Original Research Article

Genetic estimations of available quality traits for improved growth yield of pumpkin (*Cucurbita moschata* Duch) in Kumarganj, India

Abstract

Pumpkin is one of the most economically important and nutritious member of the familyCucurbitaceae. The present investigation was conducted to evaluate genetic variability, heritability and genetic advance in per cent of mean among the 30 genotypes including one check variety(NarendraAgrim) for 21 qualitative and quantitative traits. The experiment was conducted in randomized block design with three replication ,the observations were recorded on the traits like days to 50% staminate flower anthesis , days to 50% pistillate flower anthesis, node no. to first staminate flower anthesis, node no. to first pistillate flower anthesis, vinelength, no. of nodes, no. of primary branches, inter-nodal length, days to first fruit harvest, polar circumference, equatorial circumference, flesh thickness, cavity, average fruit weight, no. of fruits per plant, total soluble solids, reducing sugars, non reducing sugars, total sugars, fruit yield per plant. The analysis of variance for the design of experiments indicated highly significant difference among the genotypes for all 21 characters. The four genotypes*viz.*NDPK-17-12-1,NDPK-23,NDPK-P-6 and NDPK-32-1-2 were found significantly superior for fruit yield per plant over the check variety (NarendraAgrim).The PCV was higher than the GCV and was found highest for the trait fruit yield per plant, the presence of high heritability in broad sense along with high genetic advance in per cent of mean were observed for fruit yield per plant.Therefore,from the above obtained results it can be concluded that the characters will result in effective crop improvement for higher yield and yield contributing traits.

Keywords: Pumpkin (*Cucurbitamoschata*),Variability,GCV,PCV,heritabilityand genetic advance

Introduction

"Pumpkin (*Cucurbitamoschata*Duch. ex Poir) is a member of family cucurbitaceae, order cucurbitales and genus *Cucurbita*. It is diploid species with a chromosome no. 2n=2x=40".(Armestoet. al.,2020) [3] "Pumpkin is one of the most popular summer vegetables grown all over India on a commercial scale because of high carotene, lutein content and good keeping quality, it is considered as a vegetable of immense value.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"* (Ahmed *et al.*,2019) [1]. "In India, it is grown in states like Odisha, West Bengal, Tamil Nadu, Karnataka, Madhya Pradesh, Uttar Pradesh, Kerala, and Bihar. Pumpkin is grown in an area of 106.29 thousand hectares with annual production 2,218.40 thousand tonnes" (Anony 2021) [2]. "Heritability in a general sense, is the ratio of variation due to differences between genotypes to the total phenotypic variation for a character or trait in a population more is the variation that is heritable among the species it is better suited for different environment or has higher adaptability,heritability and genetic advance will help in determining the influence of environment for different expression of characters and this will extent the potential for selection of parents for hybridization,the adaptability could also be judged well through, genotypic and phenotypic coefficients of variation, and degree of association"(Ramjan*et al*.,2021) [10].

Materials and Methods

The experimental material comprised of 30 genotypes of pumpkin including standard check *viz.*,NarendraAgrim. The experiment was laid out in a Randomized Block Design with three replications at Main Experiment Station of Department of Vegetable Science at AcharyaNarendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P) during *Zaid* (2022),having plot size of 3×3 m accommodating 6 plants per plot with row to-row spacing of 3 m and plant-to-plant spacing of 0.50 m. Observations were recorded for 21 qualitative traits including and quantity traits like days to 50% staminate flower anthesis , days to 50% pistillate flower anthesis, node no. to first staminate flower anthesis, node no. to first pistillate flower anthesis,vinelength,no. of nodes, no. of primary branches, internodal length, days to first fruit harvest, polar circumference,equatorial circumference, flesh thickness,cavity, average fruit weight, no. of fruits per plant, total soluble solids, reducing sugars, non reducing sugars, total sugars, fruit yield per plant.The data on twenty one quantitative characters are recorded on five competitive and randomly selected plants of each genotype and in each replication. "For studying different genetic parameters and inter-relationships of twenty one qualitative and quantitative characters.The genotypic coefficients of variability and phenotypic coefficients of variability(GCV% and PCV%) were designed as per proceduresuggested by"(Burton and De vane ,1953) [4].Heritability was considered using the guidance given by Singh and Choudhary,(1985) [12].Genetic advance as a percentage of mean was calculated by the procedure given by Johnson *et al*.,(1955) [6].

Results and Discussion

Coefficient of variation is the genetic variability serves as the foundation for vegetable breeding, acting as a breeding ground for superior genotypes.Therefore, there is more potential for a character's development through selection,ifthere is more variance for that character in the breeding materials.For the purpose of evaluating the level of variability in the germplasm, the genotypic and phenotypic coefficients of variation were computed.

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 5.18 per cent (non reducing sugars) to 33.71 per cent (fruit yield per plant) for the various characters studied” [15] (Table 1).

Highest phenotypic coefficient of variation was recorded for the character fruit yield per plant (33.71) per cent followed by number of fruit per plant (31.99) per cent while, moderate to low values of PCV were observed for characters,no. of fruits (27.68),no. of primary branches (22.12),average fruit weight (18.47),vine length (18.47),cavity (15.33),flesh thickness (14.78),node no.to first staminate flower anthesis (14.04),inter-nodal length (10.78), fruit polar circumference (10.75),node no.to first pistillate flower (10.59),days to first fruit harvest (7.08),no. of nodes per plant (13.34),total soluble solids (11.16),reducing sugars (9.45), days to 50% staminate flower anthesis (6.00),days to 50% pistillate flower anthesis (5.43),total sugars (5.29),non reducing sugars (5.18).The high estimates of PCV and GCV for these characters were also reported earlier (Kumar *et al.* ,2017) [7].However,the existence of low value of GCV and PCV for remaining traits showed less response under selection(Mohsin*et al.*,2017) [8]

Genotypic coefficient variation (GCV)

It is revealed in Table 1. That, the genotypic coefficient of variation (GCV) ranged from 2.48 per cent (days to 50% pistillate flower anthesis) to 32.40 per cent (fruit yield per plant), whereas, genotypic coefficient of variation was lower for the characters like no. of nodes (9.66),polar circumference (9.51),inter-nodal length (9.36),equatorial circumference (8.74),reducing sugars (8.01),node no. to first pistillate flower anthesis (7.03),total soluble solids (6.98),days to first fruit harvest (4.64),total sugars (3.36),days to 50% staminate flower anthesis (3.23),non reducing sugars (3.02), days to 50% pistillate flower anthesis (2.48) similar findings were found by (Singh *et al*.,2019) [11].

Heritability and genetic advance

“Estimates of heritability and expected genetic advance for different characters are presented in Table 1.The broad sense heritability ranged fromlowest heritability 21.0 per cent found in case of days to 50% pistillate flower anthesis to 92.4 per cent for fruit yield per plant. Result revealed that the high heritability (>50%) estimates in broad sense were of lower magnitude except the character fruit yield per plant (92.4%), number of fruits per plant (90.40%), total number of fruits (87.50%), no. of primary branches (86.70%), average fruit weight(79.5%), fruit polar circumference (78.20%),vine length (77.9%),internodal length (75.5%).fruit equatorial circumference (73.0%),reducing sugars (72.00%).The moderate heritability characters were cavity (67.8%),flesh thickness(65.5%), node number at first pistillate flower anthesis (57.90%) and no. of nodes (52.5%).Among the twenty one characters five characters recorded lower heritability (<50%) namely node no. to first pistillate flower anthesis (44.6%), total sugars (40.3%),non reducing sugars(34.0%),days to 50% staminate flower anthesis (29.1%) and days to 50% pistillate flower anthesis (21.0%).The highest value of genetic advance in per cent of mean was shown by fruit yield per plant (64.15), while days to 50% pistillate flower anthesis had lowest value (2.34) for this parameter. The characters showing very high estimate of Ga were fruit equatorial circumference (8.90%) followed by polar circumference (8.87%) and no.of fruits (7.79%) .The moderate estimate for genetic advance resulted in case of days to first fruit harvest (3.48),internodal length (3.35) and no. of nodes per plant (4.97) while the low estimate was observed for the fruit equatorial circumference (9.92), node number at first staminate flower anthesis (9.03), days to first staminate flower anthesis (7.68), days to first pistillate flower anthesis (3.78) and days to first fruit harvest (3.46)". [15] Similar findings were also marked by earlier scientist in pumpkin (Pandey*et al.* ,2002) [9].

Conclusion-

The characters which showed high estimates of heritability and genetic advance provide a broad way for the genetic improvement in genotypes for specific characters.Thus, there exists ample scope for improvement in available germplasm to develop new improved varieties of pumpkin in future.

Table 1: Estimates of range, variability, heritability and expected genetic advance in percent of mean for the twenty one characters in pumpkin germplasm

Sl. No.	Characters	Range		Variability			Heritability in broad sense (%)	Genetic advance	Expected Ga as % of mean
		Min.	Max.	PCV%	GCV%	ECV%			
1.	Days to 50% staminate flower anthesis	36.67	43.00	6.00	3.23	5.05	29.1	1.44	3.59
2.	Days to 50% pistillate flower anthesis	38.67	45.00	5.43	2.48	4.83	21.0	0.98	2.34
3.	Node no. to first staminate flower anthesis	4.13	6.87	14.04	10.89	8.95	59.7	0.87	17.34
4.	Node no. to first pistillate flower anthesis	16.60	22.88	10.59	7.03	7.91	44.1	1.85	9.63
5.	Vine length	3.65	9.51	18.47	16.30	8.68	77.9	2.05	29.65
6.	No. of nodes per plant	25.33	44.78	13.34	9.66	9.19	52.5	4.97	14.43
7.	No. of primary branches	4.32	9.28	22.12	20.59	8.07	86.7	2.59	39.50
8.	Internodal length	13.79	22.08	10.78	9.36	5.33	75.5	3.35	16.77
9.	Days to first fruit harvest	49.00	60.00	7.08	4.64	5.34	43.1	3.48	6.28
10.	Fruit Polar circumference	42.73	64.78	10.75	9.51	5.02	78.2	8.87	17.33
11.	Fruit equatorial circumference	48.95	71.94	10.24	8.74	5.32	73.0	8.90	15.38
12.	Flesh thickness	2.90	4.80	14.78	11.96	8.67	65.5	0.73	19.95
13.	Cavity	8.90	17.71	15.33	12.66	8.73	67.8	2.88	21.48
14.	Average fruit weight	0.89	1.77	18.97	16.91	8.59	79.5	0.43	31.05
15.	Total no. of fruits	2.00	22.00	27.68	25.88	9.80	87.5	7.79	49.87
16.	Number of fruit per plant	1.00	5.13	31.99	30.42	9.91	90.4	1.76	59.58
17.	Total soluble solids	3.97	5.73	11.16	6.98	8.70	39.1	0.44	8.99
18.	Reducing sugars	5.63	7.43	9.45	8.01	5.00	72.0	0.93	14.01
19.	Non reducing sugars	46.57	53.97	5.18	3.02	4.21	34.0	1.83	3.63
20.	Total sugars	52.23	60.84	5.29	3.36	4.09	40.3	2.50	4.39
21.	Fruit yield per plant	1.38	6.65	33.71	32.40	9.30	92.4	2.35	64.15

References

1. Ahmad, G., & Khan, A. A. (2019). Pumpkin: horticultural importance and its roles in various forms; a review. *Int. J. Hortic. Agric*, *4*, 1-6.

2. Annual report 2021-22,Department of Agriculture, Cooperation and farmers' Welfare Ministry of Agriculture and Farmers' Welfare Government of India KrishiBhawan, New Delhi-110 001.

3. Armesto, J.; Rocchetti, G.; Senizza, B.; Pateiro, M.; Barba, F.J.; Domíguez, R.; Lucini, L.; Lorenzo, J.M. (2020). Nutritional characterization of (*Cucurbitamoschata* D.) Effect of variety (Ariel vs. Pluto) and farming type (conventional vs. organic).*FoodRes. Int.*2020;132:109052.

4. Burton,G.W.(1952). Quantitativeinheritanceingrasses.*Proc.6th Intern.Grassld. Cong.J.*, 1:277-283.

5. Chaudhari, D. J.; Acharya R. R.; Patel J. N.; Gohil, S. B. and Bhalala, K. C. (2017). Variability, correlation and path analysis in pumpkin (*Cucurbitamoschata*Duch. ex. Poir). *J. of Pharma. andPhyto.,* 6(6): 142-145.

6. Johnson, W. L. 1955. Elements DerexatelonsExblichkeitelahre, JenalGustar, Fisher. Kumar, P. A., Suseela, T., Dorajeerao, A. V. D., &Sujatha, R. V. (2018). Study on correlation coefficient analysis of the yield contributing characters of different pumpkin cultivars under coastal AP conditions. *J. Pharmacog Phytochem.*, 7(2), 1981-1984

7. Kumar, V., Mishra, D.P. Yadav G.C. and Dwivedi, D.K. 2017. Genetic diversity assessment for morphological, yield and biochemical traits in genotypes of pumpkin. J. Pharmacogn and Phytochem. 6 (3): 14-18.

8. Mohsin, G.M., Islam, M.S., Rahman, M.S., Ali, L. and Hasanuzzaman, M. 2017. Genetic variability, correlation and path coefficients of yield and its components analysis in pumpkin (CucurbitamoschataDuch Ex Poir) Int. J. Agril. Res. Innov. Tech., 7 (1): 8-13.

9. Pandey, S.; Singh.; J.; Upadhyay, A. K. and Ram, D. (2002). Genetic variability forantioxidantsand yield components inpumpkin.*Veg.Sci.*,29:123-126.

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

11. Singh, M. K.; Singh V. B.; Yadav G. C.; and Kumar, P. (2019). Study on variability, heritibility (narrow sence) and genetic advance analysis for growth, yield and quality traits in pumpkin (*Cucurbitamoschata*Duch. ex. Poir). *J. Pharma, Phytoche*., 8(3): 3621-3624.

12. Singh, R.K. and Chaudhary, B.D. 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi, pp. 318.

13. ThamburajS.,Singh N.,(2019). Vegetables,Tuber crops and Spices.ICAR,New Delhi.

14. Verma, A. K., Neetu, B. K. M., & Singh, V. B. (2022). Studies of genetic variability and heritability for fruit yield and its component traits in pumpkin (CucurbitamoschataDuch. ex. Poir).*PharmaInnov. J*. 2022; 11(6): 519-521

15. Aniket Kumar Verma, Neetu, Brijesh Kumar Maurya and VB Singh. Studies of genetic variability and heritability for fruityield and its component traits in pumpkin (Cucurbitamoschata Duch. ex. Poir). The Pharma Innovation Journal 2022; 11(6): 519-521