Plant Archives Vol. 26, Supplement 1, 2026 pp. 131-135 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org
DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2026.v26.supplement-1.019

GENETIC DIVERGENCE STUDY IN PUMPKIN (*CUCURBITA MOSCHATA* DUCH. EX. POIR)

Vineela Grace[1]*, Raveendra S. Jawadagi[2], Namita Bhaskar Raut[3], Dadepeera Peerajade[4] and Satyanarayana C.[5]

[1]Department of vegetable science, College of horticulture, UHS, Bagalkot, Karnataka, India
[2]Professor & Special Officer (Seeds), Seed Unit, UHS, Bagalkot, Karnataka, India
[3]Department of Vegetable Science, AICRP on Vegetables, RHREC, Kumbapur, Dharwad, Karnataka, India
[4]Department of Biotechnology and Crop Improvement, College of Horticulture, UHS, Bagalkot, Karnataka, India
[5]Department of Entomology, College of Horticulture, UHS, Bagalkot, Karnataka, India
(Date of Receiving : 14-08-2025; Date of Acceptance : 21-10-2025)

ABSTRACT

Pumpkin (*Cucurbita moschata* Duch.) is one of the most popular summer vegetable crops and belongs to the Cucurbitaceae family. A study on genetic divergences was carried out on 77 diverse genotypes of pumpkin during *rabi* 2024-2025. Genetic divergence in 77 pumpkin landraces for 19 different traits using Mahalanobis D^2 statistics and Tocher's clustering generated five clusters of the 77 pumpkin landraces. Seed index showed the maximum contribution followed by days to first harvest, fruit diameter, Days to 1st pistillate flower anthesis and carotene content in fruits. Intra cluster distance was maximum along cluster V accompanied by III, I, IV and II. The maximum inter-cluster divergence was observed between Cluster I and IV followed by Cluster I and V, Cluster I and III, Cluster IV and V. The landraces from these clusters may be selected as parents in future hybridization programs to obtain superior combinations and heterosis in segregating generation. Amongst these five clusters, cluster V exhibited highest intra-cluster diversity indicating the presence of heterogeneity among the landraces and they can be parents in hybridization programme. Cluster IV recorded the highest mean values for fruit yield per plant, fruit weight, fruit length and vine length at final harvest.
Keywords **:** Genetic divergence, Mahalanobis D^2, Tocher's cluster, hybridization

Introduction

Pumpkin (*Cucurbita moschata* Duch.) is one of the most popular summer vegetable crops, belonging to the family Cucurbitaceae. Pumpkin with diploid chromosome number 2n=2x=40 is also one of the most morphologically variable species in the plant kingdom for fruit shape, size and colour (Wu *et al*., 2011). There are 27 species under the genus Cucurbita, five of which are in cultivation. These are *C. moschata, C. maxima, C. ficifolia, C. pepo* and *C. mixta*, commonly known as Pumpkin. *C. moschata* is probably the most widely grown species of cucurbita and this species is cross compatible with *C. maxima, C.pepo* and *C.mixta* (Tindall, 1987). In India, the area under cultivation of pumpkin is It is an excellent source of minerals and vitamins for our diet, having a rich amount of beta carotene next to carrots (Kumar *et al.,* 2018).

Genetic diversity is one of the important tools to quantify genetic variability in both cross and self-pollinated crops and also important for crop improvement as well as variety development programme (Anand *et al.,* 1975 and Gaur *et al*., 1978). Multivariate analysis using Mahalanobis D^2 statistics is a valuable tool for measuring genotypic divergence among populations and evaluating the contribution of various traits to total divergence at both inter- and intra-cluster levels (Das and Gupta, 1984). This D^2 method has been widely employed by researchers to assess divergence among pumpkin genotypes. Understanding the extent and nature of variability within germplasm is essential for crop improvement.

Accordingly, the present study was conducted to assess the genetic divergence among pumpkin genotypes, with the aim of identifying diverse parents for future breeding programs.

Material and Methods

This study was conducted during the *rabi* season of 2024–25 at the Experimental Farm of the University of Horticultural Sciences (UHS), Bagalkot. The site falls under Zone-3 of region-2 in Karnataka's agro-climatic classification, located at 72º42' E longitude, 16º10' N latitude, with an altitude of 542 m above mean sea level. The experimental material comprised 77 diverse pumpkin genotypes, including four checks (Arka Chandan, Arka Suryamukhi, Indam Chakra and Kashi Harit). Each genotype was represented by six plants, with the checks replicated in each block and planted at a spacing of 3 m between rows and 1 m between plants, following an Augmented Block Design. Recommended agronomic practices and plant protection measures as per UHSB were followed to ensure optimal crop growth and health. Observations were recorded timely and appropriately on 19 horticultural traits *viz.,* vine length at final harvest (m), number of primary branches at final harvest, Days to first male and female anthesis, node at first male and female flower appearance, fruit weight (kg), fruit length (cm), fruit diameter (cm), seed index (100 seed weight), fruit rind thickness (mm), seed cavity (cm), days to first harvest, number of fruits per vine, fruit yield per plot (kg), fruit yield per hectare (tons), total soluble solids (^{0}B) and Carotene content in fruits (mg/100g). Statistical analysis of principal component was done using software of R studio and Grapes (KAU). The genetic divergence among genotypes was estimated by using D2 statistics (Mahalanobis 1936). All the genotypes used were clustered into different groups by following Tocher's method (Rao, 1952). The average intra and inter cluster distances were calculated by the formulae given by Singh and Chaudhary (1985).

Result and Discussion

Based on D^2 values, the genotypes were grouped into five highly divergent clusters (Table 1) the magnitude of D^2 values confirmed that there was considerable amount of diversity in the experimental material evaluated. Cluster I attained the highest number of genotypes, comprising 29 genotypes, subsequent to Cluster II with 25 genotypes, Cluster III with 11 genotypes, Cluster IV with 7 genotypes and Cluster V with 5 genotypes represented in table 1. The clustering pattern indicated that the genetic diversity was not fully associated with geographical diversity; hence, there was no formal relationship between geographical diversity and genetic diversity. These results conformed with Kandasamy *et al*. (2019) and Krishnamoorthy and Sampath (2019).

Intra and inter cluster distances

Studies on the intra and inter clusters D^2 values showed in table 2 revealed that highest intra-cluster distance in cluster V (D^2 = 6.071) with five genotypes accompanied by cluster III (D^2 = 5.037) with eleven genotypes, cluster I (D^2 = 4.881) with twenty-nine genotypes, cluster IV (D^2 = 4.815) and least intra-cluster distance was noticed in cluster II (D^2 = 4.608) with twenty-five genotypes. Evaluation on the inter-cluster distance shows the maximum divergence between cluster I and IV (D^2 = 9.275) closely accompanied by cluster I and V (D^2 = 8.993) and cluster I and III (D^2 = 7.500). This indicates that these clusters contain genotypes that are genetically most diverse and, therefore, could serve as promising parents in hybridization programs for the exploitation of heterosis and generation of broad genetic variability in segregating populations. Crossing between such highly divergent clusters is likely to result in hybrids with superior yield potential and desirable horticultural attributes. Whereas, cluster II and III (D^2 = 5.269) recorded the least inter-cluster distance and next lowest was between cluster III and IV (D^2 = 5.681). This indicates that, these clusters are genetically similar and less diversity was observed.

Contribution of individual character towards total divergent

The contribution of individual traits to overall divergence is summarized in Table 3. The analysis of influence on genetic divergence revealed that all 19 characters exhibited relatively uniform influence, ranging between 4.75% and 5.99%. Among them, seed index showed the maximum contribution (5.99%), subsequently days to first harvest (5.56%), fruit diameter (5.54%), Days to 1st pistillate flower anthesis (5.52%) and carotene content in fruits (5.47%). Other traits such as fruit length (5.45%), vine length at final harvest (5.41%), seed cavity (5.40%) and days to 1st staminate flower anthesis (5.43%) also contributed significantly. The least contributing trait was total soluble solids (4.75%), though its effect was still noticeable. Hence, these characters should be given importance during hybridization and selection in the segregating population.

Cluster mean

The mean values of 19 characters for 5 clusters are summarized in Table 4. For yield per plant, the highest cluster mean observed in cluster IV followed

by cluster III, II, V and I. For days to first staminate flower anthesis least cluster mean was obtained in cluster V followed by cluster III, cluster IV, cluster II and cluster I. For days to first staminate flower anthesis least cluster mean was obtained in cluster V subsequently cluster III, IV, II and I. For the node at first male flower appearance least cluster means was obtained in cluster V followed by cluster I, IV, II and III. For the node at first female flower appearance least cluster means was obtained in cluster V followed by cluster IV, III, II and I. For fruit weight and fruit length the highest mean value was observed for cluster IV succeeded by cluster V, III, II and I. For vine length at final harvest the highest mean value was observed for cluster IV followed by cluster II, V, II and I. For number of primary branches at final harvest the highest mean was noticed in cluster II followed by cluster IV, III, I and V. For fruit diameter and seed index recorded the greatest cluster mean in cluster V followed by cluster IV, III, II and I. For fruit rind thickness greatest mean within the cluster was noted in cluster V followed by cluster III, II, IV and I. For seed cavity has the maximum mean recorded in the cluster V succeeded by cluster IV, III, II and I. For days to first harvest least cluster mean was obtained in cluster I followed by cluster II, IV, III and V. For number of fruits per vine was recorded the greatest cluster mean in cluster I followed by cluster II, III, IV and V. For fruit yield per vine, fruit yield per plot and fruit yield per hectare highest cluster means were noticed in cluster IV followed by cluster III, II, V and I. Qualitative traits like TSS was recorded the greatest cluster mean in cluster II followed by cluster IV, III, V and I. Carotene content in fruits exhibited the cluster showing the maximum mean in cluster V succeeded by cluster IV, III, II and I. Therefore, initiating a hybridization program between genotypes from the respective clusters may be pursued for effective crop improvement.

Conclusion

In conclusion, the Mahalanobis D^2 analysis revealed substantial genetic diversity among the 77 pumpkin genotypes, which were grouped into five distinct clusters. The high inter-cluster distances, particularly between clusters I and VI and between clusters I and V, indicate the presence of considerable genetic divergence that can be exploited in breeding programs. The traits contributing most to this divergence seed index, days to first harvest and fruit diameter highlight key attributes influencing genetic variability. Therefore, hybridization between genotypes from these diverse clusters may be beneficial for developing superior and high-yielding genotypes with desirable agronomic traits.

Table 1 : Composition of clusters in pumpkin based on D^2 statistics

Clusters	Number of genotypes	Genotypes assigned to the cluster	Source
Cluster I	29	Check – 4	IIVR, Varanasi
		Check-3	IAHS, Bangalore
		G-45, G-33, G-55, G-29, G-57, G-35, G-22, G-13, G-27, G-14, G-20, G-54, G-49, G-78, G-44, G-52, G-40, G-46, G-24, G-53, G-60, G-36	KRCCH, Arabhavi, Karnataka
		G-63, G-69, G-68	Sirsi, Karnataka
		G-62	Andhra Pradesh, India
Cluster II	25	G-37, G-50, G-28, G-56, G-23, G-25, G-7, G-19, G-10, G-18, G-16, G-15, G-30, G-58, G-31, G-51, G-21, G-47, G-26, G-32	KRCCH, Arabhavi, Karnataka
		G-72, G-65, G-64	Sirsi, Karnataka
		G-61	Kerala, India
		G-70	Chattisghar
Cluster III	11	Check-2	IIHR, Hessarghatta
		G-12, G-2, G-4, G-1, G-9, G-11, G-8, G-17, G-5, G-6	KRCCH, Arabhavi, Karnataka
Cluster IV	7	Check-1	IIHR, Hessarghatta
		G-77, G-59, G-42, G-41, G-48, G-34	KRCCH, Arabhavi, Karnataka
Cluster V	5	G-38, G-76, G-75	KRCCH, Arabhavi, Karnataka
		G-73	Tamilnadu, India
		G-74	Sirsi, Karnataka

Table 2: Average inter and intra cluster (diagonal) distance D^2 and D values in pumpkin genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	**4.881**	6.352	7.500	9.275	8.993
Cluster II		**4.608**	5.269	6.166	7.337
Cluster III			**5.037**	5.681	6.658
Cluster IV				**4.815**	7.039
Cluster V					**6.071**

Table 3 : Per cent contribution of the different attributes affecting total divergence in germplasms of pumpkin

SI. No.	Characters	Contribution %
1	Days to 1st staminate flower anthesis	5.43
2	Days to 1st pistillate flower anthesis	5.52
3	Node at initial male flower	5.2
4	Node at initial female flower	5.13
5	Fruit weight (kg)	5.15
6	Fruit length (cm)	5.45
7	Vine length at final harvest (m)	5.41
8	Number of primary branches at final harvest	4.96
9	Fruit diameter (cm)	5.54
10	Seed index	5.99
11	Fruit rind thickness(mm)	5.27
12	Seed cavity(cm)	5.4
13	Days to first harvest	5.56
14	Number of fruits per vine	4.9
15	Fruit yield per vine	4.97
16	Fruit yield per plot (kgs)	4.97
17	Fruit yield per hectare (tons)	4.95
18	Total soluble solids (^{0}B)	4.75
19	Carotene content in fruits (mg/100g)	5.47
	Total	100.02

Table 4 : The mean of nineteen characters for eight clusters in pumpkin genotypes

SL. No	Characters	I	II	III	IV	V
1	Days to 1st staminate flower anthesis	52.08	50.77	49.79	50.51	46.47
2	Days to 1st pistillate flower anthesis	53.84	52.59	51.62	51.97	48.33
3	Node at first male flower appearance	3.89	4.09	4.51	3.97	2.73
4	Node at first female flower appearance	15.25	14.83	14.74	14.18	12.00
5	Fruit weight (kg)	1.36	3.24	3.76	6.61	4.29
6	Fruit length (cm)	22.10	32.73	35.30	41.63	35.45
7	Vine length at final harvest (m)	3.92	5.31	4.92	5.32	5.10
8	Number of primary branches at final harvest	3.80	4.47	4.15	4.37	3.10
9	Fruit diameter (cm)	14.90	17.21	21.41	23.03	23.40
10	Seed index	11.77	12.95	15.45	15.48	19.06
11	Fruit rind thickness(mm)	27.10	30.28	31.75	28.44	34.22
12	Seed cavity(cm)	9.22	12.79	18.26	18.89	19.66
13	Days to first harvest	80.61	82.47	84.78	83.56	85.40
14	Number of fruits per vine	2.33	2.19	2.04	1.48	1.42
15	Fruit yield per vine	2.70	6.40	6.84	9.14	5.53
16	Fruit yield per plot (kgs)	15.77	37.92	40.62	54.34	32.70
17	Fruit yield per hectare (tons)	8.39	20.75	22.22	29.94	17.80
18	Total soluble solids (^{0}B)	7.17	10.04	9.65	9.74	8.26
19	Carotene content in fruits (mg/100g)	0.76	0.90	1.40	1.77	1.90

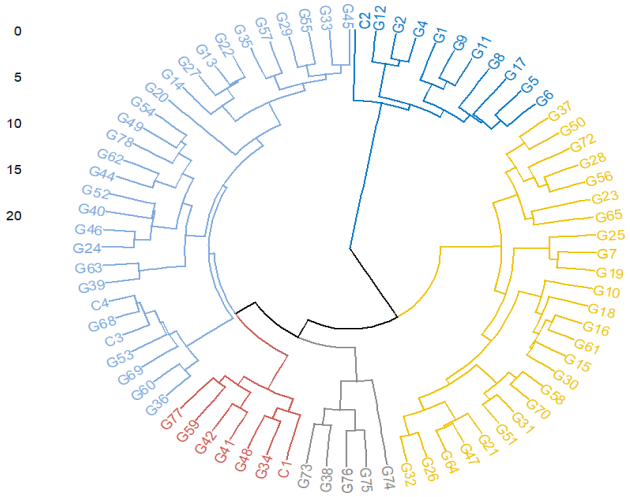

Fig. 1: Clustering pattern for divergence in pumpkin genotypes

References

Anand, I. N., Singh, J. N. and Khanna, P. P. (1975). Inter relationships and diversity in Indian colza. *Indian J. Agric. Sci.,* **45**: 253 258.

Das, P. K. and Gupta, T. D. (1984). Multivariate analysis in Blackgram. *Indian J. Genet.,* **44**(2): 243-247.

Gaur, P.C., Gupta, P.K. and Kishore, H. (1978). Studies on genetic divergence in potato. *Euphytica*. 27.361-368.

Kandasamy, R., Arivazhagan, E., Anusa, P. (2019). Genetic divergence among landraces of pumpkin (*Cucurbita moschata* Duch ex. Poir) from Tamil Nadu. *Annals of Plant and Soil Research*, **21**(4):333-336.

Krishnamoorthy, V., Sampath, S. (2019). Genetic diversity analysis in pumpkin (*Cucurbita moschata* Duch Ex. Poir). *Intern. J Chem. Stud.,* **7**(3), 3672-3676.

Kumar, R., Rajasree, V., Praneetha, S., Rajeswari, S., Tripura, U., & Sriyamuna, V. S. (2018). Per se Performance of Pumpkin Hybrids for Small Size, Thick Flesh with High Yield and Quality Traits. *Int. J. Curr. Microbiol. App. Sci*, *7*(6), 2591-2598.

Mahalanobis, P. C. (1936). On the generalized distance in statistics. *Proceedings of the National Institute of Science of India*, **2**: 49–55.

Rao, C. R. (1952). Advanced Statistical Methods in Biometrical Research. John Wiley and Sons. New York.

Singh, R. K. and Chaudhary, B. D. (1985). Biometrical methods in quantitative genetic analysis.Kalyani Publishers. New Delhi, India.318 p.

Tindall, H. D. (1987). Vegetables in the tropics. Macmillan Education, London. P.166.

Wu, J., Chang, Z., Wu, Q., Zhan, H., Xie, S. (2011). Molecular diversity of Chinese Cucurbita moschata germplasm collections detected by AFLP markers. *Sci. Hortic.,* **128**, 7-13.