



Genetic Divergence Studies in Cucumber (*Cucumis sativus* L.) Genotypes for Yield and Quality

V. Usha Rani¹, G.S. Sahu², P. Tripathy², S. Das³, M. Badu⁴,
S. Balo¹, K. Ghosh¹, N. Patel¹, G.G. Padhiary⁵

10.18805/IJARE.A-6097

ABSTRACT

Background: In an effort to identify divergent superior parents for hybridization programme, a study to examine the genetic divergence in yield and quality traits was conducted.

Methods: Thirty two cucumber genotypes were collected from different states of India and were evaluated for yield and quality characters at Bhubaneswar, Odisha during *Rabi* season of 2019.

Result: The genetic diversity of 32 cucumber genotypes was evaluated using a randomized block design. The Mahalanobis D^2 statistic revealed the presence of substantial genetic diversity among the 32 genotypes examined. In a study of 32 cucumber genotypes, clustering based on interactions in genetic distances revealed substantial genetic divergence among the groups. Genotypes from different ecogeographic regions were distributed into distinct clusters in an apparently random fashion, suggesting that there was no correlation between geographic distribution and genetic diversity. Cluster I included the most unique genotypes, suggesting that it was a major contributor to the overall genetic divergence among the five groups. Results showed that Clusters II, IV and V were all monogenomic. Cluster II, IV and V had the smallest intra-cluster distances (0.00), whereas cluster I had the largest (45.08). There was the greatest genetic distance (133.68) between cluster's I and V, suggesting that cluster V could be used in a future hybridization study. Clusters IV, V and III had the highest mean values of the five clusters for many of the characteristics. According to the ranking of D^2 value, the contribution of fruit yield per vine (16.50%) towards genetic divergence was highest. Therefore, phenotypic selection could be used to further enhance this trait.

Key words: Cluster distance, Clustering, Cucumber, Genetic diversity.

INTRODUCTION

The cucumber (*Cucumis sativus* L.), with its chromosome number of $2n = 14$, is a member of the family Cucurbitaceae, which includes 117 genera and 825 species native to warmer regions of the world. Native to the Indian sub-continent, it is now cultivated in many tropical and subtropical regions (Sebastian *et al.*, 2010). It is typically monoecious but is a strongly cross-pollinated crop. Cucumbers exhibit a wide spectrum of sexual dimorphism, including androecious, gynoeceous, hermaphrodite and andromonoecious (Bailey, 1969). India is home to numerous species of *Cucumis sativus* and allied plants, each with its own unique set of botanical and agronomic characteristics. In the South Asian region, cucumbers are planted commercially across the board. Although several landraces and wild variants of cucumber have been reported (Sebastian *et al.*, 2010), they have not been utilized to the same extent as the high-yielding cultivars. Lack of exploitable genetic variability, lack of appropriate genotypes for different cropping systems, sensitivity to biotic and abiotic stresses, lack of quality seeds of improved varieties and a narrow genetic base due to the repeated use of few parents with a high degree of pertinence in crossing programmes are the major constraints in achieving higher and profitable productivity of cucumber. Cucumber's low levels of variability have been used in successful varietal development initiatives. The output of this crop has reached

¹Faculty of Agriculture, GIET University, Gunupur-765 022, Odisha, India.

²Department of Vegetable Science, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar-751 012, Odisha, India.

³All India Coordinated Research Project on Vegetable Crops, Odisha University of Agriculture and Technology, Bhubaneswar-751 003, Odisha, India.

⁴Faculty of Agriculture, Sri Sri University, Cuttack-754 006, Odisha, India.

⁵Faculty of Agriculture, MITS Institute of Professional Studies, Rayagada-765 017, Odisha, India.

Corresponding Author: V. Usha Rani, Faculty of Agriculture, GIET University, Gunupur-765 022, Odisha, India.

Email: veerausharani@giet.edu

How to cite this article: Rani, V.U., Sahu, G.S., Tripathy, P., Das, S., Badu, M., Balo, S., Ghosh, K., Patel, N. and Padhiary, G.G. (2025). Genetic Divergence Studies in Cucumber (*Cucumis sativus* L.) Genotypes for Yield and Quality. Indian Journal of Agricultural Research. 59(3): 442-446. doi: 10.18805/IJARE.A-6097.

Submitted: 31-03-2023 **Accepted:** 01-06-2024 **Online:** 31-07-2024

a plateau, despite numerous breeding efforts. In order for a breeding program to be successful, genetic diversity and variability in the germplasm must already exist. In order to determine the extent of the variation available for yield and

yield attributing features, it is necessary to have an accurate estimation of the nature and size of diversity in a crop. A plant breeder's ability to pick superior parents for hybridization is aided by their familiarity with the genetic variation present in the available germplasm. It is expected that offspring from genetically varied parents will be more successful. "It is well-established that choosing parents with a wider range of characteristics increases the likelihood of producing offspring with high heterotic F_1 scores and a broad range of segregation-based variability. When attempting to measure phenotypic variation, multivariate analysis using Mahalanobis's D^2 statistic is a powerful tool. This study was initiated to evaluate the type and extent of genetic divergence among thirty-two cucumber genotypes in light of the foregoing. The breeder might utilize the results of a study like this to choose economically and genetically advantageous genotypes to include into the breeding plan in order to achieve the desired gains in Odisha.

MATERIALS AND METHODS

The research work was carried out during *Rabi*, 2019, at the OUAT's Department of Vegetable Science's experimental field in Bhubaneswar, Odisha with a plot size of 3.2 m × 3.0 m. A Randomized Block Design with 32 genotypes and 3 replicates was used in the study. Characters such as node at which first female flower appears, number of days to first harvest, fruit length (cm), fruit diameter (cm), average fruit weight (g), number of fruits per plant, vine length (m), TSS (OB), shelf life (days), severity of downy mildew (%) and fruit yield per vine were recorded from five randomly selected plants in each plot to reduce the likelihood of bias. (kg). Mahalanobis D^2 (1936) statistics were used in Windostat 9.30 to calculate genetic divergence (D^2) and a dendrogram, Mahalanobis Tocher distance, was created and displayed in Fig 1 and 2.

RESULTS AND DISCUSSION

D^2 analysis

D^2 values were used to divide the 32 genotypes into five quite different groups, as depicted in (Table 1). Within each cluster, D^2 values ranged from 0.00 to 45.08. Table 2 showed that the intra cluster diversity was greatest in cluster I (with 25 genotypes), next in cluster III (with 23.94) and finally in clusters II, IV and V (with 1 genotype each), where the intra cluster distance was zero. Similar results were found by Suma *et al.* (2021); Kumar *et al.* (2013) and Hasan *et al.* (2015) in cucumber and Indrajya *et al.* (2022). Genotypes that clustered together had originated from several locations. Genotypes from the same geographic location clustered separately, contrary to expectations. This revealed that there was no certain connection between spatial and genetic diversity. Materials with the same origin were clustered together, indicating that the genotypes from that origin have a diverse genetic background.

The D^2 values, which were used to determine the statistical separation of the clusters, are also depicted visually (Fig 2). The most divergent clusters were Cluster I and Cluster V ($D^2 = 133.68$), then Cluster II and Cluster V ($D^2 = 122.47$), Cluster II and Cluster IV ($D^2 = 120.70$) and Cluster I and Cluster III ($D^2 = 110.29$). It was determined, however, that the shortest distance ($D^2 = 24.55$) existed between Clusters II and III. The different genotypes indicated by maximal inter cluster distance will differ in phenotypic performance, hence it is vital to select divergent parents based on these distances in order to develop favorable hybrids and transgressive segregants in cucumber. So, in addition to selecting genotypes from clusters that have substantial inter cluster distance for hybridization, it is also conceivable to think about selecting parents based on the level of genetic divergence with reference to a particular character of interest. This means that, depending on the breeder's intentions, one may select

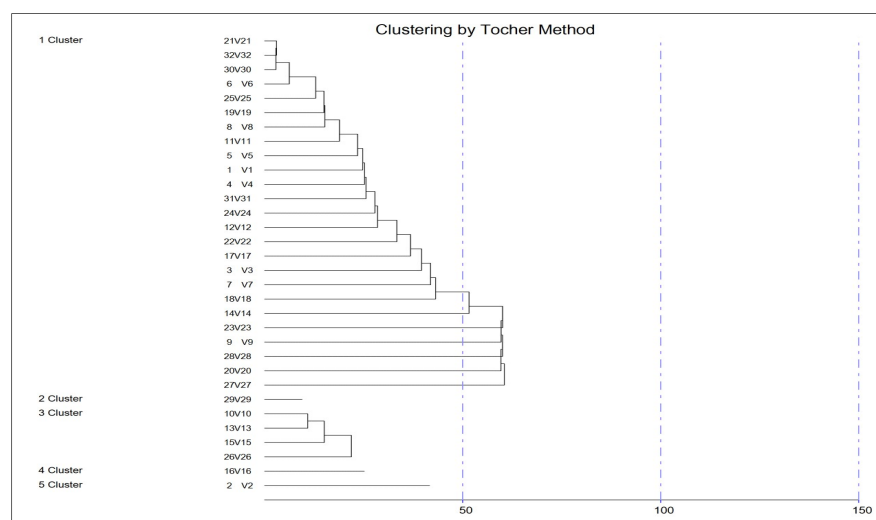


Fig 1: Clustering pattern in cucumber genotypes by tocher method.

parents that are extremely different from one another in terms of productivity, fruit size, or shelf life.

Cluster means for different characters

Table 3 displays the mean values for 12 quantitative traits of 32 genotypes of Cucumber. Mean values for node at which the first female flower appears (6.59), number of days to first female flower production (40.67), days to first harvest (40.67) and total soluble solids (4.82) were all highest for Cluster II genotypes. Cluster IV had the longest fruit length (21.31 cm), high fruit weight (210.42 g), longest vines, highest yields per plant (2.27 g) and highest total

soluble solids. (3.08). Among the five clusters, Cluster V had the highest mean cluster values for number of fruits per plant (11.89), fruit diameter (3.53), fruit shelf life (5.30), downy mildew severity (9.24 %) and the lowest mean cluster values for node at which first female flower appears (2.88) and days to first fruit harvest (35.74). Several studies, including those by Hasan *et al.* (2015), Ahirwar *et al.* (2017), Shewta *et al.* (2018) and Kumar *et al.* (2019), have highlighted the significance of cucumbers genetic diversity.

Clusters were created using the following characteristics to determine their relative contributions to the variation: fruit yield per vine (16.50%), number of fruits

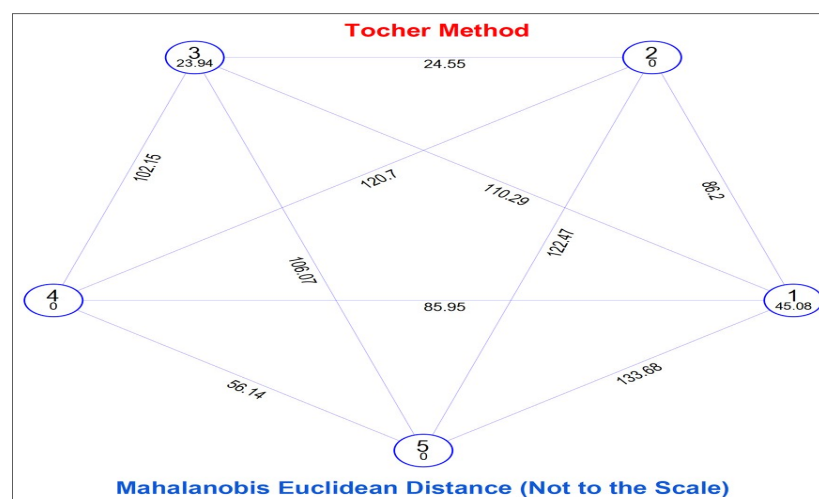


Fig 2: Mahalanobis tocher distance (not to scale).

Table 1: Clustering pattern of thirty- two genotypes of cucumber on the basis of D² statistic.

Cluster number	Number of genotypes within cluster	Genotypes in a cluster
I	25	Swarn Sheetal, Priya, Barshalaxmi, Sachin, Gangothri, Rajamata, Barsha, Rain special, Varshamangalam, Special Machar sasa, Khirasagar, Mahaprasad, Kalpatarusasa improve, Duranta, Sagar, 12 patasasa, Nandini, Barsamongal, Shubra, Gautam-910, Banki local, Bharatmata, Kheeraharalamba, Barsharani and Adimata
II	1	Kheeraharalamba
III	4	Pant Khira-1, Barsha mangalsasa, Saptarishi and Green long
IV	1	Green long S-82
V	1	Tejas

Table 2: Inter and intra cluster D-square values.

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	45.08	86.20	110.29	85.95	133.68
Cluster II	86.20	0.00	24.55	120.70	122.47
Cluster III	110.29	24.55	23.94	102.15	106.07
Cluster IV	85.95	120.70	102.15	0.00	56.14
Cluster V	133.68	122.47	106.07	56.14	0.00

Table 3: Cluster means for different characters among 32 genotypes of cucumber.

Cluster/character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
NFFFA	5.00	6.59	5.25	4.54	2.88
DFFFP	38.35	40.67	37.81	33.63	28.12
DFH	47.64	52.84	48.34	40.65	35.74
FL (cm)	14.49	15.31	15.64	21.31	19.20
FD (cm)	3.97	4.31	4.95	4.06	3.53
AFW (g)	137.34	178.53	197.63	210.42	191.05
NFP	8.31	8.22	10.08	11.02	11.89
VL (m)	2.00	2.42	2.51	3.09	2.89
TSS (°B)	3.37	4.82	4.55	3.08	4.75
SL (Days)	5.61	6.85	7.68	6.65	5.32
SDM (%)	18.03	16.39	13.16	10.42	9.24
FYPV (kgs)	1.13	1.41	1.95	2.27	2.23

Where, NFFFA= Node at which first female flower appears, DFFFP= Number of days to first female flower production, DFH= Days to first harvest, FL= Fruit length (cm), FD= Fruit diameter (cm), AFW= Average fruit weight (g), NFP= Number of fruits per plant, VL= Vine length (m), TSS= Total soluble solids (°B), SL= Shelf life, SDM (%)= Severity of downy mildew (%), FYPV= Fruit yield per vine (kg).

Table 4: Contribution of each character to divergence.

Character	No. of first rank	% Contribution
Node at which first female flower appears	43	8.50
Number of days to first female flower production	28	5.65
Days to first harvest	36	7.20
Fruit length (cm)	36	7.10
Fruit diameter (cm)	34	6.80
Average fruit weight (g)	49	9.80
Number of fruits per plant	54	10.80
Vine length (m)	28	5.60
Total soluble solids (°B)	39	7.85
Shelf life (days)	31	6.14
Severity of downy mildew (%)	40	8.06
Fruit yield per vine (kg)	83	16.50

per plant (10.80%), average fruit weight (9.80%), node at which first female flower appears (8.50%), severity of downy mildew percentage (8.06%), total soluble solids (7.15%), days to first harvest (7.20%), fruit length (7.10%) and fruit width (7.10%) displayed in Table 4. Hanchimani (2006) observed that clustering in cucumber was most affected by factors such as fruit number per vine, fruit length, average fruit weight, and yield per vine. Similar trends have been observed by previous studies who examined both the average fruit weight (Staub *et al.*, 1997; Rasheed *et al.*, 2002, in Pumpkin; Praveen Kumar, 2011, in muskmelon) and the number of fruits per vine in bottle gourd (Badade *et al.*, 2001).

CONCLUSION

Genotypes collected from different eco-geographic regions were found to be highly variable. Genotypes from clusters IV and V, which showed the highest mean for yield per plant, were also distinguished by their longer fruits, heavier average fruits, higher total number of fruits per plant, longer vines, lower incidence of downy mildew percentage and

earlier ripening". Selection from cluster I is effective for breeding programs targeting the small-fruited group and it is also effective for generating long-storage fruit varieties. High-diversity cluster genotypes may be used in a breeding program to create high-yielding varieties with desirable qualities and they may also be used in a heterosis breeding program to create F_1 hybrids with exceptional yield and quality characteristics. Screening for significant features, such as average fruit weight, fruit length and fruit production, is necessary when selecting genetically varied genotypes for hybridization. These characters can then be exploited for further development by phenotypic selection.

ACKNOWLEDGEMENT

The authors would like to thank the College of Agriculture, Department of Vegetable Science and Odisha University of Agriculture and Technology in Odisha, India for their assistance with this experiment.

Conflict of interest

All authors declare that they have no conflicts of interest.

REFERENCES

- Ahirwar, C.S., Singh, D.K. and Kushwaha, M.L. (2017). Assessment of genetic divergence in cucumber (*Cucumis sativus* L.) germplasm through clustering and principal component analysis. *International Journal of Pharmacognosy Phytochemistry*. 6(5): 804-807.
- Badade, D.S., Warade, S.D. and Gaikwad, S.K. (2001). Genetic divergence in bottle gourd. *Journal of Maharashtra Agriculture University*. 26(2): 137-139.
- Bailey, L.H. (1969). *Manual of Cultivated Plants*. Macmillan Company, New York.
- Hasan, R., Hossain, M.K., Alam, N., Bashir, A., Islam, S. and Tarafder, M.J.A. (2015). Genetic divergence in commercial cucumber (*Cucumis sativus* L.) genotypes. *Bangladesh Journal of Botany*. 44(2): 201-207.
- Hanchinamani, C.N. (2006). Genetic variability, divergence, heterosis and combining ability studies in cucumber (*Cucumis sativus* L.), Ph.D. (Hort.) Thesis, Univ. Agri. Sci., Dharwad, Karnataka, India.
- Indraja, G., Sadarunissa, S., Madhumathi, C., Tanuja, P., Sekhar, M.R. (2022). Genetic diversity and correlation coefficient studies in muskmelon (*Cucumis melo* L.). *Agricultural Science Digest*. 10: 1-5. doi: 10.18805/ag.D-5409.
- Kumar, S., Kumar, D., Kumar, R., Thakur, K.S. and Dogra, B.S. (2013). Estimation of genetic variability and divergence for fruit yield and quality traits in cucumber (*Cucumis sativus* L.) in north-western Himalayas. *Universal Journal of Plant Sciences*. 1(2): 27-36.
- Kumar, J.S., Pandit, M.K. and Pathy, T.L. (2019). Genetic variability, diversity and character association in sponge gourd [*Luffa cylindrical* (Roem.) L.]. *International Journal of Current Microbial Applied Sciences*. 8(3): 278-290.
- Kumar, P.R.B. (2011). Studies on genetic diversity in muskmelon (*Cucumis melo* L.). M.Sc. (Hort.), Thesis, College of Horticulture, Hyderabad, Andhra Pradesh.
- Mahalanobis, P.C. (1936). On the Generalised Distance in Statistics. *Proceedings of the National Institute of Sciences of India*. 2: 49-55.
- Rasheed, M., Nabi, S.A., Rasul, M. and Main, A. (2002). Genetic divergence in pumpkin (*Cucurbita moschata* Duch ex Poir). *Bangladesh Journal of Plant Breeding*. 59: 221-225.
- Sebastian, P.M., Schaefer, H., Telford, I.R.H. and Renner, S.S. (2010). Cucumber and melon have their wild progenitors in India and the sister species of *Cucumis melo* is from Australia. *Proceedings of the National Academy of Sciences*. 107(32): 14269-14273.
- Shweta, S., Kumar, R., Sharma, H.R., Sharma, J. and Gautam, N. (2018). Divergence studies for different horticultural traits in cucumber (*Cucumis sativus* L.). *International Journal of Current Microbial Applied Science*. 7(2): 1733-1741.
- Staub, J.E., Serquen, F.C., McCreight, J.D. (1997). Genetic diversity in cucumber (*Cucumis sativus* L.): An evaluation of Indian germplasm. *Genetic Resources of Crop Evolution*. 44: 315-326.
- Suma, A., Elsy, C.R., John, K.J., Pradeepkumar, T., Francies, R., Joseph, J., Santhoshkumar, A.V., Krishnan, S., Yadav, S.K. (2021). genetic diversity in indian landraces of cucumber (*Cucumis sativus* L.) based on morpho-horticultural traits. *Indian Journal of Plant Genetic Resources*. 34(3): 411-423.