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Studies of genetic variability and heritability for fruit yield and its component traits in pumpkin (*Cucurbita moschata* Duch. ex. Poir)

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Abstract

An investigation was conducted at Main Experiment Station of Department of Vegetable Science at Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P). The experimental material consisted of 28 pumpkin genotypes including three standard checks *viz.*, Arka Chandan, Azad Kaddu and Pusa Vikash was conducted in a Randomized Block Design with three replications. The germplasm of pumpkin collected from different sources to study the extent of variability, heritability and genetic advance in per cent of mean for different quantitative traits. Analysis of variance studies indicated significant differences among all the genotypes for all the characters under study**.** High magnitude of phenotypic as well genotypic coefficients of variation were observed in case of number of primary branches followed by vine length, node number at first male flower anthesis, node number at first female male flower anthesis, fruit yield per plant, average fruit weight and number of fruit per plant. This indicates possibility of obtaining higher selection response in respect of these traits. Moderate estimate of PCV and GCV were noted in case of number of fruit per plant, flesh thickness and fruit polar circumference. The occurrence of moderate values for these three parameters reveals reasonable scope of improvement through selection. However, the existence of low value of GCV and PCV for remaining traits suggested likely days to first staminate and pistallate flower anthesis, fruit polar circumference and days to first fruit harvest to showed less response under selection. High heritability along with high genetic advance in per cent of mean were recorded for most of the traits except days to first staminate and pistallate flower anthesis, days to first fruit harvest, and fruit polar and equatorial circumference. Eight traits *viz.*, node number to first staminate and pistillate flower appearance, number of primary branches, vine length, flesh thickness, number of fruit per plant, average fruit weight and fruit yield per plant, with high heritability and genetic advance are likely to provide very high selection response which are showing additive gene effect.

Keywords: Variability**,** heritability, genetic advance, GCV, PCV and genotypes

Introduction

Pumpkin (Cucurbita spp.) is an important growing vegetable crop belongs to the family Cucurbitaceae in which contain high nutritional, medicinal and economical value with chromosome number 2n=2x= 40. The word pumpkin originated from the word *pepon* which is a Greek word meaning for “large melon”, something round and large. 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) [10]. Pumpkin is relatively high in energy values, carbohydrates, good source of vitamins, especially high in carotenoid pigments and minerals (Bose and Som, 1998) [3]. It may contribute to improve the nutritional status of the people, particularly the vulnerable groups in respect of vitamin-A requirement (Satkar *et al.*, 2013) [7]. In India, it is mainly grown in Assam, West Bengal, Tamil Nadu, Karnataka, Madhya Pradesh, Uttar Pradesh, Orissa, Kerala and Bihar. The total area of pumpkin in India is 19,960 hectares whereas, the total production is 2093 (‘000 mt) with productivity of 21.71 t/ha (Annonymous, 2018) [2].

Genetic diversity is one of the important tools to quantify genetic variability in both cross and self-pollinated vegetable crops and also important for crop improvement as well as variety development programme (Anand *et al.*, 1975 and Gaur *et al.*, 1978) [1]. Multivariate analysis by means of Mahalanobis D^2 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) [4]. Many researchers have adopted this D^2 technique for measuring divergence among genotypes of pumpkin (Rashid *et al.*, 2000, Kale *et al.*, 2002 and Blessing *et al.*, 2012) [6]. An understanding of the nature and degree of variability among the germplasm is a prerequisite for its varietal improvement. Therefore, the present study was undertaken to analyse the genetic divergence among the number of pumpkin genotypes for selecting parents of diverse group for further breeding programme.

Materials and Methods

The experimental material comprised of 28 germplasm including three standard checks *viz.*, Arka Chandan, Azad Kaddu and Pusa Vikash. The experiment was laid out in a Randomized Block Design with three replications at Main Experiment Station of Department of Vegetable Science at Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P) during summer season 2019.The seeds were sown on 03/04/2019, having plot size of 3×3 m accommodating 6 plants per plot with row-to-row spacing of 3m and plant-to-plant spacing of 0.50 m. Observations were recorded for node number to first staminate flower anthesis, node number to first pistillate flower anthesis, days to first staminate flower anthesis, days to first pistillate flower anthesis, days to first fruit harvest, number of primary branches, fruit polar circumference (cm), fruit equatorial circumference (cm), vine length (m), flesh thickness (cm), number of fruits per plant, average fruit weight (Kg) and fruit yield per plant (Kg.)

The data on thirteen quantitative characters are recorded on five competitive and randomly selected plants of each genotype and in each replication. All the statistical analysis was carried out using OPSTAT statistical software. The genetic divergence among genotypes was estimated by using D^2 statistics (Mahalanobis 1936) [5]. 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) [8].

Results and Discussion

Coefficient of variation

The estimates of genotypic, phenotypic and environment coefficients of variation for thirteen characters of pumpkin germplasm evaluations are presented in Table.

Phenotypic coefficient of variation (PCV)

The estimates of coefficients of variation revealed that magnitude of phenotypic coefficients of variations (PCV) were higher than the genotypic coefficient, of variation (GCV) for all the characters indicating important role of environment. The phenotypic coefficient of variation ranged from 7.06 per cent (days to first harvest) to 37.53 per cent (number of primary branches per plant) for the various characters studied (Table 1).

Highest phenotypic coefficient of variation was recorded for the character number of primary branches per plant (37.53) per cent followed by vine length 36.19 per cent, while, moderate to high values of PCV were observed for characters, node number at first male for anthesis (29.79%), node number at first female for anthesis (27.16%), average fruit weight (24.41%), fruit yield per plant (24.27%), number of fruit per plant (21.83%), flesh thickness (19.36%) and fruit polar circumference (10.63%).However, low phenotypic coefficient of variation was observed in characters *viz.*, days to first staminate flower anthesis (8.38%), fruit equatorial circumference(8.30%), days to first pistillate flower anthesis (7.85%) and days to first fruit harvest (7.06%).

Table 1: Estimates of range, variability, heritability and expected genetic advance in per cent of mean for the thirteen characters in pumpkin germplasm

S. No.	Characters	Range		Variability			Heritability (In broad sense)%	Genetic advance	Expected g. a. as % of mean
		Min.	Max.	PCV%	GCV%	ECV%			
1	Node number at first staminate flower anthesis	3.10	9.20	29.79	27.21	12.12	83.40	3.95	65.63
2	Node number at first pistallate flower anthesis	8.50	21.30	27.16	25.91	8.14	91.00	9.10	65.26
3	Days to first staminate flower anthesis	39.20	50.30	8.38	6.45	5.35	59.20	5.73	13.12
4	Days to first pistallate flower anthesis	40.20	51.36	7.85	5.76	5.34	53.70	5.21	11.15
5	Days to first fruit harvest	57.90	76.10	7.06	4.69	5.27	44.20	5.40	8.25
6	Number of primary branches per plant	2.76	8.70	37.53	36.20	9.92	93.00	45.20	92.17
7	Fruit polar circumference (cm)	25.26	35.93	10.63	8.17	6.80	59.00	4.92	16.59
8	Fruit equatorial circumference (cm)	51.56	66.70	8.30	5.14	6.51	38.30	5.01	8.40
9	Vine length (m)	2.62	10.12	36.19	35.24	8.25	94.80	4.68	90.58
10	Flesh thickness (cm)	2.10	4.30	19.36	17.81	7.58	84.60	1.31	43.27
11	Number of fruit per plant	2.67	6.33	21.83	19.45	9.92	79.30	2.24	45.74
12	Average fruit weight (kg)	0.73	2.11	24.41	22.87	8.54	87.70	0.83	56.56
13	Fruit yield per plant (kg)	2.73	8.13	24.27	23.47	6.20	93.40	3.38	59.91

Genotypic coefficient of variation (GCV)

It is revealed in Table. That, the genotypic coefficient of variation (GCV) ranged from 5.14 per cent (days to first harvest) to 35.24 per cent (vine length), whereas, genotypic coefficient of variation was lower for the characters fruit polar circumference (8.17%), days to first staminate flower anthesis (6.45%), fruit equatorial circumference (5.14%), days to first pistillate flower anthesis (5.76%) and days to first fruit harvest (4.69%).

Environmental coefficient of variation (ECV)

The observed environmental coefficient of variation (Table) was in the range between days to first fruit harvest (5.27) per cent to node number for first staminate flower anthesis (12.12) per cent. Highest environmental coefficient of variation was recorded for the character first male for anthesis (12.12) per cent. There was moderate to low environmental coefficient of variation reported for all the characters under studied. While, moderate to high values of ECV were observed for characters number of primary branches per plant (9.92%) same as number of fruit per plant (9.92%), average fruit weight (8.54%), vine length (8.25%), node number at first female for anthesis (8.14%), flesh thickness (7.58%). fruit polar circumference (6.80%), fruit equatorial circumference 6.51%, fruit yield per plant 6.20%, days to first staminate flower anthesis (5.35%), days to first pistillate flower anthesis (5.34%) and days to first fruit harvest (5.27%).

Heritability and genetic advance

Estimates of heritability and expected genetic advance for different characters are presented in Table 1. The broad sense heritability ranged from 94.80. per cent in case of vine length to fruit equatorial circumference 38.30 per cent for lowest heritability found. Result presented in the Table 1, revealed that the high heritability estimates in broad sense were of lower magnitude except the character fruit yield per plant (93.40%), number of primary branches per plant (93.00%), node number at first female flower anthesis (91.00%), average fruit weight (87.70%), flesh thickness (84.60%), node number at first female flower anthesis (83.40%) and number of fruit per plant (79.30%). The moderate heritability character days to first staminate flower anthesis (59.20%), fruit polar circumference (59.00%) and days to first pistallate flower anthesis (53.70%). Among the thirteen characters in which found lower heritability namely days to first harvest (44.20%) and fruit equatorial circumference (38.30%) Estimate of high heritability (>50%) were recorded for all the thirteen characters except to days to first fruit harvest (44.20%) and fruit equatorial circumference (38.30%) which showed lower heritability (<50%).

The highest value of genetic advance in per cent of mean was shown by number of primary branches per plant (92.17), while days to first fruit harvest had lowest value (8.25) for this parameter. The characters showing very high estimate of Ga 40%) were number of primary branches per plant (92.17), vine length (90.58), node number at first male flower anthesis (65.63), node number at first female flower anthesis (65.26), fruit yield per plant (59.91), average fruit weight (56.56) and number of fruits per plant (43.27).

The moderate estimate for genetic advance resulted in case of fruit polar circumference (16.59), days to first staminate flower anthesis (13.11) and days to first pistillate flower anthesis (11.15) while the low estimate was observed for the fruit equatorial circumference (8.40) and days to first fruit harvest (8.25).

The traits like number of primary of primary branches, vine length (m), node number at first staminate flower anthesis, node number at first pistillate flower anthesis, fruit yield per plant (kg) and average fruit weight (kg) showed comparatively higher values of PCV, GCV, heritability (in broad sence), genetic advance and expected genetic advance as % of mean through additive gene effect and they can be improved by selection.

References

1. Anand IN, Singh JN, Khanna PP. Inter-relationships and diversity in Indian colza. Indian Journal Agriculture Sciences. 1975;45:253-258.
2. Anonymous. Indian Horticulture Database. National Horticulture Board, Ministry of Agriculture and Farmers Welfare, Government of India, Gurgaon, 2018.
3. Bose TK, Som MG. Vegetable crops in India. *Naya Prokash*, Calcutta, India, pp. 92-95.
4. Das PK, Gupta TD. Multivariate analysis in blackgram. Indian Journal Genetics. 1984;44(2):243-247.
5. Mahalanobis PC. On the generalized distance in statistics. Proceedings of the National Institute of Science of India. 1936;2:49-55.
6. Rashid MM. Genetic divergence in pumpkin. M.S. dissertation Thesis. Department of Genetic Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agril. Univ. Bangladesh, 2000, 84pp.
7. Satkar KP, Kulthe AA, Chalke PR. Preparation of bitter gourd ready-to-serve beverage and effect of storage temperature on its keeping quality. The Bioscan. 2013;8(1):115-117.
8. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. *Kalyani Publishers*. New Delhi, India, 1985, 318.
9. Sutariya DA, Patel KM, Bhadauria HS, Vaghela PO, Prajapati DV, Parmar SK. Genetic diversity for quality traits in Indian mustard (*Brassica juncea* L.) Journal Oilseed Brassica. 2011;2(1):44-47.
10. Tindall HD. Vegetables in the tropics. Macmillan Education, London, 1987, 166pp.