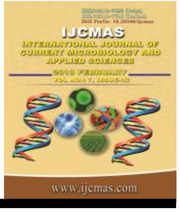
*Int.J.Curr.Microbiol.App.Sci* (2018) *7*(2): 1733-1741

*International Journal of Current Microbiology and Applied Sciences*
***ISSN: 2319-7706*** **Volume 7 Number 02 (2018)**
Journal homepage: http://www.ijcmas.com



**Original Research Article** https://doi.org/10.20546/ijcmas.2018.702.210

# Divergence Studies for Different Horticultural Traits in Cucumber (*Cucumis sativus* L.)

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## ABSTRACT

Thirty diverse genotypes of cucumber collected from different indigenous and exotic sources were planted in randomized complete block design, during kharif season of 2016 and were assessed to know the nature and magnitude of genetic divergence for different horticultural traits, using Mahalanobis $D^2$ statistics. All the characters under study showed considerable divergence and the genotypes were grouped into five clusters. Cluster II contained the maximum (12) number of genotypes, whereas cluster V contained minimum (3) genotypes. The intra cluster distance was maximum in cluster IV (3.469) and minimum in cluster III (1.776). Maximum average inter-cluster distance (6.221) was recorded between cluster III and cluster IV. Therefore, the hybridization between the genotypes of cluster III and IV can be made for getting superior hybrids or recombinants in segregating populations. Cluster III performed better for majority of traits *viz.* node number bearing first female flower, number of marketable fruits per plant, average fruit weight, harvest duration, days to marketable maturity, TSS, seed germination, seed vigour index-I and II, severity of powdery mildew, angular leaf spot and yield per plot. Maximum fruit length (21.42), minimum severity of anthracnose was recorded in cluster V (7.48), while fruit breadth was highest in cluster IV (5.50).

**Keywords**

Cucumber, Genotypes, Genetic divergence, Cluster

**Article Info**

***Accepted:***
17 January 2018
***Available Online:***
10 February 2018

## Introduction

Cucumber (*Cucumis sativus* L.) is one of the most important cucurbitaceous vegetable crops grown extensively in tropical and subtropical parts of the country. It is considered as 4th most important vegetable crop after tomato, cabbage and onion. Cucumber is a thermophilic and frost susceptible species growing best at a temperature above $20^0$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. Cucumber is thought to be indigenous to India. India is endowed with the wealth of cucumber germplasm, comprising of both wild and cultivated forms. Due to continuous cultivation of this cross-pollinated crop large variation has occurred for fruit and vegetative characters (Sharma *et al.,* 2017). The success of any breeding program depends to a large extent on the amount of genetic variability present in the population (Afangideh and Uyoh, 2007). Suitable breeding strategy can be formulated for improvement of cucumber based on the magnitude of parameters of variability. Therefore, the present study has been undertaken to estimate the extent of variability and genetic divergence in thirty genotypes of cucumber.

Assessment of genetic diversity could be suitable in crop breeding for diverse applications such as identifying diverse parental genotypes. Genetic diversity is the amount of heritable variability between varieties or populations of organisms. Variability occurs from differences in DNA sequences, biochemical characteristics like protein structure or isoenzyme properties, physiological properties like growth rate and morphological characters. Substantial effort has been directed towards collecting, preserving and evaluating genetic variability in crops (Golabadi *et al.*, 2012).

## Materials and Methods

The present study was conducted at the Experimental farm of the Department of Vegetable Science is located at an altitude of 1276 metres above mean sea level at a longitude of $77^0\ 11^{'}\ 30^{''}$ E and a latitude of $30^0\ 52^{'}\ 30^{''}$ N and is 1260 m above mean sea level and represents the mid-hill zone of Himachal Pradesh. The experimental material comprised of thirty genotypes including check cultivar K-75 collected from different exotic and indigenous germplasm of cucumber (Table 1). The experiment was laid out in Randomized Complete Block Design with three replications of each genotype. Seeds were directly sown in the field in the month of June, 2016. Three to four seeds per basin were sown at a spacing of 100 x 50 cm in a plot had size of 3.0 x 2.0 $m^2$, accommodating 12 plants per plot. After the emergence of seedlings, only one healthy plant per hill was retained. The standard cultural practices as recommended in the Package of Practices for Vegetable Crops, were followed to ensure a healthy crop stand (Anonymous, 2014).

The observations were recorded from five randomly selected plants in each replication for all characters except for fruit characters for which observations were recorded on ten randomly selected fruits per replication. Colour of fruits was observed visually after harvesting with the help of colour chart of Royal Horticultural Society, London. Seed germination of each genotype was tested in accordance with ISTA (Anonymous, 1985) and seed vigour index-I and II were calculated as per the formula given by Abdul-Baki and Anderson (1973), where, seed vigour index I = seed germination percentage × seedling length (cm) and seed vigour index II = seed germination percentage × seedling dry weight (mg). The disease severity of angular leaf spot was recorded on modified 0-9 scale of Woltman *et al.,* (2009) where absence of disease symptom was taken as 0 and leaf damage of 87-100% was scored 9. Severity of anthracnose and powdery mildew was recorded on 0-5 scale of Akem and Jovicich (2011). Here, absence of disease symptom was scored as 0 and leaf necrosis between 75-100% scored 5. For all the three diseases, the observations were recorded 65 days after sowing from ten leaves in each plant, five such vines in each replication of each genotype. Disease severity percentage was calculated by adopting the formula of McKinney (1923).

## Statistical analysis

The collected data were subjected to Analysis of Variance (ANOVA) using OP-STAT software available from HAU, Hisar and presented in table 2 and genetic divergence (D) was worked out according to Mahalanobis (1936) using SPAR-1 software available from

IASRI, New Delhi. A dendrogram was generated using Wards method and Euclidan distance as a measure of similarity with the help of SPSS software version 16 and is presented in Figure 1.

## Results and Discussion

The analysis of variance revealed highly significant differences among the genotypes for all the characters studied, indicating the existence of wide genetic divergence among them. Information on genetic diversity was also used to identify promising diverse genotypes, which may further be used in breeding programmes.

On the basis of performance of various traits, the clustering pattern of 30 diverse genotypes of cucumber has been presented in the table 3. All the genotypes were grouped into 5 clusters. Maximum number of genotypes were accommodated in cluster II (12) followed by cluster IV (7), cluster I and III (4) and cluster V (3). Genotypes from same centre of origin were placed in separate clusters, indicated wide genetic diversity among them. This may be due to frequent exchange of germplasm between different geographical regions.

Average inter and intra cluster divergence ($D^2$) values are presented in the table 4. The diagonal figures in the table represent the intra cluster distances. The intra cluster distance was maximum in cluster IV (3.469) and minimum in cluster III (1.776).

Whereas, highest (6.221) inter cluster distance was recorded between cluster III and IV and lowest (2.502) was observed between cluster I and II suggesting wide diversity between the groups. The crosses made between the genotypes from the above clusters may give transgressive segregants.

**Fig.1** Dendrogram using hierarchical cluster analysis

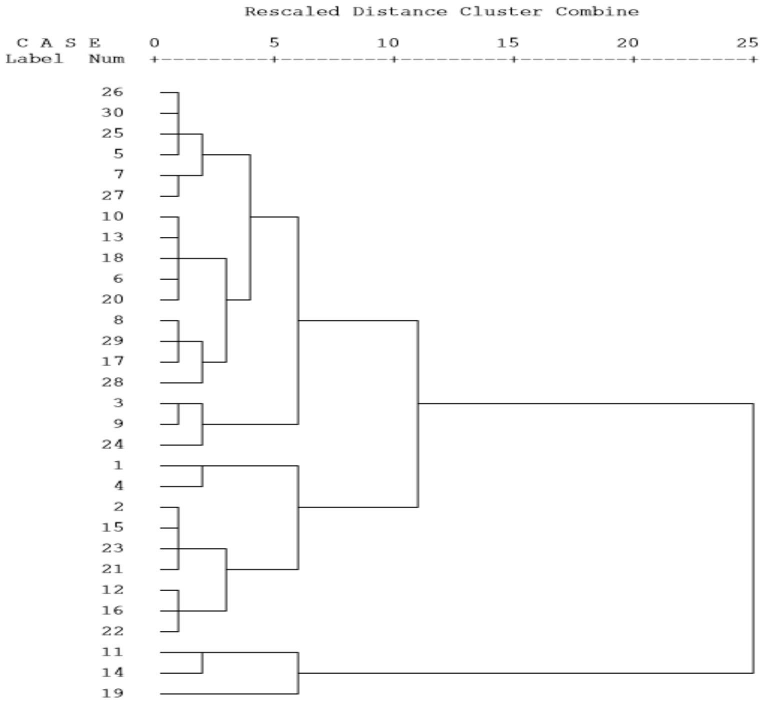

**Table.1** List of cucumber genotypes studied along with their sources

| Genotype | Source |
|---|---|
| **CGN-19533, CGN-20269, CGN-20515, CGN-20827, CGN-20930, CGN-20953, CGN-20969, CGN-21585, CGN-22930** | Centre for Crop Genetic Resources, the Netherlands |
| **PI-426170, PI-5754, PI-618894** | North Central Regional Plant Introduction Station, USA |
| **UHF-CUC-4, UHF-CUC-5, UHF-CUC-6, UHF-CUC-7, UHF-CUC-8, UHF-CUC-9, UHF-CUC-10, UHF-CUC-11, UHF-CUC-12, UHF-CUC-13, UHF-CUC-14, UHF-CUC-15, UHF-CUC-16, UHF-CUC-17, UHF-CUC-18, UHF-CUC-19, Poinsette, K-75 (Check)** | Department of Vegetable Science, UHF, Solan, HP |

**Table.2** Analysis of variance for various horticultural traits in cucumber

| Source<br>Character | Mean Sum of Squares | | | |
|---|---|---|---|---|
| | **Replications** | **Genotypes** | **Errors** | **Total** |
| **Df** | 2 | 29 | 58 | 89 |
| **Node number bearing first female** | 0.28 | 5.65* | 0.37 | 6.30 |
| **Days to marketable maturity** | 10.07 | 164.42* | 3.97 | 178.46 |
| **Number of marketable fruits/plant** | 0.09 | 4.18* | 0.18 | 4.45 |
| **Harvest duration (days)** | 0.62 | 54.22* | 3.02 | 57.86 |
| **Fruit length(cm)** | 1.28 | 16.38* | 1.25 | 18.91 |
| **Fruit breadth (cm)** | 0.26 | 0.65* | 0.10 | 1.01 |
| **Average fruit weight (g)** | 2279.71* | 4410.97* | 492.96 | 7183.64 |
| **Yield/ plot (kg)** | 0.19 | 55.39* | 1.30 | 56.88 |
| **Yield /hectare (q) [converted]** | 28.40 | 8654.93* | 202.72 | 8886.05 |
| **TSS (°B)** | 0.08* | 0.10* | 0.02 | 0.20 |
| **Seed germination (%)** | 20.81 | 120.52* | 15.33 | 156.66 |
| **Seed vigour index-I** | 2143.60 | 408017.42* | 19125.65 | 429286. |
| **Seed vigour index-II** | 68815.70 | 216697.65* | 30073.26 | 315586. |
| **Powdery mildew (%)** | 12.18* | 27.75* | 2.81 | 42.74 |
| **Anthracnose (%)** | 4.36 | 76.26* | 3.25 | 83.87 |
| **Angular leaf spot (%)** | 1.11 | 139.35* | 3.08 | 143.54 |

*Significant at 5% level of significance

**Table.3** Clustering pattern of 30 genotypes of cucumber on the basis of genetic divergence

| Cluster | Number of Genotypes | Genotypes along with their sources |
|---|---|---|
| I | 4 | CGN-20269 (the Netherlands), CGN-22930 (the Netherlands), UHF-CUC-9 (Solan), Poinsette (Solan) |
| II | 12 | CGN-20515 (the Netherlands), CGN-20827 (the Netherlands), CGN-20930 (the Netherlands), CGN-20953 (the Netherlands), CGN-20969 (the Netherlands), CGN-21585 (the Netherlands), UHF-CUC-4 (Solan), UHF-CUC-7 (Solan), UHF-CUC-11(Solan), PI-426170 (USA), PI-5754 (USA), K-75 (Solan) |
| III | 4 | UHF-CUC-8 (Solan), UHF-CUC-15 (Solan), UHF-CUC-16 (Solan), UHF-CUC-17 (Solan) |
| IV | 7 | CGN-19533 (the Netherlands), UHF-CUC-5 (Solan), UHF-CUC-10 (Solan), UHF-CUC-12 (Solan), UHF-CUC-13 (Solan), UHF-CUC-18 (Solan), UHF-CUC-19 (Solan) |
| V | 3 | UHF-CUC-6 (Solan), UHF-CUC-14 (Solan), PI-618894 (USA) |

**Table.4** Average intra and inter cluster distance ($D^2$)

| Cluster | I | II | III | IV | V |
|---|---|---|---|---|---|
| I | **2.299** | | | | |
| II | 2.502 | **2.380** | | | |
| III | 3.928 | 5.275 | **1.776** | | |
| IV | 4.546 | 3.206 | 6.221 | **3.469** | |
| V | 4.314 | 3.493 | 6.036 | 4.952 | **3.109** |

**Table.5** Cluster means for different characters among 30 genotypes of cucumber

| Characters | Clusters | | | | |
|---|---|---|---|---|---|
| | **I** | **II** | **III** | **IV** | **V** |
| Node number bearing 1st female flower | 4.53 | 5.18 | 3.75 | 6.41 | 4.89 |
| Number of marketable fruits / plant | 7.84 | 6.83 | 8.23 | 5.62 | 6.25 |
| Fruit length (cm) | 15.06 | 16.41 | 18.45 | 15.75 | 21.42 |
| Fruit breadth (cm) | 4.71 | 4.87 | 5.09 | 5.50 | 4.85 |
| Average fruit weight (g) | 251.98 | 267.00 | 314.21 | 274.35 | 224.31 |
| Days to marketable maturity | 49.43 | 48.88 | 47.43 | 60.23 | 52.02 |
| Harvest duration (days) | 23.25 | 19.68 | 28.83 | 17.90 | 18.09 |
| TSS ($^0$B) | 2.99 | 2.48 | 3.04 | 2.91 | 2.58 |
| Seed germination (%) | 89.33 | 83.94 | 99.42 | 87.57 | 86.44 |
| Seed vigour index-I | 2145.92 | 1752.05 | 2431.21 | 2042.55 | 1846.58 |
| Seed vigour index-II | 1119.22 | 1094.03 | 1431.76 | 1312.41 | 1348.14 |
| Severity of powdery mildew (%) | 14.27 | 13.19 | 9.72 | 10.70 | 14.52 |
| Severity of anthracnose (%) | 9.36 | 13.23 | 9.06 | 17.72 | 7.48 |
| Severity of angular leaf spot (%) | 9.82 | 14.81 | 5.68 | 18.59 | 6.87 |
| Yield/plot (kg) | 22.60 | 20.03 | 26.93 | 16.87 | 19.11 |

**Table.6** Mean performance of cucumber genotypes for different horticultural traits

| Genotype | NNBFF | DMM | NMF | HD | FL | FB | AFW | TSS | FC | SG* | SVI-I | SVI-II | SPM* | SA* | SALS * | YPP | YPH |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **CGN-19533** | 6.83 | 65.47 | 6.07 | 19.33 | 15.50 | 4.77 | 252.94 | 3.08 | LG (G 143 B) | 96.67 (9.89) | 1919.31 | 1735.93 | 13.00 (3.73) | 17.07 (4.24) | 13.60 (3.81) | 17.48 | 218.46 |
| **CGN-20269** | 3.26 | 44.33 | 7.55 | 19.80 | 15.67 | 4.90 | 247.67 | 2.80 | LG (G 147 A) | 85.67 (9.31) | 2243.79 | 1207.41 | 18.73 (4.44) | 9.50 (3.24) | 11.27 (3.49) | 21.48 | 268.50 |
| **CGN-20515** | 5.33 | 44.13 | 8.09 | 18.40 | 16.13 | 4.65 | 273.50 | 2.79 | LG (G 146 B) | 82.33 (9.13) | 1898.55 | 903.85 | 14.47 (3.92) | 18.83 (4.45) | 17.60 (4.31) | 23.72 | 296.54 |
| **CGN-20827** | 3.89 | 42.47 | 7.27 | 18.33 | 15.47 | 5.41 | 255.00 | 2.55 | LG (G 144 B) | 81.33 (9.08) | 1850.29 | 1473.47 | 13.33 (3.78) | 11.73 (3.57) | 11.00 (3.46) | 24.40 | 305.00 |
| **CGN-20930** | 6.83 | 45.27 | 6.98 | 19.00 | 15.28 | 5.32 | 308.47 | 2.71 | G (G 138 A) | 85.00 (9.28) | 1840.64 | 1072.10 | 13.40 (3.79) | 11.47 (3.51) | 16.27 (4.15) | 21.43 | 267.88 |
| **CGN-20953** | 5.83 | 60.87 | 7.85 | 18.67 | 15.67 | 4.58 | 285.17 | 2.71 | G (G 141 B) | 82.67 (9.15) | 1457.82 | 1165.84 | 12.83 (3.72) | 9.53 (3.25) | 17.27 (4.27) | 25.31 | 316.42 |
| **CGN-20969** | 5.67 | 44.93 | 6.44 | 18.40 | 15.47 | 4.47 | 283.33 | 3.07 | G (G 139 B) | 83.67 (9.20) | 2017.63 | 1119.94 | 13.27 (3.77) | 11.70 (3.56) | 11.00 (3.46) | 20.57 | 257.13 |
| **CGN-21585** | 5.01 | 47.13 | 6.06 | 19.33 | 16.48 | 5.34 | 263.33 | 3.19 | LG (G 152 B) | 82.33 (9.13) | 1535.27 | 1009.87 | 10.60 (3.40) | 12.77 (3.70) | 19.80 (4.56) | 15.89 | 198.67 |
| **CGN-22930** | 5.50 | 45.33 | 7.87 | 20.47 | 13.10 | 5.00 | 264.05 | 3.07 | LG (G 152 A) | 93.00 (9.69) | 2052.70 | 823.40 | 17.17 (4.26) | 10.93 (3.45) | 12.33 (3.64) | 22.96 | 287.04 |
| **UHF-CUC-4** | 3.44 | 50.47 | 4.54 | 23.33 | 16.80 | 4.57 | 263.33 | 2.79 | G (G 137 A) | 84.33 (9.24) | 1642.11 | 1240.89 | 15.63 (4.08) | 12.53 (3.67) | 17.33 (4.28) | 12.38 | 154.79 |
| **UHF-CUC-5** | 5.83 | 62.13 | 6.73 | 16.80 | 18.47 | 5.91 | 279.33 | 2.72 | LG (G 152 B) | 83.67 (9.21) | 2580.43 | 1663.84 | 6.33 (2.69) | 23.00 (4.89) | 15.80 (4.09) | 20.68 | 258.54 |
| **UHF-CUC-6** | 3.33 | 51.67 | 6.63 | 16.67 | 19.00 | 4.68 | 256.25 | 2.68 | G (G 139 A) | 95.33 (9.82) | 2180.60 | 1601.36 | 15.00 (4.00) | 8.17 (3.02) | 4.40 (2.32) | 18.52 | 231.50 |
| **UHF-CUC-7** | 4.33 | 45.33 | 6.26 | 16.33 | 17.47 | 5.13 | 276.67 | 2.93 | G (G 137 A) | 89.67 (9.53) | 1602.75 | 1167.33 | 14.47 (3.92) | 13.97 (3.87) | 6.33 (2.70) | 20.34 | 254.25 |
| **UHF-CUC-8** | 4.83 | 45.73 | 8.08 | 27.20 | 16.58 | 4.93 | 266.67 | 3.11 | G (G 137 B) | 99.33 (10.02) | 2800.87 | 1720.33 | 11.43 (3.52) | 8.90 (3.14) | 5.53 (2.54) | 25.44 | 317.96 |
| **UHF-CUC-9** | 4.50 | 46.07 | 8.16 | 28.40 | 15.90 | 4.59 | 238.33 | 3.07 | G (G 143 A) | 84.67 (9.26) | 2208.91 | 1285.72 | 9.50 (3.24) | 8.10 (3.01) | 6.67 (2.76) | 22.50 | 281.21 |

| | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **UHF-CUC-10** | 9.67 | 53.33 | 5.34 | 18.07 | 17.17 | 5.06 | 293.33 | 3.04 | G (G 142 A) | 94.00 (9.75) | 2202.76 | 1443.88 | 12.93 (3.73) | 27.07 (5.30) | 9.53 (3.25) | 18.36 | 229.46 |
| **UHF-CUC-11** | 5.22 | 57.00 | 5.94 | 23.20 | 15.08 | 5.01 | 253.75 | 2.71 | G (G 143 B) | 83.33 (9.19) | 1690.65 | 846.92 | 13.47 (3.79) | 17.50 (4.29) | 12.67 (3.69) | 19.92 | 248.96 |
| **UHF-CUC-12** | 5.33 | 50.67 | 4.04 | 15.33 | 14.67 | 6.00 | 328.92 | 2.71 | LG (G 152 A) | 84.33 (9.24) | 1695.51 | 1293.53 | 13.67 (3.82) | 14.73 (3.96) | 29.00 (5.48) | 11.43 | 142.84 |
| **UHF-CUC-13** | 5.33 | 62.00 | 5.13 | 20.80 | 15.97 | 5.51 | 255.33 | 2.87 | LG (G 144 A) | 84.00 (9.22) | 2829.07 | 1264.83 | 7.07 (2.83) | 15.97 (4.12) | 23.27 (4.93) | 20.85 | 260.63 |
| **UHF-CUC-14** | 6.33 | 57.73 | 6.33 | 17.60 | 19.83 | 5.37 | 141.50 | 2.53 | LG (G 149 C) | 80.67 (9.04) | 1557.80 | 1211.35 | 18.83 (4.45) | 10.93 (3.45) | 12.20 (3.62) | 19.68 | 246.00 |
| **UHF-CUC-15** | 3.67 | 45.60 | 8.15 | 29.20 | 18.88 | 4.79 | 307.08 | 3.03 | G (G 143 A) | 100.00 (10.05) | 2361.33 | 1155.00 | 8.80 (3.13) | 8.67 (3.10) | 6.07 (2.64) | 25.64 | 320.50 |
| **UHF-CUC-16** | 2.83 | 53.67 | 8.21 | 29.93 | 19.12 | 5.66 | 341.67 | 3.01 | G (G 141 B) | 99.33 (10.02) | 2327.61 | 1576.24 | 8.50 (3.08) | 9.50 (3.23) | 4.73 (2.39) | 27.94 | 349.21 |
| **UHF-CUC-17** | 3.67 | 44.73 | 8.49 | 29.00 | 19.23 | 5.00 | 341.44 | 3.02 | G (G 141 A) | 99.00 (10.00) | 2235.03 | 1275.46 | 10.13 (3.34) | 9.17 (3.19) | 6.40 (2.69) | 28.71 | 358.92 |
| **PI-426170** | 5.33 | 46.67 | 7.88 | 18.60 | 18.17 | 4.55 | 251.50 | 2.76 | G (G 139 A) | 86.33 (9.35) | 1860.11 | 698.28 | 12.80 (3.71) | 16.70 (4.20) | 13.40 (3.79) | 22.06 | 275.71 |
| **PI-5754** | 5.17 | 50.27 | 6.98 | 18.27 | 17.44 | 4.45 | 233.33 | 2.88 | G (G 137 A) | 83.33 (9.19) | 1819.80 | 1230.16 | 10.07 (3.32) | 9.43 (3.23) | 25.00 (5.10) | 15.00 | 187.54 |
| **PI-618894** | 5.00 | 46.67 | 5.79 | 20.00 | 25.42 | 4.50 | 275.17 | 2.54 | G (G 137 A) | 83.33 (9.19) | 1801.33 | 1231.71 | 9.73 (3.27) | 3.33 (2.08) | 4.00 (2.23) | 19.12 | 239.04 |
| **Poinsette** | 4.87 | 62.00 | 7.77 | 24.33 | 15.58 | 4.36 | 257.87 | 3.02 | G (G 139 B) | 94.00 (9.75) | 2078.27 | 1160.33 | 11.67 (3.56) | 8.90 (3.14) | 9.00 (3.16) | 23.47 | 293.33 |
| **UHF-CUC-18** | 6.67 | 60.33 | 5.62 | 18.33 | 13.84 | 5.29 | 215.17 | 3.01 | LG (G 144 C) | 83.00 (9.17) | 1440.11 | 839.21 | 10.20 (3.34) | 19.20 (4.49) | 27.53 (5.34) | 14.52 | 181.54 |
| **UHF-CUC-19** | 5.18 | 67.67 | 6.40 | 16.60 | 14.63 | 5.94 | 295.42 | 2.93 | LG (G 146 C) | 87.33 (9.39) | 1630.63 | 945.66 | 11.73 (3.57) | 7.00 (2.82) | 11.40 (3.52) | 14.79 | 184.88 |
| **K-75 (Check)** | **6.08** | **61.00** | **7.65** | **24.33** | **17.50** | **5.00** | **256.67** | **3.00** | **LG (G 144 C)** | **83.00 (9.17)** | **1808.97** | **1199.70** | **13.97 (3.87)** | **12.63 (3.69)** | **10.00 (3.31)** | **19.34** | **241.71** |
| **Range** | **2.83-9.67** | **42.47-67.67** | **4.04-8.49** | **15.33-29.93** | **13.10-25.42** | **4.36-6.00** | **141.50-341.67** | **2.53-3.19** | | **80.67-100.00** | **14410.11-2829.07** | **698.28-1735.93** | **6.33-18.83** | **3.33-27.07** | **4.00-29.00** | **11.43-28.71** | **142.84-358.92** |
| **Mean** | **5.16** | **52.02** | **6.81** | **20.80** | **16.85** | **5.02** | **268.74** | **2.88** | - | **87.82 (9.42)** | **1972.35** | **1218.79** | **12.42 (3.64)** | **12.63 (3.63)** | **13.01 (3.64)** | **20.46** | **255.81** |
| **SE (d) ±** | **0.50** | **1.63** | **0.34** | **1.42** | **0.91** | **0.26** | **18.13** | **0.12** | - | **3.20** | **112.92** | **141.59** | **1.37** | **1.47** | **1.43** | **0.93** | **11.63** |
| **C.D.$_{(0.05)}$** | **0.99** | **3.26** | **0.69** | **2.85** | **1.83** | **0.51** | **36.38** | **0.24** | - | **6.41** | **226.43** | **283.94** | **2.75** | **2.95** | **2.87** | **1.87** | **23.33** |

Where,

NNBFFF = Node number bearing first female flower, NMF = Number of marketable fruits per plant, FL = Fruit length (cm), FB = Fruit breadth (cm), AFW = Average fruit weight (g), DMM = Days to marketable maturity, HD = Harvest duration, TSS = Total soluble solids ($^0$B), FC = Fruit colour, LG = Light green, G = Green, SG = Seed germination (%), SVI-I = Seed vigor index-I, SVI-II = Seed vigor index-II, SPM = Severity of powdery mildew (%), SA = Severity of anthracnose (%), SALS = Severity of angular leaf spot (%), YPP = Yield per plot (kg) and YPH = Yield per hectare (q)

* Figures in the parenthesis are square root transformed

## Cluster means

Further, for getting the reliable conformity on the basis of cluster means, it was calculated for various horticultural traits and has been presented in the table 5. Moreover, mean performances of genotypes for different horticultural and yield traits have been presented in table 6 for getting reliable conformity about selection of parental genotypes to be used in hybridization. Genotypes of cluster III recorded lowest mean for node number bearing first female flower (3.75) along with maximum number of marketable fruits per plant (8.23), maximum average fruit weight (314.21), minimum days to marketable maturity (47.43), maximum harvest duration (28.83), highest total soluble solids (TSS) (3.04), maximum seed germination (99.42), maximum seed vigour index-I and II (2431.21, 1431.76) respectively, lowest severity of powdery mildew (9.72) and angular leaf spot (5.68). Cluster III also earned maximum yield per plot (26.93). Maximum fruit length was recorded in cluster V (21.42), while fruit breadth was highest in cluster IV (5.50). The severity of anthracnose was minimum in cluster V (7.48). Earlier workers like Sharma and Sharma (2006), Hinchinamani and Patil (2011), Punitha *et al.*, (2012), Kumar *et al.*, (2013) and Hasan *et al.*, (2015) have also indicated significance of genetic divergence in cucumber.

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**How to cite this article:**

Shweta Sharma, Ramesh Kumar, H.R. Sharma, Ajit Sharma and Nidhish Gautam. 2018. Divergence Studies for Different Horticultural Traits in Cucumber (*Cucumis sativus* L.). *Int.J.Curr.Microbiol.App.Sci.* 7(02): 1733-1741. doi: https://doi.org/10.20546/ijcmas.2018.702.210