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Genetic Diversity Analysis in Cucumber (*Cucumis sativus* L.) Based on Morphological Traits

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Evaluation of fifteen diverse genotypes of cucumber was carried out in a randomized complete block design for studying genetic divergence. Presence of wide genetic diversity, among the genotypes studied was confirmed by using Mahalanobis D^2 statistics. Based on the interactions genetic distances of cucumber genotypes had grouped into five separate clusters inferring that the genetic divergence between them was quite high. The germplasm were so divergent, that only six genotypes were grouped in cluster V and three genotypes in each cluster I and III. The two genotypes SKY/AC-270-613481 and JB/11-091-613462 were grouped as cluster II and the genotype Tripura local was so divergent in all the characters that they were allotted as a separate group as cluster IV. Cluster mean analysis proclaimed that, genotypes in cluster I recorded maximum value for vine length (3.36 m), number of leaves per plant (43.85), number of branches per plant (12.98), leaf area (144.71 cm^2), number of female flowers per plant (20.30), fruiting period (52.20 days), fruit set (89.10 %), average fruit weight (214.72 g), number of fruits per plant (19.00),

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fruit yield per plant (2.50 kg), fruit yield per ha (31.23 t/ha), rind thickness (2.79 mm) and flesh thickness (3.02 cm), whereas, same cluster I recorded minimum value for traits *viz*., internodal length (6.55 cm), days to appearance of first male flower (30.34 days), days to appearance of first female flower (31.81 days), node number at which first female flower appeared (4.00), days to first harvest (41.22 days) and number of seeds per fruit (211.69) which are negatively desirable characters in the crop production and crop improvement programme.

Keywords: Genetic diversity; cluster analysis; cucumber; yield and yield attributing traits.

1. INTRODUCTION

The Cucurbitaceae is a monophyletic family with most species being used as human food. *Cucumis sativus* L. is one of the cultivated species of the genus *Cucumis* which has been studied extensively in recent years. Cucumber is assumed to have originated in India, where it had been under cultivation for the last 3000 years [1-2]. India possesses a rich diversity of *Cucumis sativus* L. and related species, differing widely in botanical and agronomical traits. China is considered to be the secondary centre of origin [3]. Commercially cucumber is cultivated all over South Asian region. Besides large number of high yielding cultivars many landraces and wild forms have also been reported in cucumber [4] which have not been exploited to a greater extent.

The major constraints in achieving higher and profitable productivity of cucumber are lack of genetic variability, absence of appropriate genotypes for different cropping systems, sensitivity to biotic and abiotic stresses, non-availability of quality seeds of improved varieties and narrow genetic base, which has resulted in repeated usage of few parents with high degree of pertinence in crossing programmes. Many breeding attempts have been made to improve the yield level of this crop and to break the yield plateau. Genetic variability and divergence present in the germplasm are prerequisites for any breeding programme. The proper estimate of nature and magnitude of diversity in a crop is essential to infer about the extent of variation available for yield and yield attributing traits. Knowledge on genetic divergence among the available germplasm assists to a plant breeder for the selection of superior parents for hybridization programme. Genetically diverse parents are supposed to provide desirable segregants. It is an established fact that the selection of more diverse parents triggers greater chances of obtaining high heterotic F_1s and wide range of variability in the segregating generation [5]. Multivariate analysis by means of Mahalanobis's D^2 statistic is a robust tool for quantifying the degree of divergence at the phenotypic level.

After development of improved genotypes from various sources, it is necessary to evaluate their yields and other agronomic traits, and to assess nature and extent of genetic variation. For further improvement of the varieties study of the interrelationships between yield and different yield components helps in guiding the breeder in plant selection and equally important is also to characterize the potential varieties. Evaluation and characterization of genotypes are necessary to identify qualitative and quantitative characters useful for breeding and maintenance breeding programs. Moreover, documentation of diagnostic characteristics is essential for protection plant varieties as per the existing plant variety protection laws. Characterization based on morphological markers at different growth stages of the crop is practically more useful to ascertain the genuineness of a variety and to test its distinctness, uniformity, and stability. Further, for best utilization of the genotypes in development of superior varieties, an analysis of genetic diversity based on the agronomic and other morphological characters is important to identify useful parents, as F_1 crosses between divergent parents are the most responsive for genetic improvement [5].

In the present study, promising cucumber genotypes were taken to assess genetic diversity using morphological markers. The objectives of this study, to characterize the genotypes based on morphological markers and to assess the magnitude of genetic diversity of collected green gram genotypes.

2. MATERIALS AND METHODS

The experimental material comprised of fifteen diverse cucumber genotypes collected from National Bureau of Plant Genetic Resources, New Delhi and Agartala, Tripura. The genotypes are listed in Table 1. The experiment was

conducted at the Horticulture Research Station, Department of Horticulture, University of Agricultural Sciences, Gandhi Krishi Vigyan Kendra, Bengaluru - 560065. The genotypes were raised in randomized complete block design with three replications with two meter of row to row and 40 cm of plant to plant spacing was adopted. Observations were recorded on 25 morphological characters *viz*., vine length (m), number of leaves per plant, internodal length (cm), number of branches per plant, leaf area (cm^2), days to appearance of first male flower, days to appearance of first female flower, node number at which first male flower appeared, node number at which first female flower appeared, number of male flowers per plant, number of female flowers per plant, sex ratio, days to first harvest, fruiting period (days), fruit set (%), fruit length (cm), fruit diameter (cm), average fruit weight (g), number of fruits per plant , fruit yield per plant (kg), fruit yield per ha (t/ha), number of seeds per fruit, rind thickness (mm) , flesh thickness (cm) and TSS (º brix) on five randomly selected plants in all the genotypes in each replication.

Data was subjected to statistical analysis and for statistical analysis, mean of the fifteen genotypes were examined by the method summarized by Ostle [6]. To assess the genetic divergence among the landraces, Mahalanobis D^2 statistics [7] was used. Based on the genetic distance, all the genotypes were grouped into different clusters [8].

3. RESULTS AND DISCUSSION

On the basis of D^2 values, the 15 genotypes were categorized into five highly divergent clusters. The constituent of the clusters with their source are shown in (Table 2; Fig. 1). The germplasm was so divergent, that only six genotypes were grouped in cluster V and three genotypes in each cluster I and III. The two genotypes SKY/AC-270-613481 and JB/11-091-613462 were grouped as cluster II and the genotype Tripura local was so divergent in all the characters that they needed to be given the status of a separate group as cluster IV (Table 2).

This cluster comprising of one genotype with specific valuable traits and other genotypes falling in the highly divergent groups (cluster IV) will help in broadening the existing genetic base and may produce novel genotypes with seamlessly unknown combinations. The close scrutiny of Table 2 clearly showed that, although the genotypes were selected from different sources, they got grouped in different clusters *i.e.*, genotypes did not cluster according to geographical distributions. Similar results were affirmed by Hasan *et al*. [9] while working on seven genotypes of commercial cucumber Amrita and Anand [10] evaluated 19 diverse genotypes of cucumber. To establish the actual location of origin of a genotype is troublesome. To preserve the real identity of the genotypes requires great effort because of free and frequent exchange of genetic material among the crop improvement programme in the country. Furthermore, the incorporation of genes from varied sources may be one of the reasons for losing the basic geographical identity of the genotype. The dissimilarity between genetic diversity and geographical distance stipulates that forces other than geographical origins, such as spontaneous variation, natural and artificial selection, exchange of genetic stocks and genetic drift are liable for genetic diversity. In addition to this influence of environment and genotype × environment interaction on clustering pattern may be another reason for differential gene expression in the cucumber genotypes.

3.1 Cluster Mean Analysis

Cluster mean analysis of 15 genotypes (Table 3) proclaimed that, the mean value of clusters varied in magnitude for all the 25 characters and revealed the best cluster for various characters. Genotypes in cluster I recorded maximum value for vine length (3.36 m), number of leaves per plant (43.85), number of branches per plant (12.98), leaf area (144.71 cm^2), number of female flowers per plant (20.30), fruiting period (52.20 days), fruit set (89.10 %), average fruit weight (214.72 g), number of fruits per plant (19.00), fruit yield per plant (2.50 kg), fruit yield per ha (31.23 t/ha), rind thickness (2.79 mm) and flesh thickness (3.02 cm). Whereas same cluster I recorded minimum value for traits *viz*., internodal length (6.55 cm), days to appearance of first male flower (30.34 days), days to appearance of first female flower (31.81 days), node number at which first female flower appeared (4.00), days to first harvest (41.22 days) and number of seeds per fruit (211.69) which are negatively desirable characters in the crop production and crop improvement programme. Cluster II exhibited the highest mean value for number of male flowers per plant (228.27), sex ratio (13.78) and TSS (7.10 º brix). Cluster III exhibited the highest mean value for

fruit length (27.09 cm) and fruit diameter (5.27 cm), whereas lowest mean value exhibited for node number at which first male flower appeared (2.56). Results showed that, lack of parallelism between genetic diversity and geographical distance stipulates that forces other than geographical origins, such as spontaneous variation, natural and artificial selection, exchange of genetic stocks and genetic drift are liable for genetic diversity. This is an agreement with the results of Sharma and Deepa [11] Amrita and Anand [10]. In order to fulfill the aims of breeding, the breeder can select potential lines among the different clusters as a parent in hybridization programme.

3.2 Intra and Inter-cluster Distances

The cluster divergence was manifested by the high inter-cluster and low intra-cluster D^2 values (Table 4). The intra-cluster and inter-cluster D^2 values among 15 genotypes presented in Table 4 revealed that, cluster IV showed minimum intra-cluster D^2 value (0.00), whereas maximum intra-cluster D^2 value (2563.37) was shown by cluster I indicated that, very diverse genotypes are included in this cluster and the result of both natural and artificial selection forces among the genotypes. Minimum inter-cluster D^2 value was noted between the clusters II and V (616.68) specified that, close relationship among the genotypes included in these clusters. Maximum inter-cluster D^2 values were detected between the clusters I and IV (11319.16). This specified that the genotypes included in these clusters can be used as a parent in the hybridization programme to get higher heterotic hybrids from the segregating population. Punithae *et al*., [12] Amrita and Anand [10] have also explained the phenomenon of parallelism and similar intra and inter-cluster distances were worked out in 41 and 19 diverse genotypes of cucumber, respectively.

Table 1. List of genotypes used as parents with place of release and collection of cucumber in the study

Sl. No.	Genotypes / Parents	Code	Source
1	SKY/AC-247-613476	P_1	National Bureau of Plant Genetic Resources, New Delhi
2	SKY/AC-251-613477	P_2	National Bureau of Plant Genetic Resources, New Delhi
3	SKY/AC-265-613480	P_3	National Bureau of Plant Genetic Resources, New Delhi
4	SKY/AC-270-613481	P_4	National Bureau of Plant Genetic Resources, New Delhi
5	SKY/AC-316-613484	P_5	National Bureau of Plant Genetic Resources, New Delhi
6	SKY/AC-319-613485	P_6	National Bureau of Plant Genetic Resources, New Delhi
7	KP/SC-1494-613474	P_7	National Bureau of Plant Genetic Resources, New Delhi
8	JJK/10-601-595518	P_8	National Bureau of Plant Genetic Resources, New Delhi
9	JS/06-01-541367	P_9	National Bureau of Plant Genetic Resources, New Delhi
10	JB/11-028-595504	P_{10}	National Bureau of Plant Genetic Resources, New Delhi
11	JB/11-091-613462	P_{11}	National Bureau of Plant Genetic Resources, New Delhi
12	JB/11-197-613470	P_{12}	National Bureau of Plant Genetic Resources, New Delhi
13	JB/11-205-595510	P_{13}	National Bureau of Plant Genetic Resources, New Delhi
14	JB/11-217-595512	P_{14}	National Bureau of Plant Genetic Resources, New Delhi
15	Tripura local	P_{15}	Agartala, Tripura

Table 2. Distribution of cucumber genotypes in different clusters

Cluster	No. of genotypes	Sub-cluster	Genotypes
I		IA	P_1 : SKY/AC-247-613476
	3		P_3 : SKY/AC-265-613480
		IB	P_{10} : JB/11-028-595504
II	2		P_4 : SKY/AC-270-613481
			P_{11} : JB/11-091-613462
III		IIIA	P_{12} : JB/11-197-613470
	3		P_{13} : JB/11-205-595510
		IIIB	P_{14} : JB/11-217-595512
IV	1		P_{15} : Tripura local
V		VA	P_2 : SKY/AC-251-613477
			P_5 : SKY/AC-316-613484
	6		P_6 : SKY/AC-319-613485
			P_7 : KP/SC-1494-613474
		VB	P_8 : JJK/10-601-595518
			P_9 : JS/06-01-541367

Table 3. Cluster means for different traits in 15 cucumber genotypes

Cluster	Number of Elements	Sum_sq	Vine length (m)	Number of leaves/ plant	Internodal length (cm)	Number of branches/plant	Leaf area (cm^2)	Days to appearance of first male flower	Days to appearance of first female flower	Node number at which first male flower appeared	Node number at which first female flower appeared	Number of male flowers per plant	Number of female flowers per plant	Sex ratio	Days to first harvest
1	3	25.98	3.36	43.85	6.55	12.98	144.71	30.34	31.81	3.06	4.00	222.38	20.30	12.14	41.22
2	2	11.31	2.76	38.33	6.97	7.73	116.79	32.62	36.00	4.58	7.92	228.27	16.66	13.78	47.98
3	3	35.75	2.81	37.68	7.10	9.02	122.09	36.06	36.56	2.56	9.89	210.08	17.68	11.94	45.53
4	1	0.00	2.23	32.32	7.65	8.71	123.13	31.03	35.75	4.83	6.33	189.24	15.34	12.54	43.75
5	6	85.06	2.76	31.83	7.68	8.09	114.48	33.91	33.59	4.47	10.03	198.05	16.44	12.36	44.73

Table 3. Continuation…

Cluster	Number of Elements	Sum_sq	Fruiting period (days)	Fruit set (%)	Fruit length (cm)	Fruit diameter (cm)	Average fruit weight (g)	Number of fruits/plant	Fruit yield per plant (kg)	Fruit yield per ha (t/ha)	Number of seeds/ fruit	Rind thickness (mm)	Flesh thickness (cm)	TSS (º brix)
1	3	25.98	52.20	89.10	26.62	5.21	214.72	19.00	2.50	31.23	211.69	2.79	3.02	6.77
2	2	11.31	39.84	75.94	27.08	5.16	202.41	13.50	1.65	20.59	272.20	1.95	2.67	7.10
3	3	35.75	40.07	81.75	27.09	5.27	142.81	15.76	1.66	20.76	288.74	2.17	2.70	6.33
4	1	0.00	29.05	76.14	25.04	3.96	195.20	11.92	1.59	19.90	257.34	2.28	2.76	6.85
5	6	85.06	39.69	79.93	23.93	5.17	178.39	15.11	1.63	20.35	247.43	2.36	2.83	6.86

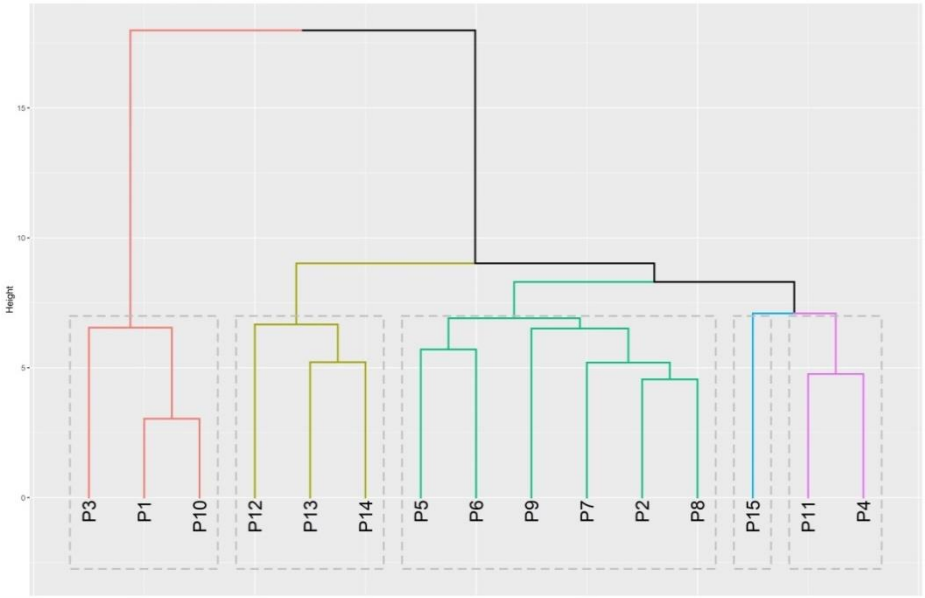

Fig. 1. Dendrogram showing relationship among cucumber genotypes

Table 4. Mean intra and inter-cluster distance (D^2) among 15 cucumber genotypes

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	2563.37	10636.27	10471.92	11319.16	10875.11
Cluster II	10636.27	475.94	1062.43	684.52	616.68
Cluster III	10471.92	1062.43	1938.92	1128.14	1255.16
Cluster IV	11319.16	684.52	1128.14	0.00	822.08
Cluster V	10875.11	616.68	1255.16	822.08	958.31

4. CONCLUSION

Considerable diversity was perceived among the genotypes used in the experiment. If a breeding programme is aimed for higher yield, then genotypes from cluster I can be selected as a parent, which showed highest mean for yield per plant along with higher average fruit weight, number of fruits per plant and other yield attributing parameters. If a breeding programme is aimed for earliness, a selection from cluster I will be highly effective as it recorded minimum value for traits *viz*., days to appearance of first male flower, days to appearance of first female flower, node number at which first female flower appeared and days to first harvest, which are negatively desirable characters in the crop production and crop improvement programme; and to breed long fruited varieties having some demand in a specific region of India, selection from cluster III will be fruitful. The genotypes of a highly divergent cluster may also be exploited in a breeding programme for the development of high yielding varieties with desirable traits and could also be exploited in heterosis breeding programme for the development of F_1 hybrids with marvelous yield, yield attributing traits and quality characters.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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