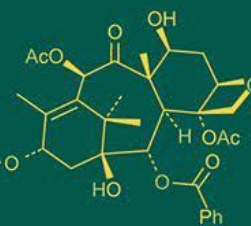
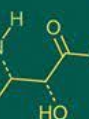
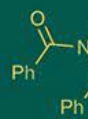
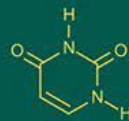
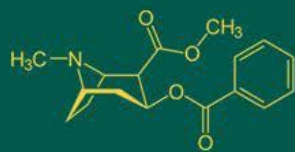


International Journal of Advanced Biochemistry Research



ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2026): 5.29
IJABR 2026; SP-10(1): 886-892
www.biochemjournal.com
Received: 15-10-2025
Accepted: 17-11-2025

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Analysis of Variability and Genetic Divergence in Horse Gram for Breeding Applications

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DOI: <https://www.doi.org/10.33545/26174693.2026.v10.i1Sk.7119>

Abstract

Horse gram (*Macrotyloma uniflorum*) is an important underutilized legume valued for its adaptability to drought-prone environments, nutritional richness and significance in traditional farming systems. Despite its resilience, productivity remains low due to limited genetic improvement. This study evaluated thirty horse gram germplasm lines during *Rabi* 2017 at RARS, Palem, to assess genetic variability and divergence using analysis of variance, variability parameters, principal component analysis and cluster analysis. Significant differences were detected for all traits except number of branches per plant and number of pods per plant. Wide variation was observed for days to 50% flowering, days to maturity, pod number, seed number, seed size and yield. Phenotypic variance exceeded genotypic variance for most traits and high heritability coupled with high genetic advance was recorded for one hundred seed weight and seed yield, indicating strong additive gene action. Principal component analysis revealed that the first three components explained 72.39% of the total variation, with seed yield contributing most strongly. K-means clustering grouped the germplasm into four distinct clusters, supported by hierarchical clustering. Divergent genotypes such as PHGG-131, PHGG-132, PHGG-157, PHGG-161, PHGG-170, PHGG-171, PHGG-183, PHGG-184, PHGG-198 and PHGG-200 were identified as potential parents. The combined findings provide a strong basis for selection and the development of improved horse gram varieties.

Keywords: Cluster, Germplasms, Genetic variability, Horse gram, PCA

Introduction

Horse gram (*Macrotyloma uniflorum* (Lam.) Verdcourt) is an important underutilized legume cultivated across diverse agro-ecological regions of the Indian subcontinent, particularly in traditional and resource-poor farming systems. It has remained an integral component of subsistence agriculture for centuries and continues to play a vital role as a food, fodder and green manure crop in several South Asian countries, including India, Nepal, Bhutan, Bangladesh, Myanmar, Sri Lanka and Malaysia (Jeswani and Baldev, 1990; Witcombe *et al.*, 2008, Kumari *et al.*, 2025) [10, 29, 13]. Known by various regional names such as Kulthi, Kollu, Ullavalu, Gahat and Mudhira, the crop has historically supported rural diets because of its ability to thrive under extreme climatic conditions, minimal cultivation inputs and low soil fertility (Bhartiya *et al.*, 2017, Kumari *et al.*, 2025) [3, 13]. India remains the largest global producer of horse gram, with major cultivation concentrated in Karnataka, Tamil Nadu, Maharashtra, Andhra Pradesh and Odisha (Kumar, 2007, Kumari *et al.*, 2025) [12, 13]. Owing to its resilience, the crop is widely adopted in dryland agriculture where other pulses fail to perform effectively.

The species is a self-pollinated diploid legume ($2n = 20, 22$ or 24) with a compact genome of approximately 398-400 Mb, contributing to its genetic stability and adaptability (Padha *et al.*, 2025; Chahota *et al.*, 2017) [19, 6]. Although the precise centre of origin continues to be debated, several classical and contemporary studies indicate India particularly southwestern India as the primary centre of domestication, with Africa serving as an important gene-rich region of the genus *Macrotyloma* (Sharma *et al.*, 2015) [22]. Wild relatives of *M. uniflorum* occur extensively across Africa, Central and Southern India, underscoring the crop's rich evolutionary base and the potential for utilizing wild germplasm in breeding programmes. Agronomically, horse gram is recognized for its exceptional drought tolerance and ability to survive in sub-humid to semi-arid climates with temperatures ranging from 25 to 30 °C and

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even up to 40 °C (Padha *et al.*, 2025) ^[19]. It is commonly cultivated as a late-season catch crop in rainfed systems and performs well on poor, gravelly and marginal soils. In addition to food and fodder uses, horse gram is valued as a green manure crop because of its substantial nitrogen-fixing ability and biomass production, making it a suitable component in sustainable cropping systems (Sivan *et al.*, 2022; Bhartiya *et al.*, 2014) ^[27, 31]. The seeds of horse gram are nutritionally rich, containing 17.9-30.4% protein, 51.9-60.9% carbohydrates, essential amino acids and minerals such as phosphorus, iron and molybdenum, along with vitamins including carotene, thiamine, riboflavin, niacin and vitamin C (Padha *et al.*, 2025; Chahota *et al.*, 2017) ^[19, 6]. The crop also contains a wide range of polyphenols and antioxidants, contributing to its various therapeutic properties. Studies have demonstrated its antimicrobial, antidiabetic, antiurolithiatic, anti-obesity and anti-ulcer activities (Ramesh *et al.*, 2011; Jayaraj *et al.*, 2000; Bhatt and Karim, 2009; Chaitanya *et al.*, 2010; Sharma *et al.*, 2015; Chahota *et al.*, 2017) ^[22, 6, 26, 9]. These multifaceted nutritional and medicinal attributes have positioned horse gram as a “future food crop” capable of contributing significantly to food and nutritional security in rural, tribal and climate-vulnerable communities. Despite its agronomic resilience and nutritional significance, horse gram has long remained neglected in mainstream crop improvement initiatives. The crop suffers from low productivity, limited availability of improved varieties and a narrow genetic base due to its cultivation mostly on marginal lands with minimal scientific intervention (Sahoo *et al.*, 2014; Sharma *et al.*, 2015; Sivan *et al.*, 2022) ^[26, 27]. This underutilization is further compounded by entrenched biases and the perception of horse gram as a minor pulse, resulting in fewer breeding programmes compared with other pulse crops. As a consequence, systematic genetic improvement efforts have lagged behind, limiting yield enhancement and adaptation to emerging climatic challenges. A comprehensive understanding of the extent of genetic variability and diversity present in available germplasm is crucial for strengthening breeding strategies aimed at developing high-yielding and climate-resilient cultivars. Evaluating genetic variability for key agromorphological traits provides insights into the potential for effective selection, especially for complex traits like yield, which exhibit polygenic inheritance and strong environmental influence (Sivan *et al.*, 2022) ^[27]. Multivariate approaches such as principal component analysis (PCA) and hierarchical cluster analysis further facilitate the identification of major sources of variation, trait associations and grouping of genotypes into distinct clusters for hybridization (Sahoo *et al.*, 2014; Padha *et al.*, 2025) ^[23, 19]. The combination of classical variability parameters with multivariate statistical tools enables a holistic understanding of the genetic structure of germplasm, thereby supporting the selection of diverse and promising parental lines. Given these gaps and opportunities, the assessment of variability, genetic divergence and trait contribution patterns in horse gram germplasm is essential for formulating effective improvement programmes. The present study integrates analysis of variance, variability parameters, PCA and hierarchical clustering to characterize genetic diversity and identify promising genotypes that can be utilized in future breeding efforts.

Material and Methods

The study was conducted during *Rabi* 2017 at the Regional Agricultural Research Station (RARS), Palem, under

Professor Jayashankar Telangana Agricultural University (PJTUAU), using a total of 30 horse gram germplasm lines. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications and the genotypes were sown at a spacing of 30 cm × 25 cm under optimal field conditions, following standard agronomic practices to ensure uniform crop establishment. Data were recorded on seven quantitative traits using standard evaluation procedures, selecting five healthy and representative plants at random from each plot in every replication. Days to 50% flowering (DF) was noted as the number of days from sowing to when 50% of the plants produced at least one open flower, while days to maturity (DM) represented the number of days to physiological maturity when about 75-80% of the pods had turned brown. The number of branches per plant (NB) was counted as all fully developed primary branches on each selected plant and the number of pods per plant (NP) was recorded as the total number of mature pods at harvest. The number of seeds per pod (NS) was estimated by counting seeds from ten randomly selected pods per plant and taking the average. The 100-seed weight (HSW) was determined by weighing 100 dried, clean seeds from the bulk seed lot of each plot using a digital precision balance. Seed yield per hectare (SYH) was calculated from the cleaned plot yield using the formula:

$$(\text{SYH (kg/ha)}) = (\text{Plot yield (kg)} / \text{Plot area (m}^2\text{)}) \times 10,000,$$

representing the genotypic productivity under field conditions. Morphological data were analyzed in R studio (R Core Team, 2016) using analysis of variance (ANOVA) to test the significance among genotypes and genetic variability parameters including phenotypic and genotypic coefficients of variation (PCV and GCV) and broad-sense heritability were estimated using the *variability* package in R. Principal Component Analysis (PCA) and hierarchical cluster analysis (Ward's method) were performed using the *FactoMineR* and *factoextra* packages to assess genetic divergence and classify the genotypes based on trait similarity.

Results and discussion

Analysis of variance and mean performance

Analysis of variance (ANOVA) was conducted to determine significant differences among accessions for each trait and to partition the observed variability into its components. The results revealed that all traits were significant or highly significant, except the number of branches per plant and the number of pods per plant, which were non-significant (Table 1). The significant variation among the germplasm entries in the present study indicates substantial genetic diversity, offering ample scope for genetic improvement. Plant breeders consistently assess genetic diversity to identify divergent parents, as crosses between genetically diverse genotypes often yield higher heterotic effects. Several studies support this concept, including reports by Sahoo *et al.* (2014) ^[23], Sivan *et al.* (2022) ^[27], Visakh and Bindu (2022) ^[28], Karthik *et al.* (2023) ^[11] and Padha *et al.* (2025) ^[19].

Mean performance revealed wide variability among the accessions: days to 50% flowering ranged from 50 days (PHGG-132) to 60.33 days (PHGG-187 and PHGG-188); days to maturity ranged from 93.33 days (PHGG-131) to

133.33 days (PHGG-170). The number of branches per plant varied from 3 (PHGG-133) to 6.67 (PHGG-157), while the number of pods per plant ranged from 13.67 (PHGG-131) to 52.67 (PHGG-185). The number of seeds per pod varied from 2 (PHGG-131) to 5.67 (PHGG-146), 100-seed weight ranged from 2.63 g (PHGG-161) to 11.33 g (PHGG-184) and seed yield ranged from 525.67 kg/ha (PHGG-161) to 1265.33 kg/ha (PHGG-198). Similar trends have been reported by Kumari *et al.* (2025) [13] and Karthik *et al.* (2023) [11]. Early-maturing accessions with higher yield, more pods per plant and a greater number of seeds per pod are particularly valuable for breeding programmes targeting short growing seasons or rapid crop turnover. These results underline the importance of selecting early-flowering and early-harvesting genotypes to meet the requirements of both farmers and plant breeders.

Genetic Variability

Genetic variability forms the foundation of any successful breeding programme, as it determines the potential for improving desirable traits (Lavudya *et al.*, 2024a) [15]. In the present study, phenotypic variance exceeded genotypic variance for all traits except seed yield (kg/ha), indicating strong environmental influence. The phenotypic (PCV) and genotypic (GCV) coefficients of variation were highest for number of branches per plant, hundred seed weight and seed yield (kg/ha), while traits such as days to 50% flowering and days to maturity exhibited lower PCV and GCV. Number of seeds per pod showed moderate GCV with relatively high PCV. Heritability estimates, combined with genetic advance as a percentage of the mean (GAM), provide insight into gene action and selection efficiency (Lavudya *et al.*, 2024a) [15]. High heritability was observed for days to maturity, hundred seed weight and seed yield (kg/ha), whereas days to 50% flowering and number of pods per plant exhibited moderate heritability; number of seeds per pod recorded low heritability. High GAM was noted for number of pods per plant, hundred seed weight and seed yield (kg/ha), while moderate GAM occurred in days to maturity and number of seeds per pod; lower GAM was recorded for days to 50% flowering and number of branches per plant. In horse gram breeding, traits with high genetic variability, heritability and genetic advance are particularly important for effective improvement. Heritability helps identify the proportion of variation that is genetically controlled, enabling the selection of superior plants from diverse populations (Lavudya *et al.*, 2024a; Lavudya *et al.*, 2023) [15, 16]. Combining heritability with GAM provides more reliable guidance for selection. In this study, PCV consistently exceeded GCV, indicating considerable environmental influence and suggesting that selection based solely on phenotype may be less reliable; thus, evaluation across multiple environments or emphasis on traits with high heritability is recommended. Similar findings on variability parameters have been reported in earlier studies. Sivan *et al.* (2022) [27] observed that PCV was higher than GCV, with heritability and GAM ranging from low to high. Visakh and Bindu (2022) [28] reported similar trends, noting moderate to high heritability along with low to high GAM. Mate *et al.* also documented higher PCV than GCV, accompanied by moderate to high heritability and GAM. Karthik *et al.* (2023) [11] found that phenotypic variance consistently exceeded genotypic variance. Similarly, Padha *et al.* (2025) [19] confirmed these patterns, recording higher PCV than

GCV with moderate to high heritability and GAM ranging from low to high.

Genetic Divergence

PCA and cluster analysis are essential multivariate tools for exploring genetic diversity, tracing crop evolution, selecting parental lines and studying environmental interactions (Sampath *et al.*, 2023; Lavudya, 2024b) [25, 17]. In this study, PCA was used to examine relationships among traits, identifying seven principal components (PCs), of which the first three had eigenvalues greater than 1 (Table 3). PC1 explained 38.12% of the total variation, followed by PC2 with 18.46% and PC3 with 15.81%. The scree plot showed that these three PCs captured the majority of the variation, making them crucial for understanding trait interrelationships, while the remaining PCs contributed minimally (Figure 1). Most traits showed positive factor loadings on PC1, except days to maturity and number of seeds per pod; on PC2, all traits were positively loaded except days to flowering; while all traits exhibited positive loadings on PC3.

Genotypes such as PHGG-131, PHGG-132, PHGG-157, PHGG-161, PHGG-170, PHGG-171, PHGG-183, PHGG-184, PHGG-198 and PHGG-200 were positioned farther from the centroid in the PCA biplot (Figure 2), indicating higher genetic divergence and greater potential for use in breeding programmes. The principal components were primarily influenced by seed yield (kg/ha), highlighting its major role in shaping the observed variability (Figure 3), whereas other traits contributed less. Biplot analysis based on the first two PCs further visualized genotype-trait relationships, showing strong positive associations among the trait vectors (Figure 4). In PCA, acute angles between trait vectors indicate positive correlations, whereas right angles indicate independence; however, correlation coefficients should be computed separately for accurate interpretation (Antony *et al.*, 2021; Lavudya *et al.*, 2024b) [2, 17]. Similar reports have been documented in earlier studies. Kumari *et al.* (2025) [13] found that the first three principal components explained 69.57% of total variation, with PC1 alone accounting for 40.55%. Rajaprakasam *et al.* (2023) [21] reported that the first two PCs together explained 93.7% of the variation. Likewise, Kumara *et al.* observed that the first three PCs accounted for 88.32% of the total variability.

Cluster analysis grouped the genotypes based on trait similarity. The elbow method identified four as the optimal number of clusters ($k = 4$) (Figure 5). K-means clustering, performed on standardized data, classified the germplasms into four distinct groups, which was further supported by hierarchical clustering using Ward's method that clearly separated the genotypes in the dendrogram. Cluster I and Cluster II each contained six germplasms, Cluster IV consisted of seven germplasms, while Cluster III had the highest number with eleven germplasms. Similar reports were observed in earlier genetic diversity studies. Sivan *et al.* (2022) [27] grouped 30 genotypes into eight distinct clusters, whereas Sahoo *et al.* (2014) [23] reported six clusters among 48 genotypes. Padha *et al.* (2025) [19] categorized 22 genotypes into four clusters, demonstrating clear genetic divergence. Likewise, Kumari *et al.* (2025) [13] employed hierarchical cluster analysis (HCA) and K-means cluster analysis (KCA) to classify 150 accessions, reinforcing previous findings and aligning with the recommendation of Yoo *et al.* (2020) [30] that HCA and

KCA are among the most widely used and effective methods for germplasm grouping. Together, the clustering and PCA results highlight substantial genetic divergence among the studied genotypes, providing a strong foundation

for selecting diverse parental lines in future horse gram breeding programmes and offering valuable resources for genetic improvement.

Table 1: Analysis of variance (ANOVA) for seven morphological traits in horse gram

Traits	Df	DF	DM	NB	NP	NS	HSW	SYH
Rep	2	14.53	63.70	2.34	65.70	1.03	21.88***	3335
Geno	29	17.55**	270.79***	2.41	294.77	3.35*	25.76***	124378 ***
Residuals	58	7.52	28.52	2.47	57.23	1.85	0.23	1702
Max	-	60.33	133.33	6.67	52.67	5.67	12.80	1287
Min	-	51.7	93.33	3	13.67	2	2.63	525.67
GM	-	56.87	110.43	4.41	37.37	3.83	11.33	998
SE	-	1.58	3.08	0.91	4.37	0.79	0.28	23.82
CD5%	-	4.48	8.73	2.57	12.36	2.22	0.79	67.42
CD1%	-	5.96	11.61	3.42	16.45	2.96	1.05	89.70

DF: Days to 50% flowering, DM: Days to maturity, NB: No. of branches per plant, NP: No. of pods per plant, NS: No. of seeds per pod, HSW: 100 seed weight, SYH: Seed yield kg / ha, Note: *, ** and *** significant at 5% 1% and 0.1% levels respectively

Table 2: Genetic parameter estimates for different traits in horse gram.

Traits	DF	DM	NB	NP	NS	HSW	SYH
EV	7.52	28.52	2.47	57.23	1.85	0.23	1701.70
GV	3.34	80.76	0.02	79.18	0.50	8.51	40892.18
PV	10.87	109.27	2.45	136.41	2.35	8.74	42593.89
ECV	4.82	4.84	35.64	20.25	35.48	6.85	4.13
GCV	3.22	8.14	3.32	23.81	18.45	41.30	20.26
PCV	5.80	9.47	35.48	31.26	39.99	41.87	20.68
H2	0.31	0.74	0.01	0.58	0.21	0.97	0.96
GA	2.09	15.91	0.03	13.97	0.67	5.93	408.16
GAM	3.67	14.41	0.64	37.37	17.54	83.94	40.89

GV: Genetic Variance, PV: Phenotypic variance, EV: Environmental Variance, GCV: Genotypic Coefficient of Variation, PCV: Phenotypic Coefficient of Variation, GA: Genetic advance, GAM: Genetic advance percent of mean, H2: Broad-sense Heritability,

Table 3: Summary of principal component analysis (PCA) and eigenvalues for morphological traits in horse gram

Principle component	EV	PV	CV
PC1	2.67	38.12	38.12
PC2	1.29	18.46	56.58
PC3	1.11		72.40
PC4	0.74	10.56	82.96
PC5	0.65	9.24	92.20
PC6	0.39	5.61	97.82
PC7	0.15	2.18	100.00

EV: Eigen values, PV: Proportional variation and CV: Cumulative variation.

Table 4: Factor loadings of principal component axes derived from PCA in horse gram

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7
DF	5.85	-0.28	0.02	7.56	-0.42	1.34	110.79
DM	-0.28	90.26	0.87	14.65	0.51	10.48	886.96
NB	0.02	0.87	0.80	3.45	0.21	0.25	27.13
NP	7.56	14.65	3.45	98.26	0.97	13.22	1264.34
NS	-0.42	0.51	0.21	0.97	1.12	0.03	4.20
HSW	1.34	10.48	0.25	13.22	0.03	8.59	476.74
SYH	110.79	886.96	27.13	1264.34	4.20	476.74	41459.42

DF: Days to 50% flowering, DM: Days to maturity, NB: No. of branches per plant, NP: No. of pods per plant, NS: No. of seeds per pod, HSW: 100 seed weight, SYH: Seed yield kg / ha.

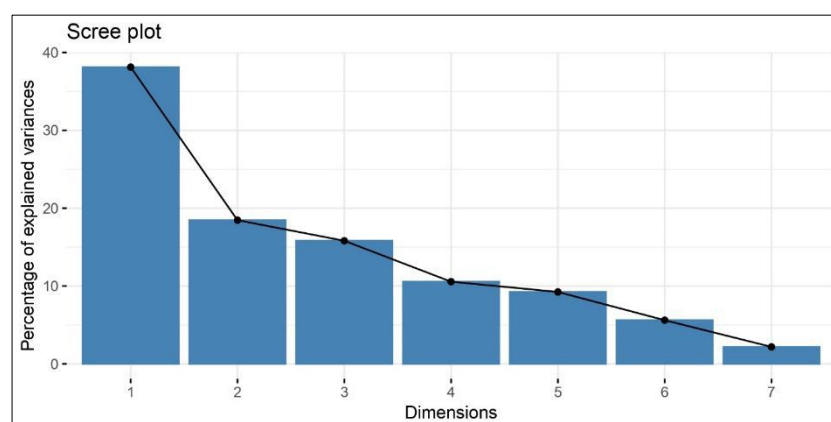
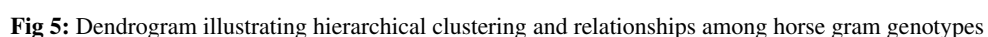
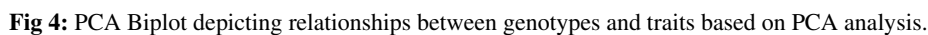
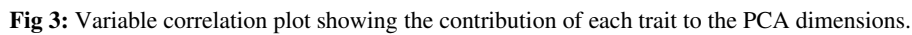
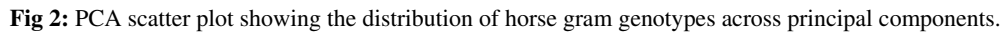


Fig 1: Scree plot showing the percentage of variance explained by each principal component.



The study revealed substantial genetic variability and divergence among the thirty horse gram germplasm lines,

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seed yield suggest predominantly additive gene action, making direct selection highly effective. Principal component analysis identified seed yield as the major contributor to overall variability, while clustering analyses clearly separated the germplasm into four distinct groups. Genotypes positioned farthest from the centroid, including PHGG-131, PHGG-132, PHGG-157, PHGG-161, PHGG-170, PHGG-171, PHGG-183, PHGG-184, PHGG-198 and PHGG-200, represent genetically diverse and superior material for use as parents in breeding programmes. The integration of variability parameters with multivariate approaches provides a comprehensive understanding of trait behaviour and genetic structure, enabling strategic parent selection for yield enhancement and adaptation. These findings contribute valuable information for designing efficient horse gram improvement programmes aimed at developing high-yielding, climate-resilient cultivars.

Conflict of interest

The authors declare that they have no conflict of interest in the publication.

Ethical approval

This article does not contain any studies with human participants or animals performed by any of the authors.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Funding

Not applicable

Grant Disclosures

Not applicable

Data Availability

The datasets produced and/or examined during this study are given as supplementary.

Credit authorship contribution statement

Maloth Ramesh: Conceptualization, Data curation, Methodology, Resources, Software, Supervision, Writing - original draft, Writing - review and editing

Acknowledgments

I sincerely thank Professor Jayashankar Telangana State Agricultural University (PJTSAU) for providing the necessary funding and research facilities that enabled the successful completion of this study.

References

1. Aatoi AWA, Kaleri MH, Fatima NA, Memon S, Mengal AA, Baloch TA, *et al.* Exploring genetic variation through line $\times$ tester analysis of sunflower (*Helianthus annuus*) genotypes for yield and oil traits under adverse environment. *Egyptian Journal of Agronomy*. 2024;46(1):131-139.
2. Antony BJ, Kachapur RM, Naidu GK, Harlapur SI. Genetic diversity study among maize (*Zea mays* L.) inbred lines. *Journal of Farm Sciences*. 2021;34(4):352-356.
3. Bhartiya A, Aditya JP, Pal RS, Bajeli J. Agro-morphological, nutritional and antioxidant properties in horsegram [*Macrotyloma uniflorum* (Lam.) Verdc.] germplasm collection from diverse altitudinal ranges of north-western Himalayan hills of India. *Vegetos*. 2017;30(1):1-9.
4. Bhartiya A, Singh S, Kumar RA, Pal RS. A traditional food legume for ensuring nutritional security in Uttarakhand hills. *Indian Farming*. 2014;64(7):45-47.
5. Bhat R, Karim AA. Exploring the nutritional potential of wild and underutilized legumes. *Comprehensive Reviews in Food Science and Food Safety*. 2009;8(4):305-331.
6. Chahota RK, Shikha D, Rana M, Sharma V, Nag A, Sharma TR, *et al.* Development and characterization of SSR markers to study genetic diversity and population structure of horsegram germplasm (*Macrotyloma uniflorum*). *Plant Molecular Biology Reporter*. 2017;35(5):550-561.
7. Chaitanya DAK, Kumar S, Reddy M, Mukherjee AM, Sumanth NSV, Ramesh DA, *et al.* Anti-urolithiatic activity of *Macrotyloma uniflorum* seed extract on ethylene glycol-induced urolithiasis in albino rats. *Journal of Innovative Trends in Pharmaceutical Sciences*. 2010;1:216-226.
8. Griffing B, Lindstrom EW. A study of the combining abilities of corn inbreds having varying proportions of corn belt and non-corn belt germplasm. *Agronomy Journal*. 1954;46:545-552.
9. Jayaraj AP, Tovey FI, Lewin MR, Clark CG. Duodenal ulcer prevalence: experimental evidence for the possible role of dietary lipids. *Journal of Gastroenterology and Hepatology*. 2000;15(6):610-616.
10. Jeswani LM, Baldev B. Advances in pulse production technology. New Delhi: Publications and Information Division, Indian Council of Agricultural Research; 1990. p. 1-350.
11. Karthik M, Wadeyar B, Soregaon CD, Ashwathama VH. Assessment of variability of horse gram (*Macrotyloma uniflorum* (Lam.) Verdc.) germplasm lines for morphological and physiological traits. *Journal of Farm Sciences*. 2023;36(2):132-135.
12. Kumar D, Vittal KPR. Production technology for horse gram in India. Jodhpur: Central Arid Zone Research Institute; 2007. p. 1-27.
13. Kumari M, Chourey SK, Arya M, Mehta PS, Bhardwaj R, Singh R, *et al.* Genetic variability studies on horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] landraces using agro-morphological traits. *Indian Journal of Plant Genetic Resources*. 2025;38(1):30-43.
14. Kumari M, Padhi SR, Chourey SK, Kondal V, Thakare SS, Negi A, *et al.* Unveiling diversity for quality traits in the Indian landraces of horsegram [*Macrotyloma uniflorum* (Lam.) Verdc.]. *Plants*. 2023;12(22):3803-3818.
15. Lavudya S, Patel MP, Kumar S, Singh A, Sakure AA, Pandya M. Identification of elite genotypes through morpho-biochemical and molecular characterization of turmeric (*Curcuma longa* L.). *South African Journal of Botany*. 2024;166:161-168.
16. Lavudya S, Patel MP, Kumar S, Singh A, Venna S, Ellandula A, *et al.* Utilizing selection indices to enhance genetic gain in turmeric (*Curcuma longa* L.).

- Electronic Journal of Plant Breeding. 2023;14(3):1215-1221.
17. Lavudya S, Thiyagarajan K, Ramasamy S, Sankarasubramanian H, Muniyandi S, Bellie A, *et al.* Assessing population structure and morpho-molecular characterization of sunflower (*Helianthus annuus* L.) for elite germplasm identification. PeerJ. 2024;12:e18205.
 18. Mate PA, Bhavsar VV, Matere BS, Girase VS. Screening of genetic variability for yield and its components in horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] local germplasm. Journal of Agriculture Research and Technology. 2022;47:78-82.
 19. Padha R, Kumar S, Kumawat R. Unveiling the genetic diversity in horsegram (*Macrotyloma uniflorum* L.) genotypes through morphological and microsatellite (SSR) markers. Scientific Reports. 2025;15(1):34861-34875.
 20. R Core Team. R: A language and environment for statistical computing. Vienna: R Foundation for Statistical Computing; 2016.
 21. Rajaprakasam S, Shanmugavel P, Chockalingam V, Jegadeesan S, Latha TKS, Ananthan SN, *et al.* Comparative metabolomic profiling of horse gram (*Macrotyloma uniflorum* (Lam.) Verdc.) genotypes for horse gram yellow mosaic virus resistance. Metabolites. 2023;13(2):165-178.
 22. Ramesh CK, Rehman A, Prabhakar BT, Vijay ABR, Aditya SJ. Antioxidant potential in sprout versus seeds of *Vigna radiata* and *Macrotyloma uniflorum*. Journal of Applied Pharmaceutical Science. 2011;1:99-103.
 23. Sahoo JL, Das TR, Baisakh B, Nayak BK, Panigrahi KK. Assessment of genetic diversity in horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.]. e-Planet. 2014;12(1):31-35.
 24. Sahoo JL, Das TR, Baisakh B, Nayak BK, Panigrahi KK. Assessment of genetic diversity in horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.]. e-Planet. 2014;12(1):31-35.
 25. Sampath L, Sasikala R, Kalaimagal T, Santhiya V, Antony B. Genetic diversity analysis in sunflower (*Helianthus annuus* L.) germplasms. Journal of Oilseeds Research. 2023;40(Special Issue):1-8.
 26. Sharma V, Sharma TR, Rana JC, Chahota RK. Analysis of genetic diversity and population structure in horsegram (*Macrotyloma uniflorum*) using RAPD and ISSR markers. Agricultural Research. 2015;4(3):221-230.
 27. Sivan S, Arya K, Nair RS, Gayathri G. Genetic variability, correlation studies, path coefficient analysis and genetic divergence in horsegram (*Macrotyloma uniflorum* (Lam.) Verdc.). Electronic Journal of Plant Breeding. 2022;13(3):1084-1091.
 28. Visakh RL, Bindu MR. Investigation on genetic variability in horse gram [*Macrotyloma uniflorum* (Lam.) Verdc.] under moisture stress condition. Journal of Pharmaceutical Innovation. 2022;11(1):600-603.
 29. Witcombe JR, Billore M, Singhal HC, Patel NB, Tikka SBS, Saini DP, *et al.* Improving the food security of low-resource farmers: introducing horsegram into maize-based cropping systems. Experimental Agriculture. 2008;44(3):339-348.
 30. Yoo C, Yoo Y, Um HY, Yoo JK. On hierarchical clustering in sufficient dimension reduction. Communications for Statistical Applications and Methods. 2020;27(4):431-443.