



ISSN (E): 2277-7695  
ISSN (P): 2349-8242  
NAAS Rating: 5.23  
TPI 2023; 12(2): 3551-3554  
© 2023 TPI

[www.thepharmajournal.com](http://www.thepharmajournal.com)

Received: 01-11-2022

Accepted: 05-12-2022

#### Khirud Panging

Assam Seed and Organic  
Certification Agency, Jorhat  
Zone, Jorhat, Assam, India

#### Gobin Chandra Bora

Department of Plant Breeding  
and Genetics, Assam  
Agricultural University, Jorhat,  
Assam, India

#### Debojit Sarma

Department of Plant Breeding  
and Genetics, Assam  
Agricultural University, Jorhat,  
Assam, India

## Genetic divergence among pumpkin (*Cucurbita moschata* Duch ex. Poir) landraces of Assam

Khirud Panging, Gobin Chandra Bora and Debojit Sarma

#### Abstract

Pumpkin (*Cucurbita moschata* Duch.) is one of the most popular summer vegetable crops and belongs to the Cucurbitaceae family. Thirty diverse pumpkin landraces representing eight districts of Assam comprised the investigation, carried out at the Instruction-cum-Research (ICR) Farm of Assam Agricultural University, Jorhat, during Rabi 2018–2019. Genetic divergence in 30 pumpkin landraces for 27 different traits using Mahalanobis  $D^2$  statistics and Tocher's clustering generated five clusters of the 30 pumpkin landraces. Diversity analysis revealed that the highest genetic diversity was evident between the cluster pairs II-V, I-V, I-V and IV-V, respectively; the landraces from these clusters may be selected as parents in future hybridization programs to obtain superior combinations and heterosis in segregating generation. The single landrace Dibrugarh-1 belonging to cluster IV stood most diverse among 30 landraces and recorded a high cluster mean for yield per plant, which can serve as a suitable parent for the hybridization programme. Landraces Karbi Anglong-1, Haflong-1, Jorhat-1, Majuli - 1 and Lakhimpur-1 belonged to the best mean cluster group V; they showed the highest intra-cluster distance, indicating the presence of heterogeneity among the landraces and they can be parents in hybridization programme.

**Keywords:** Landrace, 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. In India, it occupies an area of 99000 hectares with an annual production of 2117 metric tonnes, accounting for an average of 21.3 tonnes per hectare in 2020–21 (Anonymous, 2021) [2]. Pumpkin with  $2n=40$  chromosomes is also one of the most morphologically variable species in the plant kingdom for fruit shape, size and colour (Wu *et al.*, 2011). Assam is rich in cucurbitaceous germplasm, having a wide range of variability in respect of size, shape, and colour and even resistance to various pests and diseases. Pumpkin fruits are consumed in daily cooking and also used in sweets preparation. The fruit juice, young stems, flowers and leaves have important medicinal properties. The fruit skin has variable thickness and colour depending on the cultivars. Different fruit shapes - elongate, oval, cylindrical, elliptical and oblong are available in pumpkins. 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) [7].

Sufficient genetic variability exists among the cultivated genotypes (Aliu *et al.*, 2011) [1], offering scope for its utilization in breeding programs. The pre-requisite of any systemic breeding for increasing yield, quality, and resistance to diseases and pests is the exploration of genetic variability in available germplasm, necessitating evaluation of the local germplasm. Collecting the broad spectrum of germplasm to form a wide genetic base for selection is an immediate option for mainstreaming value-added types and choosing suitable donors for yield heterosis and open-pollinated variety development. The presence of diverse germplasm offers scope for improving economic characteristics. The present investigation aimed to evaluate the pumpkin landraces of Assam for diversity assessment using Mahalanobis  $D^2$  statistics, classifying them into different groups, and exploiting their usefulness in further breeding.

#### Materials and Methods

Thirty diverse pumpkin landraces were from eight districts of Assam *viz.*, four from each of Sivasagar, Dibrugarh, Jorhat and Majuli (Upper Brahmaputra valley zone); Karbi Anglong and Haflong (Hills zone); and three from each of Lakhimpur (North Bank Plains zone) and Kokrajhar (Lower Brahmaputra valley zone).

#### Corresponding Author:

#### Khirud Panging

Assam Seed and Organic  
Certification Agency, Jorhat  
Zone, Jorhat, Assam, India

The pumpkin germplasm was evaluated at the Instructional-cum-Research (ICR) Farm of Assam Agricultural University, Jorhat, during *Rabi* 2018–19, following the recommended Package of Practices for Assam. The experiment followed a Randomised Block Design with three replications in two-row plots. The plot size was 4.0 m x 3.75 m (2 rows of 3 m). Five random plants in each accession constituted the sample for recording the quantitative observations.

The thirty pumpkin landraces taken for genetic divergence analysis differed significantly for the characters studied.  $D^2$  statistics of Mahalanobis (1936)<sup>[8]</sup> is a routine method used in diversity analysis and classification techniques. Information on the nature and magnitude of genetic divergence would help the plant breeders choose the right parents for hybridization to obtain high heterotic expression in  $F_1$ s and a broad spectrum of variability in subsequent generations (Vivekanandan and Subramaniam, 1993)<sup>[12]</sup>. The geographical separation or genetic barrier to crossability results in genetic diversity. The present study entails genetic divergence in 30 pumpkin landraces for 27 different traits using Mahalanobis  $D^2$  statistics and clustering by Tocher's method (Rao, 1952)<sup>[11]</sup>. Mahalanobis (1936)<sup>[8]</sup> developed this model to determine the divergence among populations in terms of generalized group distance.

The characters observed were cotyledon length (mm), cotyledon breadth (mm), vine length (m), leaf blade breadth (cm), leaf blade length (cm), total chlorophyll content (mg/100 g), petiole length (cm), peduncle length (cm), days of first flowering, days to the opening of first female flower, days of maturity, no. of female flowers/plant, no. of male flowers/plant, female to the male percentage, no. of fruits/plant, fruiting per cent, fruit length (cm), fruit diameter (cm), flesh thickness (cm), single fruit weight (kg), yield/plant (kg), 100-seeds weight (g), no. of seeds/fruit, moisture content (%), carotene content ( $\mu\text{g}/100\text{g}$ ), ascorbic acid (mg/100 g) and total soluble solid (mg/100g).

## Results and Discussion

The thirty pumpkin landraces displayed marked divergence when subjected to Wilk's (A) criterion and analysis of dispersion (Table 1), taking all 27 characters together. The value of 'V' statistics estimated through Wilk's test showed significant differences among the landraces for all the characters under study.

Based on the relative magnitude of  $D^2$  statistics, the 30 pumpkin landraces fall into 5 clusters (Table 2). Among the different clusters, I consists of a maximum number of 13 landraces, followed by cluster III having six landraces, cluster II and cluster V having five landraces each, and cluster IV including a single landrace. The clustering pattern revealed that the landraces did not resolve according to their geographical origin, which might be due to the differences in adaptation, selection criteria, selection pressure and environmental conditions. These results conformed with Hosain *et al.* (2010)<sup>[4]</sup>, Naik and Prasad (2015)<sup>[9]</sup>, Rahman *et*

*al.* (2016)<sup>[10]</sup>, Kandasamy *et al.* (2019)<sup>[5]</sup>, and Krishnamoorthy and Sampath (2019)<sup>[6]</sup> in pumpkin.

The average intra- and inter-cluster  $D^2$  values among the 30 landraces are present in Table 3. The highest intra-cluster distance was apparent for cluster V (35512.0), followed by cluster III (25237.6), cluster I (19944.4) and cluster II (18017.7), indicating the homogeneous nature of the landraces within these clusters. The highest intra-cluster distance could be due to the number of diverse characters studied, which also suggests considerable variation among the landraces. Lowering the intra-cluster distances shows the closeness of the landraces belonging to the same cluster. The maximum inter-cluster distance was apparent between clusters II and V (276636.0), while the minimum inter-cluster distance was 37989.5 between I and II. The landraces belonging to clusters II and V had a wide genetic divergence and, hence intercrossing between the landraces of these groups would produce more transgressive segregates in an advanced generation. The minimum inter-cluster distance between clusters I and II revealed that the landraces belonging to these clusters would have evolved by similar evolutionary procedures even though their origins were different. Similar results were available with Dora *et al.* (2003)<sup>[3]</sup> in pointed gourd and Krishnamoorthy and Sampath (2019)<sup>[6]</sup> and Kandasamy *et al.* (2019)<sup>[5]</sup> in pumpkin. The inter-cluster distances were higher than the intra-cluster spaces, suggesting a more extensive genetic diversity among the genotypes.

Figure 1 depicts the per cent contribution of 27 characters to the total divergence. The selection and choice of parents for hybridization depend primarily on the trait contributions toward diversity. In the present investigation, the highest contribution was exhibited for ascorbic acid content (67.59%), followed by 100 seed weight (23.68%) and the number of seeds per fruit (3.45%). The per cent contribution of 100-seeds weight in pumpkin landraces was also reported earlier by Krishnamoorthy and Sampath (2019)<sup>[6]</sup>. Hence emphasis should be given to the traits such as ascorbic acid, 100-seeds weight and number of seeds per fruit for selecting the parents for the hybridization programme. The landrace *Karbi Anglong-2* showed the highest ascorbic acid content; this landrace could serve as a potential parent for the improvement program.

The individual cluster means for all 27 characters (Table 4) were assessed based on their superiority over the grand mean values. Accordingly, cluster III was superior to others for cotyledon length and breadth, petiole length, peduncle length, fruit diameter, flesh thickness, single fruit weight, yield per plant, 100- seeds weight, carotene content, ascorbic acid and total soluble solids. The number of female flowers and fruits per plant was the highest for cluster V. Cluster V had high mean values for main vine length, total chlorophyll content, peduncle length, number of female flowers, the number of fruits per plant and ascorbic acid content, while the lowest for moisture per cent. The least mean days to the first flowering and maturity were evident in cluster IV.

**Table 1:** Analysis of dispersion testing the simultaneous significance of the mean differences among the landraces

Source of variation	df	Sum of squares	Mean Squares	F Ratio	Probability
Varieties	29	-4.86E-19	-1.68E-20	-1.97E+00	0.01478 *
Error	57	4.86E-19	8.53E-21		
Total	86	0.00E+00	0.00E+00		

**Table 2:** Clustering of the thirty pumpkin landraces

Cluster	No. of genotypes	Composition
I	13	Lakhimpur-1, Jorhat-3, Karbi anglong-1, Haflong-4, Dibrugarh-2, Sivasager-4, Kokrajhar-1, Haflong-2, Sivasagar-3, Kokrajhar-3, Jorhat-4, Karbi Anglong-4, Dibrugarh-4
II	5	Haflong-1, Lakhimpur-3, Kokrajhar-2, Majuli-2, Sivasager-1
III	6	Majuli-1, Majuli-4, Sivasagar-2, Majui-3, Karbi Anglong-3, Dibrugarh-3
IV	1	Dibrugarh-1
V	5	Karbi Anglong-2, Haflong-3, Jorhat-1, Jorhat-2, Lakhimpur-2

**Table 3:** Intra- (bold) and inter-cluster distances among the Tocher's clusters

Cluster	I	II	III	IV	V
I	19944.4	37989.5	51468.5	39997.9	161568.2
II		18017.1	103380.8	101176.3	276636.0
III			25237.6	56651.1	75372.4
IV				0.0	104204.5
V					35512.0

**Table 4:** Mean trait values for the five Tocher's clusters

Cluster	Cotyledon length (mm)	Cotyledon breadth (mm)	Vine length (m)	Leaf blade breadth (cm)	Leaf blade length (cm)	Total chlorophyll content (mg/100 g)	Petiole length (cm)	Peduncle length (cm)	Days to 1 <sup>st</sup> flowering
I	12.46	6.76	5.73	29.03	25.07	15.37	14.37	10.69	43.79
II	14.10	5.39	5.79	28.15	28.12	13.25	12.07	11.19	43.10
III	13.49	6.61	5.32	27.63	23.71	12.41	13.32	12.65	43.19
IV	11.17	5.13	5.79	26.72	24.35	11.35	13.73	8.17	42.00
V	12.90	6.79	5.93	30.18	25.56	15.69	12.13	13.09	45.27

Cluster	Days to opening 1 <sup>st</sup> female flower	Days of maturity	No. Female flowers per plant	No. of male flowers per plant	Female: Male percentage (%)	No. of fruits per plant	Fruiting percentage (%)	Fruit Length (cm)	Fruit diameter (cm)
I	47.18	93.51	6.69	37.97	19.34	4.38	65.80	14.92	14.54
II	46.67	91.33	6.60	35.93	20.86	4.00	60.21	16.94	16.25
III	46.94	96.89	5.50	43.06	13.44	3.39	61.53	15.26	18.14
IV	44.67	88.33	6.00	35.00	17.32	4.00	67.14	21.07	10.86
V	47.47	92.07	7.27	32.07	25.67	4.47	57.86	13.36	14.62

Cluster	Flesh thickness (cm)	Single fruit weight (kg)	Yield per plant (kg)	100-seeds weight (g)	No. of seeds per fruit	Moisture (%)	Carotene (µg/100g)	Ascorbic acid (mg/100 g)	Total soluble solid (mg/100g)
I	2.84	0.60	2.57	13.84	233.79	87.83	6.42	15.98	8.98
II	3.32	0.87	3.44	17.45	232.27	89.68	5.60	12.25	7.86
III	3.53	1.02	3.33	16.06	211.08	87.14	6.28	21.98	9.47
IV	2.50	1.00	4.14	9.27	363.00	91.56	6.83	16.53	10.61
V	2.58	0.60	2.64	11.76	292.17	85.50	6.20	27.22	8.40

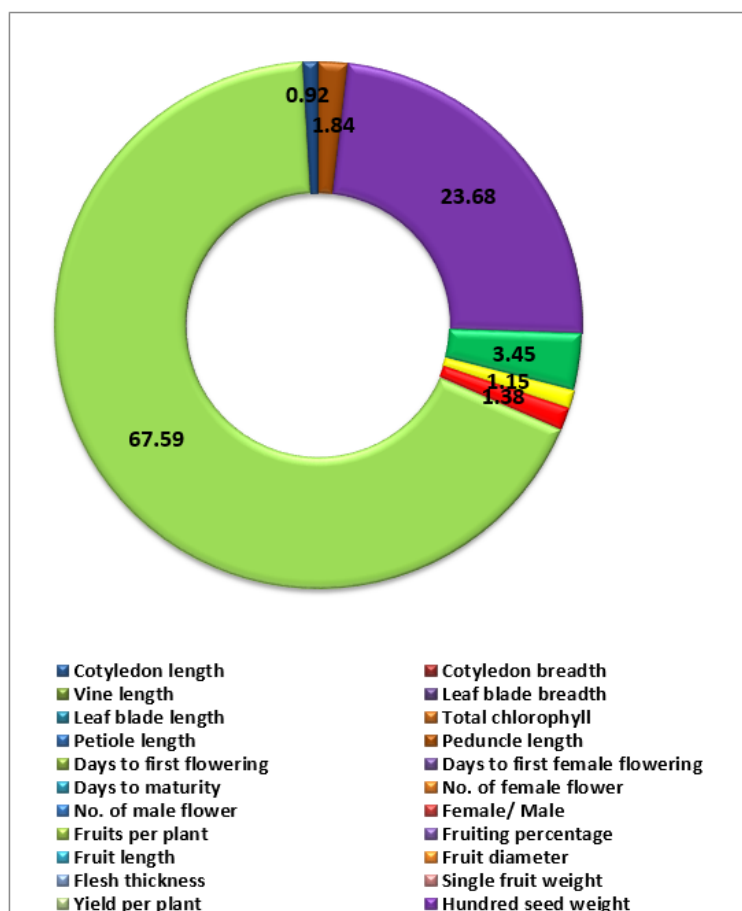


Fig 1: Percent contribution of the traits to total divergence

## Conclusion

The highest genetic diversity was evident between clusters II-V, I-VI-V and IV-V; the landraces from these clusters may be selected as parents in a future hybridization programme to obtain superior combination and consequently heterosis in segregating generation. The single landrace *Dibrugarh-1* belonging to cluster IV was the most diverse among the landraces and recorded a high cluster means for yield per plant, which could be recommended for general cultivation throughout the state. Landraces Karbi Anglong-1, Haflong-1, Jorhat-1, Majuli -1 and Lakhimpur-1 belong to the best mean cluster group V, also showing the highest intra-cluster distance, indicating the presence of heterogeneity among them, and thus, serve as parents for hybridization programme.

## References

1. Aliu SA, Haziri S, Fetahu N, Aliage I, Rusinove I, Arapi V. Morphological and nutritive variation in a collection of *Cucurbita pepo* L. growing in Kosova. *Notulae Scientia Biologicae*. 2011;3(2):119-122.
2. Anonymous. NHB STAT, Pumpkin, 2021.
3. Dora DK, Acharya GC, Das S, Behera TK. Numerical taxonomic approach: A better alternative for clustering of pointed gourd genotype. *The Orissa J Hort*. 2003;31(2):76-79.
4. Hossain MF, Rabbani MG, Hakim MA, Amanullah ASM, Ahsannullah ASM. Study on variability character association and yield performance of cucumber (*Cucumis sativus* L.). *Bangladesh Research Publication Journal*. 2010;4(3):297-311.
5. Kandasamy R, Arivazhagan E, Anusa P. Genetic divergence among landraces of pumpkin (*Cucurbita moschata* Duch ex. Poir) from Tamil Nadu. *Annals of Plant and Soil Research*. 2019;21(4):333-336
6. Krishnamoorthy V, Sampath S. Genetic diversity analysis in pumpkin (*Cucurbita moschata* Duch Ex. Poir). *Intern. J Chem. Stud*. 2019;7(3):3672-3676.
7. Kumar R, Rajasree V, Praneetha S, Rajeswari S, Tripura U, Sriyamuna VS. *Int. J Curr. Microbiol. App. Sci*. 2018;7(6):2591-2598.
8. Mahalanobis PC. A statistical study at Chinese head measurement. *J Asiatic Soc. Bengal*. 1936;25:301-377.
9. Naik ML, Prasad VM, Laxmi R. A study on character association and path analysis in pumpkin (*Cucurbita moschata* Duch ex Poir.). *Intern. J Adv. Res*. 2015;3(1):1030-1034.
10. Rahman Khan AS, Rabeya Eyasmin MH, Harunur Rashid M, Sheikh Ishtiaque, Chaki AK. Variability, heritability, character association, path analysis and morphological diversity in snake gourd. *Agriculture Natural Resources*. 2016;50:483-489.
11. Rao CR. *Advanced statistical methods in biometrical research*. John Wiley and Sons, New York. 1952, p. 374.
12. Vivekanandan P, Subramanian S. Genetic divergence in rainfed rice. *Oryza*. 1993;30:60-62.
13. Wu J, Chang Z, Wu Q, Zhan H, Xie S. Molecular diversity of Chinese *Cucurbita moschata* germplasm collections detected by AFLP markers. *Scientia Horticulturae*. 2011;128:7-13.