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Genetic divergence among landraces of pumpkin (*Cucurbita moschata* Duch ex. Poir) from Tamil Nadu

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ABSTRACT

A Study on genetic divergence was carried out on 20 genotypes of pumpkin during 2018-2019 at Vegetable Unit, Department of Horticulture, Annamalai University. The experiment was laid out in randomized block design with three replications. These genotypes were used to assess the genetic divergence. They were grouped into nine clusters by the application of clustering technique. The clusters II consisted of four number of genotypes followed by cluster I and IV comprising of three genotypes, while the clusters III, V, VI and VII has two genotypes each. Cluster VIII and IX comprising one genotype. The intra and inter cluster divergence were computed. The intra cluster divergence ranged from 0.00 to 18.48. Cluster VII showed maximum intra cluster divergence of 18.48 followed by cluster IV (17.12) and cluster II (15.63). Cluster VII and I had the minimum intra cluster divergence 0.00 followed by cluster I (11.94). The maximum inter cluster divergence was found between cluster VI and IX (24.81), while the minimum inter cluster divergence was found between clusters I and IV (14.76). Cluster IV recorded the highest mean value (11.11), while cluster IX registered the lowest mean value(6.80).

KEYWORDS: Landraces, Genetic divergence, D^2 analysis, yield, clusters and *Cucurbita moschata.*

INTRODUCTION

Pumpkin (*Cucurbita moschata* Duch. ex Poir.) is an important vegetable that belongs to the family Cucurbitaceae having chromosome number 2n=40. The name pumpkin originated from Greek word 'Pepon' used for long melon (Bahadur and Singh, 2014). In India, it occupies 78,000 hectare area with a production of 17, 14,000 metric tonnes. Pumpkin is a large, showy, yellow flowered, monoeious, highly pollinated, entamophilous species in the cucurbitaeae. Among the five cultivated species, pumpkin (*Cucurbita moschata* Duch. ex Poir.), summer squash (*Cucurbita pepo* L.), winter squash (*Cucurbita maxima*) are of great economic importance (Rana, 2014). In Tamil Nadu, maximum diversity is found for its fruit shape, fruit colour, vine length and yield characters. There are different types of fruit shape in pumpkin *viz.,* elongate, oblong, globular, elliptical, cylindrical, etc. The fruit colour varies from yellow to orange. The fruit skin ranges from smooth to slightly ribbed skin. Precise information about genetic divergence is critical for a productive breeding programme, as genetically diverse plants are known to produce high heterotic effects consequently yield desirable segregates. More the diversity better is the chance of improving economic characters under considerations in the resulting program. It also helps to know the relative distance between these strains for the characters under study. Thorough and critical information obtained through various parameters will be helpful to launch a viable improvement program. Successful breeding programme is associated with diversity of the parents within a reasonable range. Keeping these facts in view the present study was initiated using pumpkin as a test crop.

MATERIALS AND METHODS

The experiment was conducted at the Vegetable Unit, Department of Horticulture, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Cuddalore, Tamil Nadu, India. The geographical location of the research farm is having an altitude of 16 m above Mean Sea Level, latitudeof 11°24'N and longitude of 79°41'E. The pumpkin germplasm consisting of twenty genotypes collected from different districts of Tamil Nadu were selected for the experiment as summarized as CM 1 to CM20. Theexperiment was laid out in a randomized block design with three replications of each genotype.

Pits of 60 cm diameter and 30 cm depth were taken at a spacing of 2 × 1.5 m. In each pit, five seeds were sown. Sowing was done in such a way that in each replication there was a single row of two plants per accession. The cultural and management practices were adopted according to the package of practices recommended by Tamilnadu Agricultural University. Five plants in each accession were tagged for recording the biometrical observations. D^2 is the sum squares of difference between any two populations for each of the uncorrelated variables (ys), obtained by transforming correlated variables (xs) through pivotal condensation method. The square root of these D^2values gives the general distance between the two populations. The significance of the D^2 values between any two populations is determined by taking D^2values as the calculated value of $X^2$for P degrees of freedom, where P is the number of characters considered. Based on degree of divergence (D^2 values) between any two genotypes, grouping of genotypes was done by using Tocher's method (Singh *et al.,* 1977). In this method, the populations are arranged in order of their relative distances (D^2 values) from each other and a table is formed. Mahalanobis (1936) developed this model to determine divergence among populations in terms of generalized groupdistance.

RESULTS AND DISCUSSION

All the 20 genotypes were grouped into nine clusters by the application of clustering technique. The constituents of different clusters are presented in the Table.1.

Table 1: Clusters formed from twenty pumpkin genotypes

Cluster	No. of genotypes	Genotypes
I	3	CM 1,CM 7,CM 17
II	4	CM 2,CM 3,CM 10,CM 18
III	2	CM 12, CM 15
IV	3	CM 4,CM 5, CM 19
V	2	CM 16,CM 20
VI	2	CM 6,CM 13
VII	2	CM 11,CM 14
VIII	1	CM 8
IX	1	CM 9

The clusters II consisted of four number of genotypes followed by cluster I and IV comprising of three genotypes, while the clusters III, V, VI and VII had two genotypes each. Cluster VIII and IX had one genotype each. Therefore, genotypes originating at the same place might have developed different architectures. Likewise, genotypes at different places may possess similar characteristics. Thus, genetic diversity was the outcome of several factors along with a factor of geographical diversity. Similar trend of clustering pattern of diversification of genotypes based on origin was reported by Hossain *et al.* (2010), Naik and Prasad (2015), Rahman Khan *et al.*(2016).

The intra and inter cluster distance were computed and were presented in Table.2. The intra cluster distance ranged from 0.00 to 18.48. Cluster VII showed maximum intra cluster distance of 18.48 followed by cluster IV (17.12) and cluster II (15.63). Cluster VII and I had the minimum intra cluster distance 0.00 followed by cluster I (11.94). The maximum inter cluster distance was found between cluster VI and IX (24.81), while the minimum inter cluster distance was found between clusters I and IV (14.76). Minimum inter cluster distance was noticed between cluster I and IV, which explains that the genotypes in these cluster would have been evolved by similar evolutionary procedures even though their origin wasdifferent. Maximum inter cluster distance was noticed between cluster VI and IX (Table.2.). This wider distance indicated that the hybridization among the genotypes between these clusters would produce successful hybrids and desirable seggregants in further generations. The lower intra cluster distance was noticed in cluster I which shows the closeness of genotypes included in the cluster, while the highest intra cluster distance was recorded by the cluster VII. The limited gene exchange between the genotypes of the cluster may be the reason for the highest intra cluster distance. Further, selection for diverse characters could be areason for such as high intra cluster divergence. In addition to the general feature of variation and divergence indicated, this study also provides the information of the potent character that contributes to thedivergence. The most important trait found to cause maximum genetic divergence is yield vine^{-1}, number of fruits vine^{-1} and 100 seed weight. Muralidhara*et al.*(2014) andShivanandha *et al.* (2013) reported that vine length, average fruit weight and fruit girth were major characters that caused genetic divergence.

Table 2: Intra and inter cluster distances between genotypes of pumpkin

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	142.67 (11.94)	301.38 (17.36)	447.91 (21.16)	217.93 (14.76)	306.68 (17.51)	381.71 (19.53)	453.38 (21.29)	338.63 (18.40)	365.90 (19.12)
II		244.51 (15.63)	411.28 (20.28)	326.06 (18.05)	261.31 (16.16)	535.16 (23.13)	448.77 (21.18)	419.94 (20.49)	230.15 (15.17)
III			148.34 (12.17)	415.29 (20.37)	336.67 (18.34)	424.72 (20.60)	297.03 (17.23)	584.36 (24.17)	502.43 (22.41)
IV				293.37 (17.12)	303.85 (17.43)	372.87 (18.10)	422.44 (20.50)	365.79 (19.12)	371.31 (19.26)
V					219.36 (14.81)	485.59 (22.03)	349.12 (18.68)	360.07 (18.97)	304.11 (17.43)
VI						236.48 (15.37)	463.41 (21.52)	506.71 (22.51)	615.94 (24.81)
VII							341.66 (18.48)	544.01 (23.32)	520.01 (22.80)
VIII								(0.00)	405.61 (20.13)
IX									(0.00)

Values in parenthesis indicates D value, Bold value indicates intra cluster distance

Computing the cluster mean values (Table3), it was found that, the cluster I showed high values for the few characters *viz.,* vine length, number of primary branches, sex ratio, total soluble solids and yield vine^{-1}. Interestingly, it is noticed that these three characters like vine length, number of primary branches, sex ratio, total soluble solids (°Brix) and yield vine^{-1} (kg) were contributed only by asingle genotype CM 5. Hence, this genotype may serve as an ideal plant for hybridization programme for improving the yield vine^{-1}and its important component traits, since this genotype had more number of traits in a single cluster than other genotype.

Table 3: Cluster mean of 20 pumpkin genotypes for various characters

Characters	Clusters								
	I	II	III	IV	V	VI	VII	VIII	IX
Vine length (m)	7.17	6.05	5.56	6.67	5.82	6.46	5.34	4.80	5.15
Number of primary branches	10.59	9.46	9.06	9.92	9.22	9.79	8.30	8.08	7.64
Days to first male flowering	47.91	53.11	49.95	49.64	54.85	55.96	55.97	54.83	42.39
Days to first female flowering	55.26	59.30	59.22	54.72	61.59	60.04	61.56	61.95	50.13
Node number of first female flower	17.69	20.72	20.72	17.96	19.47	20.61	16.45	14.12	15.35
Sex ratio	16.15	14.35	9.37	13.52	11.59	12.33	10.04	11.65	12.15
Days to first fruit harvest	82.52	80.59	90.28	83.90	77.86	93.99	91.29	73.48	75.69
Fruit length (cm)	27.92	24.64	44.73	27.84	39.87	27.66	30.86	36.76	17.45
Fruit girth (cm)	65.13	37.05	48.92	64.14	56.37	77.77	47.10	71.60	28.66
Average fruit weight (kg)	1.93	1.81	3.73	2.12	1.44	3.96	3.67	0.93	0.827
Number of fruits vine^{-1}	5.23	5.41	2.30	5.14	5.44	2.44	2.19	7.81	6.21
100 seed weight (g)	10.66	7.36	8.45	10.37	8.30	14.09	8.59	13.03	6.84
TSS (°Brix)	5.46	4.84	3.55	4.06	3.74	3.61	3.05	3.95	3.15
Yield vine^{-1} (kg)	10.23	9.88	8.76	11.11	7.56	9.58	8.03	7.89	6.80

Based on cluster mean values, the genotypes for hybridization programme canbe selected on the character basis *viz.,* the genotype CM 5 can be selected for length of vine, more number of primary branches, high female flowers, high quality fruits with maximum total soluble solids and yield vine^{-1} (kg), which falls under cluster IV. The genotypes CM 8 had earliest female flowering and more number of fruits vine^{-1} in the cluster VIII. Similarly, the genotype CM 15, contributed days to first fruit harvest and fruit length, which fall under cluster III. The genotype CM 13, showed high values for average fruit weight, which falls in cluster VI, may be selected

as the parent for hybridization programme. The genotype CM 6 registered higher mean values for fruit girth and 100 seed weight, which falls in cluster VImay be selected as one of the parent(Table3). Among the five parents selected for hybridization programme, they fell into different divergent clusters. CM 5, CM 8 and CM 15 belongs to cluster IV, VII and III respectively, while CM 13 and CM 6 belongs to the cluster Thus from the present study, the genotypes CM 5, CM 6, CM 8, CM 13 and CM 15 were identified as suitable parents for hybridization programme to develop superior varieties in pumpkin.

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