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Short communication

Genetic diversity in indigenous germplasm of pumpkin

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There are so many vegetable crops having great importance but pumpkin (*Cucurbita moschata* Duch. ex. Poir.) is one of them which has special place due to its high productivity, nutritive value, good storability, long period of availability and better transport potentialities. Matured fruits are also used as industrial raw material for carotene production (Vucetic *et al*., 7). A wide range of genetic diversity among the parents is essential for hybridization programme. Mahalanobis D^2 analysis provides a means to quantitatively estimate the genetic diversity among crop plants (Mahalanobis, 5). Hence, such an attempt was made in the present investigation in pumpkin.

Twenty four eco-geographically different genotypes of pumpkin were collected from different parts of India, *i.e.* Uttar Pradesh (15), Uttarakhand (6), Andhra Pradesh (2) and Orrisa, and raised in randomized block design with three replication at Vegetable Research Centre of GBPUA&T, Pantnagar during summer 2006 (Feb-June) and summer 2007 (Feb-June). Each genotypes was sown in row of 7 m length accommodating 7 plants/row. The intra and inter-row spacing was 3 m × 1 m. Observations on 18 quantitative and 4 qualitative traits were recorded on 5 plants randomly selected from each genotype. The date were subjected to multivariate analysis (Rao, 6). The original mean values were transformed to normalize variables and all D^2 values were calculated. The grouping of genotypes was done by using Tocher's method as described by Rao (6). The criteria used in clustering by this method is that genotypes belonging to the same cluster should show a smaller D^2 value than those belonging to different clusters.

Analysis of variance revealed highly significant differences among 24 genotypes for 18 characters. The 24 genotypes could be grouped into 5 and 4 different clusters in 2006 and 2007, respectively (Table 2). Among the different clusters, Cluster I comprised the highest number of genotypes (11 in 2006 and 15 in 2007). Of the remaining clusters, Cluster II had 7 genotypes in both 2006 and 2007 and Cluster III had 4 genotypes in 2006 and remaining IV and V in 2006 and III and IV in 2007 were having only one genotype each. The clustering pattern indicated that geographical diversity need not necessarily be related to the genetic diversity. This could be evidenced from the study that genotypes from the same eco-geographic region did scatter in different clusters such as CM-71 and CM-83 both from Hyderabad has fallen in two different clusters. Similarly, genotypes from different eco-geographical regions like PPU-60 (Bhubneswar) and PP-113 (Gorakhpur, UP) were identified in same cluster. D^2 value was computed for all the Clusters (Table 3). Average intra-cluster distance was maximum in Cluster I in 2006 and Cluster II in 2007. The inter-cluster distance was found maximum between Cluster IV and V in 2006 and Cluster III and IV in 2007 followed by I and IV in both the years. Similar result had also been suggested by Babu *et al.* (1), and Kale *et al.* (3).

Table 1. Different genotype of pumpkin collected from different areas of India used in experiment.

Sl. No.	Genotype	Source
1	PPU – 39	Faridpur market
2	PPU – 46	Bareilly
3	PPU – 56	Pantnagar local
4	PPU – 60	Bhubneswar
5	CM – 71	Hyderabad
6	CM – 83	Hyderabad
7	PP – 113	Chopriyal village, Gorakhpur
8	PPU – 138	IIVR, Varanasi
9	PPU – 140	Deoria
10	PPU – 143	Deoria
11	PPU – 144	Padrauna
12	PPU – 146	Pathardeva, Deoria
13	PPU – 149	Baghughat, Deoria
14	PPU – 150	Tarkulawa, Deoria
15	PPU – 174	Rajgarh, Sultanpur (UP)
16	PPU – 175	Brahipur, Faizabad
17	PPU – 182	Joshimath, Chamoli
18	PPU – 185	Bansi, Siddharth Nagar (UP)
19	PPU – 189	Meskiwas, Gonda
20	PPU – 195	Bansi, Siddharth Nagar (UP)
21	PPU – 197	NBPGR, Bhowali
22	PPU – 199	NBPGR, Bhowali
23	PPU – 260	Rudrapur
24	PPU – 276	Pantnagar local

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Cluster III had the highest cluster mean for equatorial diameter of fruit (25.86), equatorial diameter of seed cavity (16.75), flesh thickness (4.55), fruit weight (9.33), fruit yield per plant (12.14) and total fruit yield per hectare (403.18). Cluster IV showed highest cluster mean for vine length (7.17), No. of primary branches per vine (15.73), node of 1st male flower appear (6.26), days to anthesis of 1st male flower (73.83), fruits per plant (1.65), 100-seed weight (20.46) and seeds per fruit (521.66). Cluster V showed the highest cluster mean for node of 1st female flower appear (15.16), sex ratio (17.94), polar diameter of fruit (44.16) and polar diameter of seed cavity (35.10), while days to anthesis of 1st female flower (67.37) in cluster II in 2006.

In 2007, cluster III showed highest cluster mean for No. of primary branches per vine (15.33), node of 1st male flower appear (5.83), days to anthesis of 1st male flower (75.13), equatorial diameter of seed cavity (15.00), fruits per plant (1.52), 100-seed weight (20.40) and seeds per fruit (514.66). Cluster IV had highest mean for vine length (7.11), node of 1st female flower appear (14.76), days to anthesis of 1st female flower (66.63), sex ratio (17.47), polar diameter of fruit (47.73), equatorial diameter of fruit (23.86), polar diameter of seed cavity (37.93) and flesh thickness (4.90) while cluster II showed highest cluster mean for fruit weight (7.01), fruit yield per plant (8.66) and total fruit yield per hectare (288.92) in 2007. From Table 4, it was evident that Cluster IV and V in 2006 and Cluster III and IV were highly divergent than other clusters. The inter-cluster distance were higher than the intra-cluster distance, which indicated the existence of substantial diversity among the parents whereas difference in clustering pattern in two years indicated the environmental differences in these two years.

Heterosis is of direct relevance for developing hybrids in both cross and self-pollinated crops. It is increasingly realized that crosses between divergent parent usually produced greater heterotic effect than those between closely related ones (Kale *et al.,* 3; Kumar *et al*., 4). The genotypes PPU-146, PPU-199, PPU-46, PPU-195, PPU-260, PPU-197 (with higher fruit yield), PPU-140 (earliness), PPU-39 (longer fruits), PPU-260 (fruits with high diameter), CM-71 (more number of fruits per plant) and PPU-260 (thicker fruit flesh) were found to be very promising with more than one desirable traits. But, when divergent parents crossed, heterosis is not found to occur always. It is, therefore, essential to explore the possible limits to parental divergence occurrence of heterosis. In this study, it was found that genotypes which grouped in Cluster IV and V, and Cluster I and IV may be chosen for hybridization programme for possible exploitation

Table 2. Cluster composition of 24 pumpkin genotypes.

Cluster	Name of genotype	
	2006	2007
I	PPU-138, PPU-143, PPU-146, PPU-149, PPU-150, PPU-175, PPU-182, PPU-185, PPU-189, PPU-195, PPU-199 (11)	PPU-39, PPU-46, PPU-56, PPU-60, CM-71, PP-113, PPU-138, PPU-143, PPU-144, PPU-146, PPU-149, PPU-189, PPU-197, PPU-199, PPU-276 (15)
II	PPU-39, PPU-46, PPU-56, CM-71, PPU-144, PPU-197, PPU-276 (7)	PPU-140, PPU-150, PPU-175, PPU-182, PPU-185, PPU-195, PPU-260 (7)
III	PPU-60, PP-113, PPU-140, PPU-260 (4)	CM-83 (1)
IV	CM-83 (1)	PPU-174 (1)
V	PPU-174 (1)	_

Values in parenthesis are number of genotypes in a particular cluster.

Table 3. Average intra and inter-cluster D ^{2} values.

Cluster	I	II	III	IV	V
I	255.17 (332.51)	382.82 (512.80)	908.60 (668.89)	952.88 (1492.42)	647.11 (-)
II		173.72 (496.55)	535.72 (933.28)	396.76 (1207.55)	757.07 (-)
III			225.61 (0.00)	482.68 (1607.35)	718.99 (-)
IV				0.00 (0.00)	1271.99 (-)
V					0.00 (-)

Values without parenthesis, based on 2006 data.

Values in parenthesis, based on 2007 data.

Table 4. Cluster mean for different characters.

Sl. No.	Character	Cluster				
		I	II	III	IV	V
1	Vine length (m)	4.42 (5.13)	5.72 (4.55)	5.17 (7.05)	7.17 (7.11)	7.08 (-)
2	No. of primary branches per vine	11.27 (11.91)	12.72 (10.45)	10.30 (15.33)	15.73 (10.60)	11.21 (-)
3	Node of 1st male flower appear	3.28 (2.18)	3.63 (1.98)	2.85 (5.83)	6.26 (2.03)	3.36 (-)
4	Node of 1st female flower appear	12.14 (12.68)	14.03 (12.14)	14.18 (11.90)	11.90 (14.76)	15.16 (-)
5	Days to anthesis of 1st male flower	63.73 (64.76)	66.07 (64.87)	63.90 (75.13)	73.83 (64.86)	61.43 (-)
6	Days to anthesis of 1st female flower	64.44 (64.74)	67.37 (65.41)	65.12 (63.70)	64.80 (66.63)	64.30 (-)
7	Sex ratio	10.69 (10.88)	11.60 (10.60)	9.98 (6.21)	6.38 (17.47)	17.94 (-)
8	Polar diameter of fruit (cm)	24.88 (25.50)	26.05 (28.42)	33.45 (29.40)	30.26 (47.73)	44.16 (-)
9	Equatorial diameter of fruit (cm)	20.12 (19.06)	17.91 (23.10)	25.86 (22.00)	20.90 (23.86)	25.36 (-)
10	Polar diameter of seed cavity (cm)	17.54 (18.20)	18.53 (19.66)	24.18 (22.40)	23.53 (37.93)	35.10 (-)
11	Equatorial diameter of seed cavity (cm)	12.72 (11.76)	10.40 (14.43)	16.75 (15.00)	14.16 (14.06)	16.30 (-)
12	Flesh thickness (cm)	3.68 (3.65)	3.75 (4.33)	4.55 (3.50)	3.36 (4.90)	4.53 (-)
13	Fruit weight (kg)	4.97 (5.09)	5.04 (7.01)	9.33 (4.43)	4.23 (6.70)	6.73 (-)
14	Fruits/plant	1.40 (1.42)	1.43 (1.26)	1.33 (1.52)	1.65 (0.98)	0.98 (-)
15	Fruit yield/plant	6.76 (7.09)	7.17 (8.66)	12.14 (6.76)	7.00 (6.63)	6.63 (-)
16	100 seed weight (g)	13.76 (16.04)	16.47 (12.21)	15.30 (20.40)	20.46 (7.60)	7.03 (-)
17	Seeds/fruit	305.66 (384.00)	429.08 (324.19)	439.25 (514.66)	521.66 (366.00)	367.00 (-)
18	Total fruit yield (q/ha)	225.48 (236.62)	239.12 (288.92)	403.18 (225.53)	233.31 (221.09)	220.09 (-)

Values without parenthesis, based on 2006 data.

Values in parenthesis, based on 2007 data.

of heterosis by devising a suitable breeding programme.

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