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Genetic divergence and cluster analysis in summer squash (*Cucurbita pepo* L.)

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Abstract

A study was conducted on 16 genotypes of Summer squash with 13 characters using Mahalanobis D² analysis. The experimental materials were evaluated during *Rabi*, 2021 at Horticultural Research Farm, Ranadevi, M.S. Swaminathan School of Agriculture, Centurion University of Technology and Management, Paralakhemundi, Odisha. The cultivars were divided into 4 different clusters, out of which 11 cultivars were under cluster I (maximum) followed by cluster III and IV having 2 cultivars each and cluster II with only one cultivar. Greater genetic variability among the genotypes belonging to various clusters is indicated by the fact that the inter cluster distance was greater than the intra cluster distance. Cluster IV has the highest intra-cluster values, whereas cluster II has the lowest. Between III and IV, there was the greatest inter cluster distance, while between I and II, the smallest. The characters contributing maximum to the total genetic divergence were number of harvest, average fruit weight, fruit girth, number of female flowers, number of male flowers in ascending order. The results obtained by D² analysis were confirmed by principal component analysis. From the present investigation, superior genotypes belonging to the most divergent groups *viz.* cluster III (Green Star and Bipin) and IV (Patty Pan and Palak Zucchini), can be used as parents to carry out hybridization work for development of hybrids in future.

Keywords: Summer squash, genetic divergence, clustering pattern, D² analysis, multivariate analysis

Introduction

Summer squash (*Cucurbita pepo* L.) is considered to be an important vegetable crop of Cucurbitaceae family having wide variability with different quantitative and qualitative characters. It is a cross pollinated, herbaceous annual crop having short internodes, bushy appearance and can be grown in temperate and sub-tropical regions with mild summer. It is also known as *zucchini*, *chappankaddu* and eaten as immature fruit. It covers a total area of 1,000,000 hectares under pumpkin, squash, and gourds with an annual production of 19,000,000 tonnes (FAO, 2006) [4]. In India, it is currently grown on 104,000 M hectares of land, producing 2183,000 MT. (Indian Horticulture, 2021).

It is one of the oldest crops still grown in America and has its origins in Northern Mexico (Tropical America) (Paris, 1996) [13]. Production of squash and pumpkin in Asia comprises half of the total area under pumpkin and squash worldwide (Al-Brifcany, 2015) [2]. The name "squash" was created by the American colonists from a member of native American languages that meant "something eaten raw." In the extremely late 1800's, "zucchini" were developed and cultivated in Italy, close to Milan. In the early 1920's, Italian immigrants brought the new, improved kind of squash back to the US. This explains the odd name since "zucchina" means "small squash" in Italian and "zucca" means "squash" in English. The same item is known as a courgette in England, Ireland, and France, but baby marrow in South Africa. Aside: In England, many kids have been tortured by being made to eat "Marrows," which resemble overgrown zucchini but are actually completely bland, soggy, and frequently difficult. Since it is a crop with a lot of nutritional value, scientists must work to better its genetic makeup. Summer squash is a cross-pollinated crop. The genotypes having high variability in size, shape and colour available in southern Odisha condition. Multivariate analysis is a useful technique for determining the extent of genotypic difference between biological populations and for learning the relative contributions of different components to the overall divergence at both the intra- and inter-cluster levels. The current study was carried out to examine the genetic divergence of 16 Genotypes of summer squash. Such a study also enables the selection of genetically divergent parents.

Materials and Methods

The experiment was conducted at Horticultural Research Farm, Ranadevi, M.S. Swaminathan School of Agriculture, Paralakhemundi during *Rabi*, 2021. The experiment was conducted in Randomized Block Design with 3 replications and 16 treatments. The seeds were sown on 22nd December 2021 having plot size 2.8×5 m accommodating 40 plants per plot with the spacing of 60×50 cm. The observations were recorded from 5 randomly selected plants in each plot for avoiding biasness for the characters like days to first flowering, days to 50% flowering, node at which first female flower appear, plant growth habit, plant height (cm), fruit length (cm), fruit girth (cm), fruit shape, average fruit weight (g), number of fruits per plant, number of female flowers, number of male flowers, number of harvest, fruit yield per plant (g) and fruit yield per plot (kg). Genetic divergence was estimated according to Mahalanobis (1936) [6] D^2 Analysis. Tocher's method (Rao, 1952) [18] was used to determine the cluster of genotypes of different group, principal component analysis (PCA) was done by Rao, 1964 [17].

Results and Discussion

For every character under investigation, the analysis of variance showed that the genotypes differ significantly. The D^2 values ranged from 11.43 to 23.45, and the scores for the principal components likewise showed that the genotypes exhibited a high level of genetic variety.

Clustering of genotypes

On the basis of genetic diversity as determined by D^2 using Tocher's approach, sixteen cultivars were divided into four distinct clusters (Table 1). The largest cluster, Cluster I, contained 11 cultivars such as Punjab Chappan Kaddu-2, Punjab Chappan Kaddu-3, Round Indian, Punjab Chappan Kaddu-1, Golden Queen, Australian Green, PusaAlankar, Black Beauty Green, Sheetal Zucchini, Heera Zucchini and KashiSubhangi. Cluster III and IV were comprised of 2 cultivars each. Green Star and Bipin were included in Cluster III. Patty Pan and Palak Zucchini were under Cluster IV. Cluster I having only one cultivar namely Orelia Zucchini.

Cluster distances

Based on the average intra- and inter-cluster distances shown in Table 2, it is clear that Cluster II had the smallest intra-cluster distance ($D_2 = 30.07$), whereas Cluster IV had the largest intra-cluster distance ($D_2 = 88.94$). According to the average inter-cluster distance, Clusters III and IV ($D_2 = 549.80$), Cluster II and IV ($D_2 = 361.60$), and Cluster I and IV ($D_2 = 257.33$) were the most divergent clusters. The genotypes distributed into different clusters randomly irrespective to geographical origin. The clustering pattern of these genotypes under the study concluded that geographic diversity may not always be associated to genetic diversity. Many genotypes received from same place have been grouped into different cluster.

Table 1: Clustering Pattern of 16 Summer squash germplasm

Cluster No.	Number of Summer squash	Name of Germplasm (with Entry Number)
I	11	Punjab chappan kaddu-1, Punjab chappan kaddu-2, Punjab chappan kaddu-3, Round Indian, Golden Queen, Australian Green, PusaAlankar, Black Beauty Green, Sheetal Zucchini, Heera Zucchini, KashiSubhangi
II	1	Orelia Zucchini
III	2	Green Star, Bipin
IV	2	Patty Pan, Palak Zucchini

Table 2: Intra Diagonal and Inter cluster average (D^2) corresponding D ($\sqrt{D^2}$) Values (in parenthesis) among groups

Cluster	I	II	III	IV
I	77.53(8.81)	130.61(11.43)	210.17(14.50)	257.33(16.04)
II		30.07 (5.48)	221.91(14.90)	361.60(19.02)
III			68.56(8.28)	549.80(23.45)
IV				88.94(9.43)

Table 3: Mean of 13 characters in different clusters of summer squash germplasm

Sl. No.	Characters	I (11)	II (1)	III (2)	IV (2)
1.	Days to first flowering	21.42	21.33	18.67*	24.50**
2.	Days to 50% flowering	28.76	27.67	25.00*	32.33**
3.	Node at which first female flower appears	6.39	4.00*	5.83	8.50**
4.	Plant height(cm)	47.72	37.13*	39.10	56.23**
5.	Fruit length(cm)	22.08	26.13**	23.72	16.22*
6.	Fruit girth(cm)	24.98	21.07*	32.52	38.82**
7.	Average fruit weight(g)	427.07	327.60*	513.13**	330.80
8.	Number of fruits plant ⁻¹	4.48	6.00**	5.33	1.50*
9.	Number of female flowers	10.48	14.33**	11.83	3.33*
10.	Number of male flowers	21.39	17.00	22.50**	7.17*
11.	Number of harvest	2.52	4.00	4.50**	1.50*
12.	Fruit yield plant ⁻¹ (g)	725.29	643.93	1308.33**	382.93*
13.	Fruit yield plot ⁻¹ (kg)	17.00	12.13	36.12**	2.43*

*and** indicate lowest and highest values respectively

Figure in the parenthesis indicate number of cultivars in a cluster

Cluster means

The cluster means of 13 quantitative characters for groups of summer squash cultivars are presented in Table 3. Cluster I comprising of 11 summer squash cultivars shows moderate expressions for all traits such as days to first flowering (21.42), days to 50% flowering (28.76), nodes at which first female flower appears (6.39), plant height (47.72), fruit length (22.08), fruit girth (24.98), average fruit weight (427.07), number of fruits plant⁻¹ (4.48), number of female flowers (10.48), number of male flowers (21.39), number of harvest (2.52), fruit yield plant⁻¹ (17.00) and fruit yield plot⁻¹ (725.29). Cluster II having 1 cultivar shows the maximum values for characters like fruit length (26.13), number of fruits plant⁻¹ (6.00) and number of female flowers (14.33) whereas minimum values for traits like node at which first female appears (4.00), plant height (37.13), fruit girth (21.07) and average fruit weight (327.60). Rest characters have moderate expressions. Two cultivars were grouped in Cluster III which were giving highest values for average fruit weight (513.13), number of male flowers (22.50), number of harvest (4.50), fruit yield plant⁻¹ (1308.33) and fruit yield plot⁻¹ (36.12). Cluster IV consisted of two cultivars which were having highest value for traits such as days to first flowering (24.50), days to 50% flowering (32.33), node at which first female flower appears (8.50), plant height (56.23) and fruit girth (38.82). In contrary lowest value was observed in fruit length

(16.22), number of fruits plant⁻¹ (1.50), number of female flowers (3.33), number of male flowers (7.17), number of harvest (1.50), fruit yield plot⁻¹ (2.43) and fruit yield plant⁻¹ (382.93).

Character contribution towards divergence

The relative contribution of 13 quantitative traits to genetic divergence among the 16 cultivars of summer squash was accessed (Table 4) by rank average of individual character over all 120 paired combinations. When choosing a cluster to select parent for hybridization, greater attention should be placed on the character contributing the most deviation. The frequency with which each component character appeared first in rank and the percentage by which it contributed to genetic divergence were also examined. Among the yield attributing traits, the maximum contribution towards divergence was made by number of harvest (36.66%) followed by average fruit weight (11.67%) and fruit girth (11.67%). Rest of the characters contributing to the divergence in order were number of female flowers (10.00%), number of male flowers (5.83%), fruit yield plot⁻¹ (5.83%), fruit yield plant⁻¹ (4.17%), days to 50% flowering (4.17%), days to first flowering (4.17%), number of fruits plant⁻¹ (2.50%), fruit length (1.67%) and node at which first female flower appears (0.83%) and plant height (0.83%).

Table 4: Relative contribution to different characters to genetic divergence in Summer squash germplasm

Sl. No	Characters	No. of first rank	% Contribution
1.	Days to first flowering	5	4.17
2.	Days to 50% flowering	5	4.17
3.	Node at which first female flower appears	1	0.83
4.	Plant height(cm)	1	0.83
5.	Fruit length(cm)	2	1.67
6.	Fruit girth(cm)	14	11.67
7.	Average fruit weight(g)	14	11.67
8.	Number of fruits plant ⁻¹	3	2.5
9.	Number of female flowers	12	10
10.	Number of male flowers	7	5.83
11.	Number of harvest	44	36.66
12.	Fruit yield plant ⁻¹ (g)	5	5.83
13.	Fruit yield plot ⁻¹ (kg)	7	4.17
Total		120	100

A potent tool for assessing genetic divergence among the test genotypes is the multivariate analysis based on Mahalanobis D² statistics (Peter and Rai, 1976; Singh and Singh, 1976; Nair and Gupta, 1976) [14, 19, 11]. Furthermore, the benefits of D² statistics for the genetic grouping of germplasm have been highlighted in published publications by Anand and Murty (1968) [3] and Ramanujam *et al.*, (1974) [16]. The multivariate grouping strategies used in the current study have produced positive findings (Table 1). It is an accepted phenomenon that hybrid derivatives from divergent parents are noted to be probably promising due to complimentary interaction between divergent genes in the parents. From the present investigation, it was recorded that Cluster III and Cluster VI both comprising of two cultivars each observed highest inter-cluster distance. So, by crossing parents of the two divergent groups gives probably promising hybrid derivatives which was due to complimentary interaction between divergent gene parents. It was also observed that traits like number of harvest, average fruit weight, fruit girth and sex number of

female flowers had contributed predominantly towards genetic divergence. Therefore, selecting parents who differed in these quantitative parameters was observed advantageous for a summer squash heterosis breeding programme. Quamruzzaman *et al.*, (2013) [15], Sultana *et al.*, (2015) [20], Oliveira *et al.*, (2016) [12], Nagar *et al.*, (2017) [9], Mohsin *et al.*, (2017) [7], Naik and Prasad (2015) [10], Ahmed *et al.*, (2016) [1], Verma *et al.*, (2020) [21] and Mohsin *et al.*, (2016) [8] reported similar findings to our present study in summer squash and pumpkin.

Selection of parents

For the better recombination the hybridization between the cultivars in cluster III (Green Star, Bipin) and IV (Patty Pan, Palak Zucchini) having more inter-cluster distance, which will be useful for improvement of the traits. Therefore selecting these genotypes as parents belonging to Cluster III and IV may be worthwhile to isolate superior genotypes.

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