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Genetic diversity analysis in pumpkin (*Cucurbita moschata* Duch Ex Poir)

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Abstract

The present study was conducted with thirty two genotypes of pumpkin collected from different indigenous source were sown in randomized block design during *Kharif* 2015 to assess the nature and magnititude of genetic divergence for growth, flowering, yield and quality traits. The collected genotypes were grouped into ten clusters and the highest (23.10) inter cluster distance was recorded between cluster IV and VII for vegetative traits. Six different cluster were obtained for yield traits and the highest (39.62) inter cluster distance was recorded between cluster V and VI for yield traits.

Keywords: Pumpkin, *Cucurbita moschata*, diversity analysis, cluster values, d^2 values

Introduction

Pumpkin (*Cucurbita moschata* Duch. ex. Poir) is an economically important cucurbitaceous vegetable. It is grown throughout the tropics of India and its occupies a prominent position due its high productivity, nutritive values, good storability, better transport quality and extensive cultivation in sub-tropical and tropical regions of the globe. It is used both immature and mature stages as vegetable and consumed as processed products. In India, it occupies an area of 19760 hectares with an annual production of 4,16,110 tonnes accounting to an average productivity of 21.06 tonnes per hectare. In Tamil Nadu, pumpkin occupies an area of 1,530 hectares with an annual production of about 37,340 tonnes and an average productivity of 24.41 tonnes per hectare in 2013-14 (Saxena and Chander, 2015) [12].

Pumpkin provides a valuable source of carotenoids that have a major role in nutrition in the form of provitamin 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 was 12.12 mg/100g of fresh weight. The concentrations of three major carotenoids were α-carotene (5.15 mg/100g), β-carotene (3.10 mg/100g) and lutein (1.50 mg/100g). The fruits also contains 92.6 per cent moisture, 4.6 per cent carbohydrates, 25 kcal, 1.4 g protein, 0.1g fat, 0.06 mg thiamine, 0.04 mg riboflavin, 2 mg vitamin C, 10 mg calcium and 0.7 mg iron in one hundred gram of edible portion (Anon., 2007) [1]. The higher dietary intake of carotenoids offers protection against vitamin A deficiency related health problems (Roy, 1973.) [10].

India is the centre of origin for many cucurbitaceous vegetables, where the cucurbits are capable of thriving and performing well even under the hot summer. Pumpkin has received little attention in crop improvement, as compared to other cucurbitaceous vegetables. Being a cross-pollinated crop, development of varieties or hybrids is possible through heterosis breeding. A precise knowledge of combining ability and gene action responsible for inheritance of yield and yield components is essential for successful crop improvement programme. Further, the development of hybrids will have the advantage of higher productivity with uniformity in size and shape.

Pumpkin, being a cross pollinated crop exhibits considerable variation for different traits. Attempts have been made to improve the local types and number of released varieties available for commercial cultivation are having large size fruits. Hence the present investigation is undertaken with the objectives to evaluate the pumpkin genotypes through D^2 analysis and classify into different groups.

Materials and Methods

The study was conducted at Department of Horticulture, Agricultural College and Research Institute, Tamil Nadu Agricultural University, Madurai, Tamil Nadu, India during *kharif* 2015.

The experimental material consisted of divers group of 32 genotypes. The details of the genotypes used for the study were CM2, CM3, CM5, CM6, CM7, CM8, CM9, CM10, CM11, CM12, CM13, CM14, CM15, CM17, CM18, CM20, CM21 were maintained in the department of horticulture, the other genotypes collected from where CM1 is Attur, Salem district, CM4 is Melur, Madurai district, CM16 is Olakkur, Villupuram district, CM19 is Gudalur, Theni district, CM22 is Gudiyatham, Vellore district, CM23 is Thirumangalam, Madurai district, CM24 id Natham, Dindugal district, CM25 is Vikravandi, Villupuram District,CM26 is Arani, Thiruvanamalai district, CM27 Sempatti, Dindugal district, CM28 is Ottamchatram, Dindugal district, CM29 is Rajapalayam, Virdhunagar district,CM30 is Tholudur, Perambalur District, CM31 is Harur, Dharmapuri district and CM 32 is Co1 variety. The seeds were sown in pits taken at a row spacing of 2.0m and intra row spacing of 2.0 m in randamized block design. The observations were recorded in five randomly selected plants from each replication for the genotypes were evaluated for following characters *viz.*, number of primary branches, vine length (cm), petiole length (cm), leaf length (cm), leaf breadth (cm), inter node length (cm), first male flower node, first female flower node, days to first male flowering, days to first female flowering, sex ratio, days to fruit maturity, number of fruits per plant, fruit length (cm), fruit diameter (cm), flesh thickness (cm), fruit weight (g), 100 seed weight (g), yield per plant (kg). Multivariate analysis was done utilizing Mahalanobis D^2 statistics and genotypes were grouped into different clusters following Tochers method as described by Rao (1952) [8].

Results and Discussion

Clustering of genotypes

Vegetative traits

The 32 genotypes were grouped into ten different clusters. The constituents of different clusters with their source are presented in the Table 1. Among clusters, it was observed that cluster IV and V were the largest with six genotypes, cluster I had four genotypes followed by cluster VIII and cluster IX that had three genotypes each and clusters II, III, VI,VII and X had two genotypes each. These results are in accordance with findings of Prasad and Singh (1997) [6].

Yield traits

The 32 genotypes were grouped into six different clusters for yield traits. The constituents of different clusters with their source are presented in the Table 2. Among clusters, it was observed that cluster I had twenty two genotypes followed by cluster V with three genotypes each and cluster II, III and IV had two genotypes each.

The clustering pattern revealed that the genotypes did not resolve according to their geographical origin. The possible reason could be, even though geographic diversity is an important factor it may not be the only determining factor for the genetic divergence. Similar findings were reported by Singh and Lal (2000) [13] in musk melon, Badade *et al*. (2001) [2] in bottle gourd and Sanwal *et al*. (2008) [11] in chow chow. Results also revealed that the factors other than geographical diversity may also be responsible for clustering of genotypes. Similar observations were reported in musk melon by Singh and Lal (2000) [13].

Intra and inter cluster distance

Vegetative traits

Average intra and inter cluster D^2 values among 32 genotypes was studied. The values showed (Table 3) that the cluster X had the maximum intra D^2 value (15.49) followed by cluster V (14.07). This is indicative of the fact that the genotypes included in these clusters are very diverse. The inter cluster D^2 value was found to be maximum between cluster IV and cluster VII (23.10). The genotypes belonging to cluster IV and cluster VII could have greater genetic divergence and hence intermating between the genotypes belonging to them would give more transgressive segregants in advanced generation. These results are confirmed with the findings of Ram (2001) [7] in pointed gourd.

Yield traits

Average intra and inter cluster D^2 values among 32 genotypes for yield trait was being studied. The values showed (Table 4) that the cluster V had the maximum intra D^2 value (20.78) followed by cluster IV (14.21). This is indicative of the fact that the genotypes included in these clusters are very diverse. The inter cluster D^2 value was found to be maximum between cluster V and VI (39.62). The genotypes belonging to cluster V and cluster VI could have greater genetic divergence and hence intermating between the genotypes belonging to them would give more transgressive segregants in advanced generation. Similar results reported by Dora *et al* (2003) [4] in pointed gourd.

Cluster mean values for different characters

Vegetative traits

The data on the mean for all the twelve characters with respect to ten clusters are summarized in the Table 5. It is obvious that different clusters exhibited distinct mean values for almost all the twelve characters studied. Cluster I possessed the highest mean values for leaf length (14.31). Cluster IV exhibited the highest mean values for fruit number of primary branches (3.11), first male flower node (11.06), days first female flowering (58.84) and sex ratio (25.81). Cluster VI showed the highest mean values for vine length (837.83), petiole length (23.78), leaf breadth (18.75) and inter node length (10.63). Cluster VII exhibited the highest mean values for yield per plant (6469.5), Cluster IX exhibited the highest mean values for first female flower node (26.53), Cluster X exhibited the highest mean values for days to first male flowering (52.73). Similar results were observed by Badade *et al* (2001) [2] in bottle gourd.

Yield traits

The data on the mean for all the eight characters for ten clusters are summarized in the Table 6**.** It is obvious that different clusters exhibited distinct mean values for almost all the eight characters studied. Cluster I possessed the highest mean values for flesh thickness (3.09). Cluster II exhibited the highest mean values for days to fruit maturity (90.66). Cluster V showed the highest mean values for fruit length (33.06), fruit diameter (68.77), fruit weight (6492.22) and 100 seed weight (20.92). Cluster VI exhibited the highest mean values for number of fruits per plant (4.4). These results are corroborated with findings of Rao *et al* (2000) [9] in cucumber.

Relative contribution of each character

Vegetative traits

The individual vegetative characters estimated the relative contribution of each character towards genetic divergence. The number of times that each character appeared in first rank is presented in Table 7. The character, sex ratio contributed the maximum percentage of 44.75 towards divergence followed by yield per plant (38.59 per cent), petiole length (4.43 per cent), number of primary branches (3.84 per cent), first male flower node (3.22 per cent) first female flower node (1.61 per cent), leaf length and days to first female flowering (1.00 per cent). The traits vine length and days to first male flowering exhibited very less contribution towards genetic divergence. The diversity for leaf breadth was observed to be nil. Similar observations were reported by Dey *et al* (2009) in bitter gourd.

Yield traits

The individual yield attributing characters estimated the relative contribution of each character towards genetic divergence. The number of times that each character appeared in first rank is presented in Table 8. The character, yield per plant contributed the maximum percentage of (36.89) towards followed by 100 seed weight (28.42 per cent), fruit weight (20.56 per cent), fruit diameter (7.25 per cent), fruit length (4.63 per cent) and flesh thickness (1.61 per cent). The trait flesh thickness exhibited very less contribution towards genetic divergence. The diversity for days to fruit maturity and number of fruits per plant was observed to be nil. The importance of fruit yield per vine in genetic divergence of was already reported by Khatum *et al*. (2010) [5] and in chow chow by Sanwal *et al*. (2008) [11].

Table 1: Composition of D^2 clusters and their geographical origin for vegetative traits in pumpkin genotypes

Cluster number	Number of Genotypes	Name of genotypes
I	4	CM1, CM2, CM3,CM5
II	2	CM16, CM19
III	2	CM13, CM24
IV	6	CM4, CM6, CM7, CM8, CM9,CM10
V	6	CM11, CM12, CM14, CM15, CM26, CM27
VI	2	CM18, CM20
VII	2	CM23, CM31
VIII	3	CM17, CM22, CM25
IX	3	CM21, CM29, CM30
X	2	CM28, CM32

Table 2: Composition of D^2 clusters and their geographical origin for yield and its related attributes in pumpkin genotypes

Cluster number	Number of genotypes	Name of genotypes
I	22	CM1, CM2, CM3, CM4, CM5, CM6, CM7, CM8, CM9, CM10,CM11, CM12, CM13, CM14, CM15, CM16, CM17, CM18, CM19, CM20,CM21, CM22
II	2	CM25, CM30
III	2	CM24, CM36
IV	2	CM28, CM31
V	3	CM23, CM27, CM32
VI	**1**	**CM29**

Table 3: Inter and intra – cluster values for pumpkin genotypes of vegetative traits in pumpkin genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	8.16	7.23	8.89	17.53	13.09	9.69	9.97	17.07	13.02	15.94
II		4.76	6.90	16.50	11.51	7.92	9.82	14.83	11.77	14.56
III			5.53	20.91	14.51	10.84	7.26	18.27	9.32	17.96
IV				9.78	14.38	15.95	23.10	13.68	25.74	14.07
V					14.07	12.60	16.72	15.22	19.30	14.73
VI						6.90	13.46	14.20	14.04	16.13
VII							8.13	21.26	10.63	19.48
VIII								13.75	21.99	14.70
IX									10.87	22.62
X										15.49

Table 4: Inter and intra – cluster D^2 values of pumpkin genotypes for yield and its related attributes in pumpkin genotypes

Clusters	I	II	III	IV	V	VI
I	14.10	13.54	14.11	18.10	27.34	25.50
II		4.60	16.24	13.64	30.09	18.77
III			8.00	15.72	31.25	26.55
IV				14.21	37.17	17.47
V					20.11	39.62
VI						0.00

Table 5: Cluster mean values of pumpkin genotypes for vegetative traits in pumpkin genotypes

Clusters	Number of primary branches per plant	Vine length (cm)	Petiole length (cm)	Leaf length (cm)	Leaf breadth (cm)	Inter node length (cm)	First male flower node	First female flower node	Days to first male flowering	Days to first female flowering	Sex ratio	Yield per plant (kg)
I	3.01	574.16	20.10	14.30	16.68	7.40	8.9	24.4	49.51	58.16	19.02	5224.91
II	2.5	755.5	21.08	12.36	16.43	8.56	9.7	25.6	48.83	56.23	18.72	4588.16
III	2.5	603.16	19.06	12.58	16.8	9.43	9.86	24.73	49.26	57.63	16.93	4769.5
IV	3.11	758.22	21.12	13.22	16.82	8.30	11.07	23.83	49.28	58.84	25.81	5304.83
V	2.63	792.83	20.41	12.62	16.95	8.6	10.5	23.55	51.41	58.16	21.40	5298.27
VI	2.96	837.83	23.78	13.73	18.75	10.63	8.7	23.33	50.16	56.7	19.5	4403.16
VII	2.76	655.5	17.95	14.15	18.05	8.95	8.7	26.36	51.8	57.13	16.58	6469.5
VIII	2.62	507.33	22.52	11.91	17.1	11.6	10.77	26.37	51.02	56.48	23.70	3602.22
IX	2.55	530.11	21.52	12.75	16.33	9.91	8.42	26.53	51.13	55.97	14.63	3424.6
X	2.2	611.5	17.86	12.31	16.45	8.33	8.3	24.7	52.73	56.56	24.11	4719.5

Table 6: Cluster mean values of pumpkin genotypes for yield and its related attributes in pumpkin genotypes

Clusters	Days to fruit maturity	No of fruits of per plant	Fruit length (cm)	Fruit diameter (cm)	Flesh thickness (cm)	Fruit weight (kg)	100 seed weight (g)	Yield per plant (kg)
I	90.07	1.93	26.80	63.60	3.09	3221.5	15.67	5047.18
II	90.66	1.5	20.9	59	2.86	2091.66	17.15	2519.66
III	88.73	1.7	31.35	61.46	2.71	2985.16	11.96	4190.33
IV	89.7	2.86	19.1	55.5	2.58	1634.5	12.52	3592
V	90.26	1.35	33.06	68.77	2.91	6492.22	20.92	6815.22
VI	83.46	4.4	17.8	44.4	2	968	15.48	3410.8

Table 7: Related contribution of vegetative traits to genetic diversity in pumpkin genotypes

S. No	Characters	Number of first ranks	Percentage of contribution towards divergence
1	Number of primary branche per plant	19	3.83
2	Vine length (cm)	2	0.40
3	Petiole length (cm)	22	4.44
4	Leaf length (cm)	5	1.00
5	Leaf breadth (cm)	0	0
6	Inter node length (cm)	4	0.81
7	First male flower node	16	3.23
8	First female flower node	8	1.61
9	Days first male flowering	2	0.40
10	Days first female flowering	5	1.01
11	Sex ratio	222	44.76
12	Yield per plant (kg)	191	38.51
	Total	496	100

Table 8: Related contribution of yield and its related attributes to genetic diversity in pumpkin genotypes

S. No	Characters	Number of first ranks	Percentage of contribution towards divergence
1	Days of fruit maturity	0	0
2	No of fruits per plant	0	0
3	Fruit length (cm)	23	4.64
4	Fruit diameter (cm)	36	7.26
5	Flesh thickness (cm)	11	2.22
6	Fruit weight (kg)	102	20.56
7	100 seed weight (g)	141	28.43
8	Yield per plant (kg)	183	36.90
	Total	496	100

Conclusion

The genotypes were grouped into ten clusters. The highest (23.10) inter cluster distance was recorded between cluster IV and VII for vegetative traits. Six different cluster were obtained for yield traits and the highest (39.62) inter cluster distance was recorded between cluster V and VI for yield traits.

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