Aniket Kumar Verma
M. Sc. Scholar, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

VB Singh
Associate Professor, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

Yogesh Kumar
M. Sc. Scholar, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

Sharvan Kumar
Ph.D. Scholar, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

Studies on genetic divergence (D^2) for fruit yield and its related traits in pumpkin (*Cucurbita moschata* Duch. ex. Poir)

Aniket Kumar Verma, VB Singh, Yogesh Kumar and Sharvan Kumar

DOI: https://doi.org/10.22271/chemi.2020.v8.i5g.10340

Abstract
An experiment was conducted at Main Experiment Station of Department of Vegetable Science at Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P). The experimental material consisted of 28 pumpkin genotypes including three standard checks *viz.,* Arka Chandan, Azad Kaddu and Pusa Vikash was conducted in a Randomized Block Design with three replications. Analysis of variance studies indicated significant differences among all the genotypes for all the characters under study. Genetic diversity was worked out using Mahalanobis D^2 statistic. Based on D^2 analysis, the genotypes were grouped into 7 distinct non-overlapping clusters. Cluster I, II and III had 6 genotypes in each clusters. Cluster IV, V and VI also had 3 genotypes and cluster VII had presented only one genotype. The maximum intra-cluster distance was in cluster V (139.09) and minimum intra-cluster distance was found for cluster VII (0.00). Clustering pattern revealed that geographical diversity was not associated with genetic diversity of genotypes. The maximum inter-cluster distance was observed between clusters III to cluster VII (503.329), which suggested that members of these two clusters are genetically very diverse to each other. The inter cluster values between cluster I to cluster VII (398.733), V to VII (325.792), II to VII (315.975), V to VI (312.753) and I to V (309.983) were also high. The minimum inter-cluster D^2 value was recorded in case of cluster III to cluster IV (174.606). The wider genetic diversity were observed in cluster clusters I to VII, V to VII, II to VII, V to VI and I to V which indicated the potentiality of these diverse genotypes collection for providing basic material for future breeding programmes.

Keywords: Divergence, cluster, breeding, cucurbita and genotype

Introduction

Pumpkin belongs to the family Cucurbitaceae having chromosome number 2n=2x= 40. There are 27 species under the genus *Cucurbita*, five of which are in cultivation. These are *C. moschata, C. maxima, C. ficifolia, C. pepo* and *C. mixta*, commonly known as pumpkin. *C. moschata* is probably the most widely grown species of *Cucurbita* and this species is cross compatible with *C. maxima, C. pepo and C. mixta* (Tindall, 1987) [14]. Pumpkin is relatively high in energy values, carbohydrates, good source of vitamins, especially high in carotenoid pigments and minerals (Bose and Som, 1998) [4]. It may contribute to improve the nutritional status of the people, particularly the vulnerable groups in respect of vitamin-A requirement (Satkar *et al.*, 2013) [11]. In India, it is mainly grown in Assam, West Bengal, Tamil Nadu, Karnataka, Madhya Pradesh, Uttar Pradesh, Orissa, Kerala and Bihar. The total area of pumpkin in India is 19,960 hectares whereas, the total production is 2093 ('000 mt) with productivity of 21.71 t/ha (Annonymous, 2018) [2].

Genetic diversity is one of the important tools to quantify genetic variability in both cross and self-pollinated vegetable crops and also important for crop improvement as well as variety development programme (Anand *et al.,* 1975 and Gaur *et al*., 1978) [1, 6]. Multivariate analysis by means of Mahalanobis D^2 statistics is useful tools in quantifying the degree of genotypic divergence among biological populations and to assess the relative contribution of different components to the total divergence both at inter and intra-cluster levels (Das and Gupta 1984) [5]. Many researchers have adopted this D^2 technique for measuring divergence among genotypes of pumpkin (Rashid *et al.,* 2000, Kale *et al.,* 2002 and Blessing *et al.,* 2012) [10, 7, 3].

Corresponding Author:
Aniket Kumar Verma
M. Sc. Scholar, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India

An understanding of the nature and degree of variability among the germplasm is a prerequisite for its varietal improvement. Therefore, the present study was undertaken to analyse the genetic divergence among the number of pumpkin genotypes for selecting parents of diverse group for further breeding programme.

Materials and Methods

The experimental material comprised of 28 germplasm including three standard checks *viz.,* Arka Chandan, Azad Kaddu and Pusa Vikash. The experiment was laid out in a Randomized Block Design with three replications at Main Experiment Station of Department of Vegetable Science at Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P) during summer season 2019. The seeds were sown on 03/04/2019, having plot size of 3×3 m accommodating 6 plants per plot with row-to-row spacing of 3 m and plant-to-plant spacing of 0.50 m. Observations were recorded for node number to first staminate flower anthesis, node number to first pistillate flower anthesis, days to first staminate flower anthesis, days to first pistillate flower anthesis, days to first fruit harvest, number of primary branches, fruit polar circumference (cm), fruit equatorial circumference (cm), vine length (m), flesh thickness (cm), number of fruits per plant, average fruit weight (kg) and fruit yield per plant (kg.)

The data on thirteen quantitative characters are recorded on five competitive and randomly selected plants of each genotype and in each replication. All the statistical analysis was carried out using OPSTAT statistical software. The genetic divergence among genotypes was estimated by using D^2 statistics (Mahalanobis 1936) [8]. All the genotypes used were clustered into different groups by following Tocher's method (Rao, 1952) [9]. The average intra and inter cluster distances were calculated by the formulae given by Singh and Chaudhary (1985) [12].

Results and Discussion

Bases on D^2 statistics values, the clustering pattern of the 28 genotypes were grouped into 7 different non-overlapping clusters (Table-1). Cluster I, II and III had same six genotypes number as well as cluster IV, V and VI also had same three genotypes number whereas cluster VII had presented only one genotype. 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 Sutariya *et al.* (2011) [13].

Intra and inter-cluster distances

The estimates of intra and inter-cluster distance represented by D^2 values are given in table-2.The minimum intra-cluster distance was found for 0.00 (cluster VII) and maximum was recorded for 139.09 (cluster V). The maximum inter-cluster distance was observed between clusters III to cluster VII (503.329), which suggested that members of these two clusters are genetically very diverse to each other. The inter-cluster values between cluster I to VII (398.733), V to VII (325.792), II to VII (315.975), V to VI (312.753) and I to V (309.983) were also high.

The minimum inter-cluster D^2 value was recorded in case of cluster I to cluster II (130.874). The higher inter-cluster distance indicated greater genetic divergence between the genotypes of those clusters, while lower inter-cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other. The intra-cluster means for thirteen characters in pumpkin are given in Table-2.

Table 1: Clustering pattern of 28 genotypes on the basis of Mahalanobis D^2 statistics

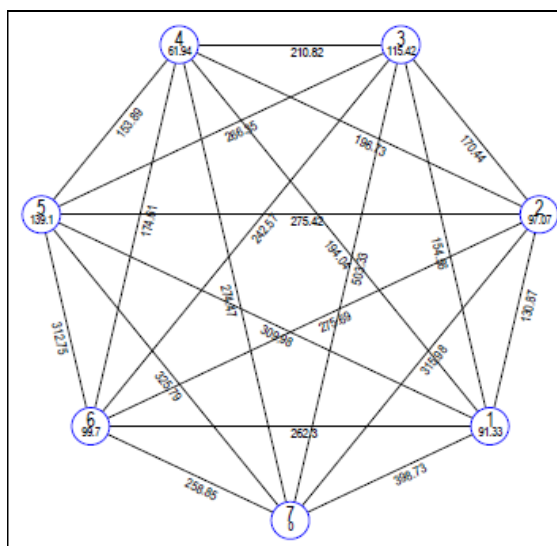| Cluster number	No. of genotypes	Genotypes in clusters
I	6	Harp-4, Azad Kaddu (C), CM-350 SPS, Arka Chandan (C), Narendra Upkar, NDPK-11
II	6	BS-13-1, NDPK-13, NDPK-7, NDPK-15, PusaVikash (C), NDPK-2
III	6	NDPK-1, CO-2 SPS, NDPK-5, NDPK-10, NDPK-9, NDPK-18
IV	3	CO-1-SPS, Harp-10, NDPK-17
V	3	NDPK-4, NDPK-16 , NDPK-8
VI	3	NDPK-3, NDPK-14, NDPK-18
VII	1	NDPK-12

Fig 2: Cluster diagram showing the average intra and inter-cluster distance; (D=D²) of pumpkin genotypes inter and intra-cluster distance

Table 2: Average of intra (bold) and inter- D² values for seven clusters

Cluster number	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
I	91.333	130.874	154.560	194.040	309.983	262.305	398.733
II		97.075	170.439	196.727	275.418	275.694	315.975
III			115.417	210.819	266.249	242.567	503.329
IV				61.936	153.887	174.606	274.475
V					139.096	312.753	325.792
VI						99.699	258.850
VII							0.000

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

Cluster	Node number at first staminate flower anthesis	Node number at first pistillate flower anthesis	Days to first staminate flower anthesis	Days to first staminate flower anthesis	Days to first fruit harvest	Number of primary branches	Fruit polar circumference (cm)	Fruit equatorial circumference (cm)	Vine length (m)	Flesh thickness (cm)	Number of fruit Per plant	Average fruit weight (kg)	Fruit yield per plant (kg)
I	5.14	12.44	42.64	46.04	66.02	4.32	27.59	60.40	4.16	3.00	3.72	1.93	5.60
II	6.28	15.36	42.92	46.70	64.61	4.16	28.81	61.03	4.09	3.21	5.84	1.60	7.08
III	6.45	9.82	43.35	46.97	64.02	4.23	29.40	58.98	4.38	2.69	5.10	1.23	5.05
IV	5.15	17.52	43.41	45.88	67.05	4.17	34.35	60.01	6.78	3.16	5.57	1.29	4.83
V	6.03	15.62	45.70	47.03	65.55	4.70	29.75	55.12	9.18	2.53	5.56	1.30	5.87
VI	7.22	15.75	44.85	48.94	67.83	8.33	31.70	59.14	4.60	4.36	4.47	1.12	4.01
VII	6.06	21.30	47.16	45.80	65.53	9.43	28.06	64.40	7.26	4.23	5.24	1.63	7.68

Cluster mean

A perusal of Table-3 showed that cluster means for different traits indicated considerable differences between the clusters. All the clusters from cluster I to cluster VII had in general medium mean performance for most of the characters, exhibiting extreme cluster means for none of the character under the study.

Cluster I showed maximum mean values for average fruit weight (1.93) while days to first staminate flower anthesis (42.64), fruit polar circumference (27.59) and number of fruit per plant (3.72) were showed minimum values for cluster I. Cluster II showed maximum mean value for number of fruit per plant (5.84) whereas number of primary branches (4.16) and vine length (4.09) were exhibited for minimum mean values. Cluster III showed minimum mean value for node number at first pistillate flower anthesis (9.82) and days to first fruit harvest. Cluster IV showed minimum mean value for node number at first staminate flower anthesis (5.15) and days to first pistillate flower anthesis (45.88) while showed maximum mean value for fruit polar circumference (34.35).Cluster V showed minimum mean value for fruit equatorial circumference (55.12) and flesh thickness (2.53)

while showed maximum mean value for vine length (9.18). Cluster VI showed maximum mean value for node number at first staminate flower anthesis (7.22), days to first pistillate flower anthesis (48.94), days to first fruit harvest (67.83) and flesh thickness (4.23) while showed minimum mean value for average fruit weight (1.12) and fruit yield per plant (4.01). Cluster VI showed maximum mean value for node number at first pistillate flower anthesis (21.30), days to first staminate flower anthesis (47.16), number of primary branches (9.43), fruit equatorial circumference (64.40) and fruit yield per plant (7.68).

Per cent contribution of the traits

Highest per cent contribution observation for the trait vine length (23.81%) followed by number of primary branches (17.20%), average fruit weight (14.55%) and fruit yield per plant (12.96%). Flesh thickness (8.99%) and number of fruit per plant (8.99%) contribute same per cent for the genetic divergence whereas node number at first pistillate flower anthesis (7.67%) and node number at first pistillate flower anthesis (5.56%) were observed. For other characters were contributed very low in Table-4.

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

S. No.	Character	Contribution (%)
1	Node number at first staminate flower anthesis	5.56
2	Node number at first pistillate flower anthesis	7.67
3	Days to first staminate flower anthsis	00.00
4	Days to first pistilate flower anthsis	00.00
5	Days to first fruit harvest	00.00
6	Number of primary branches	17.20
7	Fruit polar circumference (cm)	0.26
8	Fruit equatorial circumference (cm)	00.00
9	vine length (m)	23.81
10	Flesh thickness (cm)	8.99
11	Number of fruit per plant	8.99
12	Average fruit weight (kg)	14.55
13	Fruit yield per plant (kg)	12.96

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