



GENETIC VARIABILITY, HERITABILITY AND CHARACTER ASSOCIATION ANALYSIS IN HULL-LESS PUMPKIN (*Cucurbita pepo* subsp. *pepo* var. *styriaca*)

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Kaur K., A. S. Dhatt and J. Singh Khosa (2026): *Genetic variability, heritability and character association analysis in hull-less pumpkin (Cucurbita pepo subsp. pepo var. styriaca)*. - Genetika, Vol 58, No. 1, 43-53.

Hull-less pumpkins have been evolved due to a single recessive mutation and their consumption has numerous health benefits. The genetic variation in hull-less pumpkin is limited due to strong selection pressure for particular seed types and its cultivation in narrow geographical region. In this context, we have developed segregating populations from hull-less and hulled cultivars and selected 44 hull-less lines to broaden the genetic base of hull-less pumpkin. In the present study, 46 populations of hull-less pumpkin were characterized in terms of genetic variability, heritability and character association analysis. The morphological and biochemical characterization revealed significant variability for growth habit, quality (except dry matter), fruit, seed and oil yield. Principal component analysis (PCA) revealed eleven significant PCs which explained 82.014% of total variation. Cluster analysis performed to assess the patterns of variation and germplasm under investigation, grouped it into five clusters. Growth habit, fruit, seed and oil yield show high positive correlation with other traits.

Key words: Cluster analysis, Correlation, Mahalanobis D², Oil content, PCA

INTRODUCTION

Hull-less pumpkins have been evolved due to a single recessive mutation in Styria region of Austria (LOY, 1991; TEPNER, 2000). After the identification of hull-less mutant a number of cultivars have been developed in central Europe, North America and China, primarily for oil extraction and seed consumption (LELLEY *et al.*, 2009). The consumption of pumpkin oil and

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hull-less seeds is associated with number of health benefits related to prostate, hyperplasia, diabetic, hypertensive, tumour, bacterial, hypercholesterolemia and inflammatory actions (PATEL 2013). In India, musky pumpkin has become a popular crop due to its short growing period, nutritive value and long shelf life (PANDEY *et al.*, 2003). A wide range of diverse pumpkin germplasm was collected and utilized in breeding programmes to develop improved cultivars but no attention have been paid on hull-less trait so far (HAZRA *et al.*, 2007).

The knowledge of genetic variability and heritability for different traits is prerequisite to breed elite cultivars. The major breeding goals in hull-less pumpkin breeding programmes is to develop cultivars with bushy growth habit, high seed yield, high oil yield and resistance against various diseases (ZRAIDI *et al.*, 2003). Previous studies indicate that genetic variation in Styrian hull-less pumpkin is limited due to high selection pressure for particular seed types and its cultivation in narrow geographical region but little is known about the inheritance and correlation of various traits (LELLEY *et al.*, 2009). In the present investigation we followed mass selection and individual selection on populations obtained by crossing Lady Godiva and PCK-1 to identify hull-less lines. These lines were further characterized for various morphological and biochemical traits to estimate amount, cause and nature of the variance that is present in populations and to identify various traits influencing yield and quality traits in hull-less pumpkin. This information will be useful in broadening the genetic base and developing elite cultivars in coming years.

MATERIALS AND METHODS

Hull-less seeded lines were developed from a cross of PCK-1 x Lady Godiva (EC 664187). PCK-1 is a released variety of *Cucurbita pepo* by Punjab Agricultural University, while the latter is an introduction from USA. The experimental material comprised of 46 advance breeding lines (F₅ & F₆) of hull-less seeded pumpkin along with check varieties PCK-1 (Hulled) and Lady Godiva (Hull-less). The experiment was laid down in randomized block design (RBD) with three replications at Punjab Agricultural University, Ludhiana. Seeds of 46 genotypes were sown in the month of February in plug-trays. Upon achieving proper size seedlings were transplanted in the field by accommodating 10 plants/replication of each genotype at distance of 45 cm between plants on both edges of 1.5 m wide beds. All other cultural practices were followed as per PAU Package of Practices for the pumpkin (ANONYMOUS, 2015). The morphological and yield traits viz., vine length (cm), no. of primary branches, leaf length (cm), leaf width (cm), petiole length (cm), node no. for first female flower, node no. for first male flower, day to 50% flowering, inter-nodal length (cm), peduncle length (cm), fruit polar diameter (cm), fruit equatorial diameter (cm), fruit shape index, seed cavity (cm), flesh thickness (cm), days to harvest, no. of fruits/plant, average fruit weight (kg), fruit yield/plant (kg), fruit yield/ha (tonne), number of seeds/fruit, 100 seed weight (g), seed yield/fruit (g), seed yield/plant (g) and seed yield/hectare (kg) were recorded on five randomly selected plants from each replication. Oil content (FOLCH *et al.*, 1957) and protein content (LOWRY *et al.*, 1951), total sugar (LOEWUS 1952), starch content (CLEGG, 1956), Dry matter and ash content (AOAC, 2005) were determined using standard protocols. The above mentioned traits were subjected to Mahalanobis D² (MAHALANOBIS, 1936) by using SAS software (SAS version 9.3, 2009) to assess the genetic divergence among the genotypes and then, grouped into different clusters according to Tocher's method. The estimation of correlation among traits is done as described by AL-JIBOURI *et al.*,

(1958). Principal component analysis (PCA) was assessed in R by using ‘factoextra’ package (KASSAMBARA and MUNDT, 2020).

RESULTS AND DISCUSSION

Genetic Variability

A wide variability was observed for the majority of traits under investigation in hull-less pumpkin germplasm (Table 1).

Table 1. Range, Mean, Standard Deviation (SD), Mean Squared Error (MSE) and Coefficient of Variation (CV %) for various traits in hull-less pumpkin germplasm

Trait	Range	Mean	SD	MSE	CV%
Vine length (cm)	28.60-175.40	81.89	43.68	6.44	53.34
No. of primary branches	1.5-3.8	2.34	0.52	0.077	22.22
Leaf length (cm)	12.4-20.5	16.61	1.74	0.26	10.47
Leaf width (cm)	14.9-27	20.68	2.27	0.33	10.98
Petiole length (cm)	16.50-28.1	22.60	2.95	0.43	13.05
Node no. for first female flower	5-9	6.94	1.10	0.16	15.85
Node no. for first male flower	1-2	1.33	0.38	0.06	28.57
Day to 50% flowering	19-38	28.06	5.51	0.81	19.64
Inter-nodal length (cm)	1.5-7.5	3.70	1.79	0.26	48.38
Peduncle length (cm)	2.1-8	4.33	1.32	0.19	30.48
Fruit polar diameter (cm)	4.1-16.1	9.73	2.55	0.38	26.21
Fruit equatorial diameter (cm)	7.1-13.9	10.03	1.46	0.21	14.56
Fruit shape index	0.5-1.9	0.99	0.29	0.04	29.29
Seed cavity (cm)	7.1-14.1	10.04	1.53	0.22	15.24
Flesh thickness (cm)	1.2-3	1.48	0.31	0.04	20.94
Days to harvest	53-71.3	62.41	5.03	0.74	8.06
No. of fruits/plant	1-5	2.11	0.75	0.11	35.54
Average fruit weight (kg)	0.2-1.2	0.48	0.18	0.02	37.50
Fruit yield/plant (kg)	0.3-1.4	0.81	0.30	0.04	37.04
Fruit yield/ha (t)	10-41.8	23.79	8.81	1.30	37.03
Number of seeds/fruit	46-194	131.48	41.67	6.14	31.69
100 seed weight (g)	4.7-10.5	7.77	1.61	0.24	20.72
Seed yield/fruit (g)	4.1-15.5	10.32	3.03	0.44	29.36
Seed yield/plant (g)	5.9-41.3	20.70	8.04	1.18	38.84
Seed yield/hectare (kg)	205.1-1211.1	606.49	235.46	34.71	38.82
Sugar content (%)	2.6-7.5	6.90	2.78	0.41	42.29
Starch content (%)	2.5-11.1	6.90	2.79	0.41	40.43
Fiber content (%)	2.3-8	5.03	1.46	0.21	29.02
Dry matter (%)	92-96.3	94.66	0.90	0.13	0.95
Ash content (%)	4-7.3	5.22	0.80	0.183	15.32
Oil content (%)	15-38.3	25.38	6.54	0.96	25.77
Oil yield/ha (t)	0.3-.48	0.16	0.08	0.01	50.0
Protein (%)	1-2-2.8	2.04	0.45	0.06	22.06

Dry matter (0.95%) and leaf length (10.47 cm) exhibit minimum degree of variation while vine length (53.34 cm) and oil content (50.0%) has shown the highest variability. In present set

of germplasm, PWT-38 (53 days to harvest) and PWT-12 (71.30 days to harvest) were identified as early- and late- maturing accessions, respectively. The maximum vine length was recorded in PWT-15 (175.40 cm) while the minimum in PWT-43 (28.60 cm). Fruit yield/ha ranged from 10.0 (PWT-34) to 41.80 tonnes (PWT-25) with an average of 23.79 tonnes. The maximum oil and seed yield/ha were recorded for PWT-41. These accessions may serve as valuable useful genetic resources to breed high seed and oil yielding hull-less cultivars.

Among the 46 genotypes, PWT-27 was having orange flesh colour, whereas, PWT-5, PWT-6, PWT-21 and PWT-30 were having cream colour flesh. However, 21 genotypes were having yellow flesh colour and 20 were having light yellow (Table 2).

Table 2. Fruit flesh colour of different genotypes

Serial No.	Genotype	Flesh Colour	Serial No.	Genotype	Flesh Colour
1	PWT-1	Light Yellow	30	PWT-31	Yellow
2	PWT-2	Yellow	31	PWT-32	Yellow
3	PWT-3	Yellow	32	PWT-33	Light Yellow
4	PWT-4	Yellow	33	PWT-34	Yellow
5	PWT-5	Cream	34	PWT-35	Light Yellow
6	PWT-6	Cream	35	PWT-36	Yellow
7	PWT-7	Light Yellow	36	PWT-37	Light Yellow
8	PWT-8	Light Yellow	37	PWT-38	Light Yellow
9	PWT-9	Light Yellow	38	PWT-39	Light Yellow
10	PWT-10	Light Yellow	39	PWT-40	Light Yellow
11	PWT-11	Yellow	40	PWT-41	Yellow
12	PWT-12	Yellow	41	PWT-42	Light Yellow
13	PWT-13	Yellow	42	PWT-43	Light Yellow
14	PWT-14	Yellow	43	PWT-44	Light Yellow
15	PWT-15	Yellow	44	PWT-45	Yellow
16	PWT-16	Yellow	45	Lady Godiva	Yellow
17	PWT-17	Light Yellow	46	PCK-1	Yellow
18	PWT-18	Yellow			
19	PWT-19	Yellow			
20	PWT-20	Yellow			
21	PWT-21	Cream			
22	PWT-22	Light Yellow			
23	PWT-23	Yellow			
24	PWT-25	Light Yellow			
25	PWT-26	Light Yellow			
26	PWT-27	Orange			
27	PWT-28	Light Yellow			
28	PWT-29	Light Yellow			
29	PWT-30	Cream			

SEDLACKOVA and AVAGYAN (2022) reported the fruit weight ranging from 521.5 to 12744.7 g, fruits length 85.00 to 285.00 mm, fruits width 114 to 320 mm, fresh seed weight 17.30 to 638.50 g and 1000 seed weight 15.41 to 475.66 g. However, the results were in consistent with current experiment.

Principal component analysis, Cluster and Correlation Analysis

Principal component analysis (PCA) was performed on different traits in hull-less pumpkin germplasm and 82.014% of total variation was explained by 11 principal components (PCs) with Eigen values >1 (Table 3). The first principal component (PC1) accounted for 16.027% of the total variation, with seed yield per fruit, seed yield per plant and petiole length showing the highest positive effects (Figure 1). The second principal component (PC2) explained 13.07% of the variation, with the greatest positive contributions from fruit polar diameter and fruit weight (Supplementary Table S1).

Table 3. Eigen value and their percentage of variation for different traits in hull-less pumpkin germplasm

Eigen Vector	Eigen Value	Variation %	Total Variation %
1	5.2888	16.027	16.027
2	4.2923	13.007	29.034
3	3.4474	10.447	39.480
4	2.4306	7.365	46.846
5	2.3055	6.986	53.832
6	2.0219	6.127	59.959
7	1.9255	5.835	65.794
8	1.7061	5.170	70.964
9	1.3958	4.230	75.193
10	1.1525	3.492	78.686
11	1.0985	3.329	82.014

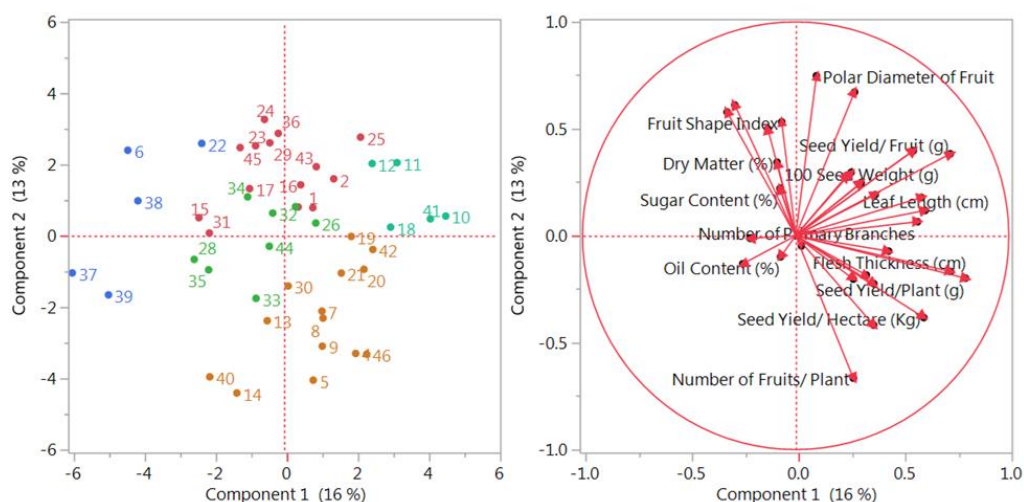


Figure 1. Principal Component Analysis

The hierarchical clustering based on Ward's method grouped 46 pumpkin accessions into five clusters. The parental lines (PCK1 and Lady Godiva) were found to be diverged from each other and grouped in separate clusters. The accessions with bushy growth habit, high oil yield, number of fruit/plant and fiber content come together in Cluster 4, whereas, thick flesh fruits, high fruit yield and seed yield accessions grouped in Cluster 5 (Figure 2). While early maturing accessions comes under Cluster 3 (Supplementary Table S2). The accessions with high sugar were grouped in Cluster 4, whereas, high dry matter and starch containing were grouped in Cluster 2.

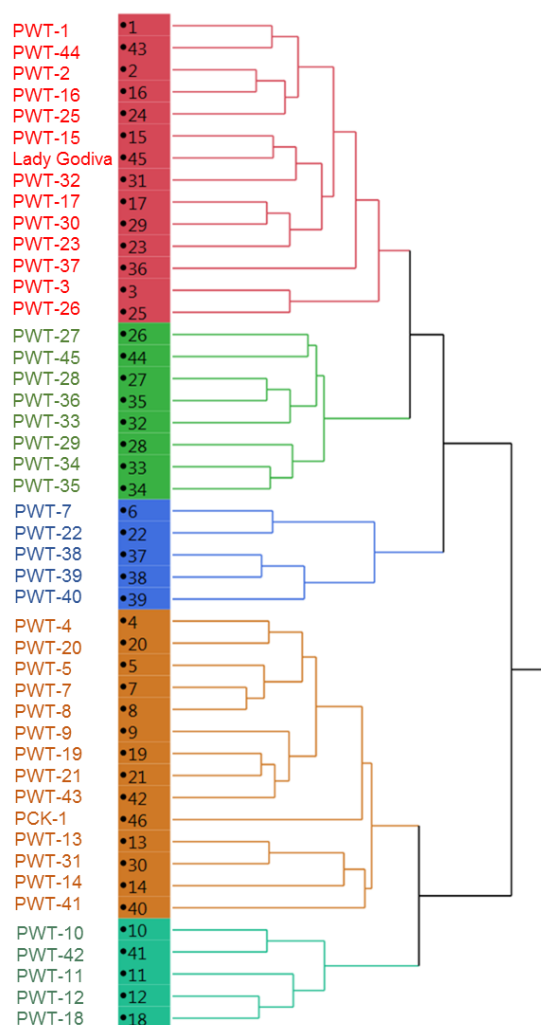
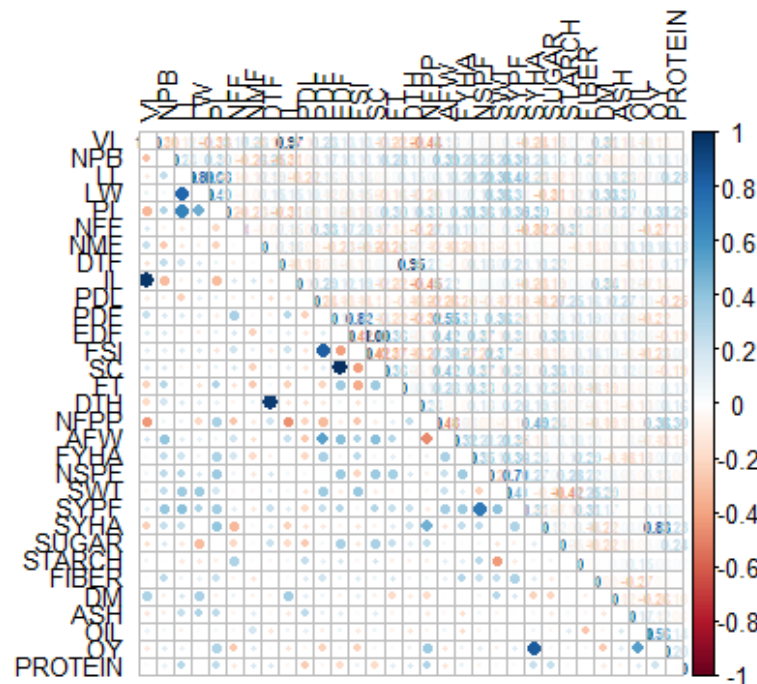


Figure 2. Hierarchical clustering based on Ward coefficient

TOMIC *et al.*, (2024) reported similar results, presenting the genotypic grouping into five different clusters based on their genetic constitution, which was independent of their geographical origins.

The Pearson correlation was calculated for various traits which indicate that oil yield and oil content are not strongly associated with other morphological and biochemical traits under investigation. Vine length showed high positive correlation with inter-nodal length, while negative with petiole length and number of fruits per plant. Seed yield/fruit show high positive correlation with number of primary branches, leaf length, leaf width, petiole length, fruit equatorial diameter, seed cavity fruit yield and oil content. Fruit yield/ hectare show high positive correlation with petiole length and fruit polar diameter (Figure 3).



VL-Vine length (cm), NPB- No. of Primary branches, LL- Leaf length (cm), LW- Leaf width (cm), PL- Petiole length (cm), NFF- Node No. for first female flower, NMF- Node No. for first male flower, DTF- Day to 50% flowering, IL- Inter-nodal length (cm), PDL- Peduncle length (cm), PDF- Fruit Polar Diameter (cm), EDF- Fruit Equatorial Diameter (cm), FSI- Fruit Shape Index, SC- Seed Cavity (cm), FT- Flesh thickness (cm), DTH- Days to Harvest, NFP- No. of fruits/plant, AFW- Average fruit weight (Kg), FYP-Fruit yield/plant (Kg), FYHA- Fruit Yield/ha (Tonne), NSPF- Number of seeds/fruit, SWT- 100 seed weight (g), SYF- Seed yield/fruit (g), SYHA- Seed yield/hectare (Kg), Sugar content (%), starch content (%), fiber content (%), Dry matter (%), Ash content (%), Oil content (%), Oil yield/ha, Protein content (%)

Figure 3. Correlation among the fifteen morphological traits of pumpkin

Table 4. Heritability (Hy), Genetic Advance (GA), Genetic Advance in percent of Mean (%GA), Phenotypic Coefficient of Variance (PCV) and Genotypic Coefficient of Variance (GCV)

Serial no.	Traits	Hy (%)	GA	% GA	PCV	GCV
1	Vine length (cm)	92.24	85.23	104.08	54.77	52.61
2	No of primary branches	23.29	0.36	15.25	31.78	15.34
3	Leaf length (cm)	78.45	3.04	18.29	11.32	10.02
4	Leaf width (cm)	73.45	3.79	18.32	12.11	10.37
5	Petiole length (cm)	70.08	4.76	21.07	14.59	12.22
6	Node of 1st female flower	35.11	1.06	15.29	21.13	12.52
8	Days to 50% flowering	77.40	9.35	33.04	20.72	18.23
9	Inter-nodal length (cm)	91.72	3.47	93.53	49.5	47.41
10	Peduncle length (cm)	79.55	2.33	53.82	32.84	29.29
11	Polar diameter (cm)	90.44	4.76	48.70	26.14	24.86
12	Equator diameter (cm)	71.54	2.50	24.87	16.88	14.28
13	Fruit shape index	81.34	0.53	53.47	31.91	28.78
14	Seed cavity (cm)	71.54	2.50	24.87	16.88	14.28
15	Flesh thickness (cm)	74.61	0.54	36.64	23.84	20.59
16	Days to harvest	73.81	8.43	13.50	8.88	7.63
17	No of fruits/plant	40.68	0.65	31.80	37.95	24.20
18	Average fruit weight (kg)	80.18	0.31	65.14	39.44	35.32
19	Fruit yield/plant (kg)	64.17	0.46	56.11	42.45	34.00
20	Fruit yield/ha (t)	64.31	13.37	56.21	42.43	34.03
21	No of seeds/fruit	76.25	71.19	54.93	34.97	30.54
22	100 seed weight (g)	62.47	2.40	30.80	23.94	18.92
23	Seed yield/fruit (g)	61.83	4.53	44.27	34.76	27.33
24	Seed yield/plant (g)	50.05	10.15	49.01	47.54	33.63
25	Seed yield/ha (kg)	50.05	297.25	49.01	47.54	33.63
26	Sugar content (%)	43.58	1.45	26.92	29.98	19.79
27	Starch content (%)	82.43	5.03	72.81	42.88	38.93
28	Fibre content (%)	74.79	2.47	49.16	31.91	27.60
29	Dry matter (%)	59.20	1.28	1.35	1.11	0.85
30	Ash content (%)	36.90	0.80	15.29	20.12	12.22
31	Oil content (%)	41.09	7.10	27.99	33.07	21.2
32	Oil yield/ha (t)	44.74	0.09	59.57	64.63	43.23
33	Protein (%)	79.41	0.79	38.49	23.53	20.97

The result provide important insights into genetic variability for quality related and agronomic traits. The genotypic and phenotypic coefficient of variation, heritability estimates, genetic advance and genetic advance in percent of mean are presented in Table 4. The phenotypic coefficients of variation were higher than the genotypic coefficient of variation for all the character studied. Out of 33 characters, oil yield per hectare and leaf length showed the highest difference between genotypic and

phenotypic coefficients of variation (GCV and PCV) in comparison to remaining characters. The characters, vine length, inter-nodal length, starch content, fruit shape index and average fruit weight showed high genetic advance in % of mean in association with high heritability.

Genotypic and phenotypic coefficient of variations and high heritability along with moderate genetic advance (GA) in percent of mean were estimated for number of nodes for first female flower. High heritability with high GA % was found in genotypes which suggested that improvement would be effective through phenotypic selection. High heritability coupled with high GA suggested that effective selection might be done. High heritability was reported for vine length and inter-nodal length and relatively high genetic advance for seed yield per hectare and vine length.

The phenotypic coefficients of variation were higher than genotypic coefficient of variation for all the character studied indicating predominance of environmental effects on the expression of these characters. Node of 1st male flower and oil yield per hectare showed the highest difference between GCV and PCV, indicating relatively higher influence of environmental effect on the expression of these characters. Genotypic and phenotypic coefficient of variations and high heritability along with moderate genetic advance (GA) in percent of mean were estimated for number of nodes for first female flower.

The research findings of current study are in partial agreement with HASSANEIN *et al.*, (2025), where, majority of the traits showed high GCV/PCV percentages. Thus, the high phenotypic variation complemented by high genotypic variation and less environmental effect specified the presence of substantial genetic variability for several traits. In the nutshell, phenotypic selection alone may be effective for improving the required traits.

CONCLUSION

It can be concluded that the germplasm lines of pumpkin developed in breeding programme, used in the present investigation has significant divergence for growth habit, quality (except dry matter), fruit, seed and oil yield. Based on Mahalanobis D^2 analysis of morphological and biochemical traits, the germplasm could be grouped into five distinct clusters. In future breeding programmes for improvement in pumpkin, the selection of parents can be effective from highly divergent groups and this selection can be focused on the above mentioned highly diverse and contrasting traits.

DATA AVAILABILITY STATEMENT

The data supporting this article are available in the online supplementary dataset.

Received, July 27th, 2025

Accepted April 10th, 2026

REFERENCES

- AL-JIBOURI, H.A., MILLER P.R., H.F. ROBINSON (1958): Genotypic and environment variances and co-variances in an upland cotton cross of interspecific origin. *Agronomy Journal* 50, 633–36.

- ANONYMOUS, (2015): Package of practices for Cultivation of Vegetables, Punjab Agricultural University, Ludhiana.11-12.
- AOAC (2005): *Official Methods of Analysis*, Association of Official Analytical Chemists, Washington, DC.
- CLEGG, K.M. (1956): The application of the anthrone reagent to the estimation of starch in cereals. *J. Sci. Food Agric* 7, 40.
- FOLCH, J., M. LEES, SLOANE-STANLEY (1957): A simple method for isolation and purification of total lipids from animal tissues. *J. Biol. Chem.* 226, 497-506.
- HASSANEIN, I.M., M.A.ABDEIN, A.A. RASHWAN, A.A. EL-SHAHENY, G.A. ZAYED (2025): Genetic Variability and Character Associations for Quantitative Traits of Squash (*Cucurbita pepo*) Genotypes. *Journal of Plant Production* 16(10), 609-14.
- HAZRA, P., A.K. MANDAL, A.K. DUTTA, H.H. RAM (2007): Breeding Pumpkin (*Cucurbita moschata* Duch. ex Poir.) for fruit yield and other characters. *International J Plant Breeding*, 1(1), 51-64
- KASSAMBARA, A., F. MUNDT (2020): Factoextra: extract and visualize the results of multivariate data analyses R Package Version 1.0.7. Available at <https://CRAN.R-project.org/package=factoextra>.
- LELLEY, T., B. LOY, M. MURKOVIC (2009): Hull-Less Oil Seed Pumpkin. In *Oil Crops*. Springer, New York 4, 469-92.
- LOEWUS, F.A. (1952): Improvement in anthrone method for the determination of carbohydrates. *Anal. Chem.* 24, 219-20.
- LOWRY, O.H., N.J. ROSEBROUGH, A.L. FARR, R.J. RANDOU (1951): Protein measurement with the Folin-phenol reagent. *J. Biol. Chem.* 193, 265-75.
- LOY, J.B. (1991): Hull-less seeded pumpkins: A new edible snack seed crop. In: J. Janick and J. E. Simon (Eds.) *Advances in New Crops*. Timber Press, Portland, 403-07.
- MAHALANOBIS, P.C. (1936): On the generalized distance in statistics. *Proc. Nat. Sci.* 2, 49-55.
- PANDEY, S., J. SINGH, A.K. UPADHYAY, D. RAM AND M. RAI (2003): Ascorbate and Carotenoid Content in an Indian Collection of Pumpkin (*Cucurbita moschata* Duch. ex Poir.). *Cucurbit Genetics Cooperative Report* 26, 51-53.
- PATEL, S. (2013): Pumpkin (*Cucurbita sp.*) seeds as nutraceutic: a review on status quo and scopes. *Mediterranean Journal of Nutrition and Metabolism* 6 (3): 183-89.
- SAS INSTITUTE (2009): Statistical analysis software system, Version 9.3. SAS Institute, Cary, NC, USA.
- SEDLACKOVA, V.H., A. AVAGYAN (2022): Morphological characteristics of selected fruit parts and naked seeds of *Cucurbita pepo* var. styriaca. *Agrobiodiversity for Improving Nutrition, Health and Life Quality*, 6(2).
- TEPPNER, H. (2000): *Cucurbita pepo* (Cucurbitaceae) – History, seed coat types, thin coated seeds, and their genetics. *Phyton* 40, 1-42.
- TOMIC, D., M. RADOVANOVIC, M. MARJANOVIC, V. DUROVIC, V. STEVOVIC, N. PAVLOVIC, D. LAZAREVIC, V. ZORNIC, M. MADIC (2024): Divergence analysis of *Cucurbita pepo* L. population for seed oil production. *Notulae Botanicae Horti Agrobotanici Cluj-Napoca* 52(4), 13907.
- ZRAIDI, A., R. OBERMAYER, R. PACHNER, T. LELLEY (2003): On the genetics and histology of hull-less character of Styrian oil-pumpkin (*Cucurbita pepo* L.). *Cucurbit Genet. Coop. Rpt* 26, 57–61.

**ANALIZA GENETSKE VARIJABILNOSTI, NASLEDNOSTI I ASOCIJACIJE
KARAKTERISTIKA BUNDEVE GOLICA
(*Cucurbita pepo* subsp. *pepo* var. *styriaca*)**

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Izvod

Golica bundeve su evoluirale zahvaljujući jednoj recesivnoj mutaciji i njihova konzumacija ima brojne zdravstvene koristi. Genetska varijacija golica je ograničena zbog jakog selekcijskog pritiska za određene vrste semena i njihovog gajenja u uskom geografskom regionu. U tom kontekstu, razvili smo segregacijske populacije iz kultivara sa i bez ljuske i odabrali 44 linije bez ljuske kako bismo proširili genetsku bazu golica bundeva. U ovoj studiji, 46 populacija golica bundeva je okarakterisano u smislu genetske varijabilnosti, nasleđivanja i analize asocijacije karakteristika. Morfološka i biohemijska karakterizacija otkrila je značajnu varijabilnost za oblik rasta, kvalitet (osim suve materije), prinos ploda, semena i ulja. Analiza glavnih komponenti (PCA) otkrila je jedanaest značajnih PC koje su objasnile 82,014% ukupne varijacije. Klaster analiza grupisala je ispitivane populacije u pet klastera. Oblik rasta, prinos ploda, semena i ulja pokazuju visoku pozitivnu korelaciju sa drugim osobinama.

Primljeno 27. VII. 2025.

Odobreno 10. IV. 2026.

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How to cite this article: Kaur K., A. S. Dhatt and J. Singh Khosa (2026): *Genetic variability, heritability and character association analysis in hull-less pumpkin (*Cucurbita pepo* subsp. *pepo* var. *styriaca*)*. - Genetika, Vol 58, No. 1, 43-53.