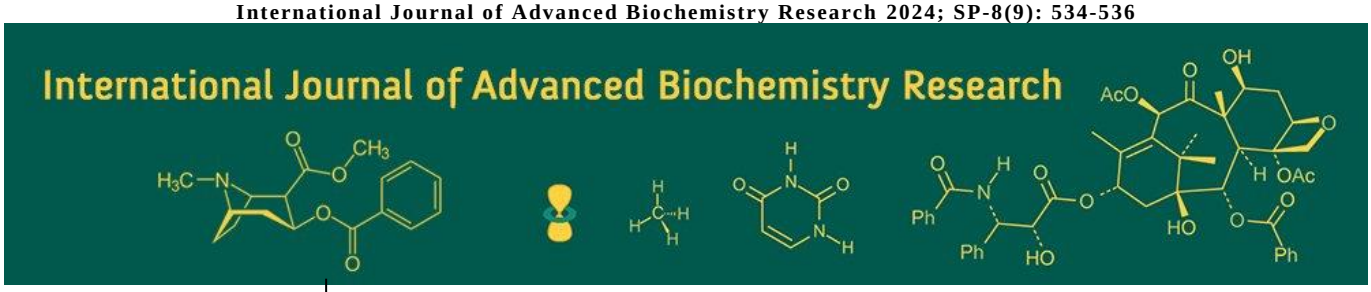


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# Estimation of genetic diversity among the genotypes of pumpkin (*Cucurbita moschata* Duch. ex Poir)

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**Abstract**
The present investigation was conducted to asses the genetic divergence in the germplasm of pumpkin. The experiment was laid out in randomized complete block design with three replication. Observations were taken for seventeen traits in 35 genotypes (including one check. The 35 genotypes were grouped into six distinct non-over lapping cluster. The minimum intra cluster distance (0.00) was found for the cluster II, cluster III, cluster IV, cluster V and cluster VI and maximum was found in cluster I (55.15). The maximum inter-cluster distance was found between cluster V and cluster VI (244.67) followed by cluster II and VI (231.40). The minimum inter cluster distance was found between cluster I and IV (93.70) followed by cluster I and V (93.80). Cluster I was superior for days to 50% pistillate flower anthesis, nodes per vine and fruit diameter. Cluster II showed maximum mean values for node to first staminate flower anthesis followed by equatorial circumference of fruit, polar circumference of fruit, fruit cavity and average fruit weight. Cluster III showed maximum mean values for days to 50% staminate flower anthesis and node to first pistillate flower anthesis. Cluster IV showed maximum mean values for number of primary branches, vine length and intermodal length. Cluster V showed maximum mean value for flesh thickness, number of fruit per plant and fruit yield per plant. Cluster VI showed maximum mean value for days to first fruit harvest. The higher inter-cluster distance indicated greater genetic divergence between the genotypes of those clusters. The diversity shown by the different genotypes that was identified using Mahalanobis $D^2$ statistics for the selection of suitable diverse parents for hybridization as an important feature for any crop improvement programme for getting desired hybrids or segregates.

**Keywords:** Pumpkin (*Cucurbita moschata)*, genetic divergence/diversity and cluster

## Introduction
Pumpkin (*Cucurbita moschata* Duch. ex. Poir) is an economically important cucurbitaceous vegetable. It occupies a prominent position due to its high productivity, nutritive values, good storability, better transport quality and extensive cultivation in subtropical and tropical regions of the globe. It is used both immature and mature stages as vegetable and consumed as processed products. Pumpkin provides a valuable source of carotenoids that have a major role in nutrition in the form of pro-vitamin A. Predominant carotenoids found in pumpkin include α-carotene, β-carotene and lutein, which gives colour to the fruits. The total carotenoids content in flesh of pumpkin is around 12.12 mg/100g of fresh weight.
Generally diverse plants are expected to give high hybrid vigour, Hence, it necessitates the study of genetic divergence among the existing varieties and germplasm collection for identification of parents for hybridization programme. The information on genetic divergence of various traits particularly of those that contribute to yield and quality would be of most useful in planning the breeding programme. $D^2$ statistics developed by Mahalanobis (1936) [2] provide a measure of magnitude for divergence between two genotypes under comparison. It considered the variation produced by any character and their consequent effect that it bears on other characters. This was first used by Mahalanobis in an anthropometric survey of the united province of India. This technique has been applied in several crops to select genotypes for further breeding programmes. Grouping of genotypes based on $D^2$ analysis will be useful in choosing suitable parental lines for heterosis breeding. Such studies are also useful in selection of parent for hybridization to recover superior transgressive segregates and it can further result into release of improved open pollinated

varieties for commercial cultivation.

## Materials and Methods

The site of experiment was Main Experimental Station of Department of Vegetable Science Farm of Acharya Narendra Deva University of Agriculture and Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.) during *Zaid* season, 2022. The experiment was conducted in Randomized Complete Block Design with three replications to assess the performance of thirty-five genotypes including 1 check. Each entry was sown in one row with 3 m, length spaced 3 m with plant to plant spacing of 0.5 m in each replication. Observation were recorded for seventeen different characters of pumpkin *i.e.*, days to 50% staminate flower anthesis, days to 50% pistillate flower anthesis, node at first staminate flower anthesis, node at first pistillate flower anthesis, number of primary branches, vine length (m), nodes per vine, internodal length (cm), days to first fruit harvest, equatorial circumference of fruit (cm), polar circumference of fruit (cm), flesh thickness (cm), fruit diameter(cm), fruit cavity (cm), average fruit weight (kg), number of fruit per plant and fruit yield per plant (kg). The genetic diversity was estimated following Mahalanobis, s (1936) [2] and generalized distance ($D^2$) extended by Rao (1952). Based on the $D^2$ values, the genotypes were grouped into clusters following the method suggested by Tocher (Rao, 1952) [4]. Intra and inter cluster distance were calculated by the method of Singh and Chaudhary (1985) [5].

## Results and Discussion

The clustering pattern of the thirty-five genotypes were grouped into six different non-overlapping cluster (Table. 1.). Cluster I had highest number of genotypes (30) whereas cluster II, cluster III, cluster IV, cluster V and cluster VI, has only one genotype in each group. The estimates of intra and inter- cluster distance represented by $D^2$ values are given in table 2. The minimum intra cluster distance (0.00) was found for the cluster II, cluster III, cluster IV, cluster V and cluster VI and maximum was found in cluster I (55.15). The minimum inter cluster distance was found between cluster I and IV (93.70) followed by cluster I and V (93.80). The maximum inter-cluster distance was found between cluster V and cluster VI (244.67) followed by cluster II and VI (231.40), which suggested that members of these clusters are genetically very diverse to each other while lower inter cluster values between the clusters suggested that the genotype of the clusters were not much genetically diverse from each other.

The relative contribution of the character toward total divergence always hints on the variability associated with that character. More is the relative contribution; maximum is the possibility of exploitation of that character in crop improvement. Highest percent contribution was observed in fruit yield per plant (9.41) followed by days to 50% staminate flower anthesis (9.08), days to 50% pistillate flower anthesis (8.40), node number to first staminate flower anthesis (8.07) and equatorial circumference of fruit (7.39) whereas vine length (1.34) followed by flesh thickness (2.02) showed lowest contribution (Table 3).

A perusal of table 4. showed that cluster means for the different characters indicated considerable differences between the clusters. The entire cluster from cluster I to cluster VI has average mean performance for most of the characters, exhibiting extreme cluster mean values for none of the characters under study. Cluster I showed maximum mean values for days to 50% pistillate flower anthesis (49.84), nodes per vine (49.19) and fruit diameter (20.61). Cluster II showed maximum mean values for node to first staminate flower anthesis (10.13) followed by equatorial circumference of fruit (62.02), polar circumference of fruit (54.70), fruit cavity (13.00) and average fruit weight (1.99). Cluster III showed maximum mean values for days to 50% staminate flower anthesis (46.33) and node to first pistillate flower anthesis (23.10). Cluster IV showed maximum mean values for number of primary branches (12.57), vine length (6.98) and intermodal length (15.71). Cluster V showed maximum mean value for flesh thickness (4.80), number of fruit per plant (5.40) and fruit yield per plant (8.97). Cluster VI showed maximum mean value for days to first fruit harvest (67.33). The pattern of distribution of genotypes in different clusters exhibited that there was no parallelism between geographical diversity and genetic diversity as genotypes of same geographical region were grouped into different cluster and vice-versa, as supported by earlier findings of Kumar *et al.* (2017) [1] and Rajput *et al.* (2021) [3]. It is suggested that hybridization among the genotypes of above said clusters would produce segregants for more than one economic character. The potential lines may picked out from different clusters and used as parents in a hybridization programme.

The overall review of the result obtained by genetic diversity study in present investigation revealed that the crosses between the entries separated by the large inter-cluster distance and having high cluster mean value for one or other character to be improved is likely to be more useful.

**Table 1:** Clustering pattern of 35 genotypes on the basis of Mahalanobis $D^2$ statistics

| Cluster number | No. of genotypes | Genotypes in clusters |
|---|---|---|
| I | 30 | NDPK-51, Narendra Agrim (C), NDPK-41, NDPK-44, NDPK 49, NDPK-50, NDPK-42, NDPK-38, NDPK-45, 2021/PUMVAR-5, NDPK-43, NDPK-25, NDPK-46, 2021/PUMVAR-3, 2019/PUMVAR-4, 2019/ PUMVAR-5, NDPK-35, NDPK-47, NDPK-40, NDPK-39, 2021/PUMVAR-1, NDPK-34, NDPK-48, 2019/PUMVAR-1, NDPK-73, 2019/PUMVAR-6, 2019/PUMVAR-3, NDPK-37, 2021/PUMVAR-4, NDPK-36 |
| II | 1 | NDPK-33 |
| III | 1 | 2021/PUMVAR-7 |
| IV | 1 | 2021/PUMVAR-2 |
| V | 1 | 2019/PUMVAR/2 |
| VI | 1 | 2021/PUMVAR-6 |

**Table 2:** Average of intra- and inter-$D^2$ values for six clusters

| Cluster number | I | II | III | IV | V | VI |
|---|---|---|---|---|---|---|
| I | 55.15 | 101.19 | 97.74 | 93.70 | 93.80 | 155.72 |
| II | | 0.00 | 183.59 | 118.63 | 193.94 | 231.40 |
| III | | | 0.00 | 133.95 | 119.15 | 110.47 |
| IV | | | | 0.00 | 156.02 | 219.36 |
| V | | | | | 0.00 | 244.67 |
| VI | | | | | | 0.00 |

**Note:** Bold figures indicate intra cluster distance

**Table 3:** Percent contribution in seventeen characters towards total genetic divergence

| S. No. | Characters | Contribution (%) |
|---|---|---|
| 1. | Days to 50% staminate flower anthesis | 9.08 |
| 2. | Days to 50% pistillate flower anthesis | 8.40 |
| 3. | Node no. to first staminate flower anthesis | 8.07 |
| 4. | Node no. to first pistillate flower anthesis | 4.54 |
| 5. | No. of primary branches | 7.23 |
| 6. | Vine length | 1.34 |
| 7. | Nodes per vine | 5.21 |
| 8. | Internodal length | 5.38 |
| 9. | Days to first fruit harvest | 6.72 |
| 10. | Equatorial circumference of fruit | 7.39 |
| 11. | Polar circumference of fruit | 6.89 |
| 12. | Flesh thickness | 2.02 |
| 13. | Fruit diameter | 2.86 |
| 14. | Fruit cavity | 6.39 |
| 15. | Average fruit weight | 6.39 |
| 16. | Number of fruit per plant | 5.55 |
| 17. | Fruit yield per plant | 9.41 |

**Table 4:** Intra-cluster group means for seventeen characters in pumpkin

| Cluster | Days to 50% staminate flower anthesis | Days to 50%pistillat flower anthesis | Node to first staminate flower anthesis | Node to first pistillat flower anthesis | No. of Primary branches | Vine Length | Nodes per Vine | Internodal Length | Days to first fruit harvest | Equatorial circumference | Polar circumference | Flesh thickness | Fruit Diameters | Fruit Cavity | Average Fruit Weight | No. of Fruit per Plant | Fruit Yield per Plant |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| I. | 45.72 | 49.84 | 5.43 | 21.52 | 8.97 | 4.78 | 49.19 | 9.80 | 65.73 | 55.53 | 50.16 | 4.40 | 20.61 | 11.80 | 1.45 | 3.26 | 4.50 |
| II. | 44.67 | 48.67 | 10.13 | 19.00 | 9.70 | 5.39 | 48.90 | 11.15 | 64.00 | 62.02 | 54.70 | 3.90 | 19.43 | 13.00 | 1.99 | 1.47 | 2.93 |
| III. | 46.33 | 49.67 | 4.80 | 23.10 | 6.67 | 4.97 | 49.17 | 10.47 | 61.00 | 53.57 | 44.01 | 2.50 | 14.47 | 8.70 | 0.89 | 5.33 | 4.62 |
| IV. | 43.67 | 48.00 | 5.47 | 19.43 | 12.57 | 6.98 | 45.80 | 15.71 | 64.33 | 43.56 | 36.15 | 4.10 | 19.17 | 12.07 | 1.46 | 3.00 | 4.34 |
| V | 45.33 | 47.00 | 5.70 | 21.10 | 9.47 | 4.92 | 44.10 | 10.72 | 60.67 | 53.61 | 52.35 | 4.80 | 17.43 | 12.27 | 1.67 | 5.40 | 8.97 |
| VI. | 45.67 | 49.33 | 6.77 | 19.40 | 6.57 | 2.57 | 41.73 | 6.35 | 67.33 | 25.33 | 47.08 | 2.20 | 13.60 | 8.07 | 0.68 | 3.90 | 2.65 |

In conclusion, the clustering analysis of thirty-five pumpkin genotypes revealed six distinct clusters, with significant variation in genetic diversity both within and between clusters. Clusters I through VI exhibited varying strengths in traits such as fruit yield and flower anthesis timing. The study found no direct correlation between geographical and genetic diversity, suggesting that hybridization among diverse clusters could enhance the improvement of multiple economic traits. The findings support selecting potential lines from different clusters for hybridization to achieve superior trait performance, leveraging the observed genetic diversity to advance crop development.

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