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Assessment of genetic diversity for qualitative and quantitative traits in pumpkin (*Cucurbita moschata*)

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Abstract

The current investigation on genetic divergence was carried out using Mahalanobis D2 statistics for yield and other qualitative and quantitative traits and five clusters were formed. Cluster I contains the maximum number of genotypes (9), followed by clusters III, and IV with 8 and 6 genotypes, respectively, and clusters II and V are monogenotypic. The intra-cluster distance was highest in cluster I (122.81) and lowest for clusters II and V (0.00), which have only one genotype, whereas, the inter-cluster distance was highest between clusters II and V (1283.61) and lowest between clusters III and IV (124.18). Cluster V records the highest mean for number of fruits per plant, fruit yield per plant, and lowest for days to 50% flowering. Maximum contribution towards genetic divergence in percent was by fruit yield per hectare (30.00), followed by node at first male flower appearance (17.33), fruit length (15.67), flesh thickness (7.67) and lowest for number of fruits per plant (0.33). Genotypes belong to clusters I and III may be used in hybridization breeding.

Keywords: Clustering; D2 analysis; genetic divergence; genetic variability; pumpkin; seed yield

Introduction

Pumpkin (*Cucurbita moschata* Duch. ex Poir.) is one of the important vegetable crops belongs to the family Cucurbitaceae with chromosome number $2n=40$. It is an annual, monoecious, climbing vine which is natural amphidiploid and cross-pollinated species which is grown all over the world for nutrition and higher return to the farmers. It is believed that pumpkin have been originated in Central America (Stuart 2004) [1]. Among the five cultivated species, pumpkin (*Cucurbita moschata* Duch. ex Poir.), summer squash (*Cucurbita pepo* L.), winter squash (*Cucurbita maxima*) are of great economic importance (Rana, 2014) [8]. Pumpkin is a nutritious, adaptable food that contains fiber, vitamins, minerals, and antioxidants. Pumpkin's health advantages are primarily related to its fiber content and micronutrients, such as beta carotene and vitamin A (Anonymous 2023) [1].

India occupies a unique position as the second-largest producer of veggies globally, following China. A total of 12.1 lakh hectares of pumpkin were grown, yielding 26.59 metric tons of product. Orissa, Uttar Pradesh, Karnataka, Chhattisgarh, Punjab, Madhya Pradesh, and Andhra Pradesh are among the Indian states with successful cultivation. The nutrient content of 100 g edible pieces of fruit is 90 ml water, 8 g carbohydrate, 1 g protein, 0.5 g fiber, 20 mg calcium, 0.8 mg iron, 210 mg beta-carotene, 0.05 mg thiamine, 0.05 mg riboflavin, 0.5 mg niacin, and 15 mg ascorbic acid (28).

Genetic diversity is one of the important pre-requisites for obtaining higher yield through hybridization programme. Morphological diversity testing is the most efficient method for identifying variability across genotypes and forming a heterotic pool. Increased diversity increases the likelihood of enhancing economic characteristics in the program.

Materials and Methods

The experiment material consists of 25 genotypes, including one check variety, Narendra Agrim. The experiment was carried out in a randomized block design with three replications during Zaid 2023 at Main Experimental Station (MES) of Department of Vegetable Science Farm of Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya, which is geographically situated at 25.56° N latitude, 82.12° E

longitude and at an elevation of 112m above the mean sea level. This area falls in sub-tropical area of Eastern India. The row to row spacing was 3.0 m apart with a plant to plant spacing of 0.60 m. The duration of experiment was from March to June, 2023 and recommended plant practices were followed to raise the healthy crops. Five guarded plants were selected at random from every genotype from each plot for the assessment of diversity. The observation was recorded on thirteen quantitative and seven qualitative traits. The data were subjected to Mahalanobis D2 statistics as per the Mahalanobis (1936) [3] method, and genotypes were grouped into different clusters following Toucher's method as suggested by Rao (1952) [9].

Results and Discussion

The statistical analysis of divergence shows significant variation within pumpkin genotypes for all the characters under study. All the 25 genotypes were grouped into five clusters (table 1). The maximum number of genotypes was found in cluster I (9 genotypes), followed by cluster III (8 genotypes) and cluster IV (6 genotypes). The remaining two clusters are monogenotypic. Monogenotypic clustering demonstrates that such genotypes may have a completely different genetic makeup from the other genotypes, resulting in the creation of a unique cluster, whereas genotypes belonging to the same cluster exhibit a close link between them.

Table 1: Clustering pattern of 25 genotypes of Pumpkin based on Mahalanobis' D2 statistics

Cluster Number	Number of Genotypes	Genotypes
I	9	VRPK-2380, VRPK-222, VRPK-2372, Narendra Upkar, VRPK-2304, VRPK-23303, VRPK-2322, Narendra Amrit, VRPK-23310
II	1	NDPK-23-4
III	8	VRPK-2309, Narendra Agrim (check), VRPK-2305, VRPK-2301, NDPK-28, NDPK-23-7, VRPK-2375, VRPK-2330
IV	6	VRPK-2360, VRPK-2362, VRPK-18-01, VRPK-2307-02, NDPK-26, NDPK-29
V	1	VRPK-123220

The intra-cluster distance between 25 genotypes ranged from 0.00 to 122.82 (Table 2). Intra-cluster distance values indicate the closeness of genotypes inside the same cluster. High intra-cluster D2 values indicate greater genetic divergence and variability across genotypes within the same cluster compared to genotypes with an intra-cluster distance of 0.00, indicating monogenotypic and less diverse. Cluster I have the highest intra-cluster distance (122.82), followed by clusters IV (99.05) and III (82.07). Murty and Arunachalam discovered that choosing parents with high genetic diversity for desirable traits significantly impacts hybridization and selection success. This investigation discovered intra-cluster variance in constituent genotypes,

which can be used to select parents for recombination breeding.

The average inter-cluster distance between genotypes ranged from 124.18 to 1283.61. Clusters II and V had the maximum inter-cluster distance, followed by clusters I and V, IV and V, III and V. The genotypic composition of cluster pairings in this study consisted of genes from the most distantly related parents, indicating the features under examination. Using genotypes from clusters separated by a high statistical distance can reveal inheritance patterns for pumpkin traits and boost crop production through hybridization. Gongopadhyay *et al.* (2008) [2], Nagar *et al.* (2017) [5], Rajput *et al.* (2021) [7] have all reported similar results.

Table 2: Average of an intra and inter-cluster D2 values for five clusters in pumpkin

Cluster number	I	II	III	IV	V
I	122.819	333.790	199.000	148.581	570.408
II		0.000	464.900	285.059	1283.619
III			82.077	124.185	363.606
IV				99.055	531.591
V					0.000

To improve yield and related characteristics in breeding programs, consider cluster means (Table 3) for seed yield per plant and key components when selecting genotypes. The result revealed that days to 50% flowering were recorded highest mean value for cluster III (61.59) followed by cluster I (60.12), cluster IV (59.58) and lowest in cluster V (51.33). The result revealed that days to node at first male flower appearance were recorded highest mean value for cluster II (6.20), cluster IV (5.01), cluster III (4.31) and lowest in cluster V (2.40). The result revealed that vine length(m) was recorded highest mean value for cluster V (4.04), cluster III (3.30), cluster IV (3.13), and lowest in cluster II (2.11). The result revealed that number of fruits per plant were recorded highest mean value for cluster V (3.53), cluster IV (3.07), cluster III (3.06) and lowest in

cluster II (2.89). The result revealed that average fruit weight (kg) was recorded highest mean value for cluster V (1.81), cluster III (1.53), cluster IV (1.38) and lowest in cluster II (0.77). The result revealed that fruit length (cm) was recorded highest mean value for cluster V (26.58), cluster III (16.09), cluster IV (15.94) and lowest in cluster II (11.45). The result revealed that fruit yield per plant (kg) were recorded highest mean value for cluster V (6.43), cluster III (4.74), cluster IV (4.24), and lowest in cluster II (2.23). The result revealed that fruit yield per hectare (q/hect) were recorded highest mean value for cluster V (357.27), cluster III (263.81), cluster IV (235.91), and lowest in cluster II (124.31). Similar results were also earlier found by Naryan *et al.* (2011) [6] and Ribeiro *et al.* (2022) [10].

Table 3: Intra-cluster group means for thirteen characters in pumpkin

Clusters	Days to 50% flowering	Node at first male flower appearance	Node at first female flower appearance	Primary branch	Inter nodal length (cm)	Vine length (m)	No. of fruits per plant	Average fruit wt. (kg)	Fruit length (cm)	Fruit diameter (cm)	Flesh thickness (cm)	Fruit yield per plant (kg)	Fruit yield per hectare (q/hect)
I	60.126	3.185	13.681	4.244	8.978	2.862	2.937	1.288	14.546	27.008	3.640	3.772	209.532
II	59.067	6.200	15.133	3.167	12.400	2.113	2.890	0.773	11.453	22.192	2.277	2.238	124.313
III	61.592	4.317	13.437	4.950	9.411	3.302	3.067	1.539	16.094	30.922	4.242	4.749	263.810
IV	59.589	5.011	13.656	4.111	8.705	3.130	3.076	1.385	15.948	28.554	3.541	4.247	235.914
V	51.333	2.400	9.200	5.900	5.800	4.047	3.533	1.817	26.583	34.567	5.267	6.432	357.279

Table 4 shows the percentage of contribution of 13 characters to the expression of genetic divergence. Fruit yield per hectare had the highest contribution (30.00),

followed by node at first male flower appearance (17.33), fruit length (15.67), flesh thickness (7.67) and lowest for number of fruits per plant (0.33).

Table 4: Per cent contribution of thirteen characters towards total genetic divergence in pumpkin

Sr. No.	Traits	Per cent Contribution
1.	Days to 50% flowering	1%
2.	Node at first male flower appearance	17.33%
3.	Node at first female flower appearance	1%
4.	Primary branch	6%
5.	Inter nodal length (cm)	5.67%
6.	Vine length (m)	1.33%
7.	No. of fruits per plant	.33%
8.	Average fruit wt. (kg)	6.33%
9.	Fruit length (cm)	15.67%
10.	Fruit diameter (cm)	5.33%
11.	Flesh thickness (cm)	7.67%
12.	Fruit yield per plant (kg)	2.33%
13.	Fruit yield per hectare (q/hect)	30%

Conclusion

This study suggests that selecting parental lines from clusters III (VRPK-2309) for number of fruits per plant, fruit yield per plant, days to 50% flowering, fruit yield per hectare, flesh thickness, fruit diameter and average fruit weight per plant could aid in future breeding programs for desired segregants.

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