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## Genetic divergence studies on growth, yield and quality traits in pumpkin (*Cucurbita moschata* Duch. Ex. Poir.) Genotypes

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### Abstract

Genetic divergence study was conducted on 33 pumpkin genotypes for thirty-seven characters at College of Horticulture, venkataramannagudem during 2022–2023. These genotypes were grouped into six clusters irrespective of geographic divergence, indicating no parallelism between geographic and genetic diversity. Cluster-I was the largest comprising 20 genotypes, followed by Cluster-II with 7 genotypes, Cluster-III with 3 genotypes. Clusters-IV, V and VI comprised one genotype each. As regards cluster means, Cluster-VI performed better in most of the biometric characters studied. Maximum inter-cluster distance was observed in Clusters-V and VI, followed by Clusters-IV and VI, and clusters-I and VI. Intra-cluster distance was highest in Cluster I.

**Keywords:** Pumpkin, genetic divergence, cluster

### Introduction

The cucurbit family is one of the largest families in the plant kingdom including the largest number of edible species. There are 27 species in the genus *Cucurbita*, of which 5 are cultivated. These are *Cucurbita moschata*, *Cucurbita maxima*, *Cucurbita ficifolia*, *Cucurbita pepo* and *Cucurbita mixta*. *Cucurbita moschata* is commonly known as pumpkin and is a widely grown *Cucurbita* species and the fruit is highly prized for its long-storing ability and high nutritional value (Jahan *et al.* 2012) [5]. This species is compatible with *C. maxima*, *C. pepo* and *C. mixta* (Tindall, 1987) [24]. Pumpkins are widely used as vegetables in both the young and mature stages and ripe fruits can be stored for 2 to 4 months (Yawalkar, 1991) [25]. Fruits with yellow and orange flesh are rich in carotene (3,332 IU), a precursor to vitamin A with abundant vitamins B and C. This can help improve the nutritional status of the population, especially vulnerable groups in terms of vitamin A requirements (Satkar *et al.* 2013) [20]. In India, pumpkins are grown on an area of 106 million hectares, with a total production of 2,218 tons and a yield of about 20.92 tons/hectare (NHB database, 2021-22). As for pumpkins, the main issue of consumer preference is the large fruit (4 to 5 kg), which is not very popular for a small family of 3 to 4 members. Furthermore, with the recent increase in the number of nuclear families in India, people prefer to buy only small and medium sized whole pumpkins rather than cut into pieces. Additionally, small fruits can be easily packed and transported without damage. Therefore, it is necessary to develop pumpkin varieties and hybrid pumpkin varieties with small to medium fruit sizes (2-3 kg). Several efforts have been made by the public and private sectors to develop high-yielding varieties and hybrids. However, the development of high-yield varieties and hybrids combined with medium-sized fruits with high beta-carotene content is still very limited. Pumpkins have received less attention in crop improvement compared to other cucurbits. Since ancient times, large amounts of genetic material have been available, but the conscious evaluation and exploitation of genetic material has only recently been realized. This is useful for the plant breeder when developing a commercially suitable variety for the market by identifying the constituent traits for which selection can be made based on improvement in yield and quality. Preliminary identification of early-maturing genotypes can be done based on characteristics such as days to appearance of first female flower, node number at which first female flower appeared, days to first fruit harvest.

Collection and evaluation of germplasm is a prerequisite for any breeding program aimed at selecting high-yielding genotypes with the desirable characteristics of high earliness, yield and

quality. Therefore, characterization of the available pumpkin germplasm was carried out to identify potential early-maturing, high-yielding cultivars of small and medium fruits as well as other cultivars. Quality parameters are improved. Furthermore, genetic advance can be used to predict selection efficiency. Mahalonobis (1936) [12]  $D^2$  statistics provide a measure of the magnitude of divergence between two groups under comparison.  $D^2$  genotype grouping will be useful in selecting suitable parental lines for heterosis breeding as well as deriving superior segregating lines from specified crosses.

### Material and Methods

Thirty-three genotypes (Table 1) of pumpkin having diverse origin were evaluated at the College of Horticulture, Venkataramannagudem, during the period November-April, 2022-23. Genotypes were evaluated using Augmented Block Design, with three blocks. Plants were grown at a spacing of 1.5 m  $\times$  1.5 m adopting the package of practices as recommended. Observations were recorded on five randomly selected plants of each genotype in each block for thirty-seven

characters, viz., vine length (cm) at final harvest ; internodal length (cm) at 45 DAS, 90 DAS and final harvest; petiole length (cm) at 45 DAS, 90 DAS and final harvest; number of branches per plant at 45 DAS, 90 DAS and final harvest; number of leaves per plant at 45 DAS, 90 DAS and final harvest; days to appearance of first male flower; node number at which first male flower appeared; days to appearance of first female flower; node number at which first female flower appeared; number of male flowers per plant; number of female flowers per plant; sex ratio (male: female); days to first fruit harvest; number of fruits per vine; number of ridges per fruit; fruit length (cm); fruit diameter(cm); flesh thickness (cm); seed cavity diameter (cm); number of seeds per fruit; test weight (g); average fruit weight (kg); fruit yield per vine (kg); estimated fruit yield (t/ha);  $\beta$ -carotene (mg/ 100 g.f.w); reducing sugars (%); non-reducing sugars (%); total sugars (%) and total soluble solids ( $^{\circ}$ brix). Genetic divergence was estimated using  $D^2$  statistics of Mahalonobis (1928) [10] and the populations were grouped into clusters as per Rao (1952).

**Table 1:** List of genotypes of pumpkin and their source

S. No	Genotype	Source
1.	IC 284761	NBPGR Regional Station, Thrissur, Kerala
2.	IC 333299	NBPGR Regional Station, Thrissur, Kerala
3.	IC 395804	NBPGR Regional Station, Thrissur, Kerala
4.	IC 599403	NBPGR Regional Station, Thrissur, Kerala
5.	IC 599408	NBPGR Regional Station, Thrissur, Kerala
6.	IC 599422	NBPGR Regional Station, Thrissur, Kerala
7.	IC 599425	NBPGR Regional Station, Thrissur, Kerala
8.	IC 599427	NBPGR Regional Station, Thrissur, Kerala
9.	IC 599435	NBPGR Regional Station, Thrissur, Kerala
10.	IC 599436	NBPGR Regional Station, Thrissur, Kerala
11.	IC 599437	NBPGR Regional Station, Thrissur, Kerala
12.	IC 613471	NBPGR Regional Station, Thrissur, Kerala
13.	IC 618053	NBPGR Regional Station, Thrissur, Kerala
14.	IC 618054	NBPGR Regional Station, Thrissur, Kerala
15.	IC 618055	NBPGR Regional Station, Thrissur, Kerala
16.	IC 618056	NBPGR Regional Station, Thrissur, Kerala
17.	IC 618057	NBPGR Regional Station, Thrissur, Kerala
18.	Coimbatore local	Coimbatore, Tamil Nadu
19.	Pollachi local	Pollachi, Tamil Nadu
20.	Mettupalyam local	Mettupalyam, Tamil Nadu
21.	Balaram local	Anakapalle, Andhra Pradesh
22.	Jogumpeta local	Anakapalle, Andhra Pradesh
23.	Kantaram local	Anakapalle, Andhra Pradesh
24.	Komira local	Anakapalle, Andhra Pradesh
25.	Jangareddygudem local	West Godavari, Andhra Pradesh
26.	Martur local	Bapatla, Andhra Pradesh
27.	Vemavaram local	Prakasam, Andhra Pradesh
28.	Vittamrajupalli local	Guntur, Andhra Pradesh
29.	Ummadivaram local	Guntur, Andhra Pradesh
30.	Dechavaram local	Palnadu, Andhra Pradesh
31.	Arka Suryamukhi (Check-1)	IIHR, Bangalore
32.	Local Cultivar-1 (Check-2)	West Godavari, Andhra Pradesh
33.	Local Cultivar-2 (Check-3)	West Godavari, Andhra Pradesh

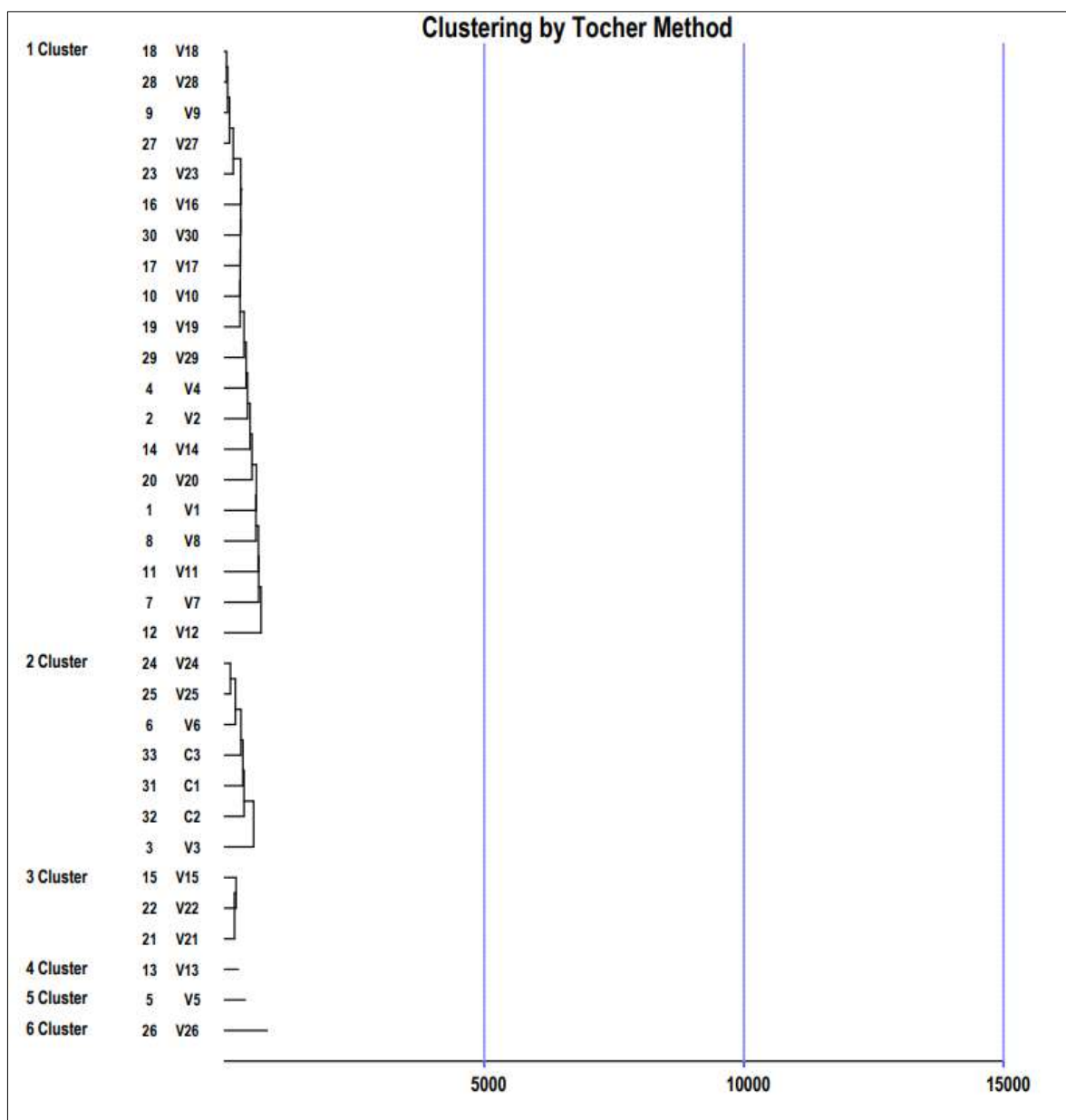
### Results and Discussion

Analysis of variance indicated that mean sum of squares in pumpkin genotypes were not highly significant for all characters except number of male flowers per plant and fruit yield per vine (kg). Having computed  $D^2$  values for all possible pairs, the thirty-three genotypes were classified into

six groups of gene constellations. These indicated a large genetic diversity (Table 2) and (Fig. 1). Maximum number of genotypes (20) grouped under Cluster-I, followed by Clusters-II and III, with 7 and 3 genotypes each. Clusters-IV, V and VI comprised one genotype each (mono-genotypic clusters).

**Table 2:** Distribution of pumpkin genotypes into different clusters

Cluster No.	Number of genotypes	Name of the genotypes
Cluster I	20	IC 284761, IC 333299, IC 599403, IC 599425, IC 599427, IC 599435, IC599436, IC 599437, IC 613471, IC 618054, IC 618056, IC 618057, Coimbatore Local, Pollachi Local, Mettupalyam Local, Kantaram Local, Vemavaram Local, Vittamrajupalli Local, Ummadivaram Local, Dechavaram Local
Cluster II	7	IC 395804, IC 599422, Komira Local, Jangareddygudem Local, Arka Suryamukhi, Local Cultivar-1, Local Cultivar-2
Cluster III	3	IC 618055, Balaram Local, Jogumpeta Local
Cluster IV	1	IC 618053
Cluster V	1	IC 599408
Cluster VI	1	Martur Local



**Fig 1:** Dendrogram showing clustering pattern for divergence in pumpkin genotypes

**Average inter and intra-cluster distances in pumpkin genotypes**

Intra and inter-cluster distances are an index of genetic diversity among clusters as shown in (Table 3) and (Fig. 2). Inter-cluster distances were greater than intra-cluster distances, revealing a considerable amount of genetic diversity among the genotypes studied. Intra-cluster distance was highest in Cluster-I (1441.37), followed by Clusters-II

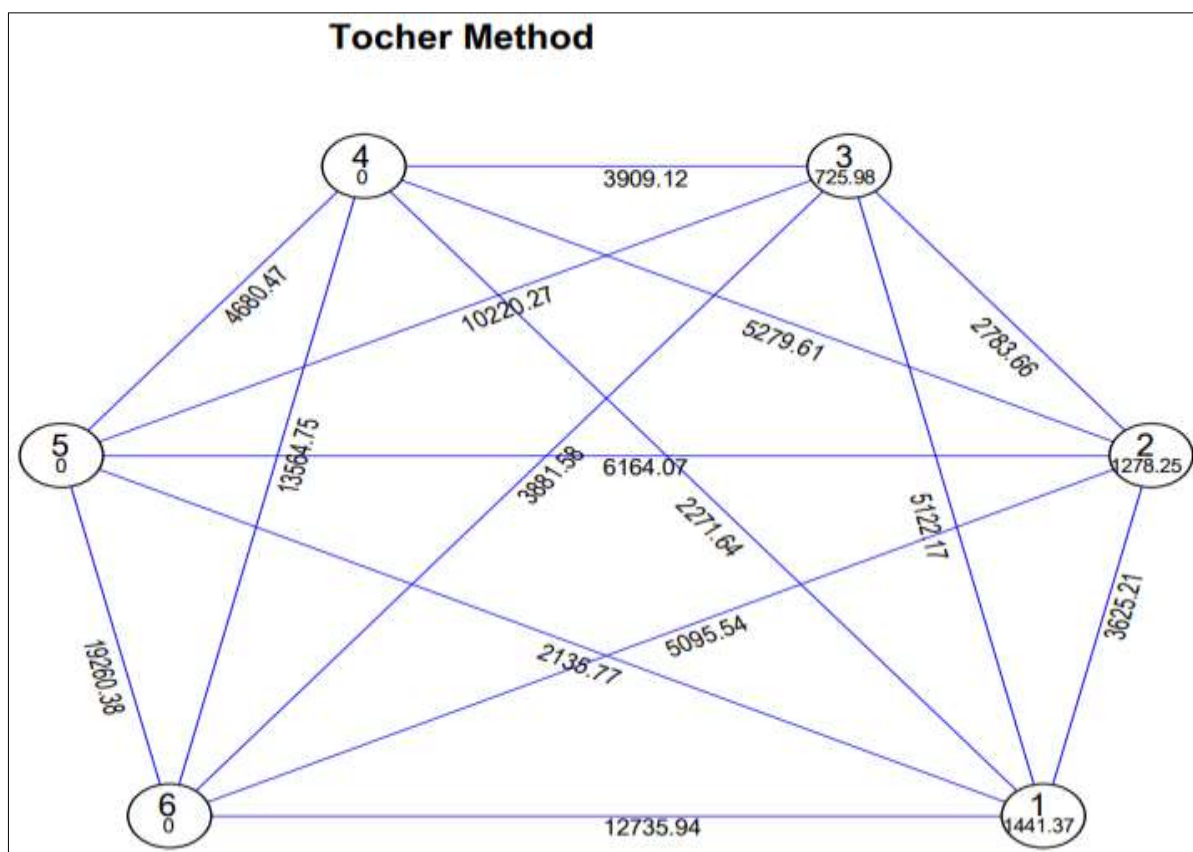
and III (1278.25 and 725.98, respectively). Highest inter-cluster distance was observed in Clusters-V and VI (19260.38), followed by Clusters-IV and VI (13564.75) and Clusters-I and VI (12735.94). Genetic distance ( $D^2$ ) between Cluster-VI was larger than in Clusters- I, IV and V. Minimum inter cluster distance was observed between Clusters-I and V (2135.77) indicating close relationship among genotypes. Data clearly indicated that the genotypes did not cluster

according to their geographical distribution. In general, the pattern of distribution of genotypes from various regions into different clusters was seen to be random. Similar observations were also reported by Lovely (2001) [9] in ash gourd, Kale *et al.* (2002) [6] and Lakshmi *et al.* (2003) [8] in pumpkin, Kandasamy (2004) [7] in melon, Maharana *et al.* (2006) [13] in ivy gourd, and by Devmore *et al.* (2007) [2] and Dey *et al.* (2007) [3] in bitter gourd. One possible reason may be that it is very difficult to establish the actual place of origin of a genotype. Free and frequent exchange of genetic material among breeders in the country makes it very difficult to maintain the real identity of a genotype. Absence of relationship between genetic diversity and geographical

distance indicates that forces other than geographical origin (such as exchange of genetic stock, genetic drift, natural mutation, spontaneous variation or natural and artificial selection) may be responsible for the genetic diversity. Another possibility may be that estimates of diversity based on characters used in the present investigation may not be sufficient to account for variability caused by some other traits of physiological / biochemical nature (which could be important in depicting the total genetic diversity in a population). Therefore, selection of genotypes for hybridization should be based on genetic diversity other than geographic divergence.

**Table 3:** Average inter and intra-cluster (diagonal) distance D<sup>2</sup> values in pumpkin genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	1441.37	3625.21	5122.17	2271.64	2135.77	12735.94
Cluster II		1278.25	2783.66	5279.61	6164.07	5095.54
Cluster III			725.98	3909.12	10220.27	3881.58
Cluster IV				0.00	4680.47	13564.75
Cluster V					0.00	19260.38
Cluster VI						0.00



Mahalanobis Euclidean Distance (Not to the Scale)

**Fig 2:** Cluster diagram showing average intra and inter-cluster D<sup>2</sup> values among pumpkin genotypes

**Cluster means of thirty-seven characters in pumpkin genotypes**

The cluster means for each of thirty-seven characters are presented in (Table 4). Cluster I included the genotypes with highest sex ratio (male: female) (2.52) and with lowest internodal length at final harvest (21.34 cm), petiole length at 45 DAS (14.27 cm), number of female flowers per plant (3.27) and number of fruits per vine (2.11). Cluster II included the genotypes with lowest days to appearance of first

female flower (57.52), number of male flowers per plant (7.09), test weight (10.26 g), estimated fruit yield (16.17 t/ha) and reducing sugars (3.28%). Cluster III included the genotypes with highest number of leaves per plant at 90 DAS (247.93) and number of leaves per plant at final harvest (317.93) and with lowest number of branches per plant at final harvest (11.67), number of female flowers per plant (3.27) and non-reducing sugars (2.39%). Cluster IV included the genotype with highest petiole length at final harvest



(21.75 cm) and number of leaves per plant at 45 DAS (94.20) and with lowest internodal length at 45 DAS (9.90), number of branches per plant at 45 DAS (4.20), number of branches per plant at 90 DAS (7.40), sex ratio (male: female) (2.24), fruit length (14.27 cm), fruit diameter (16.89 cm), number of seeds per fruit (258.80), average fruit weight (1.97 kg) and total soluble solids (3.87 °brix). Cluster V included the genotype with lowest vine length at final harvest (449.13cm), internodal length at 90 DAS (15.40 cm), petiole length at 90 DAS (18.62 cm), petiole length at final harvest (20.86 cm), number of leaves per plant at 90 DAS (214.60), number of leaves per plant at final harvest (284.60), days to first fruit harvest (88.40), number of ridges per fruit (14.00), flesh thickness (2.55 cm), seed cavity diameter (9.92 cm), fruit yield per vine (7.23 kg), beta-carotene (2.30) and total sugars (5.85%). Cluster VI included the genotype with highest vine

length at final harvest (569.66 cm), internodal length at 45 DAS (11.98 cm), internodal length at 90 DAS (19.42 cm), internodal length at final harvest (23.11 cm), petiole length at 45 DAS (16.61 cm), petiole length at 90 DAS (20.41 cm), number of branches per plant at 45 DAS (5.80), number of branches per plant at 90 DAS (9.60), number of branches per plant at final harvest (14.60), number of female flowers (4.40), number of fruits per vine (3.40), number of ridges per fruit (19.40), fruit length (23.05 cm), fruit diameter (21.38 cm), flesh thickness (3.51 cm), seed cavity diameter (12.26 cm), number of seeds per fruit (338.20), test weight (12.40 g), average fruit weight (2.90 kg), fruit yield per vine (10.77 kg), estimated fruit yield (23.96 t/ha), beta-carotene (3.15), reducing sugars (4.16%), non-reducing sugars (2.78%), total sugars (6.93%) and total soluble solids (5.39 °brix).

**Table 4:** Cluster means for growth, yield and quality traits in pumpkin genotypes

S. No	Character	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
<b>Growth characters</b>							
1	Vine length at final harvest (cm)	479.18	518.74	533.55	491.36	449.13	569.66
2	Internodal length at 45 DAS (cm)	10.38	10.92	10.87	9.90	11.21	11.98
3	Internodal length at 90 DAS (cm)	16.84	17.65	18.59	17.53	15.40	19.42
4	Internodal length at final harvest (cm)	21.34	21.92	22.24	22.39	22.38	23.11
5	Petiole length at 45 DAS (cm)	14.27	14.32	15.05	14.46	15.54	16.61
6	Petiole length at 90 DAS (cm)	18.64	19.23	19.49	18.69	18.62	20.41
7	Petiole length at final harvest (cm)	21.10	21.00	21.27	21.75	20.86	21.52
8	Number of branches per plant at 45 DAS	4.63	4.39	4.77	4.20	5.10	5.80
9	Number of branches per plant at 90 DAS	8.60	8.54	8.27	7.40	9.00	9.60
10	Number of branches per plant at final harvest	12.57	12.54	11.67	13.00	13.00	14.60
11	Number of leaves per plant at 45 DAS	75.48	73.70	87.47	94.20	77.60	68.20
12	Number of leaves per plant at 90 DAS	230.25	222.07	247.93	245.00	214.60	235.60
13	Number of leaves per plant at final harvest	300.22	288.57	317.93	317.00	284.60	305.60
<b>Floral characters</b>							
14	Days to appearance of first male flower	54.10	56.21	54.80	51.60	51.00	56.40
15	Node number at which first male flower appeared	13.17	13.59	12.20	17.40	13.00	15.80
16	Days to appearance of first female flower	57.72	57.52	61.33	69.60	58.00	65.00
17	Node number at which first female flower appeared	24.14	24.07	25.60	22.60	25.20	21.40
18	Number of male flowers per plant	8.12	7.09	8.07	7.60	8.50	10.80
19	Number of female flowers per plant	3.27	3.30	3.27	3.40	3.60	4.40
20	Sex ratio (male: female)	2.52	2.38	2.50	2.24	2.36	2.45
<b>Fruit characters</b>							
21	Days to first fruit harvest	93.44	94.37	96.13	93.20	88.40	92.80
22	Number of fruits per vine	2.11	2.38	2.27	2.60	2.20	3.40
23	Number of ridges per fruit	15.77	16.75	15.53	16.00	14.00	19.40
24	Fruit length (cm)	14.90	14.97	16.18	14.27	16.96	23.05
25	Fruit diameter (cm)	17.62	18.22	18.93	16.89	19.07	21.38
26	Flesh thickness (cm)	2.65	2.63	2.68	2.60	2.55	3.51
27	Seed cavity diameter (cm)	10.54	10.90	10.26	11.01	9.92	12.26
28	Number of seeds per fruit	279.10	303.79	299.93	258.80	279.40	338.20
29	Test weight (g)	10.60	10.26	10.60	10.31	10.71	12.40
30	Average fruit weight (kg)	2.29	2.28	2.36	1.97	2.32	2.90
31	Fruit yield per vine (kg/vine)	7.98	8.08	8.41	7.90	7.23	10.77
32	Estimated fruit yield (t/ha)	17.76	16.17	18.76	19.50	16.58	23.96
<b>Quality characters</b>							
33	β-carotene (mg/100g.f. w)	2.32	2.52	2.74	2.49	2.30	3.15
34	Reducing sugars (%)	3.41	3.28	3.68	3.35	3.32	4.16
35	Non-reducing sugars (%)	2.53	2.63	2.39	2.63	2.52	2.78
36	Total sugars (%)	5.93	5.91	6.07	5.98	5.85	6.93
37	Total soluble solids (°Brix)	4.27	4.41	4.69	3.87	4.12	5.39

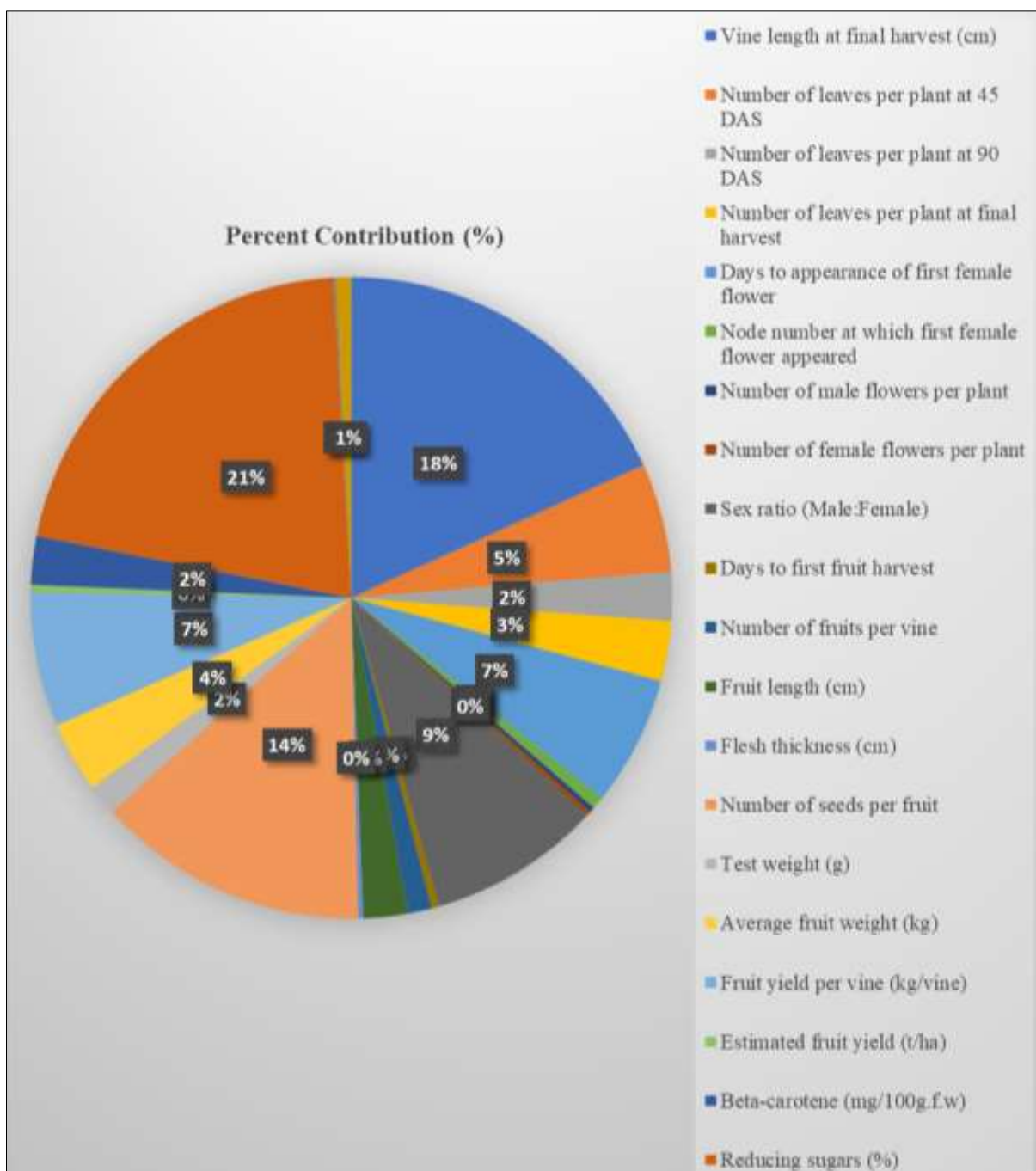
### Relative contribution of different characters towards divergence

The percent contribution towards genetic divergence by all the thirty-seven characters is furnished in the (Table 5) and (Fig. 3). The trait reducing sugars (%) had shown the highest contribution towards divergence by ranking first with a contribution of 21.03% followed by vine length (cm) at final harvest with 18.21%. The characters viz., number of seeds per fruit, sex ratio (male: female), fruit yield per vine (kg), days to appearance of first female flower, number of leaves per plant at 45 DAS, average fruit weight (kg), number of leaves per plant at final harvest, number of leaves per plant at 90 DAS, beta-carotene, fruit length (cm), test weight (g), number of fruits per vine, total soluble solids (°Brix), node number at which first female flower appeared, days to first fruit harvest,

estimated fruit yield (t/ha), flesh thickness (cm), number of male flowers per plant, number of female flowers per plant and non-reducing sugars (%) contributed 13.72, 8.72, 6.76, 6.54, 5.49, 3.57, 3.03, 2.46, 2.44, 2.25, 1.54, 1.19, 0.75, 0.64, 0.38, 0.38, 0.26, 0.25, 0.25, 0.13 per cent respectively, but however internodal length at 45 DAS (cm), internodal length at 90 DAS (cm), internodal length at final harvest (cm), petiole length at 45 DAS (cm), petiole length at 90 DAS (cm), petiole length at final harvest (cm), number of branches per plant at 45 DAS, number of branches per plant at 90 DAS, number of branches per plant at final harvest, days to appearance of first male flower, node number at which first male flower appeared, number of ridges per fruit, fruit diameter (cm), seed cavity diameter (cm) and total sugars (%) did not contribute anything to the diversity.

**Table 5:** Contribution of growth, yield and quality traits towards divergence in pumpkin genotypes

S. No	Source	Contribution (%)	Number of times ranked first
<b>Growth characters</b>			
1	Vine length at final harvest (cm)	18.21	136
2	Internodal length at 45 DAS (cm)	0.00	0
3	Internodal length at 90 DAS (cm)	0.00	0
4	Internodal length at final harvest (cm)	0.00	0
5	Petiole length at 45 DAS (cm)	0.00	0
6	Petiole length at 90 DAS (cm)	0.00	0
7	Petiole length at final harvest (cm)	0.00	0
8	Number of branches per plant at 45 DAS	0.00	0
9	Number of branches per plant at 90 DAS	0.00	0
10	Number of branches per plant at final harvest	0.00	0
11	Number of leaves per plant at 45 DAS	5.49	29
12	Number of leaves per plant at 90 DAS	2.46	13
13	Number of leaves per plant at final harvest	3.03	16
<b>Floral characters</b>			
14	Days to appearance of first male flower	0.00	0
15	Node number at which first male flower appeared	0.00	0
16	Days to appearance of first female flower	6.54	51
17	Node number at which first female flower appeared	0.64	5
18	Number of male flowers per plant	0.25	1
19	Number of female flowers per plant	0.25	1
20	Sex ratio (male: female)	8.72	68
<b>Fruit characters</b>			
21	Days to first fruit harvest	0.38	3
22	Number of fruits per vine	1.19	19
23	Number of ridges per fruit	0.00	0
24	Fruit length (cm)	2.25	36
25	Fruit diameter (cm)	0.00	0
26	Flesh thickness (cm)	0.26	2
27	Seed cavity diameter (cm)	0.00	0
28	Number of seeds per fruit	13.72	107
29	Test weight (g)	1.54	12
30	Average fruit weight (kg)	3.57	57
31	Fruit yield per vine (kg/vine)	6.76	104
32	Estimated fruit yield (t/ha)	0.38	2
<b>Quality characters</b>			
33	β-carotene (mg/100g.f. w)	2.44	19
34	Reducing sugars (%)	21.03	164
35	Non-reducing sugars (%)	0.13	1
36	Total sugars (%)	0.00	0
37	Total soluble solids (°Brix)	0.75	12



**Fig 3:** Relative contribution of characters towards genetic divergence in pumpkin

Based on these results, Mahalanobis  $D^2$  was found to be a useful tool in grouping genotypes phenotypically and geographically. Findings revealed that in pumpkin, there is a vast scope for developing new varieties with greater yield potential and to better other attributes of economic importance, using this elite germplasm. In crop improvement programmes, intercrossing among genotypes with outstanding mean performance for these characters would prove to be effective. For recovering improved progenies for growth, floral, fruit and quality characters, crosses can be attempted between the genotypes belonging to clusters I, IV and V with cluster VI as revealed by divergence studies.

**Conclusion**

Multivariate analysis considering 37 morphological traits following Mahalanobis  $D^2$  statistic revealed good diversity

among 33 genotypes of pumpkin, which were grouped into six distinct clusters. The genotypes of diverse clusters I and VI, clusters IV and VI and clusters V and VI could be used in hybridization programme either to produce highly heterotic  $F_1$ s or to generate wide range of transgressive segregants in population to develop high yielding varieties of pumpkin. The characters reducing sugars (%), vine length (cm) at final harvest and number of seeds per fruit contributed maximum towards divergence among the pumpkin genotypes.

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**References**

1. Chaudhari DJ, Acharya RR, Gohil SB, Patel NA. Genetic divergence study in pumpkin (*Cucurbita moschata*). Journal of Pharmacognosy and Phytochemistry. 2017;6(4):744-747.
2. Devmore JP, Dhonukshe BL, Apte UB, Jadhav BB. Genetic divergence in bitter gourd (*Momordica charantia* L.). South Indian Horticulture. 2007;55:20-23.
3. Dey SS, Behera TK, Munshi AD, Sirohi PS. Studies on genetic divergence in bitter gourd (*Momordica charantia* L.). Indian Journal of Horticulture. 2007;64:53-57.
4. Indraja G, Sadarunnisa S, Madhumathi C, Tanuja Priya B, Reddi Sekhar M. Genetic divergence analysis in muskmelon (*Cucumis melo* L.) International Journal of Chemical Studies. 2018;6(6):2623-626.
5. Jahan TA, Islam AKM, Rasul MG, Mian MAK, Haque MM. Heterosis of qualitative and quantitative characters in sweet gourd (*Cucurbita moschata*). African Journal of Food and Agriculture Nutrition Development. 2012;12(3):6186-199.
6. Kale VS, Patil BR, Bindu S, Paithankar DH. Genetic divergence in pumpkin (*Cucurbita moschata*). Journal of Soils and Crops. 2002;12:213-216.
7. Kandasamy R. Morphological, biochemical and molecular characterization in landraces of melon (*Cucumis melo* L.). Ph.D. thesis, Kerala Agricultural University, Thrissur; c2004. p. 141.
8. Kundu BC, Hossain MM, Khaleque MA, Mian IH. Genetic divergence in bitter gourd (*Momordica charantia*). Journal of the Asiatic Society of Bangladesh. Science. 2012;38(2):125-134.
9. Lakshmi LM, Haribabu K, Reddy GLK. Genetic divergence in pumpkin. Indian Journal of Horticulture. 2003;60:363-367.
10. Lovely B. Evaluation of genetic divergence in ash gourd. M.Sc. (Ag.) thesis, Kerala Agricultural University, Thrissur; c2001. p. 76.
11. Mahalonobis PC. A statistical study of the Chinese head measurements. Journal of Asiatic Society. 1928;25:301-377
12. Mahalonobis PC. On the generalized distances in statistics. Proceedings of National Academy of Sciences in India. 1936;2:49-55.
13. Maharana T, Mandal P, Sahoo GS, Mahapatra B. Multivariate analysis of genetic divergence in Kunduru [*Coccinia grandis* (L.) (Voigt)]. Abstracts. First International Conference on Indigenous Vegetables and Legumes, 12-15 December 2006, Hyderabad, India; c2006. p. 70.
14. More TA, Seshadri VS. Studies on genetic divergence in musk melon (*Cucumis melo* L.). Journal of Maharashtra Agricultural University. 2002;27(2):127-131.
15. Muralidhara MS, Narasegowda NC, Narayanaswamy P. Genetic divergence in pumpkin (*Cucurbita moschata*). Indian Journal of Horticulture. 2014;4(3):144-47.
16. NHB. State wise area, production and productivity of Horticulture crops during the year 2021-2022 (First Advance Estimates). National Horticulture Board, Government of India; c2022.
17. Nisha SK. Genetic studies in pumpkin (*Cucurbita moschata* Duch. ex. Poir.) through diallel analysis. M.Sc. (Hort.) Thesis, Tamil Nadu Agricultural University, Coimbatore; c1999.
18. Panging K, Chandra GB, Sarma D. Genetic divergence among pumpkin (*Cucurbita moschata* Duch. Ex. Poir.) landraces of Assam. The Pharma Innovation Journal. 2022;12(2):3551-554.
19. Panse VG, Sukhatme PV. Statistical methods for Agricultural Workers. I.C.A.R. New Delhi; c1978.
20. Rao CR. Advanced Statistical Methods in Biometric Research. John Wiley and Sons, Inc., New York; c1952. p. 390.
21. Reddy B, Begum H, Sunil N, Thirupathi Reddy M. Genetic divergence analysis in muskmelon (*Cucumis melo* L.) International Journal of Current Microbiology and Applied Sciences. 2017;6(6):2251-2260.
22. Roy SK. A simple and rapid method of estimation of total carotenoid pigment in mango. Journal of Food Science and Technology. 1973;10(1):45.
23. Satkar KP, Kulthe AA, Chalke PR. Preparation of bitter gourd ready-to-serve beverage and effect of storage temperature on its keeping quality. The Bioscan. 2013;8(1):115-117.
24. Shivanand Hegde. Studies on heterosis in ridge gourd. M.Sc. Thesis. Tamil Nadu Agricultural University, Coimbatore; c2009.
25. Srinivasan M. Studies on genetic parameters and characterization in pumpkin (*Cucurbita moschata* Duch. Ex. Poir.). M.Sc. Thesis. Tamil Nadu Agricultural University, Coimbatore; c2003.
26. Sultana S, Kawochar MA, Naznin S, Raihan H, Mahmud F. Genetic divergence in pumpkin (*Cucurbita moschata* L.) genotypes. Bangladesh Journal of Agricultural Resources. 2018;40(4):683-692.
27. Tindall HD. Vegetables in the tropics. Macmillan Education, London; c1987. p. 166.
28. Yawalkar KS. Vegetable crop in India. Agri-Horticultural Publishing House, Nagpur; c1991. p. 182-186.