



ISSN Print: 2664-844X
ISSN Online: 2664-8458
NAAS Rating (2026): 4.97
IJAFS 2026; 8(7): 379-384
www.agriculturaljournals.com
Received: 01-05-2026
Accepted: 02-06-2026

Vikrant
Division of Vegetable Science,
ICAR-Indian Agricultural
Research Institute (IARI),
New Delhi, India

Amit Kumar Mazumder
Division of Vegetable Science,
ICAR-Indian Agricultural
Research Institute (IARI),
New Delhi, India

Neha Sharma
Division of Vegetable Science,
ICAR-Indian Agricultural
Research Institute (IARI),
New Delhi, India

Avinash Tomer
Division of Vegetable Science,
ICAR-Indian Agricultural
Research Institute (IARI),
New Delhi, India

Swagata Nandi
Division of Vegetable Science,
ICAR-Indian Agricultural
Research Institute (IARI),
New Delhi, India

Bhagchand Shivran
Division of Vegetable Science,
ICAR-Indian Agricultural
Research Institute (IARI),
New Delhi, India

Corresponding Author:
Vikrant
Division of Vegetable Science,
ICAR-Indian Agricultural
Research Institute (IARI),
New Delhi, India

Agro-morphological characterization of summer squash (*Cucurbita pepo* L.) genotypes based on quantitative morphological descriptors

Vikrant, Amit Kumar Mazumder, Neha Sharma, Avinash Tomer, Swagata Nandi and Bhagchand Shivran

DOI: <https://www.doi.org/10.33545/2664844X.2026.v8.i7e.1703>

Abstract

Summer squash (*Cucurbita pepo* L.) is an economically important vegetable crop valued for its high nutritional content, short crop duration, and wide adaptability. The present study was undertaken to characterize eighteen genetically diverse summer squash genotypes using quantitative agro-morphological descriptors under the agro-climatic conditions of New Delhi, India. The experiment was conducted during the Rabi season (2024-2026) at the ICAR-Indian Agricultural Research Institute in a Randomized Complete Block Design with three replications. Morphological observations were recorded on vegetative, floral, fruit, and seed traits following UPOV and Bioversity International descriptors. Data were collected from five randomly selected plants per replication and analyzed to assess phenotypic variability among genotypes. Considerable variation was observed for growth, reproductive, fruit, and seed characteristics, indicating the presence of substantial genetic diversity. The identified variability provides valuable information for germplasm characterization, variety identification, and parental selection. The findings will support breeding programmes aimed at developing high-yielding, superior-quality, and climate-resilient summer squash cultivars.

Keywords: *Cucurbita pepo* L, agro-morphological characterization, genetic variability, germplasm evaluation, plant breeding

Introduction

Summer squash (*Cucurbita pepo* L.; $2n = 2x = 40$), a member of the family Cucurbitaceae, is one of the most economically important vegetable crops cultivated worldwide. It is valued for its tender immature fruits, rapid growth, high productivity, and adaptability to diverse agro-climatic conditions. The crop is extensively cultivated in temperate, subtropical, and tropical regions for both fresh consumption and processing. Owing to its short crop duration and continuous fruit production, summer squash has become an attractive vegetable for commercial cultivation, contributing significantly to nutritional security and farmers' income. The fruits of summer squash are rich in dietary fiber, vitamins A and C, potassium, calcium, magnesium, and several bioactive compounds with antioxidant properties. Regular consumption has been associated with improved digestive health and reduced risk of chronic diseases. Growing consumer demand for nutritious vegetables, coupled with increasing adoption of protected cultivation, has further enhanced the commercial importance of this crop.

Despite its economic significance, the genetic base of cultivated summer squash remains relatively narrow because modern breeding programs have relied on a limited number of parental lines. Continuous selection for yield, fruit quality, and market preferences has reduced genetic variability in many commercial cultivars. This limited diversity restricts breeding progress and increases vulnerability to biotic and abiotic stresses. Therefore, systematic characterization of available germplasm is essential for broadening the genetic base and identifying promising parental lines for crop improvement.

Agro-morphological characterization is the first and most fundamental step in germplasm evaluation. Morphological descriptors are inexpensive, reliable, and easily measurable, providing valuable information on genetic variability, distinctiveness, uniformity, and stability of genotypes. Such characterization facilitates germplasm conservation, variety

identification, parental selection, and breeding for improved horticultural traits. Morphological evaluation also serves as the basis for registration and protection of new plant varieties under Distinctness, Uniformity and Stability (DUS) testing.

The International Union for the Protection of New Varieties of Plants (UPOV) and Bioversity International have developed standardized descriptor lists for *Cucurbita* species, enabling uniform characterization across breeding programs. Quantitative descriptors such as cotyledon dimensions, leaf size, petiole length, floral traits, fruit dimensions, seed characteristics, and seed weight provide important information on plant growth, reproductive biology, fruit development, and seed quality. These traits are particularly useful for identifying superior genotypes possessing desirable horticultural characteristics.

Evaluation of floral traits including style length, filament length, and anther length is important because these attributes influence pollination efficiency, fruit set, and hybrid seed production. Similarly, fruit length, diameter, ribbing, and average fruit weight determine market preference and consumer acceptance, while seed size and hundred-seed weight are important indicators of seed vigor and propagation efficiency.

Although several studies have reported morphological diversity in pumpkin and winter squash, comprehensive agro-morphological characterization of summer squash germplasm under Indian agro-climatic conditions remains limited. Evaluation of diverse genotypes using standardized quantitative descriptors can provide valuable information for identifying elite breeding materials and improving selection efficiency.

Therefore, the present investigation was undertaken to characterize eighteen summer squash genotypes using quantitative agro-morphological descriptors and to assess the extent of phenotypic variability among them. The information generated from this study will contribute to germplasm characterization, facilitate the identification of superior genotypes, and provide a foundation for future breeding programmes aimed at improving yield, fruit quality, and adaptation.

Materials and Methods

Plant Material: The present investigation was conducted using eighteen genetically diverse summer squash

(*Cucurbita pepo* L.) genotypes collected from different breeding programmes and germplasm sources. The experimental material comprised advanced breeding lines and cultivated genotypes exhibiting variation in vegetative, floral, fruit, and seed characteristics. These genotypes were selected to represent a broad range of morphological diversity for characterization and evaluation.

Experimental Site

The experiment was conducted at the Research Farm of the Division of Vegetable Science, ICAR-Indian Agricultural Research Institute (IARI), New Delhi, India, during the Rabi season of 2024-2026S.

The experimental site is located at approximately 28.63° N latitude and 77.15° E longitude, at an altitude of about 228.6 m above mean sea level. The region experiences a semi-arid subtropical climate with cool winters and hot summers. The soil of the experimental field was sandy loam, well-drained, and suitable for cucurbit cultivation. Recommended agronomic practices were followed uniformly throughout the crop growth period to ensure healthy plant establishment.

Experimental Design and Crop Management

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. Each genotype was grown in a single plot consisting of an equal number of plants (specify the number, e.g., 10 plants per replication) at the recommended spacing of 2.0 m × 0.6 m (adjust if different). Standard crop management practices, including irrigation, nutrient management, weed control, and plant protection measures, were adopted uniformly for all experimental plots to minimize environmental variation. Observations were recorded on five randomly selected healthy plants from each replication, and the mean values were used for statistical analysis.

Agro-Morphological Characterization

Morphological characterization was carried out following the descriptors proposed by UPOV (International Union for the Protection of New Varieties of Plants) and Biodiversity International for *Cucurbita pepo*. Quantitative observations were recorded at appropriate growth stages using standard measuring instruments.

Table 1: The following quantitative descriptors were evaluated

	Character	Method of Measurement
1.	Cotyledon length (cm)	Measured from the base to the tip of fully expanded cotyledons using a digital ruler.
2.	Cotyledon width (cm)	Measured at the widest portion of the cotyledon.
3.	Leaf blade length (cm)	Distance from the petiole attachment to the leaf apex.
4.	Leaf blade width (cm)	Maximum width of the leaf measured across the lamina.
5.	Leaf blade silver patches	Presence or absence of silver mottling was visually recorded according to descriptor standards.
6.	Petiole length (cm)	Distance from stem attachment to the base of the leaf blade.
7.	Style length (cm)	Length from the ovary to the stigma measured in freshly opened female flowers.
8.	Filament length (cm)	Length of the filament in freshly opened male flowers.
9.	Anther length (cm)	Length of mature anthers measured using a digital Vernier caliper.
10.	Peduncle length (cm)	Measured from the fruit attachment point to the stem node.
11.	Fruit length (cm)	Measured from blossom end to stem end at marketable maturity.
12.	Fruit diameter (cm)	Maximum transverse diameter measured using a Vernier caliper.
13.	Fruit ribs	Number or prominence of ribs recorded visually according to descriptor guidelines.
14.	Average fruit weight (g)	Average weight of marketable fruits measured using an electronic balance.
15.	Seed length (cm)	Mean length of ten randomly selected mature seeds.
16.	Seed width (cm)	Maximum width of mature seeds measured using a Vernier caliper.
17.	Hundred-seed weight (g)	Weight of 100 well-filled, dried seeds recorded using a precision electronic balance.

Statistical Analysis

The recorded data were subjected to analysis of variance (ANOVA) appropriate for a randomized complete block design to determine the significance of differences among genotypes. Mean values were compared using the least significant difference (LSD) or critical difference (CD) test at the 5% probability level.

Descriptive statistics, including mean, range, standard deviation, coefficient of variation (CV), and standard error, were computed for all quantitative traits. Where appropriate, principal component analysis (PCA) and hierarchical cluster analysis (HCA) may be performed to assess genetic diversity and classify genotypes based on agro-morphological characteristics. All statistical analyses were performed using R software (version 4.x), SPSS, or SAS (specify the software used).

Based on the four multivariate analyses (correlation matrix, PCA biplot, scree plot, and hierarchical cluster analysis), the following Results and Discussion are suitable for inclusion in a research paper on summer squash (*Cucurbita pepo* L.)

morphological characterization. The interpretation is based on the uploaded figures.

Results

Correlation analysis of morphological traits (Fig-1)

Correlation analysis among the fifteen quantitative morphological characters revealed considerable variation in the degree of association among traits. Strong positive correlations were observed among several fruit-related traits, particularly fruit length, fruit diameter, and fruit weight, indicating that larger fruits tended to possess greater diameter and consequently higher fruit weight. Likewise, seed length, seed width, and 100-seed weight exhibited positive associations, suggesting coordinated seed development.

Vegetative traits such as leaf blade length, leaf blade width, and petiole length also showed moderate to strong positive correlations, indicating that vigorous vegetative growth contributes to larger leaf architecture. Cotyledon length and cotyledon width were positively associated with early seedling vigor.



Fig 1: Correlation plot

Conversely, several reproductive traits showed weak or negative correlations with vegetative characters. Some floral measurements, including style length and filament length, displayed weak associations with fruit characteristics, indicating that these reproductive structures contribute relatively independently to fruit development. The correlation matrix also revealed a few significant negative relationships, reflecting potential trade-offs among growth and reproductive traits. Overall, fruit and seed traits formed the strongest positively correlated group.

Principal Component Analysis (PCA) (Fig-2 and 3)

Principal Component Analysis reduced the fifteen morphological variables into a few principal components explaining most of the observed variability.

The scree plot indicated that the first principal component (PC1) explained 26.4% of the total variation, while the second principal component (PC2) explained 19.0%, together accounting for 45.4% of the total phenotypic variation. The remaining components contributed progressively smaller proportions of variance, indicating that the first two PCs adequately summarized the major morphological diversity among the genotypes.

The PCA biplot revealed three distinct genotype groups (K1, K2 and K3). PC1 was mainly influenced by leaf blade length, leaf blade width, petiole length, seed width, and 100-seed weight, whereas PC2 received greater contributions from fruit diameter, fruit weight, seed length, cotyledon length, and cotyledon width. Fruit length and floral traits (style length, filament length, and anther length) contributed primarily along the negative direction of PC2.

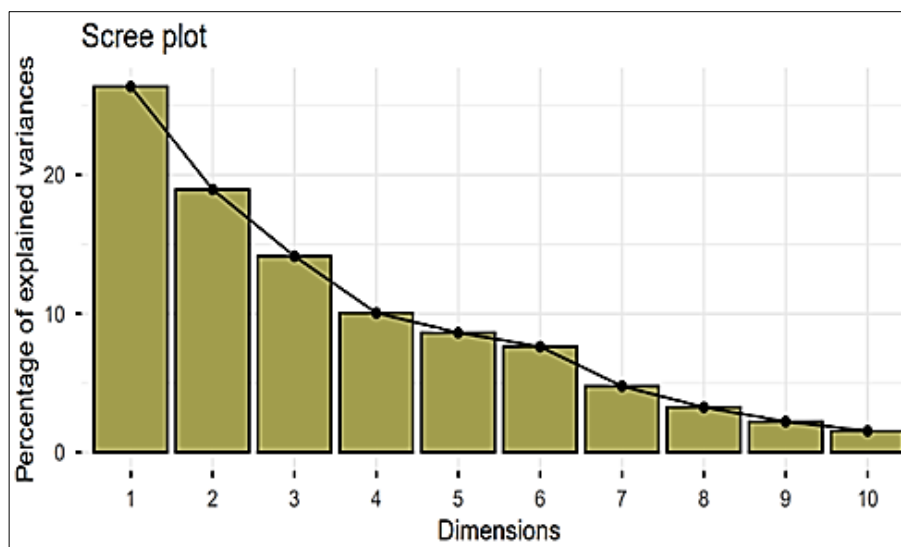


Fig 2: Scree Plot

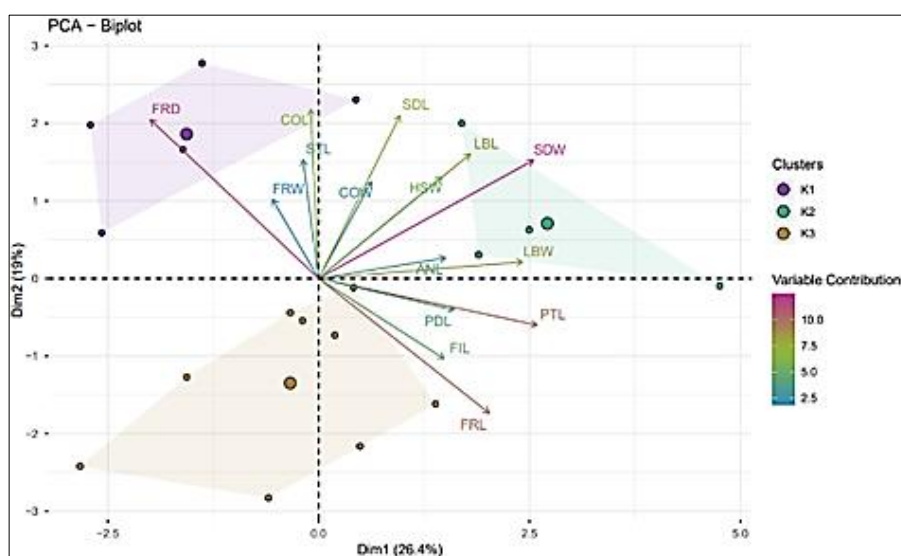


Fig 3: Biplot

The distribution of genotypes across the PCA space indicated substantial morphological diversity, with each cluster characterized by a different combination of vegetative, reproductive, and fruit traits (Hair *et al.* (2019); Mohammadi & Prasanna (2003); Ferriol *et al.* (2003) [7, 9, 6].

Cluster analysis (Fig-4)

Hierarchical clustering using Ward's method grouped the eighteen summer squash genotypes into three major clusters, demonstrating considerable genetic divergence based on morphological traits.

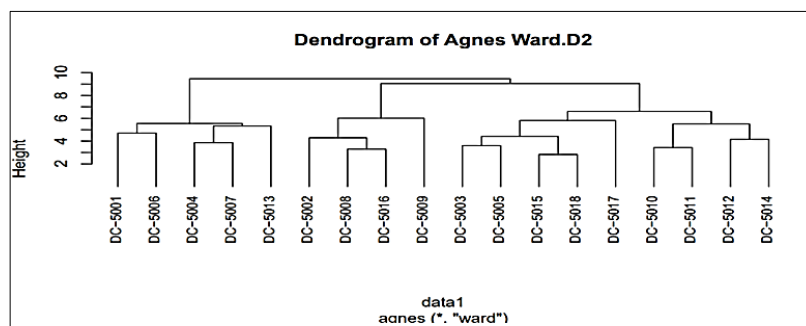


Fig 4: Cluster analysis

One cluster consisted of genotypes including DC-5001, DC-5006, DC-5004, and DC-5007, representing relatively similar vegetative and reproductive characteristics. Another cluster grouped DC-5002, DC-5008, DC-5016, DC-5009, DC-5003, DC-5005, DC-5015, DC-5018, and DC-5017,

indicating intermediate morphological similarity. The third cluster included DC-5010, DC-5011, DC-5012, and DC-5014, which were comparatively distinct from the remaining genotypes (Sneath & Sokal (1973); Ward (1963); Rohlf (2000) [13, 16, 12].

The clustering pattern suggests the existence of appreciable morphological diversity within the evaluated germplasm and identifies genetically divergent parental lines suitable for hybridization programmes.

Discussion

The present study demonstrated substantial morphological diversity among the evaluated summer squash genotypes. Significant positive correlations among fruit length, fruit diameter, and fruit weight indicate that improvement of one fruit size component is likely to result in simultaneous improvement of overall fruit yield. Similar positive relationships among seed traits suggest coordinated accumulation of seed biomass during development.

The PCA results further confirmed that fruit and vegetative characters were the major contributors to phenotypic variation. The first two principal components explained nearly half of the total variation, which is typical for quantitative morphological studies in cucurbits, where numerous traits jointly influence plant architecture and fruit characteristics. The close association of leaf size traits with seed characteristics along PC1 suggests that vigorous vegetative growth contributes to improved assimilate production and subsequent seed development.

The separation of genotypes into three distinct groups in both PCA and hierarchical clustering demonstrates broad phenotypic divergence within the germplasm. Agreement between PCA and cluster analysis strengthens the reliability

of the observed grouping. Genotypes located in different clusters are expected to possess greater genetic divergence and therefore represent promising parents for hybrid breeding aimed at exploiting heterosis and generating wider segregation in subsequent generations (Al-Jibouri *et al.* (1958); Johnson *et al.* (1955); Yadav *et al.* (2017)^[1, 8, 17].

The presence of weak or negative correlations between certain floral and fruit characters suggests that these traits may be independently inherited or differentially influenced by environmental conditions. Consequently, simultaneous improvement of reproductive and fruit traits may require careful selection strategies rather than indirect selection alone.

Overall, multivariate analysis identified fruit size, seed traits, and vegetative growth characters as the principal determinants of morphological variability in summer squash. These traits can therefore serve as reliable descriptors for germplasm characterization and as useful selection criteria in breeding programmes targeting higher yield and improved horticultural performance.

This interpretation is consistent with

- Correlation matrix (trait associations).
- PCA biplot (trait contributions and genotype grouping).
- Scree plot (26.4% and 19.0% variance explained by PC1 and PC2).
- Ward's dendrogram (three major genotype clusters).

Table 2: The phenotypic data of various agro-morphological parameters of summer squash in two replication for the season 2024-2025

GENOTYPE	Replication	Cotyledon: Length (cm)	Cotyledon: width (cm)	Leaf blade: length (cm)	Leaf blade: width (cm)	Leaf blade: silver patches	Petiole: length (cm)	Style length (cm)	Filaments length (cm)	Anthers length (cm)	Peduncle: length (cm)	Fruit: length (cm)	Fruit: diameter (cm)	Fruit: Ribs	Fruit: Weight (gm)	Seed: length (cm)	Seed: width (cm)	100 Seed weight (gm)
DC-5001	1	7.45	3.96	30.08	28.95	9	29.33	0.74	.69	.6	1.45	9.02	11.9	9	1042	1.55	0.63	159.2
DC-5002	1	6.48	3.6	31.86	27.62	9	45.33	0.76	1.38	.74	2.10	27.2	6.67	1.00	980.0	1.87	0.75	135.4
DC-5003	1	5.90	3.46	27.78	27.92	1	40.20	0.48	1.26	.96	2.10	26.5	5.7	1.00	945.0	1.27	0.60	102.6
DC-5004	1	6.18	3.50	27.82	27.72	1	33.43	1.44	.6	0.62	4.27	6.45	11.92	1.00	616.2	1.43	6.40	86.50
DC-5005	1	5.03	3.13	27.74	28.36	1	36.90	0.78	1.06	.84	2.60	24.75	5.2	9.00	500.0	1.18	0.60	86.90
DC-5006	1	7.03	3.88	27.54	24.26	9	38.93	1.26	1.18	.58	1.55	11.93	12.66	9.00	1020	1.77	5.80	96.50
DC-5007	1	6.34	3.45	26.12	28.84	1	24.10	1.06	0.62	1.26	4.48	7.84	16.68	1.00	1001.4	1.23	0.65	115.3
DC-5008	1	5.67	3.36	30.02	30.16	1	40.57	1.03	1.04	1.18	2.90	22.24	6.76	9.00	752.0	1.60	0.70	143.0
DC-5009	1	5.45	3.63	32.32	35.78	1	48.27	1.04	1.38	1.26	12.83	26.65	6.55	9.00	724.0	1.40	0.80	134.0
DC-5010	1	5.55	4.15	24.20	26.10	1	40.43	0.93	1.025	0.775	5.40	16.2	9.46	9.00	684.0	1.30	0.70	133.0
DC-5011	1	5.52	3.28	24.82	23.58	1	40.67	1.03	1.2	0.925	4.20	8.3	9.10	1.00	474.0	1.30	0.60	122.0
DC-5012	1	5.76	3.96	27.46	29.66	1	38.85	0.70	1.3	1.025	10.07	25.50	6.95	1.00	856.0	1.20	0.60	107.4
DC-5013	1	6.70	4.73	32.98	27.72	1	35.07	1.12	0.82	1.28	4.21	16.1	12.1	1.00	879.0	1.50	0.70	88.50
DC-5014	1	7.70	4.10	25.98	25.98	1	37.07	0.73	0.72	1	5.12	24.1	6.6	1.00	605	1.40	0.60	145.5
DC-5015	1	6.75	3.55	26.58	28.58	1	44.93	0.70	0.46	0.52	1.54	26.5	6.8	1.00	730	1.30	0.65	117.0
DC-5016	1	7.50	3.60	30.02	31.28	1	42.40	0.90	0.95	1.15	2.21	14.1	9.6	1.00	742	1.50	0.70	169.0
DC-5017	1	5.88	3.30	24.98	25.34	1	25.73	0.50	1.12	0.78	2.14	21.2	10.5	1.00	1105	1.10	0.50	85.00
DC-5018	1	6.75	2.91	29.70	28.02	9	36.70	0.95	0.98	0.6	2.62	23.4	7.1	9.00	747	1.30	0.60	110.0
DC-5001	2	7.62	3.85	32.50	27.50	9	28.20	0.80	0.7	0.65	1.40	9.50	11.50	9	985.0	1.60	0.60	157.6
DC-5002	2	6.54	3.50	33.10	28.70	9	43.50	0.73	1.25	0.82	2.15	26.80	6.70	1.00	950.0	1.80	0.70	134.5
DC-5003	2	5.84	3.25	26.80	26.50	1	42.10	0.55	1.2	0.94	2.20	26.60	5.75	1.00	960.0	1.30	0.65	103.5
DC-5004	2	6.10	3.60	28.90	27.50	1	34.50	1.35	0.63	0.68	4.25	6.50	12.10	1.00	650.0	1.40	0.62	87.50
DC-5005	2	5.25	3.25	27.50	26.50	1	35.60	0.82	1.1	0.9	2.50	23.80	5.60	9.00	525.0	1.20	6.30	87.60
DC-5006	2	7.10	3.60	28.20	25.50	9	37.50	1.20	1.22	0.6	1.60	12.50	13.10	9.00	990.0	1.75	5.75	97.50
DC-5007	2	6.20	3.55	27.60	27.30	1	25.30	1.10	0.7	1.12	4.65	8.50	16.50	1.00	970.0	1.40	0.70	117.5
DC-5008	2	5.80	3.40	28.50	29.20	1	38.50	1.10	1.08	1.25	3.10	21.20	7.10	9.00	780.0	1.50	0.72	142.6
DC-5009	2	5.65	3.55	33.20	33.50	1	45.80	1.12	1.35	1.3	11.50	25.60	6.70	9.00	750.0	1.45	0.77	133.5
DC-5010	2	5.50	4.00	25.50	27.30	1	41.20	1.00	1.1	0.81	5.50	16.50	9.80	9.00	660.0	1.35	0.73	130.2
DC-5011	2	5.60	3.50	26.20	24.8	1	38.50	1.10	1.15	1.02	4.5	8.5	9.6	1.00	500.0	1.25	0.64	120.4
DC-5012	2	5.85	4.10	28.10	32.00	1	36.90	0.81	1.2	1.1	11.2	26.4	7.2	1.00	820.0	1.18	0.58	105.5
DC-5013	2	6.60	4.56	30.50	28.20	1	34.50	1.15	0.9	1.25	4.35	17.2	13.5	1.00	850.0	1.55	0.68	90.50

DC-5014	2	7.92	4.00	27.50	27.10	1	36.10	0.78	0.8	1.05	5.6	25.5	7.1	1.00	620.0	1.35	0.62	143.5
DC-5015	2	6.55	3.65	26.10	30.20	1	42.20	0.75	0.5	0.55	1.42	27.5	6.5	1.00	710.0	1.33	0.64	120.5
DC-5016	2	7.25	3.55	28.50	29.50	1	40.60	0.95	1	1.1	2.4	14.5	9.4	1.00	730.0	1.45	0.75	165.5
DC-5017	2	5.75	3.40	26.50	27.50	1	27.50	0.55	1.3	0.8	2.25	22.5	10.9	1.00	1050	1.15	0.55	87.50
DC-5018	2	6.55	2.85	27.60	27.50	9	35.50	1.00	1	0.72	2.8	24.5	7.5	9.00	738.0	1.25	0.65	112.5

Conclusion

The present study revealed substantial morphological diversity among the eighteen summer squash (*Cucurbita pepo* L.) genotypes evaluated using fifteen quantitative morphological traits. Correlation analysis demonstrated strong positive associations among fruit-related traits, particularly fruit length, fruit diameter, and fruit weight, indicating that these characters can be effectively utilized for indirect selection to improve yield. Positive relationships among seed traits further suggest coordinated seed development and their potential utility in breeding programmes (Paris (2016); Ferriol *et al.* (2003); Zhang *et al.* (2018) [11, 6, 18]).

Principal Component Analysis showed that the first two principal components accounted for 45.4% of the total phenotypic variation, with major contributions from vegetative, fruit, and seed characters, confirming that these traits are the primary sources of variability among the evaluated genotypes. The PCA biplot clearly differentiated the genotypes into three groups, reflecting broad phenotypic divergence.

Hierarchical cluster analysis further classified the genotypes into three distinct clusters, supporting the PCA results and demonstrating considerable genetic divergence within the germplasm. The existence of well-separated clusters indicates the availability of diverse parental lines that can be exploited in hybridization programmes to maximize heterosis and generate superior recombinants.

Overall, the combined use of correlation analysis, PCA, and cluster analysis proved effective in identifying key morphological traits contributing to diversity and in discriminating genetically diverse genotypes. Fruit size attributes, seed characteristics, and vegetative growth traits emerged as reliable descriptors for germplasm characterization and should receive priority in selection programmes. The identified divergent genotypes provide valuable genetic resources for developing high-yielding, superior-quality summer squash cultivars with broad adaptability.

References

- Al-Jibouri HA, Miller PA, Robinson HF. Genotypic and environmental variances and covariances in an upland cotton cross of interspecific origin. *Agronomy Journal*. 1958;50(10):633-636.
- Balkaya A, Yanmaz R, Özbakır M. Morphological characterization of squash (*Cucurbita* spp.) germplasm. *Scientia Horticulturae*. 2010;124:147-153.
- Bioversity International. Descriptors for squash (*Cucurbita* spp.). Rome: Bioversity International; 2008.
- Burton GW, DeVane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*. 1953;45(10):478-481.
- Cruz CD, Regazzi AJ, Carneiro PCS. Modelos biométricos aplicados ao melhoramento genético. 4th ed. Viçosa: Universidade Federal de Viçosa; 2012.
- Ferriol M, Picó B, Nuez F. Genetic diversity of a germplasm collection of *Cucurbita pepo* using SSR markers and morphological traits. *Theoretical and Applied Genetics*. 2003;107(2):271-282.
- Hair JF, Black WC, Babin BJ, Anderson RE. Multivariate data analysis. 8th ed. Boston: Cengage Learning; 2019.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*. 1955;47(7):314-318.
- Mohammadi SA, Prasanna BM. Analysis of genetic diversity in crop plants: Salient statistical tools and considerations. *Crop Science*. 2003;43(4):1235-1248.
- Paris HS. Summer squash. In: Prohens J, Nuez F, editors. *Vegetables II: Fabaceae, Liliaceae, Solanaceae, and Umbelliferae*. New York: Springer; 2016. p. 351-379.
- Paris HS. Summer squash: History, diversity and breeding. *Plant Breeding Reviews*. 2016;40:1-62.
- Rohlf FJ. NTSYS-pc: Numerical taxonomy and multivariate analysis system. Version 2.1. Setauket (NY): Exeter Software; 2000.
- Sneath PHA, Sokal RR. Numerical taxonomy: The principles and practice of numerical classification. San Francisco: W. H. Freeman; 1973.
- Sokal RR, Michener CD. A statistical method for evaluating systematic relationships. *University of Kansas Science Bulletin*. 1958;38:1409-1438.
- UPOV. Guidelines for the conduct of tests for distinctness, uniformity and stability: *Cucurbita pepo* L. TG/119/4. Geneva: International Union for the Protection of New Varieties of Plants; 2017.
- Ward JH Jr. Hierarchical grouping to optimize an objective function. *Journal of the American Statistical Association*. 1963;58(301):236-244.
- Yadav M, Pandey S, Kumar R, Singh B. Genetic variability, correlation and path coefficient analysis for yield and its contributing traits in summer squash (*Cucurbita pepo* L.). *International Journal of Current Microbiology and Applied Sciences*. 2017;6(10):1460-1468.
- Zhang D, Lu X, Wang W, Li Y. Genetic diversity and population structure analysis in *Cucurbita pepo* using morphological and molecular markers. *Scientia Horticulturae*. 2018;240:286-293.