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Research Article

Assessment of Genetic Variation in Cucumber (*Cucumis sativus* L.) Germplasm on Correlation, Path analysis and Cluster Analysis

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Abstract

In this research, 44 genotypes with two checks Pant Khira-1 and Pointsette of cucumber (*Cucumis sativus* L.) were studied that were collected from different geographical regions. The experiment was conducted as a randomized block design (RBD) with three replications in open field condition. Average distance of inter and intra centroids cluster analysis was done to study the divergence in genotypes including checks in respect of various economic traits. The genotypes were grouped into seven non overlapping clusters. The averages inter and intra cluster distances have been presented. The distribution patterns of genotypes of cucumber into seven clusters have been analyzed. Data was collected on morphological features, yield and components of yield of cucumber which include: days to first male flowers, node number to first male flower, days to first female flowers, node number to first female flower, internodal length, days to first fruit harvest, number of fruits per plant, fruit length, fruit diameter, fruit weight, test weight, seed index, primary branches per plant, plant height and yield. The genotypic coefficients were higher in the magnitudes relative to corresponding estimates of phenotypic coefficients, which indicated high heritability of the traits under study. Number of fruits per plant (0.860**) showed positive significant correlation with yield in highly significant positive correlation, the values of direct and indirect contribution of different traits toward yield revealed the maximum direct effect of number of fruits per plant (0.837) and maximum positive indirect effect of number of fruits per plant (0.110). Therefore, Selection of superior genotypes in view point of desirable morphologic traits, with high genetic distance could be selected for hybridization programs and recognition of best genotypes for different traits to produce new elite hybrids in cucumber.

Keywords: Cucumber (*Cucumis sativus* L.), Correlation, Path analysis cluster analysis & inter and intra centroids

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Introduction

Cucumber (*Cucumis sativus* L.) is an important member of the family cucurbitaceous. The crop is of India origin, the progenitor may be closely related to the wild *Cucumis sativus* L. var. *hardwickii*, which was found in the Himalayan foothills of Nepal. Cucumber cultivation goes back to at least 3000 years in India and 2000 years in china [1]. Today cucumber is grown throughout the world in small gardens, large commercial farms and glass houses. The fruits are eaten as salad and pickle and are often consumed as cooked vegetables in various ways. It contains 0.6 g protein, 2.6 g carbohydrate, energy 12 cal, 18 mg Ca, 0.2 mg Fe, 0.02 mg thiamin, 0.02 mg riboflavin, 0.01 mg niacin, and 10 mg vitamin C per 100 g of edible portion. Very few research works relating to variability of cucumber have been conducted in India. So, intensive research efforts are needed in several areas, particularly, selection of superior genotypes. There are a lot of variability's among the existing cucumber germplasm of India [2]. An understanding of the nature and magnitude of the variability among the genetic stocks of cucumber is of prime importance for the breeder. A good knowledge of genetic wealth might also help in identifying desirable cultivars for commercial production. Because of its nature of high cross pollination, hardly any genetically pure strain is available to the growers. Estimation of genetic diversity is considered as an important factor, which is also essential prerequisite for hybridization programme for developing high yielding variety. Based on the information, the present study was undertaken to assess the variability for yield and yield attributes in cucumber.

Materials and Methods

The present investigation was conducted with average two season during July-October, 2014 and February-June, 2015 at Vegetable Research Centre, Department of Vegetable Science in G.B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand. Pantnagar is situated in the foot hills of Himalayan region (Shivalik hills) and falls under humid subtropical climate zone in narrow belt called Tarai. Geographically, Vegetable Research Centre is situated at the latitude of 29.5^{0}N, longitude 79.3^0 E and at an altitude of 243.84 meters above the mean sea level. Total 46 genotypes of cucumber (*Cucumis sativus* L.) were used as experimental material in present experiment. The genotypes were diverse with respect to morphological and important economical traits. The experiment was laid out in randomized block design with three replications. Healthy and uniform sowing of seeds was main field in plots with a spacing of 3 meters × 0.60 cm during the evening hours of during July-October, 2014 and February-June, 2015. The crops were grown with standard package of practices. The observations on various growth, yield and qualitative characters viz. observed highly significant differences for all the traits under study.

Results and Discussion

Analysis of correlation coefficient:

The results of phenotypic correlation coefficient between different characters have been presented in **Table 1**.

Table 1 Phenotypic correlation coefficient between different characters

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	**1.000**	0.081	0.437**	-0.149	0.047	-0.072	-0.012	-0.010	0.214	-0.205	0.006	0.022	0.094	-0.109	-0.101
2		**1.000**	-0.110	0.128	0.023	-0.007	-0.068	-0.053	0.014	0.069	0.054	-0.059	-0.031	-0.006	-0.030
3			**1.000**	0.006	-0.129	-0.016	0.062	-0.061	0.108	-0.112	-0.079	0.071	0.017	-0.077	-0.000
4				**1.000**	-0.053	0.010	0.014	0.119	0.099	0.000	-0.040	0.166	0.061	0.106	0.010
5					**1.000**	0.088	0.180	-0.001	-0.076	0.265*	0.200	-0.014	-0.023	-0.053	-0.289*
6						**1.000**	0.258*	0.122	-0.072	0.076	0.299*	0.004	-0.087	0.126	-0.199
7							**1.000**	0.012	0.131	0.033	-0.188	0.008	-0.038	-0.033	0.860**
8								**1.000**	-0.017	0.024	0.089	0.172	-0.105	-0.021	0.028
9									**1.000**	-0.128	-0.014	-0.015	-0.099	0.015	0.056
10										**1.000**	-0.071	-0.106	-0.104	0.003	0.517**
11											**1.000**	-0.020	0.033	0.025	-0.187
12												**1.000**	-0.008	0.100	-0.047
13													**1.000**	0.009	-0.084
14														**1.000**	-0.020
15															**1.000**

1=Days to first male flowers, 2=Node number to first male flower, 3=Days to first female flowers, 4=Node number to first female flower, 5=Internodal length (cm), 6=Days to first fruit harvest, 7=No. of fruits per plant. 8= Fruit length (cm), 9= Fruit diameter (cm), 10= Fruit weight (g), 11= Test weight (gm.), 12= Seed Index (gm.), 13= Primary branches/ Plant, 14= Plant height (met.), 15= Yield (Q/ha)
**= Significant at 1% level of significance
*= Significant at 5% level of significance

Days to first male flowers showed positive significant correlation with days to first female flowers (0.437**) in highly significant positive correlation. In the analysis days to first male flowers, numbers of fruits per plant and fruit weight correlation with showed highly significant and positive days to first female flowers, number of fruits per plant and yield (0.437**), (0.860**) and (0.517**) respectively. Node number to first male flower showed positive correlation with traits node number to first female flower (0.128), internodal length (0.023), fruit diameter (0.014), fruit weight (0.069), test weight (0.054), However negative correlation days to first female flowers (-0.110), days to first fruit harvest (-0.007), number of fruits per plant (-0.068), fruit length (-0.053), seed Index (-0.059),primary branches per plant (-0.031), plant height (-0.006) and yield (-0.030) in analysis. The positive correlation in analysis with node number to first female flower (0.006), number of fruit of per plant (0.062), fruit diameter (0.108), seed Index (0.071) and primary branches per plant (0.017) with negative correlation in the traits at internodal length (-0.129), days to first fruit harvest (-0.016), fruit length (-0.061), fruit weight (-0.112), test weight (-0.079), plant height (-0.017) and yield (-0.000). With positive correlation days to first fruit harvest (0.010), number of fruit per plant (0.014), fruit length (0.119), fruit diameter (0.099), fruit weight (0.000), seed Index (0.166), primary branches per plant (0.061), plant height (0.106), and yield (0.010) and with the negative correlation internodal length (-0.053) and test weight (-0.040). The data with positive correlation days to first fruit harvest (0.088), number of fruits per plant (0.180), fruit weight (0.265*), teat weight (0.200) with negative correlation fruit length (-0.001), fruit diameter (-0.076), seed index (-0.014), primary branches per plant (-0.023), plant height (-0.053) and yield (-0.289) with significant correlation with (0.258*) and test weight (0.299*) and showed positive correlation with non-significant with the traits in fruit length (0.122), fruit weight (0.076), test weight (0.299*), seed Index (0.004) plant height (0.126) with negate correlation fruit diameter (-0.072), primary branches per plant (-0.087) and yield (-0.199). However in pooled data this trait showed highly significant correlation with yield (0.860**) and positive correlation but non-significant with fruit length (0.012), fruit diameter (0.131), fruit weight (0.033), seed Index (0.008) and negative correlation with the test weight (-0188), primary branches (-0.038) and plant height (-0.033) and data it showed positive correlation with fruit weight (0.024), test weight (0.089), seed index (0.172), yield (0.028) and negative correlation with the traits i.e. fruit diameter (-0.017), primary branches per plant (-0.105) and plant height (-0.021). With positive correlation with plant height (0.015) and yield (0.056) with the negative correlation fruit weight (-0.128), test weight (-0.014), seed Index (-0.015) and primary branches per plant (-0.099) and data it showed highly significant correlation with yield (0.517**), positive correlation with plant height (0.003) and the negative correlation with test weight (-0.071), seed Index (-0.106), primary branches per plant (-0.104) and however data with showed positive correlation but non-significant with primary branches (0.033), plant height (0.025), yield (0.187) and negative correlation with seed index (-0.020).

Significant correlation was observation for total yield with days to first female flowers and node number to first female flower. Similar result was also observed in Bitter guard [3] and [8]. Main vine length showed/plant height showed positive and significant correlation. Similar results were also reported [10].

Days to first male flowers showed significant and positive correlation with Days to first female flowers [9] also observed highly significant and positive correlation between No. of fruits per plant and Yield (q/ha). Similar finding was also observed [4] and [11] for Days to first fruit harvest significant positive correlation was observed with Fruit diameter, Test weight and yield. If fruit weight is larger will also increase which ultimately increases the yield [5].

Path coefficient analysis

Path coefficient analysis is a mean of partitioning correlation coefficient in to direct and indirect effects of various characters. It gives idea about the contribution of each independent character on dependent character i.e. yield. Path analysis forces researchers to explicitly specify how the variable relates to one another and thus encourages the development of clear and logical theories about the process influencing a particular outcome [13]. The results of path analysis have been presented in **Table 2**.

Table 2 Path coefficient analysis for different characters on yield

	X_1	**X_2**	**X_3**	**X_4**	**X_5**	**X_6**	**X_7**	**X_8**	**X_9**	**X_{10}**	**X_{11}**	**X_{12}**	**X_{13}**	**X_{14}**
X_1	**0.010**	0.000	0.004	-0.001	0.000	-0.000	-0.000	-0.000	0.002	-0.002	0.000	0.002	0.001	-0.001
X_2	-0.000	**-0.009**	0.001	-0.001	-0.000	0.000	0.000	0.000	-0.000	-0.000	-0.000	0.006	0.000	0.000
X_3	-0.001	0.000	**-0.002**	0.000	0.000	0.000	-0.000	0.000	-0.000	0.000	0.000	-0.002	0.000	0.000
X_4	-0.000	0.000	0.000	**0.000**	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000
X_5	-0.000	-0.000	0.001	0.000	**-0.007**	-0.000	0.001	0.000	0.000	0.002	-0.001	0.000	0.002	0.000
X_6	0.001	0.000	0.000	-0.000	-0.002	**-0.024**	0.006	-0.003	0.001	-0.001	-0.007	-0.000	0.002	-0.003
X_7	-0.010	-0.057	0.052	0.011	-0.151	-0.216	**0.837**	0.010	0.110	0.028	-0.157	0.006	-0.032	-0.028
X_8	-0.000	-0.000	-0.000	0.001	0.000	0.001	0.000	**0.008**	-0.000	0.000	0.000	0.001	-0.000	-0.000
X_9	0.001	0.000	0.000	0.000	-0.000	-0.000	0.000	-0.000	**0.005**	-0.000	-0.000	-0.000	-0.000	0.000
X_{10}	-0.101	0.034	-0.055	0.000	-0.130	0.037	0.016	0.012	-0.063	**0.491**	-0.034	-0.052	-0.051	0.001
X_{11}	0.000	0.000	-0.001	-0.000	0.002	0.003	-0.002	0.001	-0.000	-0.000	**0.013**	-0.000	0.000	0.000
X_{12}	-0.000	0.000	-0.000	-0.000	0.000	0.000	0.000	-0.000	0.000	0.000	0.000	**-0.004**	0.000	-0.000
X_{13}	-0.000	0.000	-0.000	-0.000	0.000	0.000	0.000	0.000	0.000	0.000	-0.000	0.000	**-0.003**	0.000
X_{14}	-0.001	-0.000	-0.000	0.001	-0.000	0.001	-0.000	-0.000	0.000	0.000	0.000	0.001	0.000	**0.010**
X_{15}	**-0.101**	**-0.030**	**-0.000**	**0.010**	**-0.289**	**-0.199**	**0.860**	**0.028**	**0.056**	**0.517**	**-0.187**	**-0.047**	**-0.084**	**-0.020**

X_1=Days to first male flowers, X_2=Node number to first male flower, X_3=Days to first female flowers, X_4=Node number to first female flower, X_5=Internodal length (cm), X_6=Days to first fruit harvest, X_7=No. of fruits per plant. X_8= Fruit length (cm), X_9= Fruit diameter (cm), X_{10}= Fruit weight (g), X_{11}= Test weight,X_{12}= Seed Index (gm.), X_{13}= Primary branches/ Plant, X_{14}= Plant height (met.), X_{15}= Yield (Q/ha)

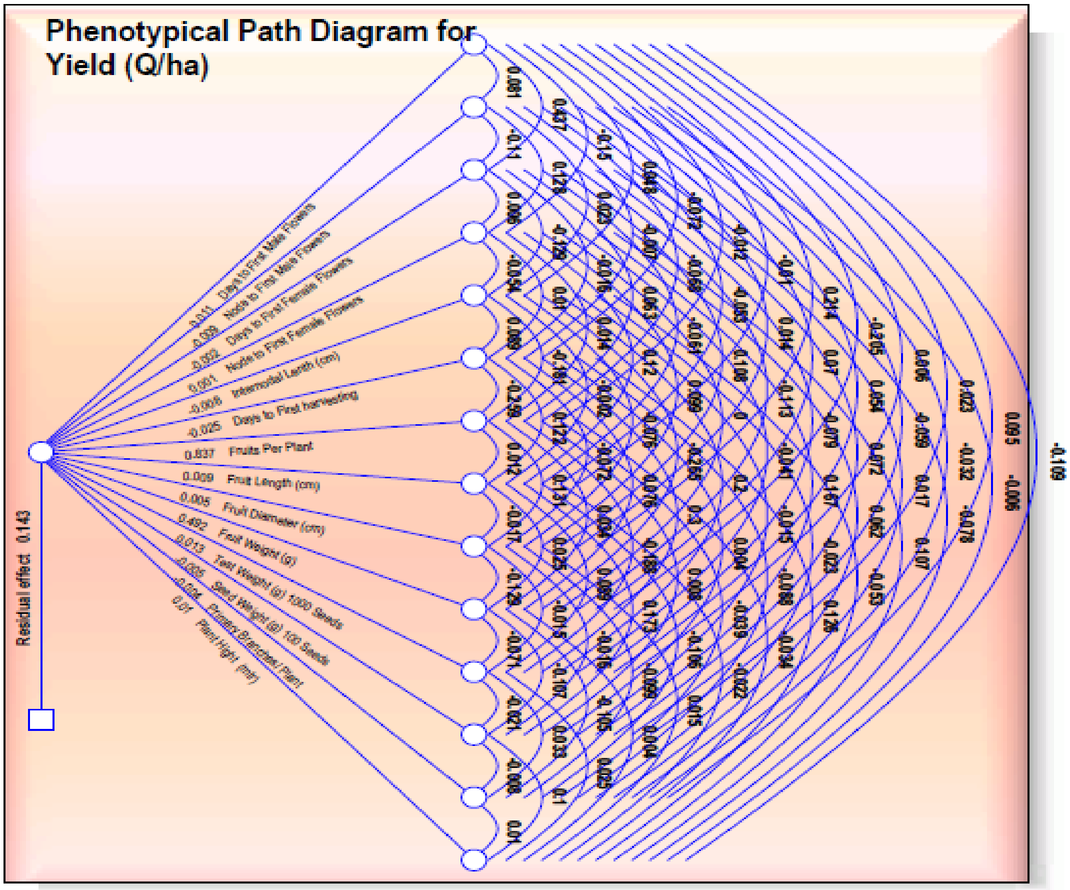

Figure 1 Path coefficient analysis for different characters on yield

Direct effect

The values of direct and indirect contribution of different traits toward yield revealed the maximum direct effect of no. of fruits per plant (0.837) followed by fruit weight (0.491), test weight (0.013), days to first male flowers (0.010), plant height (0.010), fruit length (0.008), fruit diameter (0.005) and node number to first female flower (0.000).However, days to first female Flowers (-0.002), primary branches per plant (-0.003), seed index (-0.004), internodal length (-0.007), node number to first male flower (-0.009) and days to first fruit harvest (-0.024) exerted negative direct effect on yield.

Indirect effect

The values of direct effect and indirect effect contribution of different traits toward yield revealed the maximum positive indirect effect of number of fruits per plant (0.110) followed by days to first female flowers (0.052), fruit weight (0.028), node number to first female flower (0.011), fruit length (0.010) and seed index (0.006) while it made indirect negative effect via days to first fruit harvest (-0.216) followed by test weight (-0.157), internodal length (-0.151), node number to first male flower (-0.057), primary branches per plant (-0.032), plant height (-0.028) and days to first male flowers (-0.010). Fruit weight (0.037) followed by node number to first male flower (0.034), number. of fruits per plant (0.016), fruit length (0.012), plant height (0.001) and node number to first female flower (0.000) while it exerted indirect negative effect via internodal length (-0.130) followed by days to first male flowers (-0.101), fruit diameter (-0.063), days to first female flowers (-0.055), seed index (-0.052), primary branches per plant (-0.051) and test weight (-0.034). High positive direct effect was exerted by number of fruits per plant on fruit yield per plant at both genotypic and phenotypic level, which contributed over 95% to total fruit yield.

Similar result had also been reported [6] and [12]. Days to first pistillate flower anthesis, node number to first pistillate flower appearance, fruit length, and plant height exhibited high positive direct effect upon yield but negative correlation because of indirect effect by means of other characters. Similar result had also found by [7] in bitter gourd. It is therefore suggested that these traits may be given consideration during selection programme. The value of residual effect deducting the direct and indirect effect was fairly low *i.e.* 0.2603 at phenotypic level which is in agreement with the finding of [14] The contribution of residual factors at phenotypic level was quite low indicating that most of variation in yield was explained by these variables.

Cluster analysis

The results of Average distance of inter and intra centroids have been presented in **Table 3** and Distributing pattern of 46 germplasm along with checks of cucumber into 7 clusters have been presented in **Table 4**. In analysis, the maximum intra cluster distance was noticed in cluster IV (8.81) followed by cluster II (7.37) and cluster I (5.63) whereas minimum intra cluster distance recorded in cluster III, cluster V, cluster VI and cluster VII (0.000). Maximum inter cluster distance was noticed between cluster IV and cluster VII (25.49) followed by cluster III and cluster IV (24.54), cluster IV and cluster V (23.57).

Table 3 Average distance of inter and intra centroids

Clusters	**Clusters**						
	I	**II**	**III**	**IV**	**V**	**VI**	**VII**
I	5.63	10.39	15.99	9.57	17.86	9.02	18.38
II		7.37	10.95	14.53	10.81	11.44	11.45
III			0.000	24.54	10.68	7.32	7.54
IV				8.81	23.57	18.39	25.49
V					0.000	16.13	13.74
VI						0.000	11.37
VII							0.000

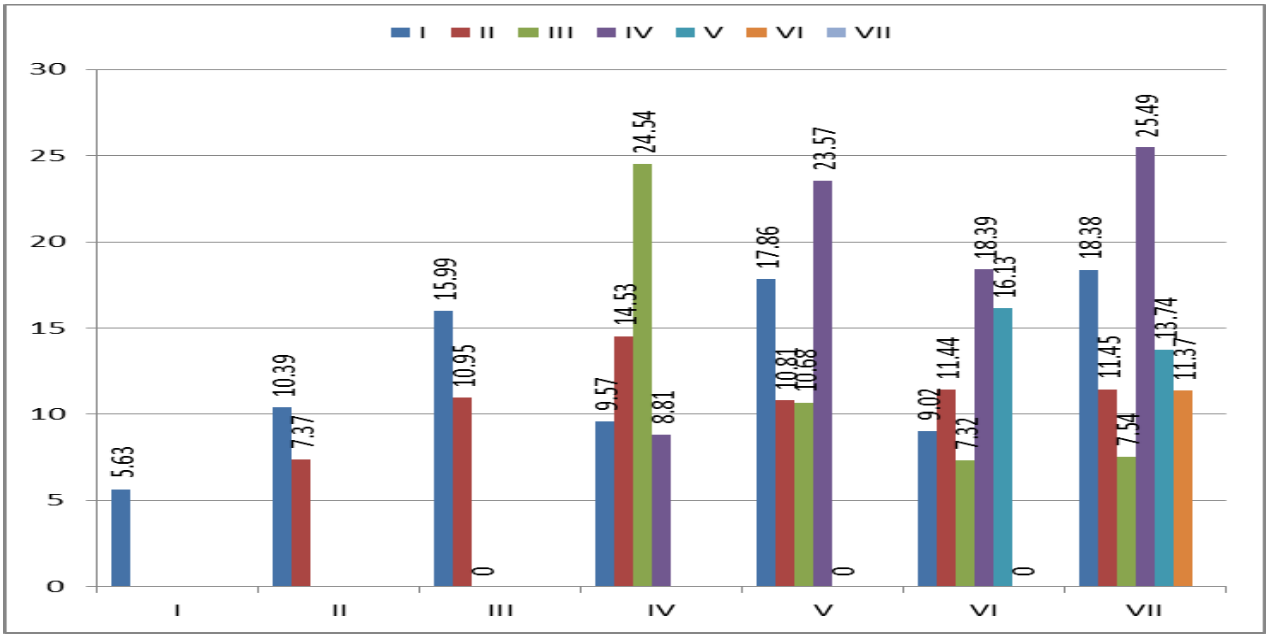

Figure 2 Average distance of inter and intra centroids

Minimum inter cluster distance was notice between cluster III and cluster VI (7.32). Maximum 24 genotypes were received by cluster II (PCUC-25, PCPGR-19, PCPGR-5370, PCPGR-34, PCPGR-22, PCPGR-138, PCPGR-45, PCPGR-06, PCUC-193, PCPGR-29, PCUC-08, PCPGR-20, Pant Khira-1, PCUC-104, PCPGR-7557, PCPGR-748, Euc-1-07, PCPGR-4343, PCPGR-7027, PCPGR-21, PCUC-832, PCUC-4302, PCUC-199 and CPGR-7176) followed by cluster I (PCUC-26, PCPGR-13, PCPGR-07, PCPGR-7657, PCPGR-04, PCUC-202, PCPGR-15, PCPGR-7795, Pointsette and PCPGR-24), cluster IV (PCPGR-103, PCPGR-7647, PCPGR-6762, PCPGR-196, PCPGR-7566, PCPGR-264, PCUC-23 and PCUC-44). Minimum only one genotype was recorded in cluster III, cluster V, cluster VI and cluster VII (PCPGR-7013, PCPGR-6006, PCUC-83 and PCPGR-7207) respectively. Were distributed into different clusters indicating the geographical diversity may not necessarily be related to genetic diversity. These findings are in agreement with [7] in cucumber.

Table 4 Distributing pattern of 46 germplasm along with checks of cucumber into 7 clusters

Cluster number	No. of germplasm	Germplasm included
I	10	PCUC-26, PCPGR-13, PCPGR-07, PCPGR-7657, PCPGR-04, PCUC-202, PCPGR-15, PCPGR-7795, Pointsette and PCPGR-24
II	24	PCUC-25, PCPGR-19, PCPGR-5370, PCPGR-34, PCPGR-22, PCPGR-138, PCPGR-45, PCPGR-06, PCUC-193, PCPGR-29, PCUC-08, PCPGR-20, Pant Khira-1, PCUC-104, PCPGR-7557, PCPGR-748, Euc-1-07, PCPGR-4343, PCPGR-7027, PCPGR-21, PCUC-832, PCUC-4302, PCUC-199 and CPGR-7176
III	1	PCPGR-7013
IV	8	PCPGR-103, PCPGR-7647, PCPGR-6762, PCPGR-196, PCPGR-7566, PCPGR-264, PCUC-23 and PCUC-44
V	1	PCPGR-6006
VI	1	PCUC-83
VII	1	PCPGR-7207

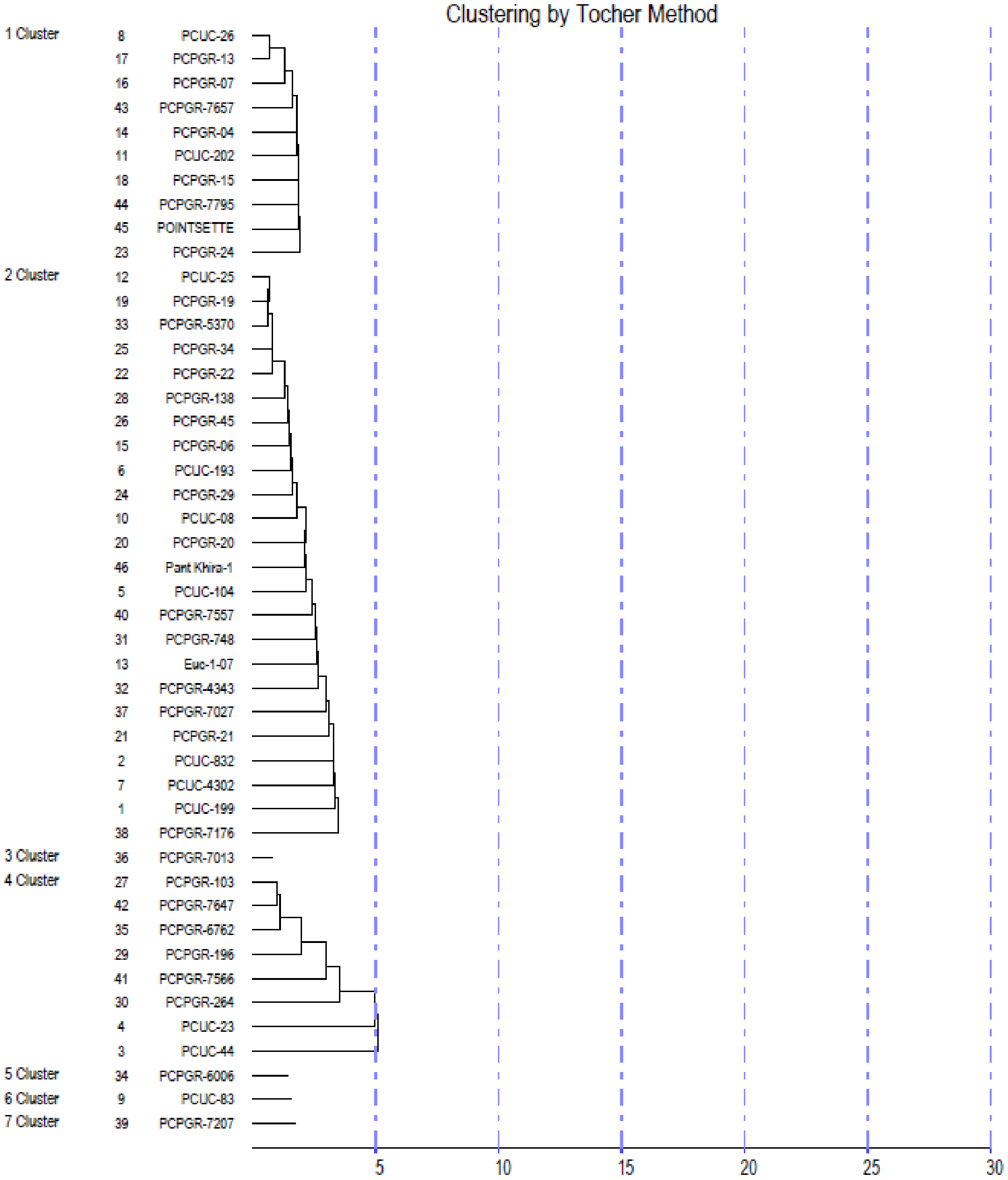

Figure 3 Dendrogram of 46 different genotypes of cucumber into 7 clusters

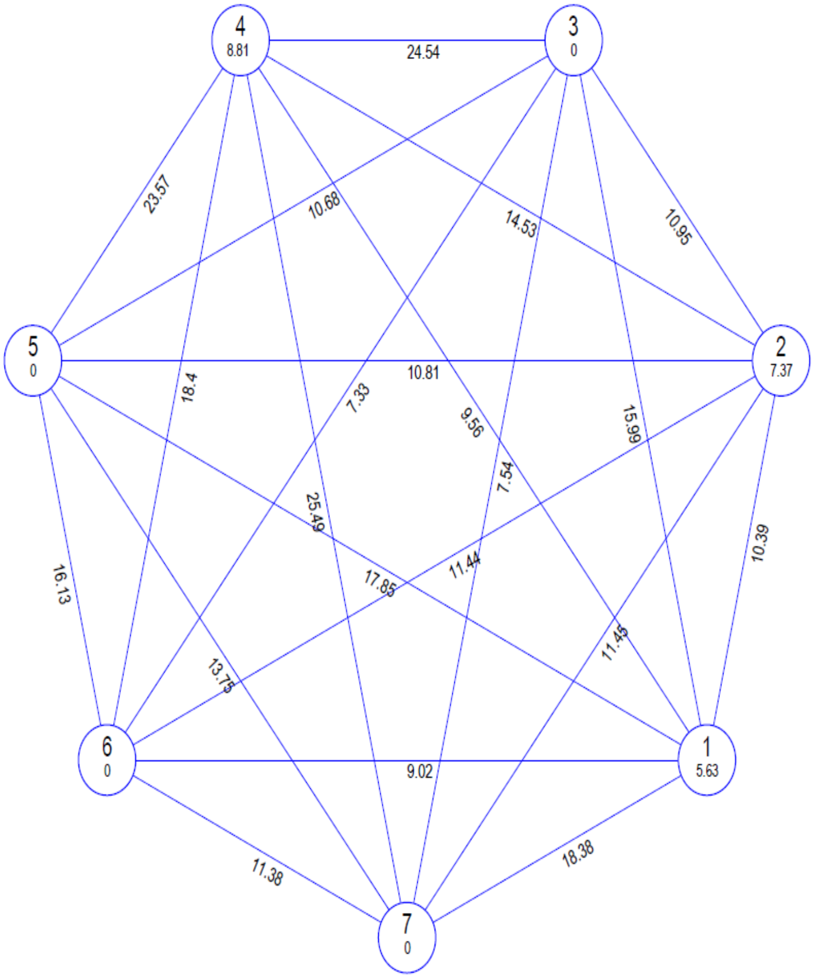

Figure 4 Mahalnobis euclidean distance by tocher method

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