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Assessment of genetic variability, heritability and genetic advance in forty-four genotypes of Pumpkin (*Cucurbita moschata* L.) for yield and yield contributing traits

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Abstract

Genetic variability is a prerequisite for effective selection and genetic improvement in crop breeding programmes. The present experiment was undertaken to estimate the magnitude of genetic variability, heritability and genetic advance for yield and yield-contributing traits in forty-four pumpkin genotypes (*Cucurbita moschata* L.). The experiment was conducted during the summer season of 2025 at the Main Experimental Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India, using a randomized block design with three replications. Eighteen quantitative traits encompassing flowering behaviour, vegetative growth, fruit yield and quality attributes were evaluated. Analysis of variance revealed highly significant differences among the genotypes for all traits, indicating the existence of substantial genetic variability within the experimental material. The phenotypic coefficient of variation exceeded the corresponding genotypic coefficient of variation for all characters, suggesting a relatively minor influence of environmental factors on trait expression. High estimates of GCV and PCV were recorded for total carotenoids, fruit yield per plot, fruit yield per plant and number of fruits per plant, reflecting the presence of considerable genetic variability for these traits. Broad-sense heritability estimates ranged from 83.70% to 99.61%, with the highest values observed for total carotenoids, dry matter content, fruit yield per plant, fruit yield per plot and number of fruits per plant. High heritability coupled with high genetic advance as percent of mean was observed for total carotenoids, fruit yield per plot, fruit yield per plant, number of fruits per plant, dry matter content, vine length, number of primary branches per plant, flesh thickness and total soluble solids, indicating the predominance of additive gene effects and the potential effectiveness of direct phenotypic selection. The combined assessment of variability parameters identified total carotenoids, fruit yield per plant, fruit yield per plot, number of fruits per plant and dry matter content as the most promising selection criteria for the development of high-yielding and nutritionally enriched pumpkin cultivars.

Keywords: *Cucurbita moschata*, genetic variability, genotypic coefficient of variation, heredity, genetic advance, fruit yield

Introduction

Pumpkin (*Cucurbita moschata* L.) is an important cucurbitaceous vegetable crop belonging to the family Cucurbitaceae with a chromosome number of $2n = 40$ (Martins *et al.*, 2015) [10]. Originating in Central and South America, it is widely cultivated in tropical and subtropical regions because of its adaptability, high productivity, and extended storage life (Jeffrey, 1990) [4]. Among cultivated *Cucurbita* species, *C. moschata* is the most extensively grown in tropical climates due to its superior heat tolerance and adaptability (Lee *et al.*, 2003; Kiramana *et al.*, 2017) [8, 6]. Pumpkin is valued for its nutritional and economic importance. The fruits are rich in carbohydrates, minerals, vitamins, dietary fibre, and carotenoids, particularly β -carotene, which serves as a precursor of vitamin A. In addition, pumpkin contains appreciable amounts of ascorbic acid and other antioxidant compounds that contribute to human health (Tamburaj and Singh, 2001) [16]. Owing to its nutritional richness and diverse uses, pumpkin has become an important vegetable crop for both consumers and farmers. The success of any crop improvement programme depends on the availability of genetic variability. Assessment of genetic variability provides information on the extent of diversity present in a population and facilitates the identification of superior genotypes such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation

(PCV), heritability, and genetic advance is essential for designing effective selection strategies. High heritability coupled with high genetic advance generally indicates the predominance of additive gene action and greater effectiveness of selection.

Therefore, the present experiment was undertaken to assess the genetic variability, heritability, and genetic advance among forty-four pumpkin genotypes for yield and yield contributing traits and to identify promising genotypes for future breeding programmes.

Materials and Methods

The present experiment was conducted during the summer season of 2025 at the Main Experimental Station, Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India. The experimental site is located at 25.6° N latitude and 82.12° E longitude with an altitude of 113 m above mean sea level. The soil was sandy loam in texture with a slightly alkaline reaction (pH 7.5–8.5).

The experimental material comprised forty-four pumpkin genotypes, including fortythree test genotypes and one check variety (Kashi Harit). The experiment was laid out in a randomized block design with three replications. Seeds were sown directly in the field at a spacing of 3.0 m × 0.6 m in plots measuring 3.0 m × 3.0 m. Five plants were maintained for each genotype in every replication. Observations were recorded on five randomly selected plants from each genotype for eighteen quantitative traits, namely days to 50% female flowering, days to first male flower anthesis, days to first female flower anthesis, node at first female flower appearance, number of primary branches per plant, internodal length, vine length, number of fruits per plant, average fruit weight, fruit length, fruit diameter, flesh thickness, ascorbic acid content, dry matter

content, total soluble solids, total carotenoids, fruit yield per plant and fruit yield per plot. Biochemical traits were estimated following standard procedures described by Ranganna (1997)^[14]. The data were subjected to analysis of variance following Panse and Sukhatme (2000). Genotypic and phenotypic coefficients of variation were estimated according to Burton and DeVane (1953)^[2], while broad-sense heritability and genetic advance were computed following Allard (1960)^[1] and Hanson *et al.* (1956)^[3], respectively. Correlation and path coefficient analysis were performed using the methods proposed by Pearson (1909)^[13] and Dewey and Lu (1959), respectively. Genetic divergence was estimated using Mahalanobis D² statistics (Mahalanobis, 1936)^[9], and principal component analysis was carried out according to Pearson (1901)^[12].

Results and Discussion

Analysis of Variance

The analysis of variance revealed highly significant differences among the forty-four pumpkin genotypes for all eighteen quantitative traits studied (Table 1), indicating the presence of substantial genetic variability within the experimental material. The existence of significant variation for flowering, vegetative, yield and quality traits suggests a broad genetic base that can be effectively exploited for crop improvement. Genetic variability is a prerequisite for successful selection, as it provides opportunities for identifying superior genotypes and developing improved cultivars. Similar findings were reported by Srikanth *et al.* (2017)^[18], Ramjan *et al.* (2021), Rakesh Kumar *et al.* (2022)^[7], Kumar *et al.* (2023), Neha *et al.* (2025)^[11] and Vikash Babu *et al.* (2025)^[17], who observed significant differences among pumpkin genotypes for economically important characters, indicating considerable scope for genetic improvement.

Table 1: Analysis of variance (mean squares) for eighteen characters in pumpkin.

Sl. No	Characters	Replication	Genotypes	Error
	d.f	2	43	86
1	Days to 50% female flowering	0.70	15.02**	0.84
2	Days to first male flower anthesis	0.03	15.37**	0.43
3	Days to first female flower anthesis	0.70	14.52**	0.42
4	Node at first female flower appearance	0.010	3.065**	0.146
5	Number of primary branches / plant	0.003	1.239**	0.026
6	Internodal length (cm)	0.017	4.814**	0.121
7	Vine length (m)	0.006	0.701**	0.014
8	Number of fruits / plant	0.003	1.089**	0.007
9	Average fruit weight (kg)	0.003	0.077**	0.003
10	Fruit length (cm)	0.40	11.88**	0.31
11	Fruit diameter (cm)	1.49	19.77**	1.21
12	Flesh thickness (cm)	0.010	0.825**	0.019
13	Ascorbic acid (mg/100 g)	0.250	1.922**	0.046
14	Dry matter content (%)	0.04	16.81**	0.07
15	Total soluble solids (°Brix)	0.043	6.841**	0.063
16	Total carotenoids (mg/100 g)	0.001	0.216**	0.000
17	Fruit yield / plant (kg)	0.001	3.276**	0.015
18	Fruit yield / plot (kg)	0.55	82.85**	0.42

Note: Significant at 1% level of probability.

Genotypic and Phenotypic Coefficient of Variation

The estimates of mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as percent of mean are presented in Table 2. The PCV values were slightly higher than the corresponding GCV values for all the traits, indicating that environmental

influence on trait expression was relatively small. The narrow differences between GCV and PCV for most characters suggest that the observed variation was predominantly genetic in nature and that phenotypic selection would be effective for their improvement. High GCV and PCV values were recorded for total carotenoids (40.18 and 40.26%), fruit yield per plot (35.63

and 35.90%), fruit yield per plant (35.44 and 35.68%) and number of fruits per plant (29.83 and 30.11%), indicating the presence of substantial genetic variability for these traits. Such high variability may be attributed to differences in genetic constitution, reproductive efficiency and assimilate partitioning among the genotypes. Since fruit yield is a complex trait governed by several component characters, the existence of wide variability for yield-related traits provides greater opportunities for achieving genetic gain through selection. Similar results were reported by Srikanth *et al.* (2017)^[18], Ramjan *et al.* (2021), Rakesh Kumar *et al.* (2022)^[7], Kumar *et al.* (2023), Neha *et al.* (2025)^[11] and Vikash Babu *et al.* (2025)^[17], who also observed high GCV and PCV for fruit yield and associated traits in pumpkin.

Moderate GCV and PCV were observed for dry matter content, vine length, number of primary branches per plant, flesh thickness, total soluble solids, internodal length, fruit length and average fruit weight, indicating the presence of appreciable variability and the possibility of further improvement through selection. In contrast, relatively low GCV and PCV values were observed for days to 50 per cent female flowering, days to first male flower anthesis, days to first female flower anthesis, fruit diameter and ascorbic acid content, suggesting comparatively lower variability for these characters. Similar trends have been reported by Ramjan *et al.* (2021), Rakesh Kumar *et al.* (2022)^[7] and Neha *et al.* (2025)^[11].

Heritability and Genetic Advance

Heritability estimates provide information regarding the proportion of total variation attributable to genetic factors, whereas genetic advance indicates the expected improvement from selection. In the present study, broad-sense heritability ranged from 83.70% to 99.61% (Table 2). The highest heritability was recorded for total carotenoids (99.61%), followed by dry matter content (98.76%), fruit yield per plant

(98.63%), fruit yield per plot (98.49%), number of fruits per plant (98.14%) and total soluble solids (97.29%). The high heritability observed for these traits indicates that their expression was largely governed by genetic factors and less influenced by environmental conditions. Similar findings were reported by Ramjan *et al.* (2021), Rakesh Kumar *et al.* (2022)^[7], Kumar *et al.* (2023), Neha *et al.* (2025)^[11] and Vikash Babu *et al.* (2025)^[17].

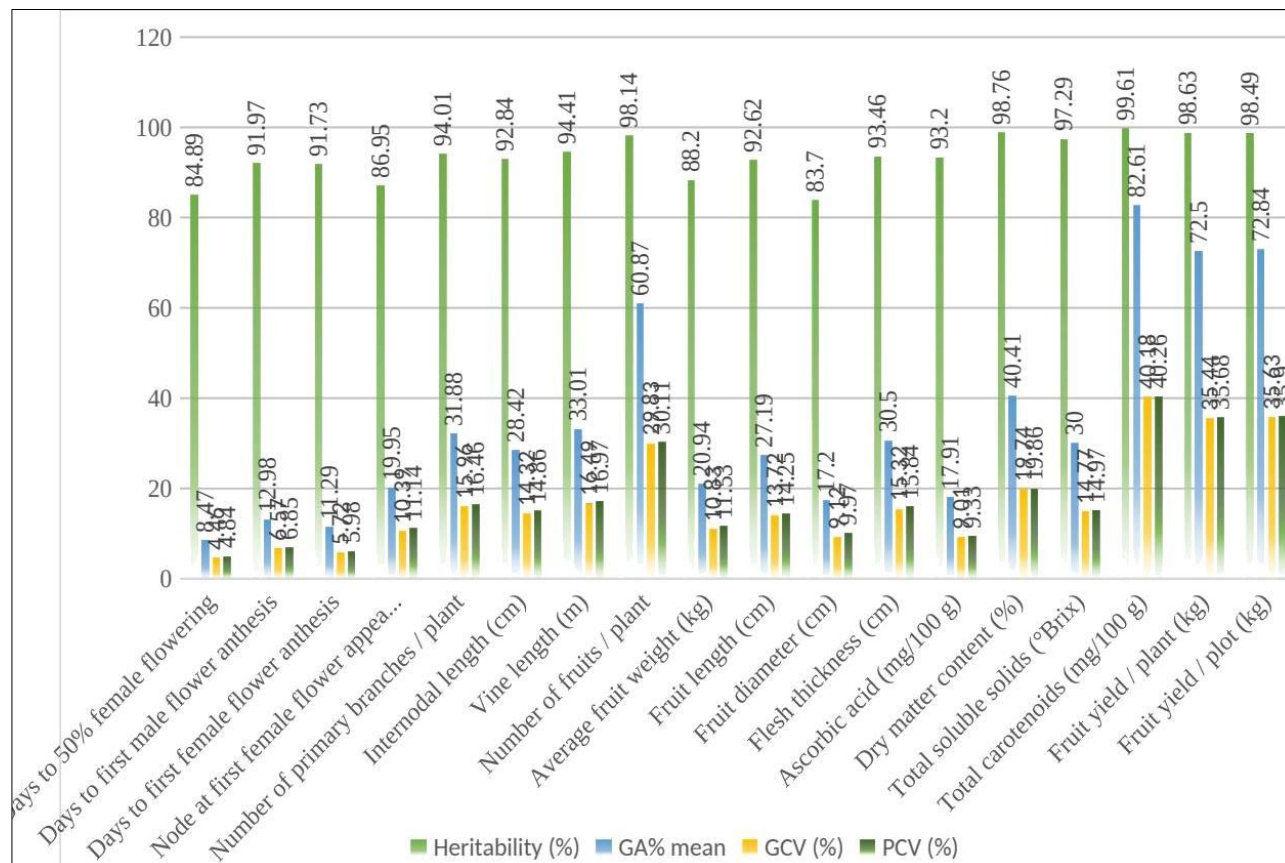
Genetic advance as percent of mean ranged from 8.47% for days to 50 per cent female flowering to 82.61% for total carotenoids. High genetic advance as percent of mean was recorded for total carotenoids (82.61%), fruit yield per plot (72.84%), fruit yield per plant (72.50%), number of fruits per plant (60.87%), dry matter content (40.41%), vine length (33.01%), number of primary branches per plant (31.88%), flesh thickness (30.50%) and total soluble solids (30.00%). High heritability coupled with high genetic advance indicates the predominance of additive gene action and suggests that these traits can be effectively improved through direct phenotypic selection. Such traits are generally considered reliable selection criteria because the observed variation is largely heritable and the expected response to selection is high. Similar conclusions were drawn by Johnson *et al.* (1955)^[5], Srikanth *et al.* (2017), Ramjan *et al.* (2021), Rakesh Kumar *et al.* (2022)^[7], Kumar *et al.* (2023), Neha *et al.* (2025)^[11] and Vikash Babu *et al.* (2025)^[17].

Among the studied characters, total carotenoids, fruit yield per plant, fruit yield per plot, number of fruits per plant and dry matter content exhibited high GCV, high heritability and high genetic advance as percent of mean. These traits therefore possess substantial exploitable genetic variability and are likely to respond effectively to selection. Consequently, they may be considered important selection indices for the development of high-yielding and nutritionally superior pumpkin genotypes.

Table 2: Mean, range, GCV(%), PCV(%), GA(%) and contribution (%) for eighteen characters in pumpkin. Figure 1. Graph of GCV%, PCV%, Heritability (%) and Genetic advance % of mean.

Characters	Mean	Range		Heritability (%)	GA % mean	GC V (%)	PC V (%)	% Contribution
		Min	Max					
Days to 50% female flowering	48.7	45.3	54.4	84.89	8.47	4.46	4.84	8.18
	3	7	8					
Days to first male flower anthesis	33.9	30.9	38.3	91.97	12.9	6.57	6.85	7.00
	5	7	5		8			
Days to first female flower anthesis	37.8	35.1	42.5	91.73	11.29	5.72	5.98	6.68
	7	0	3					
Node at first female flower appearance	9.50	8.03	12.6	86.95	19.9	10.3	11.1	6.84
			8		5	9	4	
Number of primary branches / plant	3.98	3.01	5.71	94.01	31.8	15.9	16.4	5.77
					8	6	6	
Internodal length (cm)	8.74	7.02	12.1	92.84	28.4	14.3	14.8	5.21
			0		2	2	6	
Vine length (m)	2.90	2.01	4.04	94.41	33.0	16.4	16.9	6.03
					1	9	7	
Number of fruits / plant	2.01	1.00	3.33	98.14	60.8	29.8	30.1	4.58
					7	3	1	
Average fruit weight (kg)	1.44	1.15	1.78	88.20	20.9	10.8	11.5	6.24
					4	3	3	
Fruit length (cm)	14.3	11.5	19.1	92.62	27.1	13.7	14.2	6.23
	2	3	0		9	2	5	
Fruit diameter (cm)	27.2	22.2	33.0	83.70	17.2	9.12	9.97	7.24
	6	0	1		0			
Flesh thickness (cm)	3.38	2.25	4.36	93.46	30.5	15.3	15.8	5.79
					0	2	4	
Ascorbic acid (mg/100 g)	8.78	7.12	10.2	93.20	17.9	9.01	9.33	6.79
			5		1			
Dry matter content (%)	11.9	7.15	16.2	98.76	40.4	19.7	19.8	3.87

	7		4		1	4	6	
Total soluble solids (°Brix)	10.1	8.12	13.8	97.29	30.0	14.7	14.9	5.20
	8		7		0	7	7	
Total carotenoids (mg/100 g)	0.67	0.23	1.42	99.61	82.6	40.1	40.2	2.92
					1	8	6	
Fruit yield / plant (kg)	2.94	1.23	5.19	98.63	72.5	35.4	35.6	3.47
					0	4	8	
Fruit yield / plot (kg)	14.7	6.08	26.0	98.49	72.8	35.6	35.9	1.96
	1		5		4	3	0	



Conclusion

The present study revealed the existence of substantial genetic variability among the forty-four pumpkin genotypes for all the traits studied, as evidenced by the significant differences observed in the analysis of variance. The higher magnitude of PCV than GCV for all characters indicated the influence of environmental factors on trait expression, although the differences were generally narrow, suggesting that most of the variation was genetic in nature. High GCV and PCV were observed for total carotenoids, fruit yield per plant, fruit yield per plot and number of fruits per plant, indicating the presence of considerable variability for these traits.

High heritability coupled with high genetic advance as percent of mean was recorded for total carotenoids, fruit yield per plant, fruit yield per plot, number of fruits per plant, dry matter content, vine length, number of primary branches per plant, flesh thickness and total soluble solids, suggesting the predominance of additive gene action and greater effectiveness of direct selection. Therefore, these traits may be considered reliable selection criteria for the improvement of yield and nutritional quality in pumpkin. The findings of the present experiment provide valuable information for the selection of superior genotypes and their utilization in future pumpkin breeding programmes aimed at developing high-yielding and nutritionally enriched cultivars.

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