www.ThePharmaJournal.com

The Pharma Innovation



ISSN (E): 2277- 7695 ISSN (P): 2349-8242 NAAS Rating: 5.23 TPI 2021; SP-10(11): 2566-2571 © 2021 TPI www.thepharmajournal.com Received: 13-09-2021 Accepted: 23-10-2021

Devesh Tiwari

Ph.D., Scholar, Department of Vegetable Science, A.N.D. University of Agriculture and Technology Kumarganj Ayodhya, Uttar Pradesh, India

GC Yadav

Associate Professor, Department of Vegetable Science, A.N.D. University of Agriculture and Technology Kumarganj Ayodhya, Uttar Pradesh, India

Corresponding Author Devesh Tiwari Ph.D., Scholar, Department of Vegetable Science, A.N.D.

University of Agriculture and Technology Kumarganj Ayodhya, Uttar Pradesh, India

Genetic diversity assessment in pumpkin for quantitative traits

Devesh Tiwari and GC Yadav

Abstract

The present investigation was carried out with the aim to assess the genetic diversity among the parents and their off-springs. The study was conducted during Zaid, 2020 (Y1) and Zaid, 2021 (Y2). The present investigated shows that the analysis of variance revealed that mean squares due to genotypes were found significant for all the traits in the both seasons (Y_1, Y_2) and over seasons (Pooled). The moderate phenotypic as well as genotypic coefficients of variation observed in case of fruit yield per plant, number of fruits per plant, non-reducing sugars and node number to first male flower appearance during both seasons (Y1, Y2) and over seasons (Pooled), vine length, flesh thickness, internodal length, number of primary branches per plant, node number to first female flower appearance, β-carotene, reducing sugar and average fruit weight during both seasons (Y1 and Y2). The estimates of high heritability coupled with high genetic advance as per cent of mean were observed for fruit yield per plant, non-reducing sugars, number of fruits per plant, node number to first male flower appearance and flesh thickness during Y1 and Y₂ while, number of primary branches per plant, β -carotene and reducing sugars during Y₁. High heritability coupled with moderate genetic advance was observed for total soluble solids during Y_1 and Y₂. Moderate heritability coupled with high genetic advance were observed for non-reducing sugars during over seasons (pooled) which indicating the additive gene action for these traits and the phenotypic selection could be relied upon.

Keywords: Pumpkin, fruit yield, PCV, GCV, Heritability (broad sense) and genetic advance

Introduction

Pumpkin (*Cucurbita moschata* Duch. ex. Poir) is one amongst foremost important vegetable crop of family (gourd) Cucurbitaceae. It's has been grown throughout the world due to having its good nutritional/medicinal value and also higher returns to the farmers. The centre of origin of pumpkin is believed to be central Mexico. Pumpkin is a sexually propagated, herbaceous annual vegetable allopolyploid having chromosome number 2n=2x=40. Plant stem is an angular, hairless five ridged, trailing and branched. Trailing vine strikes roots at nods. Leaves are deeply or shallowly lobed not pinnatifid. Fruits have diuretic and vermetic action. Seeds are non-bitter in test, tasty and nutritious. The flowers are yellow coloured and large in size with showy companulate corolla. Ovary is inferior, syncarpous and tricarpellary. Corolla is companulate, gamopetalous, lobed. Pumpkin are monoecious, highly cross pollinated, entamophilous with three anthers. The word pumpkin was originated from Greek word *pepon*, which means "large melon", something large and round.

Pumpkin showed more variability in their fruit size, colour, shape, fruit yield and also other agronomic attributes (Singh, 2005 and Singh *et al.*, 2005) ^[19, 21]. Like other gourds pumpkin is summer season crop and hence it may be cultivated throughout the year in central and southern states of the country. The phenotypic appearance of the plant is mainly controlled by the genetic makeup and surrounding the environment. The genetic variance of any quantitative character is composed of additive variance (heritable) and non-additive variance and include dominance and epitasis (non-allelic interaction). That's why; it becomes essential to partition the observed phenotypic variability into its heritable and non-heritable components with suitable parameters such as phenotypic and genotypic coefficient of variation, heritability and genetic advance. After that, genetic advance can be used to predict the efficiency of selection.

Materials and Methods

The experimental materials for the present study comprised of nine promising and diverse inbreds and varieties of pumpkin selected on the basis of genetic variability from the germplasm stock maintained in the Department of Vegetable Science, A.N.D.

University of Agriculture & Technology, Kumarganj, Ayodhya (U.P.) India. The selected parental lines *i.e.* Narendra Agrim (P₁), Narendra Amrit (P₂), Narendra Upkar (P₃), NDPK-7-24 (P₄), NDPK-76-1 (P₅), NDPK-2-1 (P₆), NDPK-39-2 (P₇) NDPK-41-2 (P₈), and NDPK-43-3 (P₉) were raised and crossed in the all possible combinations, excluding reciprocals, during *Zaid*, 2019 to develop 36 F₁ hybrid seeds and evaluated during *Zaid*, 2020 and *Zaid*, 2021.

Observations were recorded on fourteen economic traits including biochemical analysis *viz.*, node number to first male flower, node number to first female flower, days to first male flower anthesis, days to first female flower anthesis, days to first fruit harvest, vine length (m), internodal length (cm), number of primary branches per plant, equatorial circumference of fruit (cm), polar circumference of fruit (cm), flesh thickness (cm), average fruit weight (kg), number of fruits per plant, fruit yield per plant (kg), ascorbic acid (mg/100g), total soluble solids (%), β – carotene, dry matter content (%), reducing sugars (%), non-reducing sugars (%).

Result and Discussion

Mean squares (Table 1) due to replications, genotypes, parents, hybrids and parents *vs.* hybrids for fourteen quantitative traits and seven quality traits were worked out to test the significance of differences among the genotypes *Zaid*, 2020 (Y_1), *Zaid*, 2021 (Y_2) and over seasons (Pooled) are presented.

The estimates of phenotypic coefficients of variations (PCV) were higher than genotypic coefficients of variations (GCV) for all characters during both seasons (*Zaid*, 2020 and 2021) and over seasons (pooled). Above-mentioned findings are also in close by conformity with the earlier researchers *viz.*, Rana *et al.* (1986) ^[17]; Chigwe and Saka (1994) ^[5]; Babu *et al.* (1996) ^[1]; Rios *et al.* (1996) ^[18]; Kumaran *et al.* (1997) ^[11]; Gwanama *et al.* (2002) ^[8]; Pandey *et al.* (2002) ^[16], Dhatt and Singh (2008) ^[6], Chaudhari *et al.* (2017) ^[4], Srikanth *et al.* (2017) ^[22], Kumar *et al.* (2017b) ^[10], Kumar *et al.* (2018), Singh *et al.* (2019) ^[20] and Suresh *et al.* (2020) ^[23].

The moderate phenotypic as well as genotypic coefficients of variation were observed in case of fruit yield per plant, number of fruits per plant, non-reducing sugars and node number to first male flower appearance during both seasons (Y1, Y2) and over seasons (Pooled), vine length, flesh thickness, internodal length, number of primary branches per plant, node number to first female flower appearance, β carotene, reducing sugar and average fruit weight during both seasons (Y_1, Y_2) , whereas PCV was moderate for vine length, flesh thickness, number of primary branches per plant, βcarotene, internodal length, node number to first female flower appearance, average fruit weight, reducing sugar during over seasons (pooled) and only PCV was moderate for dry matter content during both seasons (Y_1, Y_2) and over seasons (Pooled). Mohanty and Mishra (1999) ^[14]; Mohanty (2002); Laxmi et al. (2002)^[12] and Dhatt and Singh (2008)^[6] also reported the PCV was greater than GCV for all the

characteristics. The moderate PCV and GCV showed that variation could be attributed due to differences in experimental material and growing environments. While, the rest characters showed low estimates of phenotypic as well as genotypic coefficients of variation.

Heritability (broad sense) of a character is important to the breeder since it indicates the possibility and extent to which improvement is possible through selection. It also indicates direction of selection pressure to be applied for a trait during selection because it assesses the relationship between parents and their progeny, hence widely used in determining the degree to which a character can be transferred from parents to offspring. High heritability, on the other hand, isn't adequate to make efficient selection in advanced generations unless it's accompanied by substantial amount of genetic advance (Burton, 1952)^[3]. Estimate of high heritability along with high genetic advance in per cent of mean provides great possibility for further enhancement in advance generations.

The heritability estimates for different traits ranged from 3.40 to 91.20 per cent. High estimates of heritability were observed for node number to first male flower appearance, number of primary branches per plant, flesh thickness, number of fruits per plant, fruit yield per plant, total soluble solids, reducing sugars and non-reducing sugars during Y_1 and Y_2 , node number to first female flower appearance, internodal length, average fruit weight, ascorbic acid, β-carotene, dry matter content and total sugars during Y₂ exhibited high heritability, which revealed that these traits are governed by additive gene action and phenotypic selection would be effective for improvement of these traits. The earlier researchers viz., Doijode and Sulladmath (1986); Rana et al. (1986)^[17] and Mohanty (2000)^[15] also reported high heritability for either of the traits. However, the moderate estimates of heritability observed for number of fruits per plant, β-carotene and nonreducing sugars.

The estimates of high heritability along with high genetic advance as per cent of mean were observed for fruit yield per plant, non-reducing sugars, number of fruits per plant, node number to first male flower appearance and flesh thickness during Y_1 and Y_2 while, number of primary branches per plant, β-carotene and reducing sugars during Y1. High heritability coupled with moderate genetic advance was observed for total soluble solids during Y1 and Y2. Moderate heritability coupled with high genetic advance were observed for non-reducing sugars during over seasons (pooled) which indicating the additive gene action for these traits and the phenotypic selection could be relied upon. Mangal et al. $(1979)^{[13]}$; Rana *et al.* (1986)^[17]; Kumaran *et al.* (1997)^[11]; Bindu *et al.* (2000)^[2]; Kumar *et al.* (2018); Singh *et al.* (2019) ^[20] have reported high heritability with high genetic advance and Mohanty and Mishra (1999) [14] informed moderate heritability along with high genetic advance and Dhatt and Singh (2008) ^[6] have informed high heritability accompanied by moderate to high genetic advance for the majority of the aforementioned characteristics.

Source of Variation	d.f.	Node number to first male flower appearance	Node number to first female flower appearance	Days to first male flower anthesis	Days to first female flower anthesis	Days to first fruit harvest	Vine length (m)	Internodal length (cm)	Number of primary branches per plant	Equatorial circumference of fruit (cm)	Polar circumference of fruit (cm)
Replications	2	0.75	3.94	0.29	64.51	26.03	0.26	0.11	0.03	75.23	74.83
Genotypes	44	3.66**	9.53**	8.33*	12.22**	16.11*	0.66**	2.26**	1.82**	37.78**	16.28*
Parents	8	8.22**	27.04**	5.99	21.33**	34.61**	0.61**	4.02**	2.71**	54.91**	14.66
Hybrids	35	2.72**	5.16**	9.11*	9.31	11.09	0.68**	1.91**	1.67**	34.30**	12.63
Parents vs. Hybrids	1	0.17	22.03**	0.00	41.27*	43.54*	0.21	0.61	0.02	22.62	156.89**
Error	88	0.20	1.01	4.94	6.42	9.31	0.06	0.20	0.11	13.71	9.13

Table 1: ANOVA (mean squares) for a set of 9×9 diallel cross in pumpkin during 2020 (Y₁)

Source of Variation		Flesh thickness	Average fruit	No. of fruits	Fruit yield per	Ascorbic acid	Total soluble	B Caratana	Dry matter	Reducing	Non-reducing	Total Sugars
Source of variation	u.1.	(cm)	weight (kg)	per plant	plant (kg)	(mg/100)	solids (%)	p – Carotene	Content (%)	sugars (%)	sugars (%)	(%)
Replications	2	0.06	0.01	0.04	0.08	1.01	1.29	0.50	0.04	0.08	0.00	0.01
Genotypes	44	0.34**	0.14**	0.64**	2.83**	0.66**	0.84**	0.87**	1.23**	0.27**	0.26**	0.57**
Parents	8	0.65**	0.16**	0.45**	2.05**	1.04**	1.31**	1.27**	2.77**	0.15**	0.39**	0.32**
Hybrids	35	0.28**	0.14**	0.54**	1.83**	0.59**	0.76**	0.80**	0.91**	0.25**	0.24**	0.57**
Parents vs. Hybrids	1	0.00	0.06*	5.61**	44.07**	0.19	0.00	0.14	0.01	2.00**	0.07**	2.78**
Error	88	0.02	0.01	0.02	0.08	0.06	0.06	0.05	0.11	0.01	0.01	0.05

*, ** Significant at 5 per cent and 1 per cent probability levels, respectively.

Table 2: ANOVA (mean squares) for a set of 9×9 diallel cross in pumpkin during 2021 (Y₂)

Source of Variation	d.f.	Node number to first male flower appearance	Node number to first female flower appearance	Days to first male flower anthesis	Days to first female flower anthesis	Days to first fruit harvest	Vine length (m)	Internodal length (cm)	Number of primary branches per plant	Equatorial circumference of fruit (cm)	Polar circumference of fruit (cm)
Replications	2	0.61	4.45*	0.20	64.82	28.49	0.46	0.05	0.18	93.17	94.34
Genotypes	44	3.88**	10.07**	9.05*	13.45*	17.42*	0.70**	2.47**	1.93**	40.08**	17.40**
Parents	8	8.72**	28.71**	6.70	23.07**	37.44**	0.65**	4.26**	2.88**	58.27**	15.83
Hybrids	35	2.88**	5.44**	9.84*	10.25	12.00	0.73**	2.11**	1.77**	36.38**	13.28*
Parents vs. Hybrids	1	0.18	23.09**	0.00	48.51*	47.02*	0.22	0.73	0.03	23.95	174.48**
Error	88	0.32	1.40	5.67	7.77	10.95	0.09	0.34	0.18	18.02	8.47

Source of Variation	d f	Flesh thickness	Average fruit	No. of fruits	Fruit yield per	Ascorbic acid	Total soluble	β-	Dry matter	Reducing	Non-reducing	Total
Source of variation	u.1.	(cm)	weight (kg)	per plant	plant (kg)	(mg/100)	solids (%)	Carotene	Content (%)	sugars (%)	sugars (%)	Sugars (%)
Replications	2	0.09	0.04	0.05	0.09	1.63	1.54	0.81	0.06	0.12	0.00	0.01
Genotypes	44	0.37**	0.16**	0.74**	3.23**	0.69**	0.90**	0.91**	1.30**	0.28**	0.27**	0.60**
Parents	8	0.71**	0.19**	0.52**	2.35**	1.08**	1.39**	1.32**	2.95**	0.16**	0.40**	0.33**
Hybrids	35	0.31**	0.16**	0.62**	2.07**	0.62**	0.81**	0.83**	0.96**	0.26**	0.25**	0.59**
Parents vs. Hybrids	1	0.00	0.07	6.44**	51.04**	0.20	0.00	0.15	0.01	2.07**	0.08**	2.89**
Error	88	0.03	0.02	0.04	0.12	0.09	0.07	0.11	0.21	0.02	0.01	0.09

*, ** Significant at 5 per cent and 1 per cent probability levels, respectively.

Source of Variation	d.f.	Node number to first male flower appearance	Node number to first female flower appearance	Days to first male flower anthesis	Days to first female flower anthesis	Days to first fruit harvest	Vine length (m)	Internodal length (cm)	Number of primary branches per plant	Equatorial circumference of fruit (cm)	Polar circumference of fruit (cm)
Environments	1	3.44**	16.17**	192.34**	184.49**	396.37**	0.91**	3.42**	2.87**	188.06**	142.34**
Blocks within Environments	4	0.68*	4.20**	0.24	64.66**	27.26*	0.36**	0.08	0.10	84.20**	84.58**
Genotypes	44	7.55**	19.60**	17.38**	25.51**	33.52**	1.36**	4.73**	3.76**	77.85**	33.66**
Parents		16.95**	55.75**	12.69*	44.38**	72.03**	1.26**	8.28**	5.60**	113.16**	30.41**
Hybrids	35	5.60**	10.61**	18.95**	19.36**	23.09**	1.41**	4.02**	3.44**	70.67**	25.90**
Parents vs. Hybrids	1	0.35	45.12**	0.00	89.64**	90.54**	0.43*	1.34*	0.06	46.57	331.14**
Treatment vs. Environments	44	0.00	0.00	0.00	0.16	0.01	0.00	0.00	0.00	0.01	0.03
Parent vs. Environments	8	0.00	0.01	0.01	0.01	0.02	0.00	0.00	0.00	0.02	0.08
Hybrids vs. Environments		0.00	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.01	0.01
Parents vs. Hybrids X Environments		0.00	0.00	0.00	0.14	0.03	0.00	0.00	0.00	0.00	0.23
Error	176	0.26	1.21	5.30	7.10	10.13	0.08	0.27	0.15	15.87	8.80

Table 3: ANOVA (mean squares) for a set of 9×9 diallel cross in pumpkin over seasons (Pooled)

*, ** Significant at 5 per cent and 1 per cent probability levels, respectively.

Source of Variation		Flesh thickness (cm)	Average fruit weight (kg)	No. of fruits per plant	Fruit yield per plant (kg)	Ascorbic acid (mg/100)	Total soluble solids (%)	β- Carotene	Dry matter Content (%)	Reducing sugars (%)	Non-reducing sugars (%)	Total Sugars (%)
Environments	1	0.81**	1.29**	2.37**	9.29**	0.85**	1.89**	0.64**	2.50**	0.20**	0.11**	0.60**
Blocks within Environments	4	0.08*	0.02	0.04	0.09	1.32**	1.42**	0.66**	0.05	0.10**	0.00	0.01
Genotypes	44	0.72**	0.30**	1.38**	6.06**	1.36**	1.74**	1.78**	2.53**	0.56**	0.54**	1.18**
Parents	8	1.37**	0.36**	0.98**	4.40**	2.12**	2.71**	2.59**	5.72**	0.31**	0.79**	0.65**
Hybrids	35	0.59**	0.30**	1.17**	3.90**	1.22**	1.57**	1.64**	1.87**	0.52**	0.49**	1.17**
Parents vs. Hybrids	1	0.00	0.13**	12.03**	94.98**	0.40*	0.00	0.29	0.02	4.07**	0.16**	5.68**
Treatment vs. Environments	44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Parent vs. Environments	8	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Hybrids vs. Environments	35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Parents vs. Hybrids X Environments	1	0.00	0.00	0.01	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Error	176	0.02	0.01	0.03	0.10	0.08	0.07	0.08	0.16	0.01	0.01	0.07

Table 3: Contd...

*, ** Significant at 5 per cent and 1 per cent probability levels, respectively.

Traits Comp of variation	onent on	Node number to first male flower appearance	Node number to first female flower appearance	Days to first male flower anthesis	Days to first female flower anthesis	Days to first fruit harvest	Vine length (m)	Internodal length (cm)	Number of primary branches per plant	Equatorial circumference of fruit (cm)	Polar circumference of fruit (cm)
	Y1	15.46	11.92	5.83	6.79	5.61	13.44	12.17	12.05	8.37	6.88
PCV (%)	Y ₂	15.86	12.22	5.93	7.03	5.74	13.80	12.83	12.38	8.78	6.67
Ē	Pooled	15.61	12.04	5.88	6.94	5.72	13.62	12.23	12.58	8.65	6.80
	Y1	14.25	10.22	2.51	3.26	2.48	11.62	10.67	10.96	5.08	3.13
GCV (%)	Y ₂	14.03	10.02	2.41	3.11	2.33	11.42	10.54	10.78	4.72	3.40
	Pooled	10.94	6.80	1.52	1.27	1.89	6.74	8.18	8.30	3.78	2.28
ECV (%)	Y1	6.01	6.12	5.26	5.96	5.03	6.76	5.86	5.01	6.65	6.13

http://www.thepharmajournal.com

	Y ₂	7.39	6.99	5.41	6.31	5.25	7.74	7.31	6.09	7.40	5.73
	Pooled	11.13	9.94	5.68	6.83	5.40	11.83	9.09	9.45	7.78	6.40
h ² (brood	Y1	84.90	73.60	18.60	23.10	19.60	74.70	76.80	82.70	36.90	20.70
II- (DIOad	Y ₂	78.30	67.30	16.60	19.60	16.40	68.50	67.50	75.80	29.00	26.00
selise) (%)	Pooled	49.10	31.90	6.70	3.40	10.90	24.50	44.70	43.60	19.10	11.30
Genetic	Y1	27.04	18.07	2.23	3.23	2.26	20.69	19.26	20.53	6.36	2.93
advance (% of	Y ₂	25.57	16.93	2.02	2.83	1.94	19.49	17.85	19.33	5.24	3.57
mean)	Pooled	15.79	7.92	0.81	0.48	1.28	6.87	11.27	11.29	3.40	1.58
	Y1	7.35	16.47	42.26	42.53	60.58	3.83	7.76	6.87	55.66	49.27
General Mean	Y ₂	7.76	16.95	43.95	44.18	63.00	3.95	7.99	7.08	57.33	50.72
	Pooled	7.64	16.69	43.07	43.37	61.81	3.89	7.90	6.95	56.44	50.00

Table 4: Contd...

Traits compor	ient of	Flesh thickness	Average fruit	No. of fruits	Fruit yield per	Ascorbic acid	Total soluble	β- Carotene	Dry matter	Reducing	Non-reducing	Total
variation	1	(cm)	weight (kg)	per plant	plant (kg)	(mg/100 gm)	solids (%)	(mg/100 gm)	Content (%)	sugars (%)	sugars (%)	Sugars (%)
	Y1	12.90	11.72	18.06	19.22	9.20	10.47	11.88	10.89	11.75	15.50	10.20
PCV (%)	Y ₂	13.23	12.24	18.26	19.30	9.59	10.62	12.43	11.52	12.03	15.48	10.69
	Pooled	13.08	11.96	18.23	19.15	9.42	10.48	12.41	11.24	11.91	15.47	10.45
	Y1	11.78	10.57	16.92	18.36	8.07	9.41	10.76	9.50	10.89	14.64	8.85
GCV (%)	Y ₂	11.63	10.24	16.81	18.24	7.83	9.36	10.45	9.12	10.74	14.62	8.56
	Pooled	7.08	7.70	12.96	11.57	5.75	7.16	9.58	6.96	6.65	12.97	7.09
	Y1	5.24	5.06	6.31	5.69	4.40	4.60	5.03	5.33	4.42	5.08	5.08
ECV (%)	Y2	6.31	6.70	7.13	6.31	5.53	5.01	6.72	7.03	5.40	5.08	6.40
	Pooled	11.00	9.15	12.81	15.26	7.45	7.65	7.88	8.83	9.88	8.43	7.68
1-2 (h	Y1	83.50	81.30	87.80	91.20	77.10	80.70	82.00	76.00	85.90	89.20	75.20
(04)	Y ₂	77.20	70.00	84.70	89.30	66.70	77.70	70.70	62.70	79.80	89.20	64.10
(%)	Pooled	29.30	41.40	50.60	36.50	37.30	46.70	59.60	38.30	31.20	70.30	46.00
Courselies a deserve	Y1	22.18	19.65	32.65	36.12	14.61	17.41	20.07	17.06	20.79	28.49	15.81
Genetic advance $\binom{0}{2}$ of mean)	Y2	21.06	17.65	31.88	35.50	13.19	17.00	18.10	14.87	19.78	28.45	14.13
(% of mean)	Pooled	7.89	10.21	18.99	14.40	7.24	10.09	15.25	8.87	7.66	22.42	9.91
General Mean	Y1	2.80	1.99	2.68	5.21	5.57	5.42	4.84	6.41	2.71	1.99	4.71
	Y2	2.91	2.13	2.86	5.58	5.69	5.59	4.94	6.60	2.77	2.03	4.80
	Pooled	2.85	2.07	2.77	5.40	5.63	5.50	4.91	6.49	2.74	2.01	4.75

References

- Babu VS, Gopalkrishnan TR, Peter KV. Variability and divergence in pumpkin (*Cucurbita moschata* Poir.) J Trop. Agric 1996;34:10-13.
- 2. Bindu S, Mahakal KG, Kale PB, Sakahre SB, Chitra KR. Genetic variability in pumpkin (*Cucurbita moschata* Duch. ex Poir.). Ann. Pl. phys 2000;14:66-68.
- 3. Burton GW. Quantitative inheritance in grasses. Proc. 6th Internat. Grassld. Cong. J 1952;1:277-283.
- Chaudhari DJ, Acharya RR, Patel JN, Gohil SB, Bhalala KC. Variability, correlation and path analysis in Pumpkin (*Cucurbita moschata* Duch. ex. Poir.). Journal of Pharmacognosy and Phytochemistry 2017;6(6):142-145.
- Chigwe CFB, Saka VW. Collection and characterization of Malawi pumpkin germplasm. Zimbabwe J Agril. Res 1994;32:139-147.
- 6. Dhatt AS, Hardevinder Singh. Genetic variability, correlation and path coefficient analysis in pumpkin. Crop Improvement 2008;35:91-94.
- 7. Doijode SD, Sulladmath UV. Genetics of certain vegetative and flowering characters in pumpkin (*C. moschata*). Agricultural Science Digest 1988;8:203-206.
- Gwanama C, Nichterlein K, Lungu D, Simabwachi W. Variation of fruit beta-carotene content of tropical pumpkin [*Cucurbita moschata* (Duchsne) Piorot] land races in Zambia. Pl. Genet. Resources Newsletter 2002;129:44-46.
- Kumar V, Mishra DP, Yadav GC, Dwivedi DK. Genetic diversity assessment for morphological, yield and biochemical traits in genotypes of pumpkin. Journal of Pharmacognosy and Phytochemistry 2017a;6(3):14-18.
- Kumar V, Mishra DP, Yadav GC, Yadav S, Kumar S. Determining relationships between yield and biochemical traits in pumpkin. The Pharma Innovation Journal 2017b;7(1):14-18.
- 11. Kumaran SS, Natarajan S, Thamburaj S. Genetic variability in pumpkin (*Cucurbita moschata* Duch. ex Poir.). South Indian Hort 1997;45:10-12.
- 12. Lakshmi LM, Haribabu K, Reddy GLK. Genetic variability studies in pumpkin (*Cucurbita moschata* Duch. ex Poir.). J Res. ANGRAU 2002;30:82-86.
- 13. Mangal JL, Pandita ML, Sidhu AS. Variability and correlation studies in pumpkin (*Cucurbita moschata* Duch. Poir.). Haryana J Sci 1979;8:82-86.
- Mohanty BK, Mohanty SK, Mishra RS. Genetics of yield and yield components in pumpkin (*Cucurbita moschata*). The Indian Journal of Agricultural Sciences 1999;69(11):325-328.
- 15. Mohanty BK. Studies on variability and selection parameters in pumpkin (*Cucurbita moschata* Duch. ex Poir.). South Indian Hort 2000;48:111-113.
- 16. Pandey S, Singh J, Upadhyay AK, Ram D. Genetic variability for antioxidants and yield components in pumpkin (*Cucurbita moschata* Duch. ex poir.). Veg. Sci 2002;29:123-126.
- 17. Rana TK, Vashishtha RN, Pandita ML. Genetic variability and heritability studies in pumpkin (*Cucurbita moschata* Poir.). Haryana J Hort. Sci 1986;15(1-2):71-75.
- Rios H, Batista O, Fernandez A. Characteristics and potential of Cuban germplasm of pumpkin (*Cucurbita moschata* Poir Duch). Cultivos Tropicales 1996;17:88-91.
- 19. Singh A, Singh SP, Singh V, Singh NK. Genetic Expression of Inbreds and F₁ Hybrid of Pumpkin

(*Cucurbita moschata* Duch. ex Poir.) in Off and Main Season Crops in the Abstracts of National Seminar on Cucurbits held in between 22-23 September at Govind Ballabh Pant University of Agriculture & Technology. Pantnagar 2005, 125.

- Singh MK, Singh VB, Yadav GC, Kumar P. Studies on variability, heritability (narrow sense) and genetic advance analysis for growth, yield and quality traits in pumpkin (*Cucurbita moschata* Duch. ex. Poir). Journal of Pharmacognosy and Phytochemistry 2019;8(3):3621-3624.
- Singh V. Studies on Floral Biology and Genetic Markers and their Implication in Crop Improvement of Pumpkin (*Cucurbita moschata* Duch. ex Poir.). Ph.D. Thesis, Sumbmitted to Narendra Deva Univ. of Agri. & Tech. Kumarganj, Faizabad (U.P.) 2005.
- 22. Srikanth M, Bharad SG, Thulasiram LB, Potdukhe NR. Studies on genetic variability, heritability and genetic advance in pumpkin (*Cucurbita moschata* Duch ex Poir.). Int. J Curr. Microbiol. App. Sci 2017;6(6):1416-1422.
- 23. Suresh D, Kumar R, Kumar A. Evaluation of parents and hybrids for yield and marketable quality characters in pumpkin (*Cucurbita moschata* poir.) Int. J Curr. Microbiol. App. Sci 2020;9(7):753-762.