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Genetic Divergence Studies in Cucumber

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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

Cucumber is an important vegetable crop belonging to family Cucurbitaceae which is the most widely cultivated in the tropical and sub-tropical areas of the world. Immature cucumber fruits can be either consumed as raw or in the form of pickle. In addition to its cooling properties, immature fruits are considered useful for people suffering from constipation, jaundice, and indigestion. In Himachal Pradesh, cucumber is commercially grown from March-May which makes the fruits available to the consumers from June-October, when there is non-availability of fruits in plains. Thirty two diverse genotypes of cucumber were evaluated in Randomized Complete Block Design with three replications including standard check cultivar i.e Solan Srijan at Horticultural Research and Training Station and Krishi Vigyan Kendra Kandaghat It is concluded from the present investigation that for the improvement of various horticultural traits in cucumber, it would be better to carry out hybridization between genotypes from cluster IV (S-30, Sel-3A, Grani Collection, Kothi Deora Collection and Solan Srijan) and cluster II (FAM-2, Ujawala Summer Long-45, Bajrol Collection and Kothon Collection) in order to obtain better recombinants.

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Keywords: Cucumber; genetic divergence; vegetable crop.

1. INTRODUCTION

Cucumber (*Cucumis sativus* L.) is an important vegetable crop that belongs to the family Cucurbitaceae. It is most widely cultivated in the tropical and sub-tropical areas of the world. After watermelon, cucumber is the most cultivated cucurbit and it stands fourth among the group of important vegetables after tomato, cabbage and onion. About 30 species of the genus *Cucumis* have been identified in two distinct geographical regions: South-East of the Himalayas and the African continents. From these regions, the South-East of Himalayas forms part of the Asian group with chromosome x=7 to which cucumber belongs. There is evidence that cucumbers have been domesticated for 3000 years in India, and probably for 2000 years in eastern Iran and China. (Tyagi 2020). It has been evolved from the wild progenitor *Cucumis hardwickii* in Indo-Chinese region [1-4]. It had spread eastwards to China and westward to Asia Minor, North Africa and Southern Europe from India [5]. Immature cucumber fruits can be either consumed as raw or in the form of pickle. It is considered as low energy and high water content vegetable. In addition to its cooling properties, immature fruits are considered useful for people suffering from constipation, jaundice, and indigestion. It contains 96.3 g moisture, 0.4 g protein, 0.1 g fat, 0.4 g fibre, 2.5 g carbohydrates, 13 kcal, 10 mg calcium, 25 mg phosphorus, 1.5 mg iron, thiamine 0.03 mg and 0.2 mg vitamin C per 100 grams of edible part [6]. In Himachal Pradesh, cucumber is commercially grown from March-May which makes the fruits readily available to the consumers from June-October, when there is non-availability of fruits in plains. The farmers get high remunerative prices for the produce as it is cultivated as an offseason vegetable crop in the mid hills of Himachal Pradesh.

Existence of genetic diversity is important for any effective crop improvement programme. Genetic divergence studies helps to know the adaptability of different varieties in a particular agro-climatic condition. It also plays a crucial role in determining the potential for future yield improvement. To initiate any crop improvement program, it is essential to have variation in the existing germplasm. Selection, which is a fundamental and traditional method, is effective for improving traits influenced by additive and additive × additive gene actions. However, for traits influenced by non-additive gene actions that do not respond well to selection, it becomes necessary to partition the non-additive component of genetic variance into additive and non-additive variances through hybridization or crossing of parents with desirable attributes Rao [7] This can be achieved through genetic divergence studies. Mahalanobis D^2 multivariate analysis (Mahalanobis 1936) is a valuable tool for quantitatively estimating the genetic divergence between different population [7]. It helps to identify suitable genotypes for utilization in hybridization programs. Additionally, grouping of genotypes based on Tocher's method can be particularly useful in selecting reliable parents for obtaining superior segregants.

2. MATERIALS AND METHODS

The current study was carried out to evaluate thirty- two genotypes of cucumber along with Solan Srijan, as a standard check variety for yield and various yield attributing traits at the Horticultural Research & Training Station and Krishi Vigyan Kendra, Kandaghat, Dr YS Parmar University of Horticulture and Forestry, District-Solan, Himachal Pradesh, India during Kharif season of 2022. The experiment was planted in a Randomized Complete Block Design (RCBD) with three replications and various traits were examined *viz*., days taken to first female flower appearance, node number bearing first female flower, days to marketable maturity, number of primary branches per plant, fruit length (cm), fruit breadth (cm), average fruit weight (g), number of marketable fruits per plant, harvest duration (days), vine length (cm), hundred seed weight (g), total soluble solids (°B), ascorbic acid content (mg/100g), severity of downy mildew (%) and marketable fruit yield per plant (kg) & per hectare (ha).

Genetic divergence (D^2 analysis): The genetic divergence in cucumber was estimated by Mahalanobis D^2 statistics as suggested by Rao [7]. The calculation of D^2 analysis involved following steps:

i) A set of uncorrelated linear combination linear (y's) was obtained by pivotal condensation of the common dispersion matrix Rao [7] of the set of correlated variable (x's).
ii) Using the relationship between y's and x's the mean value of different genotypes for

different characters (x_1 to x_{15}) were transformed into the mean values of an uncorrelated linear combination (y_1 to y_{15}).

iii) The D^2 values between i^{th} and j^{th} genotype for K characters were calculated as:

$$D^2 ij = \sum_{i=1}^{k} (yit - yjt)^2$$

Where,
yit is uncorrelated mean value of i^{th} genotype for 't' characters
yjt is uncorrelated mean value of j^{th} genotype for 't' characters
D^2ij is D^2 between i^{th} and j^{th} accessions

Group constellation: Treating D^2 as the generalized statistical distance between a pair of populations (genotypes), all populations were grouped into number of clusters according to method described by Rao [7]. TNAU STAT software was used to calculate the gentic diversiy under this experiment.

The criterion used in clustering by this method was that, any two genotypes belonging to the same cluster, at least on an average, show a small D^2 value than those belonging to two different clusters. In other words, if genotypes V_1 and V_2 are close together and genotypes V_3 is distant from both as shown by their generalized distance then V_1 and V_2 will be grouped, in same the cluster.

Intra and inter cluster genetic distances: Intra and inter cluster genetic distances (d) where computed square root of average intra and inter cluster D^2 values *i.e.* $d = \sqrt{D^2}$.

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

Sr.No.	Genotype	Source
1.	Bajrol Collection	Village-Bajrol, Block-Solan
2.	CH-2	SKUAST, Jammu
3.	CH-3	SKUAST, Jammu
4.	Dyarag Bukhar Collection	Village-Dyarag Bukhar, Block-Solan
5.	FAM-2	SKUAST, Jammu
6.	Grani Collection	Village-Grani, Block-Solan
7.	Green Express	SKUAST, Jammu
8.	Him Palam Kheera-1	CSKHPAU, Palampur
9.	Jagdamba	NDUAT, Faizabad
10.	Jokhri Collection	Village-Jokhri, Block-Solan
11.	Kheera Prasad-37	NDUAT, Faizabad
12.	Kheera Prasad-44	NDUAT, Faizabad
13.	Kothi Deora Collection	Village-Kothi Deora, Block-Solan
14.	Kothon Collection	Village-Kothon, Block-Solan
15.	Mahatama Kheera-40	NDUAT, Faizabad
16.	Mansar Collection	Village-Mansar, Block-Solan
17.	NDUAT-2	NDUAT, Faizabad
18.	Nirmala Collection	Village-Dedgharat, Block-Kandaghat
19.	PKH-11	PAU, Ludhiana
20.	PKH-12	PAU, Ludhiana
21.	Pusa Barkha	IARI, New Delhi
22.	Rano Collection	Village-Rano, Block-Solan
23.	S-30	SKUAST, Jammu
24.	S-3-A	SKUAST, Jammu
25.	Sadanand Collection	Village-Rahon, Block-Solan
26.	Sel-3A	SKUAST, Jammu
27.	Shunnu Collection	Village-Shunnu, Block-Solan
28.	Summer Special-33	SKUAST, Jammu
29.	Swaran IIVR	IIVR, Varanasi
30.	Ujawala Summer Long-45	NDUAT, Faizabad
31.	K-75	Department of Vegetable Science,UHF, Nauni
32.	Solan Srijan (Check)	Department of Vegetable Science,UHF, Nauni

3. RESULTS AND DISCUSSION

Significant variations among genotypes were obtained through the analysis of variance for the fifteen parameters studied. The clustering pattern of the thirty-two genotypes based on genetic divergence is presented in Table 2. By calculating D^2 values for all possible combinations of genotypes, thirty-two cucumber genotypes were classified into five distinct clusters, indicating a wide diversity among the parents [8]. The largest cluster, Cluster-I, consisted of 14 genotypes (CH-2, CH-3, S-3-A, PKH-11, PKH-12, Jagdamba, Kheera Prasad-44, Mahatama Kheera-40, Him Palam Kheera-1, Mansar Collection, Nirmala Collection, Rano Collection, Shunnu Collection and K-75). Cluster-III comprised of eight genotypes (Green Express, Summer Special-33, Swaran IIVR, Kheera Prasad-37, Pusa Barkha, Dyarag Bukhar Collection, Jokhri Collection and Sadanand Collection), while Cluster-IV included five genotypes (S-30, Sel-3A, Grani Collection, Kothi Deora Collection and Solan Srijan). Cluster-II consisted of four genotypes (FAM-2, Ujawala Summer Long-45, Bajrol Collection and Kothon Collection), while Cluster-V consisted of one genotype (NDUAT-2). The majority of genotypes were distributed among Clusters I followed by Clusters III, IV, II and V. Similar findings were obtained by Hossain et al. [9], Manohar and Murthy [10], Kumar et al. [11], Kumawat et al. [12] and Thapa [13] who also observed genetic diversity in cucumber based on D^2 analysis and classified the germplasm into different clusters.

The practical significance of grouping cucumber genotypes into clusters and estimating intra and inter- cluster distances among them, lies in providing an index of genetic diversity among the clusters. The average distances within and between clusters are provided in Table 3. The values on the diagonal of the table indicate the distances within each cluster. The intra cluster distance ranged from 0 (cluster V) to 15.73 (cluster II). The inter cluster distance was highest (30.00) between cluster II and IV, and lowest (18.06) between cluster I and V. Genotypes belonging to the same cluster show minimal variation in the measured traits. It is theoretically not expected to obtain superior hybrids or segregants by crossing genotypes from the same cluster. However, there is a general understanding that greater divergence between genotypes is associated with higher levels of heterosis. Cluster II (15.73) recorded the highest average intra-cluster distance, followed by cluster III and cluster IV (15.55), while cluster I (15.06) observed the lowest intra-cluster distance. Therefore, it would be advantageous to carry out crosses between genotypes from distant clusters in order to obtain highly heterotic crosses.

Table 2. Clustering pattern of thirty-two cucumber genotypes on the basis of genetic divergence

Cluster	Number of Genotypes	List of genotypes
I	**14**	CH-2, CH-3, S-3-A, PKH-11, PKH-12, Jagdamba, Kheera Prasad-44, Mahatama Kheera-40, Him Palam Kheera-1, Mansar Collection, Nirmala Collection, Rano Collection, Shunnu Collection, K-75
II	**4**	FAM-2, Ujawala Summer Long-45, Bajrol Collection, Kothon Collection
III	**8**	Green Express, Summer Special-33, Swaran IIVR, Kheera Prasad-37, Pusa Barkha, Dyarag Bukhar Collection, Jokhri Collection, Sadanand Collection
IV	**5**	S-30, Sel-3A, Grani Collection, Kothi Deora Collection, Solan Srijan
V	**1**	NDUAT-2

Table 3. Average intra (Diagonal) and inter-cluster (Lower half Diagonal) distance

Cluster	I	II	III	IV	V
I	**15.06**				
II	21.66	**15.73**			
III	21.65	21.10	**15.55**		
IV	20.90	30.00	20.14	**15.55**	
V	18.06	27.32	19.97	19.97	**0**

Table 4. Cluster means for different characters among thirty-two genotypes of cucumber

Characters	I	II	III	IV	V
Days taken to first female flower appearance	53.43	51.83	50.83	43.87	50.00
Node number bearing first female flower	5.62	9.03	5.52	3.10	3.49
Days to marketable maturity	61.69	60.58	58.92	50.33	56.33
Number of primary branches per plant	3.46	3.65	3.21	4.78	4.96
Fruit length (cm)	17.02	16.74	15.48	20.20	17.62
Fruit breadth (cm)	4.62	4.40	4.61	5.21	5.14
Fruit weight (g)	255.00	254.17	235.93	295.22	256.16
Number of marketable fruits per plant	6.93	5.98	8.61	10.47	7.18
Harvest duration (days)	21.00	18.67	21.21	30.60	21.67
Vine length (m)	275.79	280.73	300.80	337.16	317.74
Hundred seed weight (g)	2.18	1.12	1.79	2.54	2.37
TSS (^{o} B)	2.28	1.73	1.93	3.09	2.75
Ascorbic acid content (mg/100g)	2.89	2.73	2.90	3.95	3.28
Marketable fruit yield per plant (kg)	1.91	1.86	1.80	2.75	2.36

The largest inter-cluster distance was found between cluster II and IV, followed by cluster II and V. Crosses between parents from clusters with significant inter-cluster distances are expected to generate desirable recombinants in subsequent generations, which can be further developed into conventional homozygous varieties. The smallest inter-cluster distance was observed between clusters I and V. These findings indicate that genotypes from distant clusters possess a significant level of diversity. The hybridization of genotypes possessing a wide genetic base is expected to lead the highest level of heterotic performance and ultimately will yield desirable transgressive recombinants. This is because a broad genetic base is essential for the success of any crop improvement program.

In Table 4 average values of different traits for each cluster have been presented. Among the five clusters, cluster IV showed highest mean values for various characters namely, fruit length (20.20 cm), fruit breadth (5.21 cm), fruit weight (295.22 g), number of marketable fruits per plant (10.47), harvest duration (30.60 days), vine length (337.16 cm), hundred seed weight (2.54 g), total soluble solids (3.09 °B), ascorbic acid content (3.95 mg/100g) and marketable fruit yield per plant (2.75 kg). On the other hand, cluster I exhibited higher mean values for days taken to first female flower appearance (53.43) and days to marketable maturity (61.69). Cluster II observed the maximum value for node number bearing first female flower (9.03), while cluster V showed higher mean values for number of primary branches per plant (4.96). Clusters III did not show superior values for any character. Hybridization programs involving genotypes with a broad genetic base and desirable traits can result in the production of superior segregants for various traits, including yield. Cluster IV recorded the lowest mean for days taken to first female flower appearance (43.87), followed by cluster V (50.00), cluster III (50.83), cluster II (51.83) and cluster I (53.43). For the character, node number bearing first female minimum mean value was observed in cluster IV (3.10) followed by cluster V (3.49), cluster III (5.52), cluster I (5.62) and cluster II (9.03). Cluster IV had the lowest mean for the days to marketable maturity (50.33), followed by cluster V (56.33), cluster III (58.92), cluster II (60.58) and cluster I (61.69). With regard to, number of primary branches per plant maximum mean value was reported for cluster V (4.96), followed by cluster IV (4.78), cluster II (3.65), cluster I (3.46) and cluster III (3.21). Maximum fruit length was shown for cluster IV (20.20) followed by cluster V (17.62), cluster I (17.02), cluster II (16.74) and cluster III (15.48), whereas fruit breadth was recorded highest in cluster IV (5.21) followed by cluster V (5.14), cluster I (4.62), cluster III (4.61) and cluster II (4.40). In respect of maximum fruit weight, cluster IV (295.22) observed highest value followed by cluster V (256.16), cluster I (255.00), cluster II (254.17) and cluster III (235.93). For number of marketable fruits per plant maximum mean was inscribed in cluster IV (10.47), followed by cluster III (8.61), cluster V (7.18), cluster I (6.93) and cluster II (5.98). Harvest duration marked with maximum in cluster IV (30.60) was followed by cluster V (21.67), cluster III (21.21), cluster I (21.00) and cluster II (18.67). For vine length higher mean was observed for cluster IV (337.16), followed by cluster V (317.74), cluster III (300.80), cluster II (280.73)

and cluster I (275.79). Highest total soluble solids was recorded in cluster IV (3.09) followed by cluster V (2.75), cluster I (2.28), cluster III (1.93) and cluster II (1.73), whereas highest ascorbic acid content was observed in cluster IV (3.95), followed by cluster V (3.28), cluster III (2.90), cluster I (2.89) and cluster II (2.79). Maximum hundred seed weight mean value showed in cluster IV (2.54) followed by cluster V (2.37), cluster I (2.18), cluster III (1.79) and cluster II (1.12). Maximum yield per plant was recorded in cluster IV (2.75) followed by cluster V (2.36), cluster I (1.91), cluster II (1.86) and cluster III (1.80). Previous studies by Manohar and Murthy [10], Kumar et al. [11], Hasan et al. [14], Sharma et al. [15], Patil et al. [16] and Thappa [13] had also highlighted the importance of genetic divergence in cucumber.

For the improvement of various horticultural traits in cucumber, it would be better to carry out hybridization between genotypes from cluster IV (S-30, Sel-3A, Grani Collection, Kothi Deora Collection and Solan Srijan) and cluster II (FAM-2, Ujawala Summer Long-45, Bajrol Collection and Kothon Collection) in order to obtain better recombinants.Genetically diverse parents are likely to produce high heterotic effects and the distantly related parents with in the same species when utilized in cross breeding programme are likely to produce a wide spectrum of variability [17].

Considering the significance of this crop, there is a need to enhance and develop varieties that are well-suited to specific agro-ecological conditions. Selection, which is a fundamental and traditional method, is effective for improving traits influenced by additive and additive × additive gene actions. However, for traits influenced by non-additive gene actions that do not respond well to selection, it becomes necessary to partition the non-additive component of genetic variance into additive and non-additive variances through hybridization or crossing of parents with desirable attributes. This can be achieved through genetic divergence studies Exploring genetic diversity helps to develop new cultivars with improved traits such as disease resistance, yield, flavor, and nutritional content. Additionally, studying environmental factors and their impact on cucumber variability could lead to more resilient varieties adapted to changing climate conditions. Furthermore, investigating the potential health benefits of specific cucumber varieties could provide insights into their medicinal properties and nutritional value.

4. CONCLUSION

For traits where direct selection is not feasible, hybridization between genetically diverse parents based on their mean performance becomes necessary to obtain superior hybrids or transgressive segregants with a wide range of traits. Studies on genetic divergence play a crucial role in this context. The genetic divergence analysis in this study categorized the thirty-two genotypes into five clusters. Among these clusters, hybridization between cluster II and IV is expected to yield favorable results in terms of obtaining superior recombinants or segregants for improving traits such as days taken to first female flower appearance, node number bearing first female flower, days to marketable maturity, fruit weight, number of marketable fruits per plant, and marketable fruit yield per plant.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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