

Studies on Genetic Divergence in Cucumber (*Cucumis sativus* L.) under Subtropical Conditions of Garhwal Himalaya

K.N. Shah¹, D.K. Rana² and Vivek Singh³

¹ Department of Horticulture, H.N.B. Garhwal University, Srinagar (Garhwal), Uttarakhand, India, 246174.

Abstract

A study was conducted during *zaid* season 2015, at Horticultural Research Centre, Department of Horticulture, H.N.B. Garhwal University, Srinagar (Garhwal), Uttarakhand, to evaluate the nature and magnitude of genetic divergence in 13 cucumber genotypes. The results revealed that there is a wide genetic diversity among the 13 genotypes of cucumber. The genotypes were grouped into 4 clusters based on Mahalanobis D^2 statistics using Tocher's method. The clustering pattern of genotypes revealed that among the 4 clusters, maximum numbers of genotypes were found in cluster I and III which comprises 5 genotypes each, while cluster IV was found to be mono-genotypic. Intra clusters distance was highest in II (70.365), while lowest in cluster I (49.748). The inter cluster D^2 values were maximum between cluster II and IV (93.131), whereas, minimum distance observed between cluster I and II (66.512) cluster III was the most diverse as many clusters showed high inter cluster distances with it. From the present studies, cluster I secured first rank which observed maximum mean value for 11 characters followed by clusters II, indicating presence of most promising genotypes in them and these can be extensively used for further breeding programmes to generate new material.

Key words: Cucumber, Genetic, Genotype, Divergence, Mahalanobis and Cluster.

1. Introduction

Cucumber (*Cucumis sativus* L.) is one of the most important cucurbitaceous vegetables grown throughout the world in tropical and sub-tropical climatic conditions. It is an ideal summer vegetable crop chiefly grown for its edible tender fruits, preferred as a salad ingredient, pickles and as a cooked vegetable. The genetic improvement in yield of any crop is possible only if enough genetic diversity exists. Genetic diversity studies are being conducted in various crops to access suitability of different varieties in specific agro-climatic

conditions (Chadha and Bhushan 2013, Mishra *et al.* 2013 and Rawat *et al.* 2014). The concept of D^2 as measures of divergence was first introduced by Mahalanobis (1928). Mahalanobis D^2 statistic has been widely used to determine the extent of genetic diversity in the material irrespective of the number of populations. The uses of Mahalanobis D^2 statistic for estimating genetic divergence have been emphasized by Chohata *et al.* (1994) because it permits precise comparison among all the possible pair of populations in any group before effecting actual crosses. For the selection of parents for hybridization, genetic divergence among the population is necessary for heterotic effect. Keeping above points in view, 13 genotypes were evaluated for the study of genetic divergence in cucumber.

2. Materials and Methods

The experiment was conducted during *zaid* season, 2015 at Horticultural Research Centre, Department of Horticulture, HNB Garhwal University, Srinagar (Garhwal), Uttarakhand, India. Srinagar (Garhwal) is located in Alaknanda valley (30° 12' 0" to 30° 13' 4" latitude North and 78° 0' 45" to 78° 0' 50" East longitude and 540 m above MSL). This region exhibits a semi-arid, subtropical climate with dry summer and rigorous winter with occasional dense fog in the morning up to 10 am from January to mid-March and June to mid-August. The materials for the present investigation consist of 13 genotypes *viz.*, GP-1, HP-1, HP-2, K-90, Mandal, New Manipur-1, New Manipur-2, PB- Naveen, RAJ-1, RAJ-2, Seven Star, SPP-63 and Swarna Purna collected from different region of India. The experiment was laid out in Randomized Block Design with three replications. The whole area of experimental site was divided into three blocks of equal size and each block possessed 13 plots. Each plot measured 4.50 × 2.0 m² area. The seedling were transplanting at four leaf stage *i.e.*, 25-30 days after sowing. Transplanting of seedlings was done in evening hours in each experimental plot at the

spacing of 1.50 x 0.50 cm. After transplanting, a light irrigation was given for the proper establishment of the seedlings. All the cultural activities and plant protection measures recommended for the successful crop. Five plants were randomly selected from each plot per replication for recording the data on the following observations *viz.*, days to first seed germination, days to 50 % seed germination, length of vine (cm), diameter of vine (mm), number of primary branches/vine, number of nodes/vine, days taken to opening of first male flower, number of nodes bearing first male flower, days taken to opening of first female flower, number of nodes bearing first female flower, percent of fruit setting, days to first fruit harvest, number of fruits/ vine, length of fruit (cm), diameter of fruit (cm), average weight of fruit (g), fruit yield/vine (kg), number of locules/vine, duration of harvesting (days), carbohydrate (g/100g), protein (g/100g), vitamin C (mg/100g), TSS (°Brix), calcium (mg/100g) and phosphorus (mg/100g). The data obtained from selected plants under each treatment were subjected for statistical analysis. The genetic divergence analysis was carried out by using the method given by Mahalanobis (1936), clustering of genotypes by Rao (1952) and inter and intra clustering by Singh and Choudhary (1977).

3. Results and discussion

The analysis of variance revealed substantial amount of variability for the 25 traits studied signifying sufficient scope to identify desirable genotypes. Based on the relative magnitude of D^2 values 13 genotypes were grouped into 4 different clusters (Table 1 and Fig. 1).

Table 1. Cluster composition of 13 varieties of cucumber

Cluster	Number of genotype	Genotypes
I	5	K-90, SPP-63, PB-Naveen, Seven Star and HP-2
II	2	Mandal and RAJ-1
III	5	Swarna Purna, New Manipur, New Manipur-1, New Manipur-2, HP-1 and GP-1
IV	1	RAJ-2

The clustering pattern of genotypes revealed that among the 4 clusters, maximum numbers of genotypes were found in cluster I (K-90, SPP-63, PB-Naveen, Seven Star and HP-2) and III (Swarna Purna, New Manipur-1, New Manipur-2, HP-1 and GP-1) which comprises 5 genotypes each. The

cluster II includes two genotypes namely Mandal and RAJ-1, while cluster IV (RAJ-2) was found to be mono-genotypic. The resultant three clusters showed considerable genetic diversity. Genotypes from different geographical regions were grouped in same cluster indicating no relationship between geographical 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) in cucumber, Khan (2006) and Kabir *et al.* (2009) in pointed gourd.

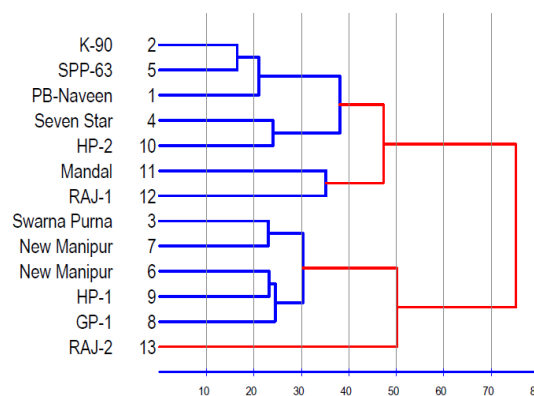


Fig 1. Dendrogram showing clustering by Tocher's Methods

The intra and inter cluster D^2 values are given in Table 2 and Fig. 2. Intra clusters distance was highest in cluster II (70.365) followed by cluster III (50.397) and lowest in cluster I (49.748). The clusters IV had no intra cluster distance (zero) as they are represented by single genotypes.

Table 2. Average intra and inter cluster D^2 values.

Cluster	I	II	III	IV
I	49.748	70.574	66.512	89.602
II		70.365	82.804	93.131
III			50.397	80.258
IV				0.000

The inter cluster D^2 values were maximum between cluster II and IV (93.131). The minimum distance observed between cluster I and II (66.512) that indicates the less diversity between them. Cluster III was the most diverse as many clusters showed high inter cluster distances with it. Therefore, the genotypes falling in these clusters were genetically more divergent. Inter-crossing the genotypes from this cluster may generate wider variability and is expected to throw high yielding transgressive

segregants in a population improvement programme.

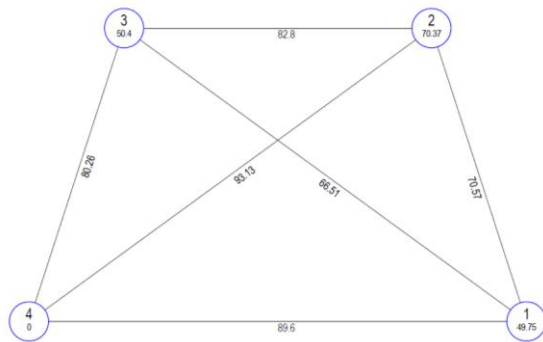


Fig. 2: Mahalanobis D² distances in cucumber

Character wise mean were calculated for all the genotypes spread over four clusters and rank was assigned based on individual score (Table 3). The best cluster mean was given as first rank and the clusters that followed were given 2nd, 3rd and 4th for all the characters. From the present studies, cluster I secured first rank which observed maximum mean value for 11 characters followed by clusters II, indicating presence of most promising genotypes in them and these can be extensively used for further breeding programmes to generate new material. These results are in agreement with the result of **Kumar et. al. (2013)** in cucumber.

4. Conclusion

On the basis of obtained results, it can be concluded that more importance should be given to improve number of nodes per vine, vine length, number of primary branches, early flowering and fruiting and number of fruit per vine while selection of high yielding genotypes in cucumber. Therefore, the genotypes falling in clusters III were genetically more divergent. Inter-crossing the genotypes from this cluster may generate wider variability and is expected to throw high yielding transgressive segregants in a population improvement programme.

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Table 3. Cluster mean for 25 parameters in cucumber

Cluster		1st Seed Germination	50% Seed Germination	Length of vine (cm)	Diameter of vine (cm)	No. of primary branches/ Vine	No. of nodes/ vine	Days taken to opening 1st male flower	No. nodes bearing 1st male flower	Days taken to opening 1st female flower	No. nodes bearing 1st female flower	% of fruit setting	Days to 1st fruit harvest
I	Mean	6.60	7.93	217.23	7.10	6.86	24.92	33.26	3.38	35.13	4.81	90.89	50.86
	Rank	1	1	1	4	3	1	4	4	4	4	3	4
II	Mean	5.83	7.66	197.40	8.47	7.63	21.86	35.76	4.59	37.61	5.94	92.25	51.69
	Rank	4	2	2	1	1	3	3	2	3	2	2	3
III	Mean	6.26	7.93	189.78	7.65	6.62	23.54	36.10	4.16	38.54	5.68	89.39	53.88
	Rank	3	1	3	3	4	2	2	3	2	3	4	2
IV	Mean	6.33	7.66	155.03	7.91	7.52	16.99	40.73	6.84	43.37	8.87	92.36	54.39
	Rank	2	2	4	2	2	4	1	1	1	1	1	1

Table 3. Cluster mean for 25 parameters in cucumber

Cluster		No. of fruits/ vine	Fruit yield/ vine (kg)	Length of Fruit (cm)	Weight of Fruit (g)	Diameter of Fruit (cm)	No. of Locules/ fruit	Duration of Harvesting	Carbohydrate (g/100g)	Protein (g/100g)	Vitamin C (mg/100g)	TSS (°Brix)	Calcium (mg/100g)	Phosphorus (mg/100g)	Overall Score	Rank
I	Mean	14.18	2.35	22.99	169.26	3.66	3.46	64.87	2.41	0.36	6.72	4.71	9.43	23.51	87	3
	Rank	3	3	1	2	3	3	1	3	1	3	2	3	2		
II	Mean	20.55	2.57	20.08	125.25	3.81	3.33	64.25	2.48	0.35	7.27	4.05	8.65	24.28	77	1
	Rank	1	2	3	4	2	4	2	1	2	1	4	4	1		
III	Mean	12.54	1.94	16.33	157.06	4.12	3.53	62.01	2.29	0.32	6.83	4.97	10.64	21.54	96	4
	Rank	4	4	4	3	1	2	3	4	3	2	1	1	3		
IV	Mean	14.87	3.01	21.54	203.37	2.70	4.00	61.52	2.47	0.29	6.51	4.60	10.41	20.49	80	2
	Rank	2	1	2	1	4	1	4	2	4	4	3	2	4		