.15	43.87	46.87	83.10	29.46
VII							24.20	41.99	31.75	35.69	47.46
VIII								26.88	36.80	55.01	43.40
IX									24.95	49.82	37.52
X										0.00	69.85
XI											0.00

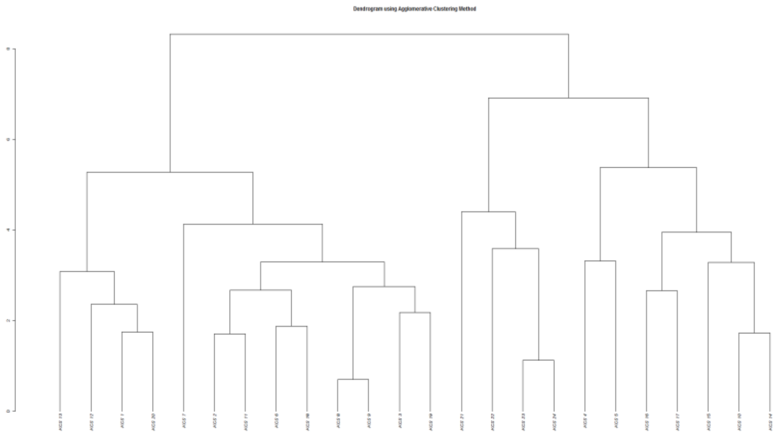
Table.3 Distribution of 24 cucumber genotypes in different clusters

Cluster No	Number of genotypes	Name of genotypes
I	5	KCS-1, KCS-2, KCS-3, KCS-14 andKCS-15
II	2	KCS-8 andKCS-9
III	2	KCS-18 andKCS-19
IV	2	KCS-17 andKCS-23
V	2	KCS-11 andKCS-16
VI	2	KCS-21 andKCS-24
VII	2	KCS-6 andKCS-20
VIII	3	KCS-4, KCS-5 andKCS-10
IX	2	KCS-12 andKCS-13
X	1	KCS-7
XI	1	KCS-22

Table.4 Cluster means for different characters among 24 genotypes of cucumber

Cluster/Traits	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)
1	223.20	3.93	37.20	11.53	20.58	11.54	10.55	171.53	1.81	8.03
2	248.74	4.33	38.50	8.50	20.49	11.46	11.37	178.75	2.04	9.04
3	256.08	4.33	29.66	12.50	19.74	12.09	10.00	182.20	1.82	8.10
4	196.83	4.00	36.00	14.66	22.49	11.58	6.88	182.99	1.26	5.59
5	203.92	4.89	36.83	11.83	20.92	9.53	9.75	176.00	1.72	7.63
6	236.58	3.02	38.33	20.33	21.63	11.62	5.38	182.48	0.98	4.36
7	215.08	3.83	33.67	9.66	18.05	11.10	11.75	159.74	1.87	8.31
8	255.44	4.44	46.33	14.00	21.59	13.49	8.50	196.33	1.67	7.40
9	240.33	4.33	38.17	12.16	17.86	9.66	8.75	143.33	1.25	5.56
10	200.16	6.66	27.00	7.00	18.77	10.67	12.38	175.68	2.18	9.67
11	212.16	2.00	26.66	17.33	21.88	10.67	7.25	182.50	1.32	5.88

Fig.1 Diagram showing average intra and inter-cluster distances (D2) of 24 genotypes of cucumber



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 (VIII and X) appeared to be most promising to combine the desirable characters. Earlier workers like Ram (2001), 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 genotypes KCS-18 and KCS-19 of cluster III could be selected for vine length wherein KCS-17 and KCS-23 of cluster IV could be selected for fruit length.

The genotypes KCS-4, KCS-5 and KCS-10 in cluster VIII were promising for the characters fruit circumference and fruit weight. The genotype KCS-22 in cluster XI could be selected for earlier days to first female flowering. In cluster X, the genotypeKCS-7 could be selected for number of primary branches, node at which first female flower appear, number of fruits per plant, yield per vine and yield per hectare if used in hybridization programme.

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