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Genetic variability, heritability and genetic advance in pumpkin (*Cucurbita moschata* Duch Ex Poir)

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ABSTRACT

The investigations were carried out to evaluate the 64 genotypes (28 F_1, 28 F_2 and 8 parental lines) of pumpkin ((Cucurbita moschata Duch. Ex Poir.)'at Department of Vegetable Science, Kalyanpur, CSA. University of Agriculture and Technology, Kanpur (U.P.) during Zaid 2021. The experiments were laid out in randomized complete block design with three replications. The data were recorded for 19 characters including total fruit yield per plant and its component traits. Analysis of variance showed that there was highly significant variation for all the characters studied. In F_1 generation, the highest genotypic as well as phenotypic coefficients of variations were observed for fruit yield/plant. In F_2 generation, the highest genotypic as well as phenotypic coefficients of variation were observed for fruit yield/plant and average fruit weight. In F_1, high heritability in narrow sense coupled with high genetic advance as per cent of mean were observed for equatorial circumference of fruit, polar circumference of fruit and seeds/fruit while in F_2, high heritability coupled with high genetic advance as per cent of mean were observed for seeds/fruit. High estimate of heritability along with high genetic advance in per cent of mean provides good scope for further improvement in advance generations.

Keywords: Pumpkin, genetic variability, heritability and genetic advance.

INTRODUCTION

Pumpkin (*Cucurbita moschata* Duch ex Poir) is an economically important vegetable crop. It is hardy in nature and rich in carotene content and also has very good keeping quality. It is a herbaceous annual sexually propagated vegetable having an identical genomic structure *i.e.* AABB which indicates that it is an amphidiploid. It comprises about 27 species of both wild and cultivated having same chromosome number of 2n = 40.Among these species only five species *Cucurbita moschata, Cucurbita maxima, Cucurbita ficifolia, Cucurbita pepo* and *Cucurbita mixta* are commonly cultivated. These species are considered to be originated in Central America. Because of its wider adaptability and versatility, pumpkin is grown throughout the world either in outdoors or indoors. In India, the total area covered by pumpkin is 0.104 million hectares whereas, the total production is 2.183 million tonnes with productivity 20.99 tonnes/ha (Anonymous 2020). Pumpkin is relatively high in energy and carbohydrates and a good source of vitamins, especially high carotenoid pigments and minerals. The colour of pumpkin is derived from the orange pigments *i.e.* carotene content abundant in fruits. It may certainly contribute to improve nutritional status of the people, particularly the vulnerable groups in respect of vitamin A requirement. Pumpkins are very versatile in their uses for cooking. Most of the parts of pumpkin are edible, including the fleshy shell, seeds, leaves, and even the flowers. Parameters of genotypic and phenotypic coefficient of variation (GCV & PCV) are useful in detecting the amount of variability present in the available genotypes. Heritability and genetic advance help in determining the influence of environment in expression of the characters and the extent to which improvement is possible after selection (Srikanth *et al.* 2017). High heritability (narrow sense) coupled with high genetic advance as per cent of mean suggested that selection would be highly effective and efficient for characters. The present investigation was, therefore, under taken to ascertain magnitude and extent of heritability and genetic advance in pumpkin.

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MATERIALS AND METHODS

The investigations were carried out to evaluate the 64 genotypes (28 F_1, 28 F_2 and 8 parental lines) of pumkin *viz*: Azad Pumpkin - 1 (P_1), P-35-16 (P_2), P-40-16 (P_3), Narendra Agrim (P_4), NDPK-7-24 (P_5), Kashi Harit (P_6), DVRP-2-5 (P_7), and Punjab Samrat (P_8). The 8 parental lines and their 28 $F_1$and F_2 were grown in a randomized complete block design with three replications during *Zaid* 2021 at the Main Experiment Station, Department of Vegetable Science, Kalyanpur, CSA University of Agriculture and Technology, Kanpur (U.P.). Each 28 F_1, F_2 and parents were grown in rows spaced 3 meters apart with a plant to plant spacing of 0.50 meter. All the recommended agronomic package of practices and plant protection measures were followed to raise good crop. Observations were recorded on nineteen quantitative traits *viz.*, days to first male flower appearance, days to first female flower appearance, node numbers to first male flower appearance, node numbers to first female flower appearance, vine length, internodal length, branches plant^{-1}, days to first harvest, average fruit weight, fruits/plant, equatorial circumference of fruit, polar circumference of fruit, flesh thickness, total soluble solids, dry matter content, moisture content, seed/fruit, Specific gravity and fruit yield/plant. The data recorded from 28 F_1, 28 $F_2$and 8 parental lines on nineteen characters were subjected to estimate nature and magnitude of the recorded data which were analysed by (Panse and Sukhatme 1954) for analysis of variance. The genotypic and phenotypic coefficient of variance was calculated as per the formula suggested by Burton (1952) and heritability in narrow sense (Kempthorne, 1957) and genetic advance in per cent of mean (Johnson *et al.,* 1955).

RESULT AND DISCUSSION

Analysis of variance

The Mean sum of squares due to genotypes were further divided into parents, parents *vs* F_1, F_2 and parents *vs* F_2 population. In F_1, highly significant variances were recorded among the treatments for days to first male flower appears, days to first female flower appears, node number to first male flower appears, node number to first female flower appears, vine length, intermodal length, primary branches/plant, days to first harvest, average fruit weight and fruits/plant (Table- 1). Variances due to parents were found highly significant for all the characters except node number to first male flower appearance. The variances due to F_1's were highly significant for all the traits studied and variances due to parent *vs* F_1, were highly significant for all the characters except specific gravity. In F_2, highly significant variances were observed among the treatments, parents, F_2 and parent *vs* F_2 for all the characters except node number of male flower appearance and flesh thickness due to parents, total soluble solids due to F_2 and node numbers to first male flower appearance, polar circumference of fruit and specific gravity due to parent *vs* F_2.

Coefficient of variation

The estimates of phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) for all the characters presented (Table 2). In F_1 generation, the highest genotypic as well as phenotypic coefficients of variation were observed for fruit yield/plant. The moderate GCV as well as PCV were observed for number of seeds per fruit followed by average fruit weight, fruits/plant, dry matter content, vine length and polar circumference of fruit. The low GCV as well as PCV were observed for remaining characters. In F_2 generation, the highest genotypic as well as phenotypic coefficients of variation were observed for fruit yield/plant and average fruit weight. The moderate GCV as well as PCV were observed for fruits/plant followed by vine length and seeds/fruit. The low GCV as well as PCV were observed for remaining characters. Similar findings were reported by Ramjan (2021): Singh *et al* (2019): Mohsin *et al.* (2017): Sampat and Krishnamoorthy (2018).

Heritability and genetic advance

Estimates of heritability in narrow-sense (h^2_{ns}) have been classified by Kempthorne and Curnow (1961) into three categories *viz*., high (> 30%), medium (10-30%) and low (<10%).In F_1, the high heritability in narrow-sense (>30%) were observed for days to first male flower appearance (63.86), followed by days to first female flower appearance (56.48), polar circumference of fruit

Table 1: Analysis of variance (Mean sum of squares) for parents, F_1 s and F_2in 8 x 8 diallel cross of pumpkin for 19 characters

Source of variation	Replicates	Treatments	Parents	F_1's	Ps. Vs. F_1's	Error	Replicates	Treatments	Parents	F_2	Ps. Vs. F_2	Error
	Parents and F_1s						Parents and F_2s					
df	2	35	7	27	1	70	2	35	7	27	1	70
1	1.69	46.00**	56.61**	43.67**	34.77**	1.11	0.86	55.27**	56.61**	52.14**	130.54**	1.89
2	4.54	66.66**	37.09**	74.83**	53.16**	2.18	1.22	42.01**	37.09**	40.65**	113.31**	3.24
3	0.66**	0.54**	0.13	0.38**	7.69**	0.13	0.14	0.49**	0.13	0.59**	0.19	0.06
4	0.73	4.91**	7.04**	3.60**	25.24**	0.57	0.56	3.82**	7.04**	2.27**	23.13**	0.84
5	0.25	1.08**	0.76**	1.07**	3.59**	0.11	0.1	1.57**	0.76**	0.51**	35.91**	0.13
6	0.18	1.24**	2.11**	0.92**	3.77**	0.12	2.81**	1.82**	2.11**	1.43**	10.17**	0.5
7	0.55	1.96**	0.54*	1.47**	25.09**	0.21	0.12	1.56**	0.54	1.58**	8.29**	0.31
8	2.13	72.68**	33.60**	78.09**	199.86**	1.84	0.04	23.80**	33.60**	21.16**	26.32**	1.8
9	0.03	0.37**	0.18**	0.26**	4.57**	0.02	0.01	0.31**	0.18**	0.09**	7.11**	0.02
10	0.01	0.76**	0.63**	0.57**	6.61**	0.04	0.001	0.85**	0.63**	0.58**	9.60**	0.04
11	1.2	105.26	118.68**	89.49**	437.25**	1.33	0.19	51.76**	118.68**	26.46**	266.57**	1.03
12	6.69	83.49	62.78**	72.09**	536.11**	2.32	4.6	33.52**	62.78**	27.17**	0.03	2.75
13	0.05*	0.07*	0.01	0.05**	1.11**	0.01	0.01	0.04**	0.01	0.01**	0.96**	0.01
14	0.01	0.66	0.32**	0.24**	14.52**	0.03	0.02	0.26**	0.32**	0.02	6.03**	0.02
15	0.2	1.9	0.37	2.16**	5.55**	0.29	0.12	0.65**	0.37**	0.41**	9.01**	0.08
16	0.2	1.9	0.37	2.16**	5.55**	0.29	0.12	0.65**	0.37**	0.41**	9.01**	0.08
17	101.68	2453.51	1440.45**	2426.77**	10266.93**	133.87	24.15	1156.77**	1342.90**	1138.41**	349.56*	80.98
18	0.01	0.12	0.02**	0.01**	0.001	0.01	0.01	0.01**	0.01*	0.01**	0.001	0.004
19	0.21	11.48	3.61**	7.39**	177.06**	0.43	0.09	6.51**	3.60**	1.54**	161.00**	0.23

**, ** Significant at 5% and 1%*

(47.78), equatorial circumference of fruit (45.62), seeds/fruit (44.16), node numbers of first female flower appearance (38.70), days to first harvest (33.26), dry matter content and moisture content (30.16)(Table 3). The moderate estimate of heritability in narrow-sense were observed in specific gravity (27.72) followed by intermodal length (20.66), vine length (19.94), node numbers of first male flower appearance (18.75), fruits/plant (17.62), average fruit weight (15.19) and fruit yield/plant (12.47). The remaining characters showed low estimate of heritability in narrow-sense (h^2_{ns}). In F_2, the high heritability in narrow-sense (>30%) were observed for polar circumference of fruit (62.49) followed by number of seeds per fruit (59.03), days to first female flower appearance (53.38), equatorial circumference of fruit (52.46), days to first male flower appearance (51.82), days to first harvest (37.43), node numbers of first female flower appearance (36.70). The moderate estimate of heritability in narrow- sense were observed in specific gravity (28.53) followed by node numbers of first male flower appearance (19.35), moisture content (18.44), dry matter content (18.43) and intermodal length (16.55), branches/plant (14.02) and fruits/plant (10.70). All remaining characters showed low estimate of heritability in narrow-sense (h^2_{ns}). Similar findings had been also reported by Wani *et al.* (2008), Sampat and Krishnamoorthy (2018) and Ramjan (2021).

Table 2: Estimates of genetic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for nineteen characters in pumpkin

Characters	F_1		F_2	
	GCV	PCV	GCV	PCV
Days to first male flower appear	8.74	9.06	8.90	9.36
Days to first female flower appear	9.19	9.64	6.70	7.49
Node numbers to first male flower appearance	7.69	10.70	7.23	8.65
Node numbers to first female flower appearance	5.91	6.98	4.51	6.12
Vine length (cm)	10.45	12.05	17.19	19.34
Internodal length (cm)	6.71	7.75	7.47	10.94
Branches/plant	9.18	10.70	8.16	10.73
Days to first harvest	7.38	7.66	3.91	4.36
Average fruit weight (kg)	14.46	15.39	20.65	23.02
Fruits/plant	13.36	14.34	19.63	20.91
Equatorial circumference of fruit (cm)	9.99	10.18	7.88	8.11
Polar circumference of fruit (cm)	10.23	10.66	6.87	7.73
Flesh thickness (cm)	5.55	7.07	4.85	5.94
Total soluble solids (^{0}Brix)	7.31	7.76	4.64	5.15
Dry matter content (%)	10.87	13.54	6.37	7.53
Moisture content (%)	0.78	0.98	0.47	0.55
Seeds/fruit	17.44	18.88	13.76	15.23
Specific gravity (g/cm^3)	5.15	8.24	4.20	8.01
Fruit yield/plant (kg)	22.03	23.28	35.85	37.80

In F_1, high estimate of genetic advance in per cent of mean (>20%) was observed for fruit yield/ plant (42.93%), followed by seeds/ fruit (33.16%), average fruit weight (28.00%), fruits/plant (25.62%), polar circumference of fruit (20.23%) and equatorial circumference of fruit (20.20%), Moderate estimate of genetic advance in percent of mean (10-20%) was observed for vine length (18.65%) followed by days to first female flower appearance (18.03%), dry matter content (17.99%)days to first male flower appearance (17.36%), number of primary branches per plant (16.22%), days to first harvest (14.65%), total soluble solids (14.18%), intermodal length (11.98%), node number to first female flower appearance (10.32%). All remaining characters showed low estimate of genetic advance in per cent of mean. In F_2, high estimate of genetic advance in per cent of mean (>20%) was observed for fruit yield per plant (70.05%), followed by average fruit weight (38.18), fruits/plant (37.95%), vine length (31.46%) and seeds/fruit (25.59%). Moderate estimate of genetic advance in percent of mean (10-20%) was observed for days to first male flower appearance (17.43%), equatorial circumference of fruit (15.75), number of primary branches per plant (12.79%), polar circumference of fruit (12.56%), node number to first male flower appearance (12.44%), days to first female flower appearance (12.33%),dry matter content (11.10%)and intermodal length (10.50%). The remaining characters showed low estimate of genetic advance in per cent of mean.Wani *et al.* (2008), Sampat and Krishnamoorthy (2018) and Ramjan (2021).

Table 3: Estimation of heritability (ns) and expected genetic advance as per cent of mean for 19 characters in 8 x 8 diallel cross in pumpkin

Characters	Mean performance			Heritability (ns)		Genetic advance		Genetic advance in % of mean	
	Parent	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
1	45.34	43.97	47.98	63.86	51.82	7.69	8.26	17.36	17.43
2	51.78	50.10	54.25	56.48	53.38	9.10	6.62	18.03	12.33
3	5.31	4.67	5.21	18.75	19.35	0.55	0.65	11.39	12.44
4	21.25	20.08	22.36	38.70	36.70	2.10	1.51	10.32	6.83
5	5.11	5.55	3.72	19.94	7.29	1.02	1.27	18.65	31.46
6	9.44	8.99	8.70	20.66	16.55	1.09	0.93	11.98	10.50
7	7.41	8.57	8.08	4.87	14.02	1.35	1.02	16.22	12.79
8	68.37	65.10	69.56	33.26	37.43	9.64	5.00	14.65	7.21
9	1.98	2.47	1.36	15.19	5.00	0.66	0.57	28.00	38.15
10	3.21	3.80	2.49	17.62	10.70	0.94	1.01	25.62	37.95
11	55.15	59.99	51.37	45.62	52.46	11.90	8.22	20.20	15.75
12	46.67	52.03	46.63	47.78	62.49	10.28	5.86	20.23	12.56
13	2.37	2.61	2.14	3.13	-0.20	0.23	0.18	8.98	8.15
14	5.61	6.50	6.18	9.45	9.85	0.89	0.52	14.18	8.61
15	6.30	6.85	7.00	30.16	18.43	1.21	0.76	17.99	11.10
16	93.70	93.15	93.00	30.16	18.44	1.21	0.76	1.30	0.82
17	141.25	164.70	136.71	44.16	59.03	52.89	35.23	33.16	25.59
18	0.99	0.99	0.95	27.72	28.53	0.07	0.04	6.62	4.54
19	6.32	9.40	3.38	12.47	9.52	3.74	2.83	42.93	70.05

On the other hand, in F_1 high heritability coupled with high genetic advance were observed for equatorial circumference of fruit (45.62, 20.20%), polar circumference of fruit (47.78, 20.23%) and seeds/fruit (44.16, 33.16%). The high heritability coupled with moderate genetic advance were observed for days to first male flower appearance (63.86, 17.86%), followed by days to first female flower appearance (56.48, 18.03%), node number to first female flower appearance (38.70, 10.32%), days to first harvest (33.26, 14.65%), dry matter content (30.16, 17.99%). The moderate heritability coupled with moderate genetic advance were observed for node number to first male flower appearance (18.75, 11.39%), vine length (19.94, 18.65%). The moderate heritability along with high genetic advance were observed for fruits/plant (17.62, 25.62%), average fruit weight (15.19, 28.00%) and fruit yield per plant (12.47, 42.93%).The high heritability along with low genetic advance were observed for moisture content (30.16, 1.30%). On the other hand in $F_{2,}$ high heritability coupled with high genetic advance were observed for seeds/fruit (59.03, 25.59%).The high heritability coupled with moderate genetic advance were observed for days to first male flower appearance (51.82, 17.43%), followed by days to first female flower appearance (53.38, 12.33%), equatorial circumference of fruit (52.46, 15.75%), polar circumference of fruit (62.49, 12.56%). The moderate heritability coupled with moderate genetic advance were observed for node number to first male flower appearance (19.35, 12.44%) followed by intermodal length (16.55, 10.50%), primary branches/plant (14.02, 12.79%), dry matter content (18.43, 11.10%). The moderate heritability along with high genetic advance were observed for fruits/plant (10.70, 37.95%). The low heritability along with high genetic advance were observed for fruit yield/plant (9.52, 70.05%) followed by average fruit weight (5.00, 38.15%) and vine length (7.29, 31.46).Similar findings were also reported by Wani *et al.* (2008), Akter *et al.* (2013) and Ramjan (2021).

Based on the above findings in F_1 generation, the high genotypic as well as phenotypic coefficients of variation were observed for fruit yield/plant. The fruit yield/plant and average fruit weight in F_2 revealed higher variability in terms of the above mentioned characters. High heritability (narrow sense) coupled with high genetic advance as per cent of mean were observed for equatorial circumference of fruit, polar circumference of fruit and number of seeds per fruit in F_1 whereas, seeds/fruit in F_2which were governed by additive gene action and therefore, selection may be highly effective for these characters.

REFERENCES

Akter, S., Rasul, M. G. A., Islam, Aminul and. Hossain, M. M., (2013) Genetic variability, correlation and path coefficient analysis of yield and quality traits in pumpkin(*Cucurbita moschata* Duch ex Poir.) *Bangladesh Journal of Plant Breeding and Genetics* **26**(1): 25-33

Anonymous. (2020) Indian Horticulture Database. National Horticulture Board, Ministry of Agriculture, Government of India, Gurugram.

Burton, G.W. (1952) Quantitative inheritance in grasses. Proc. 6th *International Grassland Congress***1**: 277-283

Johnson, H.W.; Robinson, H.F. and Comstock, R.E. (1955) Estimates of genetic and environmental variability in soybean. *Agronomy Journal* **74**: 314-318.

Kempthorne, O. (1957)An Introduction to genetical statistics. *John Wiley and Sons, Inc.,* New York., U.S.A.

Kempthorne, O. and Curnow, R.N. (1961) The partial diallel cross. *Biometrics***17**: 229-250.

Mohsin, G.M. Islam, M.S,. Rahman, M.S. L. Ali and Hasanuzzaman, M. (2017) Genetic variability, correlation and path coefficients of yield andits components analysis in pumpkin (*Cucurbita moschata* Duch Ex Poir)*International Journal of Agricultural Research, Innovation and Technology* **7** (1): 8-13.

Panse, V.G. and Sukhatme, P.V. (1954) Statistical Methods for Agriculture Workers. Indian Council of Agricultural Research, New Delhi

Ramjan, M.D. (2021) Characterization of pumpkin (*Cucurbita moschata* Duch. Ex. Poir.) germplasm through genetic variability, heritability and genetic advance. *Electronic Journal of Plant Breeding***12**(1): 91 - 96.

Sampath, S. and Krishnamoorthy, V. (2018)Genetic variability, correlation and path analysis in pumpkin (*Cucurbita moschata* Duch. ex. Poir)*International Journal of Current Microbiology and Applied Sciences* **6**(6): 3027-3035.

Singh, M.K.; Singh, V.B. Yadav, G.C. and Kumar, P.(2019) Studies on variability, heritability (Narrow sense) and genetic advance analysis for growth, yield and quality traits in pumpkin (*Cucurbitamoschata* Duch. ex. Poir), *Journal of Pharmacognosy and Phytochemistry* **8**(3): 3621-3624

Srikanth, M., Bharad, L.B. Thulasiram and Potdukhe, N.R. (2017) Studies on genetic variability, heritability and genetic advance in pumpkin (*Cucurbita moschata* Duch ex Poir.)*International Journal of Current Microbiology and Applied Sciences* ***6***(6): 1416-1422

Wani, K.P.; Ahmed, N. and Hussain, K. (2008) Gene action studies in bottle gourd. *The Indian Journal of Agricultural Sciences***78** (3): 258-260