

Analysis of Genetic Diversity among a Collection of Pumpkin (*Cucurbita moschata* Duch. Ex. Poir) Genotypes

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ABSTRACT

In the summer of 2023, twenty-two pumpkin genotypes were evaluated for nineteen qualitative and morphological characters. Statistically significant differences were recorded for all traits studied, pointing to the presence of rich genetic variability. In most cases, the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV), reflecting environmental influence along with genetic control. The highest PCV and GCV values were obtained for number of fruits per vine, vine length, average fruit weight and vitamin-C. These traits also expressed high heritability coupled with genetic advance, suggesting their reliability for

effective selection. Correlation studies indicated that fruit yield was positively and significantly related to average fruit weight and number of fruits per vine. Results of path analysis further confirmed the direct significant influence of vine length, fruit weight and fruit number on yield. Based on cluster analysis, the genotypes were grouped into three distinct clusters, Cluster I having twelve accessions, Cluster II nine, while Cluster III was represented by a single genotype. The largest intra-cluster distance was in Cluster II, whereas the maximum inter-cluster distance was observed between Clusters II and III. Cultivar VNR 14 among the assembled genotypes stood out for its early flowering and fruit set, higher fruit yield and superior TSS. This genotype can be utilized as a promising parent in future breeding programs to exploit heterotic potential and develop improved cultivars.

Keywords Heritability, Genetic advance, Correlation analysis, Cluster diversity, Pumpkin (*Cucurbita moschata*).

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INTRODUCTION

Pumpkin botanically known as (*Cucurbita moschata* Duch. Ex. Poir.) is one of the widely grown summer vegetable crops in India with significant economic and nutritional importance. India ranks second in pumpkin production among other countries world-wide,

contributing 2.2 million tonnes annually (FAOSTAT 2024). The crop is a rich source of essential nutrients like Vitamin A, B, C and E and its seeds are valued for their amino acid and mineral content (Batoool *et al.* 2022 and Liu *et al.* 2023). Despite its importance, the full yield potential of available genotypes in India remains underexploited due to the use of poor-yielding varieties and a high incidence of pests and diseases (Halder and Rai 2020, Bisht *et al.* 2025). Although the country possesses vast genetic diversity within the *Cucurbita* genus, a thorough understanding of this diversity's genetic architecture is lacking (Neha *et al.* 2025). A systematic research approach is therefore required to assess the genetic constituents of yield and its contributing traits to guide effective plant breeding. In the present experiment attempts have been made to analyze the genetic diversity among 22 collected pumpkin genotypes by evaluating its yield, yield related traits and biochemical components in terms of range, PCV, GCV, heritability ($h^2\%$), genetic advance, correlation and path co-efficient analysis of different traits to identify promising lines and strategies for crop improvement.

MATERIALS AND METHODS

The research was conducted at the Agricultural Experimental Farm of the University of Calcutta, West Bengal, India in the summer of 2023. The experiment was laid out in a Randomized Block Design (RBD) with three replications, utilizing 22 distinct pumpkin genotypes sourced from various locations across West Bengal. The field was prepared with power tillers and pits were filled with a mixture of farmyard manure, topsoil and fertilizers. A basal fertilizer dose was applied with subsequent top dressing throughout the season.

Observations were recorded from five randomly selected plants of each genotype. A total of nineteen morphological and biochemical traits were analyzed. Quantitative traits including vine length, number of nodes to the first female flower, sex ratio and key yield attributes like average fruit weight, number of fruits per vine and total yield were accounted for. Biochemical analysis for total soluble solids (TSS), ascorbic acid, beta-carotene and sugar content using standard methods were performed and recorded.

RESULTS AND DISCUSSION

Genetic variability, heritability and genetic advance

In the present investigation, involving twenty-two cultivars, the analysis of variance showed highly significant difference for all the nineteen characters. The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were calculated, with PCV values slightly higher than GCV values, suggesting a minimal influence of environmental factors. Traits with high PCV and GCV values included number of fruits per vine (PCV: 67.06%, GCV: 62.15%), vine length at 60 DAS (PCV: 59.32%, GCV: 58.75%), average fruit weight (PCV: 54.42%, GCV: 52.90%) and vitamin-C (PCV: 53.09%, GCV: 52.87) (Table 1). The high values for these traits demonstrate significant potential for genetic improvement through selective breeding. Our findings are in conformity to those of Ingole *et al.* (2021) and Tiwari and Yadav (2021).

Heritability explains how much of the similarity between parents and their offspring is due to genetics, while genetic advance tells us how much improvement we can expect in a trait after selecting the best individuals. Heritability indicates how strongly genes influence a particular trait and how likely it is to be passed on to the next generation. Therefore, using heritability coupled with genetic advance gives a more accurate idea about how effective selection will be. This is because genetic advance depends on the amount of genetic variation present, the influence of the environment on trait expression and how strictly selection is applied. However, a trait with high heritability does not always show a high genetic advance (Ananda *et al.* 2023). In this study, heritability ranged from 99.92% for number of fruits per vine to 29.89% for days taken to germination (Table 1). Traits with high heritability coupled with high genetic advance were noted for fruits per vine (h^2 99.92%, G. A. 95.44%), average fruit weight (h^2 99.86%, G. A. 94.78%), fruit cavity volume (h^2 98.94%, G. A. 91.35%), beta-carotene content of the pulp (h^2 99.73%, G. A. 70.44%), vitamin-C (h^2 99.15%, G. A. 68.45%), 100 seed weight (h^2 97.09%, G. A. 77.25%) and polar diameter of the fruit (h^2

Table 1. Key Genetic Parameters for Pumpkin Genotypes.

Character	Grand mean	Range	P. C. V	G. C. V	E. C. V	h ² (%)	G. A. as% of Mean
1. Days taken to germination	6.53	5.0-10.4	18.58	10.15	15.55	29.89	11.44
2. Vinelength 60 DAS	229.18	94.5-335.3	59.32	58.75	5.79	99.09	61.05
3. Node no..to which first female flower appears	18.77	13.6-26.3	17.92	17.13	5.23	91.47	33.76
4. Days to first female flower appearance	44.56	38.6-53.6	17.88	14.83	6.22	77.59	56.10
5. Sex ratio	14.38	5.62-21.20	24.21	23.06	7.38	90.71	45.24
6. Inter-nodal length (cm)	9.72	6.4-15.9	22.84	20.28	10.51	78.81	37.09
7. Days to first fruit harvest	79.96	55.1-97.9	18.03	17.42	4.63	93.41	34.69
8. Average fruit weight(kg)	0.94	1.95-2.00	54.42	52.90	10.11	99.86	94.78
9. Polar diameter of the fruit (cm)	7.76	5.6-16.3	35.04	34.67	5.08	97.90	70.68
10. Equatorial diameter of the fruit (cm)	8.84	5.5-18.2	35.54	34.84	6.99	96.13	70.38
11. Fruit cavity volume (cc)	340.13	165.8-750.1	49.72	49.46	5.11	98.94	91.35
12. No.of seeds per fruit	320.77	218.7-436.1	17.79	17.24	4.37	93.96	34.43
13. 100 seed weight (g)	4.26	2.2-9.7	38.62	38.05	6.59	97.09	77.25
14. total soluble solids (TSS)	3.92	2.3-5.1	14.90	13.54	6.23	82.54	25.34
15. Betacarotene content of the pulp.	2.08	0.95-3.21	34.29	34.24	1.78	99.73	70.44
16. Total sugar content of the pulp	4.82	2.7-7.6	23.20	22.24	6.59	91.92	43.94
17. Vitamin C(mg/100 ml)	0.03	0.013-0.09	53.09	52.87	4.89	99.15	68.45
18. No. of fruits per vine	11.60	4.53-19.35	67.06	62.15	18.45	99.92	95.44
19. Yield	10.53	3.8-18.2	34.33	28.99	18.38	71.33	50.45

97.90%, G. A. 70.68%) which suggests additive gene action and are highly responsive to direct selection. Significant gains can be achieved by simply selecting individuals with superior performance for these traits. Conversely, traits with high heritability but moderate to low genetic advance, such as days to first fruit harvest (h^2 93.41%, G. A. 34.69%), number of seeds per fruit (h^2 93.96%, G. A. 34.43%), node number to which first female flower appears (h^2 91.47%, G. A. 33.76%), total soluble solids (h^2 82.54%, G. A. 25.34%) and inter-nodal length (h^2 78.81%, G. A. 37.09%) were mostly under non-additive gene action which requires hybridization for effective improvement. These findings do conform to those of Neha *et al.* (2025) and Ezin *et al.* (2022).

Correlation

Correlation analysis was performed to determine the degree of association among the measured morphological and yield-contributing traits. Phenotypic and genotypic correlation studies revealed that fruit yield had significant positive correlation with number of fruits per vine (0.609, 0.526) and average fruit weight (0.601, 500), while days taken to germination (0.528) had a significant positive genotypic correlation with

fruit yield (Table 2, Table 3). This finding indicates that selecting for higher fruit number or weight will lead to an increase in overall yield. Conversely, any identified negative correlations highlight traits where simultaneous improvement would be challenging, requiring careful consideration in selection strategies. A significant negative correlation was observed between fruit yield and sex ratio of flowers (male: female) (-0.501, -0.618). Similar results were reported by Rai *et al.* (2023).

Path analysis coefficient

Path coefficient analysis helps separate correlation into direct and indirect effects, revealing how different traits influence yield. It provides a clearer understanding of cause-effect relationships among variables, though results should be interpreted carefully considering possible limitations. The analysis showed maximum positive direct effect on fruit yield through traits like number of fruits per vine (2.98), followed by average fruit weight (2.86) and vine length (2.27), while polar diameter of the fruit (-1.12) exhibited highest negative direct effect towards fruit yield followed by days to first female flower appearance (-1.00) (Table 4). Thus, it may be

Table 2. Phenotypic correlation coefficient among different characters in pumpkin.

Traits	1	2	3	4	5	6	7	8	9
1	1.000	-0.199	-0.205	-0.169	0.067	-0.129	-0.112	0.083	0.237
2		1.000	0.452*	0.030	-0.345	0.153	0.036	0.394	0.465*
3			1.000	0.059	0.040	0.011	-0.280	0.219	0.011
4				1.000	0.356	0.160	0.151	0.074	0.043
5					1.000	-0.018	-0.093	-0.140	-0.146
6						1.000	0.128	-0.138	-0.030
7							1.000	-0.043	0.438*
8								1.000	0.665**
9									1.000
10									
11									
12									
13									
14									
15									
16									
17									
18									
19									

Table 2. Continued.

Traits	10	11	12	13	14	15	16	17	18	19
1	0.026	-0.157	-0.069	0.01	0.111	0.021	-0.208	0.072	0.046	0.078
2	0.215	0.581**	0.440*	0.311	0.228	0.143	-0.149	-0.197	-0.148	0.209
3	-0.136	0.388	0.409	0.286	-0.055	-0.253	0.110	-0.024	-0.316	-0.551**
4	0.102	-0.162	-0.133	0.189	-0.103	0.329	0.133	0.128	-0.205	-0.165
5	-0.034	-0.315	-0.191	-0.031	-0.071	0.237	0.193	0.222	-0.386	-0.501*
6	0.044	-0.019	-0.274	-0.145	-0.066	0.306	-0.033	-0.106	-0.123	-0.268
7	0.620**	-0.132	-0.277	0.039	0.277	0.580**	0.040	0.181	-0.110	-0.519*
8	0.465*	0.644**	0.482*	0.337	0.167	-0.135	-0.252	-0.107	-0.481*	0.601**
9	0.655**	0.513*	0.372	0.448*	0.379	0.341	-0.163	-0.050	-0.243	0.317
10	1.000	0.311	0.053	0.282	0.424*	0.608**	-0.180	0.233	-0.463*	-0.069
11		1.000	0.774**	0.458*	0.329	-0.134	-0.058	-0.219	-0.291	0.223
12			1.000	0.433*	0.297	-0.270	0.057	-0.181	-0.097	0.267
13				1.000	0.174	0.104	0.374	0.076	-0.271	0.002
14					1.000	0.055	-0.220	0.160	-0.122	0.208
15						1.000	-0.096	0.072	-0.168	-0.307
16							1.000	0.255	-0.028	-0.304
17								1.000	0.077	-0.082
18									1.000	0.609**
19										1.000

Note: * significant at 5% and ** significant at 1% levels of significance respectively.

1.Days taken to germination, 2.Vine length 60 DAS, 3.Node no. to which first female flower appears, 4.Days to first female flower appearance, 5. sex ratio, 6. Inter- nodal length (cm), 7. Days to first fruit harvest, 8.Average fruit weight (kg), 9. Polar diameter of the fruit (cm), 10. Equatorial diameter of the fruit (cm), 11. Fruit cavity volume (cc), 12.No. of seeds per fruit , 13.100 seed weight (g),14. Total soluble solids (TSS), 15. Beta carotene content of the pulp., 16.Total sugar content of the pulp, 17.Vitamin C (mg/10, 0ml), 18. No. of fruits per vine 19.Yield.

suggested that selection of characters having higher positive and direct effect on total fruit yield per plant might be accounted for bringing about improvement

in the ultimate output, i.e. increased yield potential of the genotypes under study. Similar findings were observed by Kumar *et al.* (2024) and Verma *et al.*

Table 3. Genotypic correlation coefficient among different characters in pumpkin.

Traits	1	2	3	4	5	6	7	8	9
1	1.000	-0.300	-0.402	-0.380	0.261	-0.279	-0.163	0.042	0.471*
2		1.000	0.475*	0.098	-0.356	0.161	0.034	0.424*	0.463*
3			1.000	0.055	0.029	-0.008	-0.293	0.237	0.014
4				1.000	0.758**	0.126	0.253	-0.061	0.107
5					1.000	0.042	-0.065	-0.127	-0.158
6						1.000	0.112	-0.193	-0.064
7							1.000	-0.036	0.449*
8								1.000	0.706**
9									1.000
10									
11									
12									
13									
14									
15									
16									
17									
18									
19									

Table 3. Continued.

Traits	10	11	12	13	14	15	16	17	18	19
1	0.028	-0.247	-0.204	-0.043	0.248	0.057	-0.335	0.136	0.463*	0.528*
2	0.221	0.593**	0.461*	0.313	0.268	0.146	-0.162	-0.197	-0.180	0.250
3	-0.147	0.407*	0.435*	0.307	-0.106	-0.264	0.111	-0.020	-0.335	-0.246
4	0.209	-0.314	-0.350	0.299	-0.253	0.543**	0.115	0.238	-0.288	-0.444*
5	-0.031	-0.336	-0.203	-0.008	-0.109	0.246	0.229	0.222	-0.467*	-0.618**
6	0.023	-0.012	-0.323	-0.176	-0.110	0.349	-0.077	-0.106	-0.131	-0.371
7	0.641**	-0.132	-0.286	0.019	0.312	0.601**	0.030	0.188	-0.113	-0.120
8	0.489*	0.667**	0.481*	0.345	0.217	-0.143	-0.250	-0.099	-0.517*	0.500*
9	0.668**	0.518*	0.385	0.457*	0.423*	0.345	-0.168	-0.048	-0.266	0.384
10	1.000	0.322	0.059	0.287	0.494*	0.619**	-0.173	0.237	-0.528*	-0.072
11		1.000	0.790**	0.466*	0.362	-0.133	-0.062	-0.220	-0.339	0.260
12			1.000	0.440*	0.322	-0.273	0.059	-0.186	-0.053	0.395
13				1.000	0.186	0.108	0.415	0.083	-0.274	0.044
14					1.000	0.071	-0.250	0.169	-0.109	0.347
15						1.000	-0.096	0.073	-0.194	-0.375
16							1.000	0.262	-0.084	-0.387
17								1.000	0.077	-0.099
18									1.000	0.526*
19										1.000

Note: * significant at 5% and ** significant at 1% levels of significance respectively.

1. Days taken to germination, 2. Vine length 60 DAS, 3. Node no. to which first female flower appears, 4. Days to first female flower appearance, 5. sex ratio, 6. Inter-nodal length (cm), 7. Days to first fruit harvest, 8. Average fruit weight (kg), 9. Polar diameter of the fruit (cm), 10. Equatorial diameter of the fruit (cm), 11. Fruit cavity volume (cc), 12. No. of seeds per fruit, 13. 100 seed weight (g), 14. Total soluble solids (TSS), 15. Beta carotene content of the pulp, 16. Total sugar content of the pulp, 17. Vitamin C (mg/100 ml), 18. No. of fruits per vine, 19. Yield.

(2023) in *Cucurbita moschata*.

Genetic divergence

To assess the total genetic variability across all mea-

sured traits, Mahalanobis D² analysis was employed, which effectively groups genotypes into distinct clusters based on their overall divergence (Mahalanobis 1936). The resulting cluster distances (inter-cluster

Table 4. Direct and indirect effect of component character on fruit yield in pumpkin.

Traits	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	0.13	-0.08	-0.06	0.00	0.13	-0.02	-0.04	0.07	-0.53	0.01	0.02	0.06	-0.00	0.12	-0.00	-0.11	-0.08	0.92
2	-0.04	2.27	0.07	-0.00	-0.19	0.016	0.00	0.79	-0.52	0.15	-0.05	-0.13	0.05	0.13	-0.02	-0.05	0.12	-0.35
3	-0.05	0.13	0.16	-0.00	0.01	-0.00	-0.08	0.44	-0.01	-0.10	-0.03	-0.12	0.04	-0.05	0.04	0.039	0.01	-0.66
4	-0.05	0.02	0.00	-1.00	0.40	0.01	0.06	-0.11	-0.12	0.14	0.02	0.10	0.04	-0.12	-0.08	0.04	-0.15	-0.57
5	0.03	-0.09	0.00	-0.00	0.53	0.00	-0.01	-0.23	0.17	-0.02	0.03	0.06	-0.00	-0.05	-0.03	0.08	-0.14	-0.92
6	-0.03	0.04	-0.00	-0.00	0.02	0.10	0.03	-0.35	0.07	0.01	0.00	0.09	-0.02	-0.05	-0.05	-0.02	0.06	-0.25
7	-0.02	0.00	-0.04	-0.00	-0.03	0.01	0.27	-0.06	-0.50	0.44	0.01	0.08	0.00	0.15	-0.09	0.01	-0.12	-0.22
8	0.00	0.11	0.03	0.00	-0.06	-0.01	-0.00	2.86	-0.79	0.33	-0.06	-0.14	0.05	0.10	0.02	-0.08	0.06	-1.02
9	0.06	0.12	0.00	-0.00	-0.08	-0.00	0.12	1.31	-1.12	0.46	-0.04	-0.11	0.07	0.21	-0.05	-0.05	0.03	-0.52
10	0.00	0.06	-0.02	-0.00	-0.01	0.00	0.17	0.91	-0.75	0.69	-0.03	-0.01	0.04	0.24	-0.09	-0.06	-0.15	-1.04
11	-0.03	0.16	0.06	0.00	-0.17	-0.00	-0.03	1.24	-0.58	0.22	-0.09	-0.23	0.07	0.18	0.02	-0.02	0.14	-0.67
12	-0.02	0.12	0.06	0.00	-0.10	-0.03	-0.07	0.89	-0.43	0.04	-0.07	-0.29	0.07	0.16	0.04	0.02	0.12	-0.10
13	-0.00	0.08	0.04	-0.00	-0.00	-0.01	0.00	0.64	-0.51	0.19	-0.04	-0.13	0.16	0.09	-0.01	0.14	-0.05	-0.54
14	0.03	0.07	-0.01	0.00	-0.05	-0.01	0.08	0.40	-0.47	0.34	-0.03	-0.95	0.02	0.49	-0.01	-0.08	-0.11	-0.21
15	0.00	0.04	-0.04	-0.00	0.13	0.03	0.16	-0.26	-0.38	0.42	0.01	0.08	0.01	0.03	-0.15	-0.03	-0.04	-0.38
16	-0.04	-0.04	0.01	-0.00	0.12	-0.00	0.00	-0.46	0.18	-0.11	0.00	-0.01	0.06	-0.12	0.01	0.35	-0.17	-0.16
17	0.018	-0.05	-0.00	-0.00	0.11	-0.01	0.05	-0.18	0.05	0.16	0.02	0.05	0.01	0.08	-0.01	0.09	-0.65	0.15
18	0.06	-0.04	-0.05	0.00	-0.25	-0.01	-0.03	-0.96	0.30	-0.36	0.03	0.01	-0.04	-0.05	0.03	-0.02	-0.05	2.98

1. Days taken to germination, 2.Vine length 60 DAS, 3. Node no. to which first female flower appears, 4. Days to first female flower appearance, 5. sex ratio, 6. Inter- nodal length (cm), 7. Days to first fruit harvest, 8. Average fruit weight (kg), 9. Polar diameter of the fruit (cm), 10. Equatorial diameter of the fruit (cm), 11.Fruit cavity volume (cc), 12. No. of seeds per fruit , 13. 100 seed weight (g), 14.Total soluble solids (TSS), 15. Beta carotene content of the pulp., 16. Total sugar content of the pulp, 17.Vitamin C (mg/10, 0ml), 18. No. of fruits per vine.

Table 5. Average Inter- and Intra-Cluster D² Values.

Clusters	I	II	III
I	306.569	491.516	462.770
II		315.076	1173.719
III			110.000

D²) are crucial for identifying the most genetically distinct parents, as crossing accessions from the farthest clusters is predicted to yield maximum hybrid vigor (heterosis) and the best potential for new high-performing varieties (Gunasekaran *et al.* 2023).

The genetic divergence study grouped the 22 genotypes into three clusters which indicated satisfactory level of divergence among the clusters. Cluster I was the largest having 12 genotypes followed by cluster II with 9 genotypes and cluster III having only 1 genotype. The genotypes distributed randomly among the different clusters irrespective of their geographic origin. Intra cluster distance was high in cluster II (315.076) followed by cluster I (306.569), and cluster III (110.000). The maximum inter-cluster distance was recorded between cluster III and clus-

Table 6. Grouping of Pumpkin genotypes in Clusters,

Clusters	Number of Genotypes	Name of Genotypes
I	12	Arjuna, Baidyabati, Bhim, Chameli, Dev, Deva 549, EW 137, GM Birbal, Hali Sahar, Kalo Hira, Kashi Harit, NS 9527
II	9	Kanchan, Krishna, KSP 1570 mask, Momtaj, P-18, Paradise, Rana BSS 749, Sultan, Subham Tile Kumro
III	1	VNR-14

ter II (1173.719), followed by the distance between cluster II and cluster I (491.516) (Table 5). This high divergence between cluster III (VNR-14) (Table 6) and the genotypes in cluster II identifies VNR-14 as a promising parental line for future hybridization programs aimed at maximizing hybrid vigor or heterosis.

CONCLUSION

The findings of this investigation provide a data-driven framework for an effective pumpkin breeding program. The identified genotypes and traits can serve as a valuable gene pool for future crop improvement.

By leveraging direct selection for traits with high heritability and strategic hybridization between genetically divergent parents, it is possible to develop superior varieties that address the current challenges of low yield and poor quality.

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