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Research Note

Studies on genetic divergence in pumpkin

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Abstract

Twenty five cultivars of Pumpkin are evaluated systematically during *kharif* season of 2013-14. Analysis of variance studies indicates significant differences among all the genotypes for all the characters under study. Majority of the characters like fruit diameter, seed cavity length, flesh thickness, placenta weight exhibit moderate PCV, GCV values and fruit weight exhibits higher GCV and PCV values. All the characters exhibited high broad sense heritability. High heritability coupled with high GCA for the characters fruit weight, fruit diameter, seed cavity length suggesting that they can be improved through direct selection due to predominant additive variation. Genetic diversity worked out using Mahalanobis D^2 statistics. Based on D^2analysis, the genotypes were grouped into 5 different clusters, where the cluster V possessed higher number (8) of genotypes followed by the cluster I (5) cluster IV (5), III (3), II(2) and VI (2). The maximum inter-cluster distance was observed between the clusters III, VI and cluster II, III that of minimum in between the Clusters V and Cluster VI.

Keywords

Genetic diversity,Genetic advance, Heritability,Genetic variability,D^2analysis.

Pumpkin belongs to the family Cucurbitaceae having chromosome number 2n= 40. There are 27 species under the genus Cucurbita, five of which are in cultivation. These are *C. moschata*, *C. maxima*, *C. ficifolia*, *C. pepo and C. mixta*, commonly known as Pumpkin. *C. moschata* is probably the most widely grown species of cucurbita and this species is cross compatible with *C. maxima*, *C.pepo and C.mixta* (Tindall, 1987). Pumpkin is relatively high in energy and carbohydrates and a good source of vitamins, especially high carotenoid pigments and minerals (Bose and Som, 1998). It may contribute to improve the nutritional status of the people, particularly the vulnerable groups in respect of vitamin A requirement. In India, the area under cultivation of pumpkin is 0.36 million ha, with a total production of 3.50 million tonnes/annum, productivity is about 9.72 tonnes/ha (NHB data, 2013). Though a fairly common crop, to-date there is no released variety of pumpkin with high yield potential and good quality in India.

Genetic diversity is one of the important tools to quantify genetic variability in both cross and self-pollinated crops and also important for crop improvement as well as variety development programme (Anand et al., 1975 and Gaur et al., 1978). Multivariate analysis by means of Mahalanobis D2 statistics is useful tools in quantifying the degree of genotypic divergence among biological populations and to assess the relative contribution of different components to the total divergence both at inter and intra-cluster levels (Das and Gupta 1984). Many researchers have adopted this D2 technique for measuring divergence among genotypes of pumpkin (Rashid 2000, kale et al., 2002 and blessing et al., 2012). An understanding of the nature and degree of variability among the germplasm is a prerequisite for its variety improvement. Therefore, the present study was undertaken to analyze the genetic divergence of a number of pumpkin genotypes for selecting parents of diverse group for further breeding programme.

The experiment was conducted at Experimental Research Field, Department of Horticulture, Allahabad School of Agriculture, SHIATS and Allahabad during kharif season 2013 with 25 genotypes of pumpkin. The experiment is laid out in Randomized Block Design (RBD) with three replications. The seed are sowed at 8/8/2013, having plot size of 1×2 m accommodating 10 plants per plot with row-to-row spacing of 2m and plant-to-plant spacing of 1m. Recommended doses and application methods of manure and fertilizers were applied in the experimental field (Chattopadhyay et al., 2007). Bamboo stick support was given to the growing plants and allowed them to creep on a rope nets. Necessary intercultural operations and irrigation were done during the crop period to ensure normal growth and development of the plants. Control measures were taken against red pumpkin beetle at seedling stage and fruit fly at fruiting stage (Chattopadhyay et al., 2007). Observations were recorded for node number of 1st male flower, node number of first female flower, days to first male flower, days to first female flower, fruit weight (g), fruit length (cm), fruit diameter (cm), seed cavity length (cm,), seed cavity width (cm), flesh thickness (cm), placenta weight (g), days to first fruit harvest, number of fruits per vine, vine length (cm), fruit yield (kg/vine). The data on fifteen quantitative characters are recorded on five competitive and randomly selected plants in each genotype and in each replication, except number of fruits per plant, fruit weight and fruit yield per plant which arc recorded on whole genotype basis.

All the statistical analysis was carried out using OPSTAT statistical software Phenotypic and genotypic co-efficient of variability, broad sense heritability (h2) and expected genetic advance were estimated as suggested by Burton (1952), Hanson et al. (1956) and Johnson et al. (1955) respectively. The genetic divergence among genotypes was estimated by using D2 statistics (Mahalanobis 1936). All the genotypes used were clustered into different groups by following Tocher's method (Rao, 1952). The average intra and inter cluster distances were calculated by the formulae given by Singh and Chaudhary (1985).

The genetic parameters for different characters are presented in Table 1. In general, the values of phenotypic co-efficient of variations were higher magnitude than that the corresponding genotypic co-efficient of variations for all the characters showing that the environment had an important role in influencing the expression of these characters, but in present study almost similar trend and similar magnitude of PCV and GCV showed that environment did not much influence the estimates of genetic performance. Majority of the characters except placenta weight, days to first fruit harvest, vine length recorded smaller differences between PCV and GCV values as they were less influenced by the environment indicating reliability of selection based on these traits. The estimates of PCV and GCV were moderate for seed cavity length, seed cavity width, number of fruits per vine indicating phenotypes reflected the genetic worth of the genotypes.

Moderate PCV and low GCV values were observed for seed cavity width, seed cavity length, fruit

diameter, vine length Low PCV and GCV values were observed for days to first male flower, days to first female flower, fruit length, days to first fruit harvest, node no of first male flower indicating limited scope for improvement for these traits using these genotypes. The results were supported by Yadav et al. (2010). High heritability estimates were found for the characters, viz. placenta weight, vine length, days to first fruit harvest, fruit diameter, fruit yield advocating that the selection based on phenotypic performance of these characters would be more operative and these were witnessed by Yadav et al. (2010) and Kumar et al. (2011). High genetic advance as per-cent of mean (GAM) was observed placenta weight, fruit yield, vine length, fruit diameter, number of fruits per vine. Characters like node no of first male flower, days to first male flower, node number of first female flower, days to first female flower, fruit length, seed cavity length, flesh thickness displayed low GAM values.

All the characters exhibited high broad sense heritability values viz., fruit weight 33%, fruit length 54%, fruit diameter 81%, seed cavity length 48%, seed cavity width 48%, flesh thickness 25%, placenta weight 94%, days to first fruit harvest 82%, number of fruits per vine 58%, vine length 90% and fruit yield 72% suggesting that the selection based on phenotypic performance of these traits would be more effective. High genetic advance as per cent of mean (GAM) is observed for the characters fruit diameter 20.81%, seed cavity length 11.65%, seed cavity width 15.67%, flesh thickness 12.68%, days to first fruit harvest 13.90%, number of fruits per vine 17.07%, vine length 30.61% and fruit yield 40.14%. The character placenta weight 52.43%, fruit length 6.80% exhibit moderate and low level of GAM respectively.

High heritability coupled with high genetic advance as per cent of mean is observed for the characters like placenta weight, fruit yield, vine length, fruit diameter, number of fruits per vine, fruit weight, seed cavity length, seed cavity width, flesh thickness indicating that these traits are under the strong influence of additive gene action and hence simple selection based on phenotypic performance of these traits would be more effective. High heritability and moderate GAM values is observed for the character, days to first fruit harvest, fruit length indicating the influence of non-additive gene action and considerable influence of environment on the expression of these traits. This trait could be exploited through manifestation of dominance and epistatic components through heterosis.

Based on D2 values, the genotypes were grouped into six highly divergent clusters (Table 2) the magnitude of D2 values confirmed that there was considerable amount of diversity in the experimental material evaluated. Cluster-5 contained highest number of genotypes (8), while cluster-VI and cluster-II had lowest number of genotypes (2).

Cluster mean: A perusal of results of cluster mean (Table 3) revealed the cluster I with 5 genotypes exhibited highest fruit length (16.64), average fruit weight (1.55), seed cavity length (12.31) and lowest mean value for node number at first male flower appearance (5.23), days to first female flower appearance (39.70). Cluster II had two genotypes, which exhibited highest in node number of first male (5.73) and female flowers appearance (17.75) and lowest in fruit length (15.01). Cluster III was characterized by highest in placenta weight (410.74), lowest in flesh thickness (2.15) while the cluster IV had maximum in days to first fruit harvest (66.54) and lowest in fruit yield yield (4.36). Cluster V with eight genotypes exhibited highest in seed cavity width (6.34) and lowest in average fruit weight (1.23), placenta weight (203.67). Cluster VI with 2 genotypes exhibited highest in days to first female flower appearance (45.83) while lowest in fruit diameter (14.40), seed cavity width (5.15), vine length (230.76), number of fruits per vine (1.88). None of the cluster contained genotypes with all the desirable traits, which could be directly selected and utilized. Similar results were also reported by Khatum et al., 2010 in snake gourd. All the minimum and maximum scluster mean value was distributed in relatively distant clusters. While studying the genetic divergence in Pumpkin genotypes thereby underlining the fact that the hybridization between genotypes of different cluster is necessary for the development of desirable genotypes (Figure1). Based on the per se performance of the best genotypes within the clusters, there may be directly selected or may be used as potential parents in hybridization programme.

Intra and inter cluster distances: The 25 lines were grouped into 6 clusters based on D2 values (Table 4). The cluster-II displayed the least intra cluster distance, while the maximum intra cluster distance was recorded for cluster IV. The highest inter cluster generalized distance was found between cluster-III and cluster-VI followed by clusters-II and III. The involvement of genotypes belonging to cluster III and VI, II and III, and III and V in hybridization would help in achieving novel recombinants (Joshi et al., 2008 in pointed gourd).

Contribution of individual character towards total divergent: The contribution of each trait to total divergence is presented in Table 5. Among the traits studied placenta weight contributed maximum divergence (36.67%) followed by vine length (20.33%), fruit yield (6.67%), fruit diameter (5.67%). The traits viz., placenta weight, vine length, fruit yield, fruit diameter contributed 69.34% towards total divergence. Hence, these characters should be given importance during hybridization and selection in the segregating population.

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Table 1.The genetic parameters for various characters in Pumpkin

S. No.	Character	Range	Mean	PCV (%)	GCV (%)	h^2 (%)	GA	GAM
1	Node number of 1st male flower	4.96-7.30	5.52	15.40	1.39	1.3%	0.01	0.26
2	Node number of 1st female flower	15,00-19.26	17.26	8.79	4.41	25%	0.79	4.56
3	Days to first male flower	27.10-31.20	28.74	4.71	2.32	24%	0.68	2.35
4	Days to first female flower	37.86-45.83	41.30	6.15	4.72	59%	3.08	7.45
5	Fruit weight (g)	0.95-2.17	1.29	25.16	14.40	33%	0.22	16.99
6	Fruit length (cm)	13.80-17.73	15.67	6.07	4.48	54%	1.07	6.80
7	Fruit diameter (cm)	13.16-20.16	16.24	12.46	11.22	81%	3.38	20.81
8	Seed cavity length (cm)	9.36-13.86	11.37	11.69	8.13	48%	1.33	11.65
9	Seed cavity width (cm)	5.10-8.36	5.98	15.77	10.95	48%	0.94	15.67
10	Flesh thickness (cm)	1.86-3.63	2.39	24.81	12.36	25%	0.30	12.68
11	Placenta weight (g)	188.16-425.06	269.15	26.96	26.19	94%	141.11	52.43
12	Days to first fruit harvest	57.63-79.30	63.38	8.28	7.47	82%	8.81	13.90
13	Number of fruits per vine	1.88-2.50	2.18	14.21	10.85	58%	0.37	17.07
14	Vine length (cm)	206.50-361.13	271.70	16.59	15.70	90%	83.16	30.61
15	Fruit yield (kg/vine)	2.26-8.78	5.64	27.11	22.98	72%	2.27	40.14

Table 2.Clustering pattern of 25 genotypes of pumpkin by Ward's method

Cluster	No. of genotypes	Genotypes
I	5	VRP-6, HARP-10, VRPK-11-01, KPS-01, VRPK-11-02
II	2	PUSA VIKASH, SWARNA AMIT
III	3	VRPK-02, VRPK-09-01, VRPK-15
IV	5	VRPK-171, VRPK-113, PUNJAB SAMRAT, PPU-72, VRPK-38
V	8	VRPK-51, VRPK-113-01, VR-14, VRPK-222-02, ARKA CHANDAN, VRPK-72-11-02, CO-02, KASHI HARIT
VI	2	CM-350, VRPK-207-02

Table 3.Mean values of clusters for fifteen characters in for 25 Pumpkin genotypes

S.NO	Character	I	II	III	IV	V	VI
	No of genotypes	5	2	3	5	8	2
1	Node number of first male flower	5.23	5.73	5.54	5.46	5.65	5.70
2	Node number of first female flower	17.18	17.75	16.46	17.34	17.30	17.75
3	Days to first male flower	28.33	28.43	29.25	28.36	28.71	30.35
4	Days to first female flower	39.70	42.25	39.10	42.35	41.09	45.83
5	Average fruit weight (g)	1.55	1.15	1.24	1.23	1.23	1.23
6	Fruit length (cm)	16.64	15.01	15.85	15.62	15.24	15.51
7	Fruit diameter (cm)	17.56	19.63	17.25	16.49	14.50	14.40
8	Seed cavity length (cm)	12.31	10.96	12.21	11.61	10.59	10.68
9	Seed cavity width (cm)	5.94	5.23	6.34	5.84	6.34	5.15
10	Flesh thickness (cm)	2.23	3.40	2.15	2.24	2.41	2.40
11	Placenta weight (g)	291.02	215.88	410.74	307.28	203.67	221.50
12	Days to first fruit harvest	60.95	60.68	60.34	66.54	62.01	74.30
13	Number of fruits per vine	2.23	2.10	2.36	2.08	2.23	1.88
14	Vine length (cm)	310.66	328.66	240.51	249.53	268.92	230.76
15	Fruit yield (kg/vine)	7.31	4.92	6.40	4.36	5.53	4.72

Table 4.Average intra (bold) and inter-cluster D^2 values for six clusters among twenty five genotypes of Pumpkin

Cluster	I	II	III	IV	V	VI
I	79.202	124.279	158.027	138.478	152.533	232.057
II		42.017	271.497	172.871	121.505	158.849
III			67.908	142.026	277.151	296.881
IV				91.22	154.963	153.316
V					77.58	130.049
VI						56.343

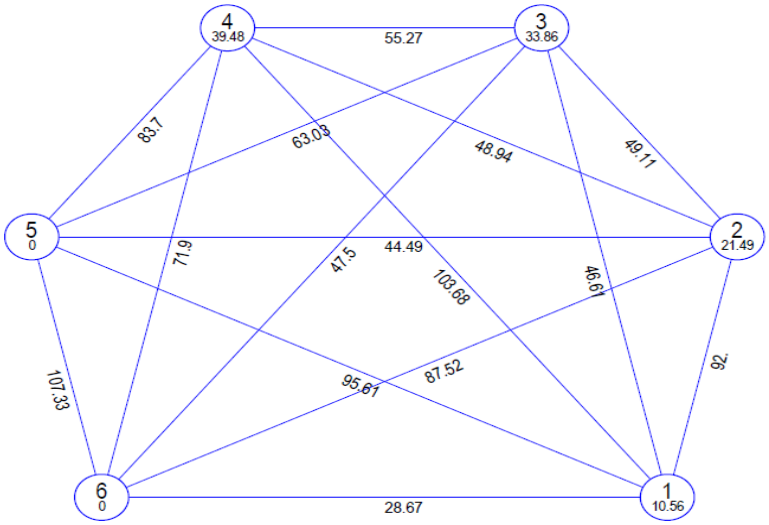

Figure1. Cluster diagram showing the average intra and inter cluster distances ($D = D^2$) of pumpkin genotypes Inter and intra-cluster distance.

Table 5.Percent contribution of different characters towards diversity in 25 genotypes of pumpkin

S. No.	Character	Times ranked 1st	Per cent contribution
1	Node number of first male flower	0	0.00
2	Node number of first female flower	0	0.00
3	Days to first male flower	0	0.00
4	Days to first female flower	1	0.33
5	Average fruit weight (g)	2	0.67
6	Fruit length (cm)	2	0.67
7	Fruit diameter (cm)	17	5.67
8	Seed cavity length (cm)	0	0.00
9	Seed cavity width (cm)	3	1.00
10	Flesh thickness (cm)	0	0.00
11	Placenta weight (g)	110	36.67
12	Days to first fruit harvest	20	6.67
13	Number of fruits per vine	4	1.33
14	Vine length (cm)	61	20.33
15	Fruit yield (kg/vine)	20	6.67