

**RESEARCH ARTICLE :**

# Analysis of genetic divergence for yield contributing traits in Pumpkin (*Cucurbita moschata* Duch. ex Poir.)

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**SUMMARY :** Genetic divergence among 23 pumpkin genotypes was estimated using Mahalanobis's  $D^2$  statistic. Analysis of variance studies indicates significant differences among all the genotypes for all the characters under study. Based on  $D^2$  analysis, the genotypes were grouped into 6 different clusters, where cluster II contained the highest number of genotypes (6) followed by I (5), III (5), IV (4), VI (2) and cluster V contained the lowest (1). Clustering pattern revealed that geographical diversity was not associated with genetic diversity *i.e.*, genotypes collected from same location were grouped into different clusters. The maximum intra-cluster distance was observed for cluster VI (6.07) and the minimum for cluster I (4.67). The maximum inter-cluster distance was observed between cluster V and VI (8.31) and that of minimum was observed in between the cluster I and II (5.80). Cluster V recorded the highest mean values for the characters vine length at 90 days (m), number of primary branches at 90 days, sex ratio, days to fruit harvest, fruit set %, fruit length (cm), rind thickness (cm), flesh thickness (cm), test weight (100 seed wt.(g).)

**KEY WORDS :**

Cluster,  $D^2$  analysis, Genetic diversity, Pumpkin

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## **BACKGROUND AND OBJECTIVES**

Pumpkin (*Cucurbita moschata* Duch ex. Poir) being an important Cucurbitaceous vegetable crop cultivated under tropical, sub-tropical and temperate regions all over the world Central Mexico is considered as centre of origin of pumpkin and now is widely grown in most tropical countries. India is the center of origin of many cucurbitaceous vegetables, where the cucurbits are capable of thriving and performing well even under the hot

summer. Pumpkin is very nutritious due to its high content of vitamin A. Much emphasis on alleviating vitamin A deficiency through vegetables like pumpkin, a cheaper source of carotene rich vegetable is laid by WHO (Anonymous, 2008).

The knowledge pattern of inheritance of various characters are important consideration while determining the most approximate breeding procedure applicable to any particular crop. Information on genetic

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divergence among the available germplasm is vital to a plant breeder for an efficient choice of parents for hybridization. Based on Mahalanobis (1936)  $D^2$  statistics. This analysis helps in assessing genetic divergence among the parents and the relative contribution of different characters to the total divergence. It is also useful in assigning genotypes to specific heterotic groups to create segregating progenies with maximum genetic variability for further breeding purposes. Information on the selection of local pumpkin genotypes on the basis of diversity is inadequate in Akola conditions keeping the above facts in view, the present investigation was undertaken to estimate the nature and magnitude of genetic diversity and traits contributing towards genetic divergence among 23 genotypes of pumpkin for further utilization in breeding programme.

## RESOURCES AND METHODS

Experiment was conducted at Main Garden, Department of Horticulture, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (Maharashtra) during summer season in randomized block design with 23 genotypes of pumpkin (*Cucurbita moschata* Duch. ex Poir) collected in Vidarbha region of Maharashtra (AKP-1 to AKP-22 and one check Arka Chandan) replicated thrice. All recommended cultural and management practices were followed to raise the healthy crop. Five competitive plants were selected randomly in each row for recording the observations on 21 parameters viz., vine length (m) 90 DAS, number of primary branches 90 DAS, node at first

male flower appears, node at first female flower appears, days to first male flower appears, days to first female flower appears, sex ratio (%), inter nodal length (cm), days to first harvest, fruit set (%), number of fruits per vine, fruit yield per vine (kg), average fruit weight (kg), fruit length (cm), fruit diameter (cm), fruit yield per hectare (tonnes), rind thickness (cm), flesh thickness (cm), fruit cavity (cc), number of seeds per fruit, test weight (100 seed weight (g)). The statistical data were analysed using WINDOSTAT version 9.1 software. The genetic divergence among genotypes was estimated by using  $D^2$  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).

## OBSERVATIONS AND ANALYSIS

The analysis of variance showed significant differences among the 23 genotypes for all 21 characters under study indicating the presence of notable genetic variability among the genotypes. Twenty three genotypes were grouped into six divergent clusters on the basis of cluster analysis (Table 1). Cluster II contained highest number of genotypes (6), followed by cluster I (5) and cluster III (5), while Cluster V was composed of only one genotype. The clustering patterns of genotypes reveal that the genotypes collected from the same region did not form a single cluster. This indicates that geographic diversity is not always related to genetic diversity. These

**Table 1 : Clustering pattern of 23 Pumpkin genotypes**

Cluster	No. of genotypes						
I	5	AKP-1	AKP-2	AKP-4	AKP-6	AKP-3	
II	6	AKP-5	AKP-20	AKP-9	AKP-7	AKP-8	AKP-10
III	5	AKP-12	AKP-13	AKP-11	AKP-14	AKP-17	
IV	4	AKP-16	AKP-19	AKP-18	Arka Chandan		
V	1	AKP-15					
VI	2	AKP-21	AKP-22				

**Table 2 : Average intra (bold) and inter-cluster  $D^2$  values for six clusters among 23 Pumpkin genotypes**

Cluster	I	II	III	IV	V	VI
I	(21.80) 4.67	(33.64) 5.80	(48.58) 6.97	(44.62) 6.68	(63.04) 7.94	(68.06) 8.25
II		(26.31) 5.13	(37.69) 6.14	(39.69) 6.30	(56.85) 7.54	(48.30) 6.95
III			(29.81) 5.46	(38.06) 6.17	(56.85) 7.54	(49.84) 7.06
IV				(31.58) 5.62	(57.76) 7.60	(55.50) 7.45
V					0.00	(69.05) 8.31
VI						(36.84) 6.07

results corroborate the view of Rashid (2000) in pumpkin and Kundu *et al.* (2008) in bitter gourd. This result indicated that the genotypes that have originated from the same place may have different genetic architecture.

### Inter and intra cluster distance in pumpkin genotypes :

The average inter and intra cluster distances ( $D = \sqrt{D^2}$ ) are presented in Table 2. Cluster VI had the maximum intra cluster distance ( $D = 6.07$ ) followed by cluster IV ( $D = 5.62$ ). The least intra cluster distance observed in cluster I ( $D = 4.67$ ). The other clusters like cluster II ( $D = 5.13$ ), and cluster III ( $D = 5.46$ ) showed medium inter cluster distance. Indicating their independent identity and importance due to the unique characters possessed by the strains in the clusters. The highest inter cluster generalized distance was found between cluster-V and cluster-VI followed by clusters-III and cluster V. The involvement of genotypes belonging to cluster V and VI, and cluster III and V in hybridization would help in achieving novel recombinants.

### Cluster mean for yield and its attributes :

Mean performance of six clusters for 21 characters

are shown in Table 3. Maximum mean (3.35) for vine length at 90 days (m) was observed in cluster V and minimum mean (2.85) observed in cluster VI. Number of primary branches at 90 days showed maximum mean (3.36) in cluster V and minimum mean observed in cluster VI. Sex ratio was observed maximum mean (12.52) in cluster V and productive minimum mean recorded in cluster VI. While maximum mean (2.87) for node at first female flower appear was observed in cluster I and minimum mean (2.30) was observed in cluster VI. Similarly maximum mean (15.26) for node at first male flower appear was observed in cluster III and minimum mean (2.30) was observed in cluster VI. The cluster III recorded highest mean for days to first male and female flower and cluster I recorded lowest mean for days to first male and female flower. Cluster III was characterised by highest mean (4.96) inter nodal length (cm) and cluster II recorded lowest mean (4.11) inter nodal length. Cluster V included highest mean (111.66) for days to fruit harvest and cluster VI included lowest mean (93.89) for days to fruit harvest. While cluster V comprised of highest mean (70.37) fruit set % and cluster IV comprised of lowest mean (45.52) fruit set %. Cluster I comprise of maximum number of fruits per vine (3.37)

**Table 3 : Mean values of clusters for twenty one characters in 23 Pumpkin genotypes**

Sr. No.	Character	I	II	III	IV	V	VI
1.	Vine length at 90 days (m)	3.11	3.10	3.18	2.90	3.35	2.85
2.	Number of primary branches at 90 days	3.13	3.22	3.09	3.00	3.36	2.97
3.	Sex ratio	11.43	11.58	10.83	11.94	12.52	10.49
4.	Node at first male flower appear	2.87	2.65	2.33	2.31	2.40	2.30
5.	Node at first female flower appear	11.90	12.29	15.26	13.52	14.06	11.57
6.	Days to first male flower appear	48.83	49.93	52.64	50.34	50.51	52.46
7.	Days to first female flower appear	55.37	57.87	61.98	59.69	60.68	59.24
8.	Inter nodal length (cm)	4.31	4.11	4.96	4.48	4.44	4.83
9.	Days to fruit harvest	101.42	95.09	97.33	98.11	111.66	93.89
10.	Fruit set %	51.00	50.41	47.05	45.52	70.37	60.84
11.	Number of fruits per vine	3.37	2.90	2.90	1.79	1.33	2.44
12.	Yield per vine (kg)	8.75	10.22	10.04	8.41	11.82	12.06
13.	Average fruit weight (kg)	3.03	3.22	2.95	3.03	3.53	4.50
14.	Fruit length (cm)	21.62	27.58	25.76	26.05	32.22	27.68
15.	Fruit diameter (cm)	16.78	22.03	20.42	22.54	13.72	23.89
16.	Fruit yield per ha (tonnes)	42.77	51.09	50.23	44.80	59.11	60.32
17.	Rind thickness (cm)	0.37	0.31	0.35	0.44	0.59	0.25
18.	Flesh thickness (cm)	3.36	3.44	4.04	4.09	5.25	4.02
19.	Tss ( <sup>o</sup> Brix)	5.09	4.53	4.18	4.61	5.00	4.51
20.	Number of seeds per fruit	199.54	164.78	191.11	202.322	189.100	317.56
21.	Test weight (100 seed wt) (g)	13.08	14.28	13.22	11.28	14.80	13.40

and cluster V comprise of minimum number of fruits per vine (1.33). For yield per vine (kg) cluster VI (12.06) showed highest and cluster IV showed lowest. Cluster VI showed highest mean (4.50) average fruit weight (kg) and cluster III showed lowest mean (2.95) average fruit weight (kg). Cluster V having maximum fruit length (32.22) and cluster I having minimum fruit length (21.62). Cluster VI comprised of highest mean (23.89) in fruit diameter (cm) and lowest mean (13.72) in cluster V. Cluster VI comprise highest mean (60.32) fruit yield per ha (tonnes) and cluster I comprised lowest mean (42.72). Similarly cluster V recorded maximum mean (0.59) for rind thickness (cm) and flesh thickness (cm) (5.25), while minimum mean (0.25) recorded in cluster VI for rind thickness (cm) and cluster I for flesh thickness (cm) (3.36). Cluster I noted highest mean (5.09) Tss (<sup>o</sup>Brix) and cluster III noted lowest mean (4.18) Tss (<sup>o</sup>Brix). Cluster VI showed highest number of seeds (317.56) per fruit, whereas cluster II recorded lowest number of seeds (164.78) per fruit. Highest test weight (100 seed wt) (g) was recorded in cluster V and lowest test weight (100 seed wt) (g) was recorded in cluster IV. While studying the genetic divergence in Pumpkin genotypes Wide range of genetic divergence was noticed among

the studied genotypes, and this divergence of the genotypes may be taken into account for selecting the parents for hybridization and future improvement programme of this crop through breeding.

### Contribution of individual character towards total divergent :

The clusters have been formed based on the

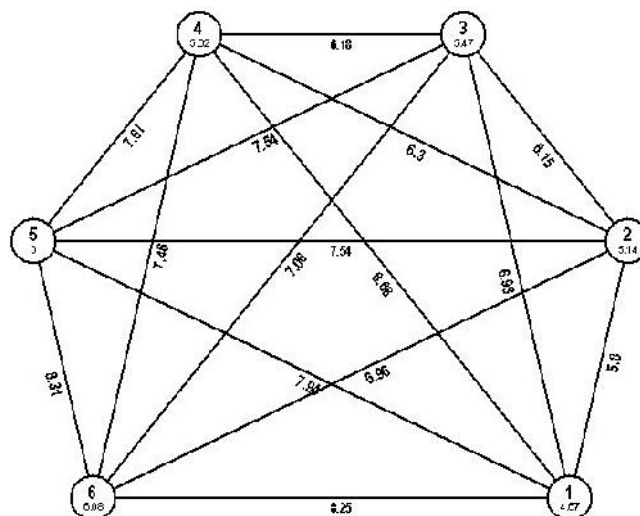


Fig. 1 : Cluster diagram showing the average Inter and intra-cluster distance ( $D = D^2$ ) of 23 Pumpkin genotypes

Table 4 : Per cent contribution of different characters towards diversity in 23 Pumpkin genotypes

Sr. No.	Character	Times Ranked 1 <sup>st</sup>	Per Cent contribution
1.	Vine length at 90 days (m)	0	0.00
2.	Number of primary branches at 90 days	0	0.00
3.	Sex ratio	0	0.00
4.	Node at first male flower appear	0	0.00
5.	Node at first female flower appear	3	1.19
6.	Days to first male flower appear	1	0.40
7.	Days to first female flower appear	0	0.00
8.	Inter nodal length (cm)	14	5.53
9.	Days to fruit harvest	0	0.00
10.	Fruit set %	29	11.46
11.	Number of fruits per vine	31	12.25
12.	Yield per vine (kg)	16	6.32
13.	Average fruit weight (kg)	4	1.58
14.	Fruit length (cm)	15	5.93
15.	Fruit diameter (cm)	24	9.49
16.	Fruit yield per ha (tonnes)	2	0.79
17.	Rind thickness (cm)	38	15.20
18.	Flesh thickness (cm)	3	1.19
19.	Tss ( <sup>o</sup> Brix)	1	0.40
20.	Number of seeds per fruit	63	24.90
21.	Test weight (100 seed wt.) (g)	9	3.56

contribution of different characters to the divergence (Table 4 and Fig. 1). Among these characters number of seeds per fruit (24.90%) to total genetic diversity followed by rind thickness (cm) (15.20), number of fruits per vine (12.25%), fruit set % (11.46%), fruit diameter (cm) (9.49%), yield per vine (kg) (6.32%), fruit length (cm) (5.93%), inter nodal length (cm) (5.53%) and test weight (100 seed wt.) (3.56%). However, average fruit weight (kg) (1.58%), flesh thickness (cm) (1.19%), first female flower appear (1.19%), fruit yield per ha (tonnes) (0.79%), TSS (<sup>o</sup>Brix) (0.40%), days to male flower appear (0.40%) have meagerly contributed to the diversity. While, vine length @ 90 days (cm), number of primary branches @ 90 days, sex ratio, node @ first male flower appear, days to first female flower appear and days to first harvest had zero contribution to the total genetic diversity.

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## REFERENCES

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**Mahalonobis, P.C.** (1936). *On the generalized distance in Statistics*. Proceedings, National Institute of Science, India **2**: 49-55.

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

**Rao, C.R.** (1952). *Advanced Statistical Methods in Biometrical Research*. John Wiley and Sons, New York. pp. 45-110.

**Rashid, M.M.** (2000). Genetic divergence in pumpkin. MS Thesis. Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur. p 85.

**Kundu, B.C.** (2008). Morpho-biochemical diversity and heterosis in bitter gourd (*Momordica charantia* L.). Ph.D. Dissertation. Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur.

## WEBLIOGRAPHY

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Anonymous (2008). World Health Organization, [www.who.int/vmnis/vitamina/en/](http://www.who.int/vmnis/vitamina/en/)

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