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Genetic divergence study in pumpkin (*Cucurbita moschata* Duch. Ex. Poir)

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Abstract

A study on genetic divergences was carried out on 40 diverse genotypes of pumpkin. These forty genotypes were grouped into fourteen clusters. Total sugar content contributed maximum to total genetic divergence followed by fruit weight, fruit yield per plant, β -carotene, flesh thickness, first male flowering node, test weight of 100 seeds, equatorial circumferences of fruit and number of seeds per fruit. Intra cluster distance was maximum along cluster VI followed by V, I, III and II. The maximum inter-cluster divergence was observed between cluster IX and XIV followed by cluster X and XIII, cluster X and cluster XIV and cluster X and XII. Cluster IX recorded the highest mean values for fruit yield per plant, least mean values for days to harvest and flesh thickness. Cluster X recorded the highest mean values for equatorial circumferences of fruit and flesh thickness. Cluster XIII recorded least mean values for days to opening first female flower and highest mean values for polar circumferences of fruit and cluster IV recorded highest mean values for test weight of 100 seeds and total sugar content.

Keywords: Genotypes, TSS, Genetic divergence, Flesh thickness, β -carotene

Introduction

Pumpkin is an important cucurbitaceous vegetable, grown under wide range of agro-climatic conditions all over the world. The monoecious character, conspicuous and solitary flowers, large seed number per fruit and wide variability for yield, size and shape of fruit make this crop congenial for commercial breeding. Pumpkin have an advantage over other vegetables as the fruit can be stored for up to six months before being consumed and hence can play an important role in maintaining nutritional levels during the long dry seasons (2). 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. Hence, present study was planned to generate information on the genetic diversity present in 40 pumpkin genotypes.

Material and Methods

The experiment comprising of 40 diverse genotypes was laid out in a randomized block designs with two replications during *kharif* 2016 at Main Vegetable Research Station, AAU, Anand. Each plot consisted of single row of seven plants and the spacing was 2 m \times 1 m inter row and intra row distance, respectively. The package of practices was followed as per the recommendation for raising good and healthy crop. Three plants were selected excluding border plants for recording the observation. Data were recorded on sixteen characters as indicated in Table 3. Genetic diversity between groups was estimated by using D^2 statistics given by (1) following the procedure given by (4). All the sixteen traits were correlated and transformed into uncorrelated linear combinations through Rivotal condensation method using the error variance-covariance dispersion matrix. The mean values of the uncorrelated linear combination were computed to calculate D^2 values between all possible pairs of genotypes. The grouping of genotypes was done by using Tocher's method as described by (4). The criterion used in clustering by this method is that varieties belonging to same cluster should show a smaller D^2 value than those belonging to different clusters.

Result and Discussion

D^2 analysis revealed that the presence of considerable diversity among 40 genotypes of pumpkin, which ranged from 70.09 to 5021.24. These 40 genotypes were grouped into 14

cluster based on similarity of D^2 values (Table 1). The cluster I was the largest having 11 genotypes followed by cluster II with 7 genotypes and cluster III with 6 genotypes. The clusters V, VI, VII, VIII and XII contained 2 genotypes each. However, clusters IV, IX, X, XI, XIII and XIV were monogenotypic and contained only one genotype. The clustering pattern indicated that the genetic diversity was not fully associated with geographical diversity; hence, there was no formal relationship between geographical diversity and genetic diversity.

Similarly fifty seven diverse genotypes of pumpkin were grouped into fifteen clusters by (5). Twenty five diverse genotypes of pumpkin were grouped into five different clusters by (3). (6) Carried out a similar type of genetic divergence study in fifty genotypes of pumpkin and grouped them into three clusters using Tocher's method.

Intra cluster distances (Table 2) revealed, cluster VI with two genotypes shared maximum intra-cluster distance ($D^2 = 440.30$) followed by cluster V ($D^2 = 433.36$) with two genotypes, cluster I ($D^2 = 393.11$), cluster III ($D^2 = 341.56$), cluster II (330.27), cluster XII (322.85), cluster VII (289.63) and VIII (199.91) with two genotypes each. However, present study showed that there is comparatively high intra-cluster distance among cluster VI, cluster V, cluster I and cluster III indicating the presence of sufficient amount of diversity with genotypes of respective clusters. So there is scope for selection within the clusters.

Based on distance between cluster, *i.e.* inter-cluster distance (Table 2) the maximum divergence was observed between cluster IX and XIV ($D^2 = 4311.82$) followed by cluster X and XIII ($D^2 = 4271.52$), cluster X and XIV ($D^2 = 4226.11$), cluster X and cluster XII ($D^2 = 4201.30$), cluster II and XIV ($D^2 = 3836.84$), cluster VIII and cluster X ($D^2 = 3663.02$), cluster I and cluster XIV ($D^2 = 3648.36$), cluster X and cluster XI ($D^2 = 3535.32$), cluster I and XII ($D^2 = 3131.29$), cluster IX and XII ($D^2 = 3101.95$), cluster XI and cluster XIV ($D^2 = 3078.33$), cluster IV and cluster XIV ($D^2 = 2956.23$), cluster II and cluster XII ($D^2 = 2922.88$) and cluster V and cluster X ($D^2 = 2882.94$). While, statistical distance was least between cluster III and cluster XI ($D^2 = 492.78$). Hence, inclusion of

genotypes from highly diverse clusters in hybridization programme can result into highly heterotic hybrids.

The mean values of 16 characters for 14 clusters are summarized in Table 3. For yield per plant, the highest cluster mean observed in cluster IX followed by cluster X, cluster VIII and cluster XI. For days to opening first male flower, the least cluster mean was obtained in cluster I followed by cluster V, cluster VI and cluster IX. For days to opening first female flower, the least cluster mean was obtained in cluster XIII followed by cluster IX, cluster I and cluster II. For first male flowering node, least cluster means was obtained cluster in V followed by cluster XIII, cluster II and cluster I. For first female flowering node, least cluster mean was obtained cluster V followed by cluster XIII, cluster VI and cluster IX. For number of fruits per plant, the highest mean value was observed in cluster XI (1.32) followed by cluster IX, cluster X and cluster VII. For days to harvesting, the least cluster mean was obtained in cluster IX followed by cluster I, cluster XIII and cluster IV. For polar circumferences of fruit, the highest mean value was recorded for cluster XIII followed by cluster VII, cluster II and cluster VI. For equatorial circumferences of fruit, the highest mean value was depicted for cluster X followed by cluster IX, cluster VIII and cluster XI. For average fruit weight, the highest mean value was observed for cluster X followed by cluster IX, cluster VIII and cluster XI. For flesh thickness, the highest mean value was recorded for cluster IX followed by cluster VIII, cluster X and cluster XI. For number of seeds per fruit, the highest mean value was recorded for cluster XIV followed by cluster VII, cluster X and cluster XIII. For test weight of 100 seeds, the highest mean value was depicted for cluster IV followed by cluster X, cluster XI and cluster XII. For total soluble solids, the highest mean value was observed in cluster VI followed by cluster XI, cluster VIII and cluster VI. For total sugar content, the highest mean values was recorded for cluster XIII followed by cluster XI, cluster VII and cluster VI. For β -carotene content, the highest mean value was recorded for cluster VII followed by cluster IV, cluster III and cluster I. Hence, employment of hybridization programme between genotypes of respective clusters could be attempted for successful crop improvement.

Table 1: Distribution of 40 genotypes of pumpkin on the basis of D^2 -statistics

Sr. No	Cluster	Number of genotypes	Name of genotypes	Sources
1	I	11	GPPK 11, GPPK 38, GPPK 78, GPPK 92, GPPK 93, GPPK 137, GPPK 140, GPPK 151, GPPK 156	MVRS, AAU, Anand
			CM -350	Vellanikkara, Kerala
			Pusa Vishwas	IARI, New Delhi
2	II	7	GPPK 3, GPPK 9, GPPK 29, GPPK 41, GPPK 52, GPPK 54, GPPK 123	MVRS, AAU, Anand
3	III	6	GPPK 63, GPPK 75, GPPK 87, GPPK 96, GPPK 174, AP-1	
4	IV	1	GPPK 153	
5	V	2	GPPK 9, GPPK 146	
6	VI	2	GPPK 44, GPPK 131	
7	VII	2	GPPK 53, GPPK 110	
8	VIII	2	GPPK 7, GPPK 80	
9	IX	1	GPPK 20	
10	X	1	GPPK 71	
11	XI	1	GPPK 101	
12	XII	2	GPPK 85, GPPK 86	
13	XIII	1	GPPK 24	
14	XIV	1	GPPK 74	

Table 2: Average intra-cluster and inter-cluster value for 40 genotypes of pumpkin

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	393.11	978.12	785.90	518.78	1460.08	1418.50	1980.42	2207.20	543.36	779.05	1863.43	3131.29	2787.55	3648.36
II		330.27	1257.88	1275.46	553.72	1661.41	2560.85	1299.72	750.94	2159.70	750.63	2922.88	1723.74	3836.84
III			341.56	702.63	1050.22	492.78	588.91	1220.72	1004.73	1287.16	1473.01	1316.64	1397.78	1623.56
IV				0	1640.98	1049.35	1161.69	2241.33	922.63	1134.69	1633.74	2788.27	2790.27	2956.23
V					433.36	1104.60	2193.52	598.72	1090.70	2882.94	538.75	1608.35	678.24	2577.78
VI						440.30	634.63	816.29	1479.18	2187.51	1210.21	811.01	1051.71	1197.38
VII							289.63	1855.42	2020.94	1340.16	2584.38	1366.49	2164.08	1191.18
VIII								199.91	1684.93	3663.02	606.63	1013.81	500.50	1912.58
IX									0	1226.90	1439.36	3101.95	2507.40	4311.82
X										0	3525.32	4201.30	4271.52	4226.11
XI											0	2032.06	1147.73	3078.33
XII												322.85	643.10	591.37
XIII													0	1286.53
XIV														0

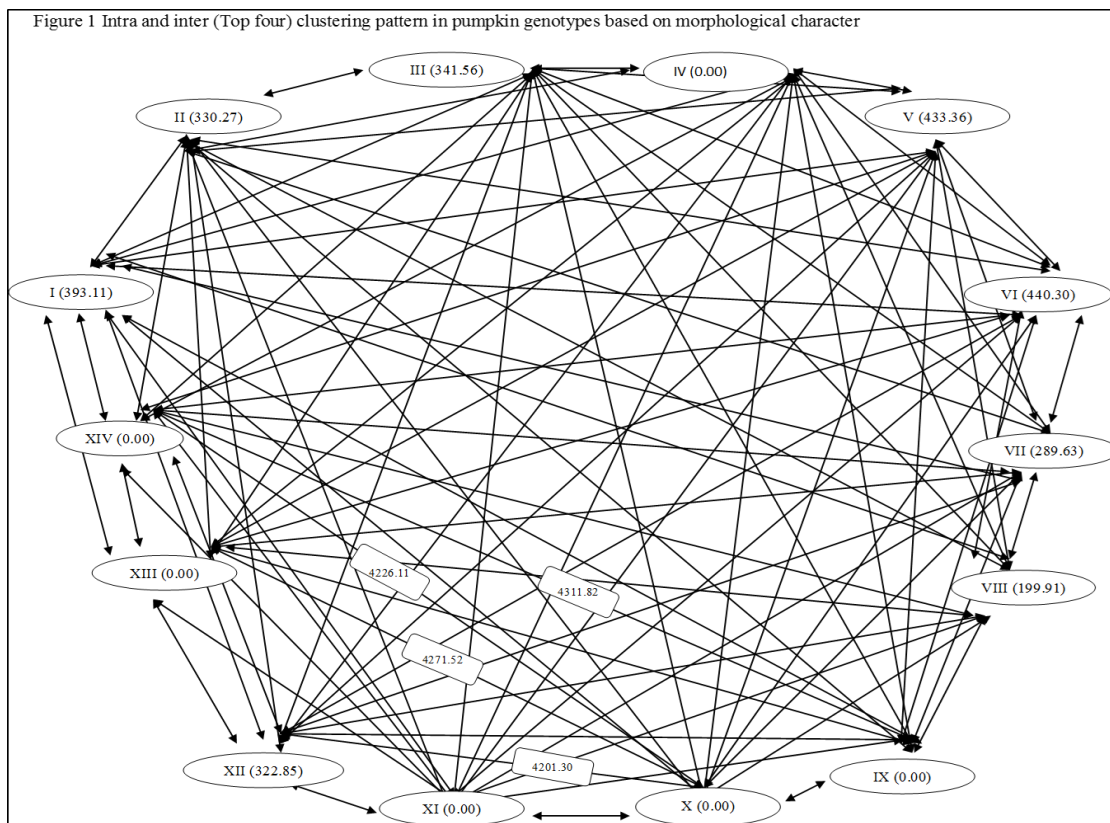


Fig 1

Table 3: Cluster means of different characters in pumpkin

Cluster	FYP	DOFM	DOFF	FMFN	FFFN	NOF	DTH	PCF	ECF	FW	FT	NOS	TW	TSS	TS	β-Car
I	3.94	42.78	49.50	12.18	14.95	0.94	89.16	72.95	62.57	4.06	28.32	296.01	14.95	4.89	0.75	2.91
II	4.69	44.06	50.40	11.97	15.44	1.01	102.24	78.35	62.14	4.67	30.98	310.14	15.90	4.85	1.01	2.00
III	4.09	45.98	52.30	13.53	16.35	0.98	97.17	73.69	65.80	4.26	28.53	321.47	17.82	4.87	1.51	3.03
IV	2.29	47.20	52.00	16.20	19.40	0.60	94.20	63.83	72.66	3.33	26.60	295.66	20.89	6.15	1.02	3.10
V	3.64	42.85	50.25	10.35	13.60	0.75	104.35	73.16	68.66	4.44	27.95	289.08	16.62	5.15	1.39	2.13
VI	5.78	43.30	49.55	10.60	13.90	1.05	95.95	76.16	70.00	5.40	36.25	315.00	16.20	6.05	1.79	3.06
VII	5.96	51.15	53.45	16.40	18.15	1.10	108.60	84.50	68.83	5.46	36.30	391.83	17.46	5.62	1.83	3.62
VIII	7.27	48.05	52.35	14.90	16.65	1.15	96.85	75.08	79.25	6.41	44.65	331.25	16.20	5.70	2.07	2.68
IX	7.59	43.60	49.40	13.20	14.40	1.20	88.30	66.83	79.66	6.55	45.30	220.33	19.20	5.35	1.36	2.62
X	7.30	45.70	51.30	13.00	16.20	1.10	99.90	73.33	83.33	6.87	43.20	328.00	20.57	4.45	0.67	3.45
XI	7.01	50.50	58.60	17.30	16.50	1.32	108.10	71.00	73.33	5.73	39.50	300.50	20.01	5.90	1.06	2.76
XII	4.41	43.85	51.60	12.25	15.55	1.00	105.20	68.91	68.75	4.60	31.95	182.83	17.85	5.50	2.35	2.50
XIII	3.95	44.50	48.20	11.10	13.90	0.80	89.80	89.17	72.16	5.15	29.60	323.50	17.62	4.45	2.60	2.61
XIV	2.68	49.80	55.70	15.40	17.70	0.65	107.00	70.83	60.33	3.61	23.50	403.00	17.52	4.20	1.61	2.42
S.Em	0.96	3.56	4.05	1.69	1.94	0.16	9.34	7.05	6.56	0.55	4.85	49.32	1.81	0.72	0.18	0.36
CD at 5%	2.71	NS	NS	4.78	NS	NS	NS	NS	NS	1.57	13.71	NS	NS	NS	0.52	1.01
CV %	36.62	14.08	14.09	23.34	22.06	29.65	17.04	16.76	17.44	21.16	27.30	28.57	19.24	25.30	24.95	23.37
R ²	0.41	-	-	0.22	-	-	-	-	0.13	0.50	0.29	0.10	0.14	-	0.84	0.39
CV _b	30.73	-	-	12.44	-	-	-	-	6.73	21.11	17.59	9.60	7.82	-	57.94	18.78

FYP : Fruit yield per plant, DOFM : days to opening first male flower, DOFF : days to opening first female flower, FMFN : first male flowering node, FFFN : first female flowering node, NOF : number of fruits per plant, DTH : days to harvest, PCF : polar circumferences of fruit, ECF : equatorial circumferences of fruit, FW : fruit weight, FT : flesh thickness, NOS : number of seed per fruit, TW : test weight of 100 seeds, TSS : total soluble solids, TS : total sugar content and β-Car : β-carotene

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