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Genetic divergence studies in pumpkin (*Cucurbita moschata* Duch. ex Poir.) for growth and yield traits

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Abstract

The present study was conducted with the aim to assess the diversity among the lines of pumpkin and their offspring with the help of Mahalanobis D^2 analysis. The trials were conducted during three seasons and pooled analysis of data was carried out. The observations were recorded for fourteen growth and yield traits. The present investigation was revealed that the clustering pattern for the twenty one genotypes was grouped into five different non-overlapping cluster in pooled analysis. The minimum intra cluster distance (0.00) was found for all the clusters except in cluster I and III and maximum was found in cluster III followed by cluster I in pooled analysis. The minimum inter-cluster distance was found between cluster II and maximum inter cluster distance was calculated between cluster III and IV. Cluster II showed maximum mean value for four characters viz., days to first male flower anthesis, days to first female flower anthesis, node number to first male flower appear, days to first fruit harvest and number of primary branches per plant. In pooled analysis, highest per cent contribution towards clustering of genotypes was showed by average fruit weight. The study further concluded that the much diversity was observed among the genotypes (lines and off-springs) for growth and yield traits.

Keywords: Pumpkin, genetic divergence, growth characters and marketable fruit yield

Introduction

Pumpkin (*Cucurbita moschata* Duch. ex. Poir) is one of the most important vegetable crops of family cucurbitaceae grown throughout the world not only for providing better nutrition to the consumers but also higher returns to the farmers. It is originated from central Mexico. Pumpkin is a herbaceous annual, sexually propagated vegetable with chromosome number $2n=2x=40$. The word pumpkin was originated from the Greek word *pepon*, which means "large melon", something round and large. Robinson and Decker-Walters (1999)^[7] concluded that in genus *Cucurbita*, there are 5 cultivated and 10 wild species. Seshadri and More (2009)^[8] also stated that the recent recognition of synonyms and taxonomic changes have reduced the number of *Cucurbita* species to 15 or even less. The five cultivated species are *C. argyrosperma* (earlier *C. mixta*), *C. pepo*, *C. maxima*, *C. moschata* and *C. ficifolia*. In India, pumpkin and squashes were introduced from South America by foreign navigators and emissaries. *Cucurbita moschata* is more widely cultivated than other four cultivated species in our country.

Pumpkin is relatively high in energy and carbohydrates with a good source of vitamins, especially high carotenoids pigments and minerals. It may certainly contribute to improve nutritional status of the people, particularly the vulnerable groups in respect of vitamin A requirement. Night-blindness is a serious problem of South Asian countries. Encouraging the mass people to take more pumpkin can easily be solved the problem. The total area of pumpkin in India is 78000 hectares whereas, the total production is 1.71 million tonne with productivity 21.97 MT/ha (Anonymous, 2018).

Genetic diversity has been considered as a pre-requisite for obtaining high yielding progenies through hybridization. For getting high heterosis or for recovering transgressive segregants, parents chosen for hybridization need to be genetically diverse or distant. The importance of genetic diversity has long been appreciated by breeders and it has been proved in many crops that diversity between the parents used in hybridization programme was the key to success in most of the cases. It is commonly found that the level of heterosis exhibited by a hybrid is a function of the genetic divergence between the parents.

Materials and methods

The experiments of the present research work was conducted during *Kharif*, 2015 (E₁), *Rabi*

2015-16 (E_2) and *Zaid*, (E_3) of 2016 at Main Experiment Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture & Technology, Narendra Nagar (Kumarganj), Ayodhya (U.P.) which falls under humid sub-tropical climate and is located in between 24.47° and 26.56° N latitude, and 82.12° and 83.58° E longitude at an altitude of 113 m above the mean sea level. The experimental materials for the present study comprised of six promising and diverse inbreds and varieties of pumpkin selected on the basis of genetic variability from the germplasm stock maintained in the Department of Vegetable Science, N.D. University of Agriculture & Technology, Kumarganj, Ayodhya (U.P.) India. The selected parental lines *i.e.* Narendra Upkar (P_1), NDPK-120 (P_2), Narendra Agrim (P_3), NDPK-39-2 (P_4), Kashi Harit (P_5) and NDPK-11-3 (P_6) were raised and crossed with the all possible combinations, excluding reciprocals in diallel mating design, during *Zaid*, 2015 to get 15 F_1 hybrid seeds for the study of diversity for fourteen quantitative traits.

Observations were recorded on fourteen economic traits *viz.*, days to first female flower anthesis, days to first male flower anthesis, node number to first male flower appearance, node number to first female flower appearance, days to first fruit harvest, vine length (m), internodal length (cm), number of primary branches per plant, fruit weight (kg), number of fruits per plant, equatorial circumference of fruit (cm), polar circumference of fruit (cm), flesh thickness (cm) and fruit yield per plant (kg).

Genetic divergence of forty genotypes of vegetable pea was worked out using Mahalanobis (1936) D^2 statistics. The eighteen quantitative characters in pumpkin were included for these analyses.

Result and discussion

The studies of genetic divergence among the 21 genotypes (parents and their off springs) of pumpkin were carried out by using Mahalanobis D^2 statistics for three seasons and over seasons.

The clustering pattern for the twenty one genotypes was grouped into five different non-overlapping cluster in pooled analysis (Table 1). In pooled analysis Cluster I had highest number of genotypes (10) followed by cluster II (4) and cluster IV (3). Whereas, cluster V and cluster III presented only two genotypes in each group in pooled analysis.

This indicated presence of considerable diversity in the genotype. The major clusters in the reveal genetic divergence analysis contained frequently the genotypes of heterogenous origin. Although, the genotypes of same origin or geographic region found to be grouped simultaneously in the same cluster. The instance of grouping of genotypes of different origin or geographic region in same cluster were frequently observed. This recommended that there is no parallelism between genetic and geographic diversity.

The estimates of intra and inter- cluster distance represented by D^2 values are given in table 2 for E_1 , E_2 , E_3 and over seasons (pooled). The minimum intra cluster distance (0.00) was found for all the clusters except in cluster I and III and

maximum was found in cluster III followed by cluster I. The minimum inter-cluster distance was found between cluster II and IV followed by cluster I and V, cluster I and IV, cluster I and II, cluster III and V, cluster IV and V. However, maximum inter cluster distance was calculated between cluster III and IV followed by cluster II and III, cluster II and V and cluster IV and V in pooled analysis.

Lower inter cluster values between the clusters suggested that the genotypes of the clusters were not much genetically diverse from each other, while the higher inter cluster distance indicated greater genetic divergence between the genotypes of those clusters. These results are in close conformation with the findings of Nayak and Prasad (2015)^[6].

A perusal of table 3 showed that cluster means for the different traits indicated considerable differences between the clusters. The entire cluster from cluster I to cluster V had average mean performance for most of the characters, exhibiting extreme cluster mean values for none of the characters under study. Cluster II showed maximum mean value for four characters *viz.*, days to first male flower anthesis, days to first female flower anthesis, node number to first male flower appear, days to first fruit harvest and number of primary branches per plant. Cluster IV showed maximum mean value for six characters namely equatorial circumference of fruit, polar circumference of fruit, vine length, average fruit weight, number of fruits per plant and fruit yield per plant. Cluster number V recorded maximum value for node number to first female flower appear and intermodal length. Cluster I recorded maximum value for flesh thickness (Srikanth *et al.*, 2017)^[10].

Cluster IV showed minimum mean values for days to first male flower anthesis, days to first female flower anthesis, node number to first male flower appear and days to first fruit harvest in pooled analysis. Cluster II showed minimum values for node number to first female flower appear, equatorial circumference of fruit, polar circumference of fruit, internodal length, vine length and average fruit weight in pooled analysis. Cluster V showed minimum values for number of primary branches per plant, flesh thickness and number of fruits per plant in pooled analysis. Cluster III recorded minimum values for fruit yield per plant in pooled analysis. These results are in corroborated to the findings of Chaudhari *et al.*, (2017)^[2] and Kandasamy *et al.*, (2019)^[3].

In pooled analysis, highest per cent contribution towards clustering of genotypes was showed by average fruit weight followed by number of fruits per plant, number of primary branches per plant, equatorial circumference of fruit, pericarp thickness, node number to first female flower appear, polar circumference of fruit and Days to first male flower anthesis. These results are in close conformation with the findings of Shivananda (2013)^[9].

The overall review of the results 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 values for one or other character will be helpful in the improvement of pumpkin.

Table 1: Distribution of twenty one genotypes (Lines/F₁ hybrids)

Cluster No.	Number of genotype				Name of genotype							
	E ₁	E ₂	E ₃	pooled	E ₁		E ₂		E ₃		pooled	
1	5	2	6	10	P ₁ × P ₂ , P ₃ × P ₆ , P ₁ × P ₃ , P ₁ × P ₆ , P ₅ × P ₆		P ₁ × P ₃ , P ₂ × P ₅		P ₁ × P ₂ , P ₁ × P ₃ , P ₂ × P ₄ , P ₂ × P ₆ , P ₃ × P ₄ , P ₂ × P ₅		P ₁ × P ₂ , P ₅ × P ₆ , P ₁ × P ₆ , P ₁ × P ₄ , P ₁ × P ₃ , P ₁ × P ₅ , P ₄ , P ₃ , P ₁ , P ₂	
2	3	7	3	4	P ₁ × P ₄ , P ₂ × P ₆ , P ₂ × P ₅		P ₁ × P ₄ , P ₂ × P ₆ , P ₃ × P ₅ , P ₄ × P ₅ , P ₃ × P ₄ , P ₃ × P ₆ , P ₂ × P ₃		P ₅ , P ₆ , P ₁		P ₂ × P ₃ , P ₂ × P ₄ , P ₅ , P ₆	
3	4	3	5	2	P ₄ × P ₅ , P ₄ × P ₆ , P ₁ × P ₅ , P ₃ × P ₅		P ₁ × P ₅ , P ₄ × P ₆ , P ₁ × P ₂		P ₁ × P ₆ , P ₂ × P ₃ , P ₁ × P ₄ , P ₃ × P ₆ , P ₄ × P ₅		P ₂ × P ₅ , P ₂ × P ₆	
4	5	6	3	3	P ₂ × P ₄ , P ₁ , P ₂ × P ₃ , P ₅ , P ₆		P ₁ × P ₆ , P ₂ × P ₄ , P ₅ × P ₆ , P ₁ , P ₃ , P ₂		P ₄ × P ₆ , P ₅ × P ₆ , P ₃ × P ₅		P ₃ × P ₄ , P ₃ × P ₆ , P ₃ × P ₅	
5	4	3	4	2	P ₂ , P ₄ , P ₁ × P ₃ , P ₃ × P ₄		P ₅ , P ₆ , P ₄		P ₂ × P ₅ , P ₃ , P ₂ , P ₄		P ₄ × P ₅ , P ₄ × P ₆	

Table 2: Intra and inter clusters D² values for five clusters in pumpkin for three seasons (E₁, E₂, E₃) and over seasons (pooled).
Season-E₁ (Kharif, 2015)

	Cluster -1	Cluster -2	Cluster -3	Cluster -4	Cluster -5
Cluster -1	210.95	400.48	818.10	382.22	355.32
Cluster -2		0.00	1654.94	116.11	996.26
Cluster -3			167.40	1634.64	413.14
Cluster -4				0.00	962.18
Cluster -5					0.00

Season-E₂ (Rabi, 2015-16)

	Cluster -1	Cluster -2	Cluster -3	Cluster -4	Cluster -5
Cluster -1	246.83	883.97	1109.93	491.93	2855.51
Cluster -2		258.41	533.22	1900.51	951.59
Cluster -3			0.00	2526.97	903.28
Cluster -4				79.55	4793.67
Cluster -5					273.09

Season-E₃ (Summer season, 2016)

	Cluster -1	Cluster -2	Cluster -3	Cluster -4	Cluster -5
Cluster -1	196.41	377.00	799.00	329.64	320.85
Cluster -2		0.00	1552.89	130.99	908.49
Cluster -3			161.21	1518.88	452.59
Cluster -4				0.00	805.33
Cluster -5					0.00

Over Seasons

	Cluster -1	Cluster -2	Cluster -3	Cluster -4	Cluster -5
Cluster -1	5.84	10.41	14.76	10.22	10.18
Cluster -2		0.00	21.09	8.91	15.69
Cluster -3			8.68	32.09	13.90
Cluster -4				0.00	15.66
Cluster -5					0.00

Table 3: Cluster mean for different economic traits in for three seasons (E₁, E₂, E₃) and over seasons.

Cluster/Character	Days to first male Flower anthesis				Days to first female flower anthesis				Node No. to first male flower appear				Node No. to first female flower appear				Days to first fruit harvest			
	E ₁	E ₂	E ₃	pooled	E ₁	E ₂	E ₃	pooled	E ₁	E ₂	E ₃	pooled	E ₁	E ₂	E ₃	pooled	E ₁	E ₂	E ₃	pooled
Cluster -1	39.72	88.77	37.55	49.23	41.84	86.49	39.20	50.916	4.41	5.10	4.35	4.50	18.13	12.23	16.95	16.26	57.55	108.27	54.44	69.37
Cluster -2	38.22	92.73	47.53	102.16	39.58	91.40	49.30	99.62	4.35	6.05	4.55	6.63	16.44	10.27	16.95	12.37	56.86	112.68	67.94	122.78
Cluster -3	39.99	97.65	39.32	85.34	44.44	95.49	44.22	84.38	3.81	6.18	3.81	6.02	16.99	11.03	16.99	12.78	62.11	118.29	60.55	104.66
Cluster -4	48.20	102.08	42.55	39.40	49.52	98.99	41.54	42.27	4.55	7.28	5.55	4.29	16.95	12.37	20.33	16.92	67.83	121.07	59.22	58.42
Cluster -5	41.45	106.07	39.87	44.72	41.91	103.14	42.18	45.62	4.98	7.80	4.61	4.85	19.00	13.85	18.26	18.21	61.08	126.10	57.75	63.47

Contd.

Cluster/Character	Number of primary branches per pant				Equatorial circumference of fruit				Polar circumference of fruit				Flesh thickness				Internodal length (cm)			
	E ₁	E ₂	E ₃	pooled	E ₁	E ₂	E ₃	pooled	E ₁	E ₂	E ₃	pooled	E ₁	E ₂	E ₃	pooled	E ₁	E ₂	E ₃	pooled
Cluster -1	9.01	9.82	10.13	9.24	57.80	54.01	55.65	55.70	49.94	47.46	48.84	48.06	2.71	2.55	2.73	2.69	6.96	5.07	6.55	7.28
Cluster -2	10.37	7.24	7.15	9.66	56.86	52.99	50.13	47.64	49.12	45.17	44.82	40.47	2.75	2.68	2.40	2.57	6.74	6.19	7.40	6.03
Cluster -3	8.77	10.07	8.77	8.77	62.11	51.10	58.29	54.15	49.81	45.95	50.42	45.77	2.47	2.70	2.47	2.55	8.97	6.06	8.77	6.75
Cluster -4	7.15	7.85	5.35	9.26	67.83	50.35	54.95	56.59	44.21	39.03	48.60	48.95	2.40	2.41	2.81	2.63	7.60	7.08	8.47	7.46
Cluster -5	7.11	8.60	8.33	6.59	61.08	46.53	54.98	49.35	45.14	33.61	48.55	44.77	2.70	2.45	2.69	2.49	8.17	6.67	7.30	7.91

Contd.

Cluster/ Character	Vine length (m)				Average fruit weight (kg)				Number of fruits per plant				Fruit yield per plant (kg)			
	E ₁	E ₂	E ₃	pooled	E ₁	E ₂	E ₃	pooled	E ₁	E ₂	E ₃	pooled	E ₁	E ₂	E ₃	pooled
Cluster -1	4.03	2.05	3.74	3.46	2.06	1.56	2.01	1.83	3.02	3.80	3.55	2.82	6.27	5.92	7.18	5.20
Cluster -2	3.41	2.82	3.45	2.25	1.75	1.49	2.08	1.23	3.25	2.69	2.29	2.73	5.71	4.09	4.75	3.41
Cluster -3	3.94	2.33	4.24	3.00	1.85	1.39	2.03	1.60	2.52	2.60	2.77	2.69	4.69	3.62	5.63	4.37
Cluster -4	3.15	2.51	4.22	3.84	1.91	1.47	2.25	2.00	2.04	2.16	2.46	3.04	3.88	3.09	5.55	6.13
Cluster -5	2.73	2.43	3.56	3.01	1.76	1.23	2.01	1.95	2.44	2.65	2.93	2.33	4.29	3.31	5.95	4.52

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

S. No.	Characters	Per cent contribution			
		E ₁	E ₂	E ₃	Pooled
1.	Days to first male flower anthesis	30.48	64.29	31.43	0.48
2.	Days to first female flower anthesis	1.43	0.00	0.48	0.00
3.	Node number to first male flower app.	1.90	0.00	2.86	0.00
4.	Node number to first female flower app.	1.90	0.00	3.33	1.43
5.	Days to first fruit harvest	1.43	0.48	1.90	0.00
6.	Number of primary branches per plant	20.00	21.43	20.95	10.48
7.	Equatorial circumference of fruit (cm)	0.00	2.38	0.48	3.81
8.	Polar circumference of fruit (cm)	0.95	1.43	0.95	0.95
9.	Flesh thickness (cm)	0.00	2.38	0.00	2.38
10.	Internodal length (cm)	15.71	2.38	11.43	5.24
11.	Vine length (m)	7.62	0.00	8.57	0.00
12.	Average fruit weight (Kg)	9.05	1.43	8.10	40.00
13.	No. of fruits per plant	7.62	1.43	7.14	35.24
14.	Fruit yield per plant(kg)	1.90	2.38	2.38	0.00

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