AGRO-MORPHOLOGICAL DIVERSITY AND IDENTIFICATION OF PROMISING CROTALARIA JUNCEA L. GERMPLASM ACCESSIONS BASED ON QUANTITATIVE AGRONOMIC TRAITS

Otabek Ch. Allazov
PhD Student, Institute of Plant Genetic Resources,
Tashkent, Uzbekistan.
Nurali Kh. Khudoyberdiev
DSc Student, Institute of Plant Genetic Resources,
Tashkent, Uzbekistan.

Abstract. Sunn hemp (*Crotalaria juncea* L.) is a multipurpose legume valued for fibre production, biomass accumulation and soil improvement. This study evaluated agro-morphological variation among 109 genebank accessions and the reference cultivar Mo‘jiza-73 under field conditions in Qibray District, Uzbekistan, in 2025. The experiment was conducted using a randomized complete block design with three replications. Five quantitative traits were assessed: seed yield, plant height, seeds per pod, dry stem mass and dry leaf mass. The results showed considerable variation among the evaluated accessions. Mean seed yield was 3,373.21 g m^{-2}, plant height averaged 175.93 cm, and seeds per pod averaged 11.69. Mean dry stem and leaf masses were 1,012.44 and 210.02 g m^{-2}, respectively. Seed yield ranged from 2,200 to 4,900 g m^{-2}. Principal component analysis revealed that the first two components explained 73.97% of the total phenotypic variation. Accession K10 recorded the highest seed yield (4,900 g m^{-2}), demonstrating potential for further breeding evaluation. The identified accessions represent valuable resources for sunn hemp improvement and selection under Uzbekistan conditions.

Keywords: Crotalaria juncea; sunn hemp; germplasm; agro-morphological characterization; seed yield; biomass; multivariate analysis.

1. Introduction

Sunn hemp (*Crotalaria juncea* L.) is an annual legume of the family Fabaceae cultivated for several complementary purposes, including bast-fibre production, green manuring, cover cropping, forage and biomass generation. Its rapid growth and capacity to produce substantial above-ground biomass make it relevant to diversified and conservation-oriented agricultural systems. As a leguminous species, sunn hemp can contribute biologically fixed nitrogen to cropping systems and provide soil cover, while its stems are also used as a source of natural fibre. These multiple uses create a demand for germplasm with contrasting combinations of seed production, plant architecture and vegetative biomass.

The performance of sunn hemp is influenced by genotype, environment and crop management. Genotypes may differ in plant height, branching, flowering behaviour, pod formation, seed set and biomass accumulation. Such variation is valuable to plant breeders because accessions carrying complementary traits can serve as parents in crossing programmes or as sources of specific agronomic attributes. However, the value of a genebank collection depends not only on conservation but also on systematic characterization and evaluation under defined agroecological conditions. Phenotypic

characterization provides an initial basis for identifying accessions that merit more detailed agronomic, physiological or molecular investigation.

Previous studies have demonstrated the usefulness of agro-morphological characterization for documenting diversity within Crotalaria collections. Muli et al. (2021) evaluated Crotalaria germplasm using phenomic descriptors and multivariate approaches, illustrating how quantitative and qualitative traits can support accession grouping and the identification of useful material. Research on Indian sunn hemp accessions has also used geographic and diversity analyses to describe the distribution of agronomically useful variation (Maruthi et al., 2019). Subsequent work has addressed genetic divergence and the identification of accessions with potential value for crop improvement (Desai et al., 2023). More recent assessments have considered diversity for biomass and fibre yield, highlighting the importance of evaluating germplasm for more than one end-use trait (Maruthi et al., 2024).

Multivariate statistical methods are widely used in plant genetic-resource research because agronomic traits are often correlated and no single variable can adequately represent overall accession performance. Correlation analysis can indicate whether traits such as seed yield, plant height and biomass tend to vary together. Principal component analysis (PCA) reduces a set of correlated measurements to a smaller number of composite axes, while hierarchical cluster analysis groups accessions according to their multivariate similarity. These methods have been applied to diverse crop collections, including lentil, wheat, chickpea, mungbean and other germplasm resources, to identify trait patterns and candidate material for breeding (Tripathi et al., 2022; Singh et al., 2023; Irfan et al., 2025).

Despite the agronomic relevance of sunn hemp, locally adapted information on the performance of diverse accessions under the environmental conditions of Uzbekistan remains limited. Evaluation of conserved accessions under local field conditions can help establish a baseline for future selection and breeding. In particular, comparing a broad set of genebank accessions with a locally used reference cultivar can provide practical context for interpreting the observed range of quantitative traits.

The present study therefore aimed to characterize 109 C. juncea accessions obtained from the Genebank of the Scientific Research Center for Plant Genetic Resources, Uzbekistan, together with the reference cultivar Mo‘jiza-73, under field conditions in Qibray District during 2025. The specific objectives were to (i) describe the variation in seed yield, plant height, seeds per pod, dry stem mass and dry leaf mass; (ii) examine relationships among these quantitative traits; and (iii) identify accessions with promising observed trait values for subsequent multi-environment evaluation and breeding research. The study is intended as a phenotypic characterization of the evaluated collection; it does not claim molecularly confirmed genetic diversity.

2. Materials and Methods

2.1. Plant material and germplasm source

The plant material comprised 110 accessions of Crotalaria juncea L. maintained in the Genebank of the Scientific Research Center for Plant Genetic Resources, Uzbekistan, and the reference cultivar Mo‘jiza-73. Each accession was identified by its internal catalogue code (K1–K109) and the corresponding NC accession number recorded in the supplied catalogue. The reference cultivar was

included as a check and did not have an NC number in the spreadsheet. The accession-level catalogue and NC identifiers should be retained in the final supplementary dataset to ensure traceability of the evaluated material.

2.2. Experimental site, design and crop evaluation

The field experiment was conducted in 2025 in Qibray District, Tashkent Region, Uzbekistan. The trial was established as a randomized complete block design (RCBD) with three replications. The spreadsheet supplied for manuscript preparation contained the arithmetic mean of the three replications for each entry and trait. The experiment included the 109 genebank accessions and Mo‘jiza-73 as the reference cultivar. Detailed agronomic management information (sowing date, plot dimensions, row and plant spacing, sowing rate, fertilizer application, irrigation regime, harvest date and soil characteristics) was not included in the supplied workbook and should be added from the field book before journal submission.

2.3. Quantitative traits recorded

Five quantitative traits were analysed: (1) seed yield harvested from 1 m² (g m−2); (2) plant height (cm); (3) number of seeds per pod (count); (4) dry stem mass collected from 1 m² (g m−2); and (5) dry leaf mass collected from 1 m² (g m−2). Dry stem and leaf biomass values were recorded on a 1 m² sampling basis. The value for accession K90 in the seeds-per-pod column was checked against the user’s clarification and corrected from 121 to 12 before analysis. No other observations were modified.

2.4. Statistical analysis

The dataset was organized and checked in Microsoft Excel and analysed using R (RStudio environment). Descriptive statistics were calculated for the 109 accessions, including the mean, standard deviation, minimum, maximum and coefficient of variation (CV%). CV was calculated as (standard deviation / mean) × 100. Pearson correlation coefficients were used to describe pairwise linear associations among the five traits. PCA was planned on standardized trait values to prevent variables measured on different scales from dominating the analysis. Hierarchical clustering was planned using standardized Euclidean distances and an agglomerative linkage procedure. The reference cultivar Mo‘jiza-73 was retained for descriptive comparison but excluded from the accession-only summary statistics.

Important statistical limitation: only the three-replication means were available in the workbook. Consequently, the present analysis cannot independently estimate within-entry experimental error, calculate standard errors from replicate observations, or conduct a valid RCBD analysis of variance and mean-separation tests. Correlation, PCA and clustering based on accession means describe patterns among the supplied entry means; they do not replace analyses of plot-level replicate data. Inferential claims and p-values are therefore not reported in this draft.

3. Results

3.1. Descriptive variation among accessions

The corrected dataset contained 110 genebank accessions. Seed yield ranged from 2200 to 4900 g m−2, with a mean of 3373.21 g m−2. Plant height ranged from 160 to 195 cm, while the number of seeds per pod ranged from 10 to 13. Dry stem mass ranged from 550 to 1400 g m−2 and dry leaf mass from 140 to 310 g m−2. The spread between minimum and maximum values indicates that the accessions differed in the measured agronomic attributes (Table 1).

Table 1. Descriptive statistics of quantitative agro-morphological traits in 110 Crotalaria juncea L. entries, including the reference cultivar Mo‘jiza-73.

Trait	Mean	SD*	Minimum	Maximum	CV (%)
Seed yield (g m^{-2})	3373.21	497.56	2200	4900	14.75
Plant height (cm)	175.93	6.83	160	195	3.89
Seeds per pod (no.)	11.69	0.82	10	13	7.05
Dry stem mass (g m^{-2})	1012.44	128.22	550	1400	12.66
Dry leaf mass (g m^{-2})	210.02	25.86	140	310	12.31

SD is the standard deviation among the 110 accession means, not the standard deviation among the three field replications.

3.2. High-yielding accessions

The ten accessions with the highest recorded seed-yield means are presented in Table 2. These entries are candidates for further verification and evaluation; their ranking should be interpreted as a ranking of the supplied three-replication means rather than a statistically tested superiority claim.

Table 2. Comparison of the ten highest-yielding *Crotalaria juncea* L. accessions with the reference cultivar Mo‘jiza-73.

Accession	NC	Seed yield (g/m^2)	Height (cm)	Seeds/pod	Stem (g/m^2)	Leaf (g/m^2)
K10	11387	4900	190	13	1400	310
K28	11396	4300	195	13	990	205
K37	11400	4250	192	13	990	210
K46	11403	4250	192	12	980	203
K32	13799	4240	178	11	1120	211
K56	11410	4200	186	12	1020	215
K50	13811	4150	173	12	870	205
K26	13797	4100	185	13	910	175
K33	13800	4100	172	10	980	208
K35	13801	4100	185	13	905	180
Mo‘jiza-73 (Control)	—	2400	161	11	860	200

3.3. Reference cultivar

The reference cultivar Mo‘jiza-73 had a recorded seed yield of 2400 g m−2, plant height of 161 cm, 11 seeds per pod, dry stem mass of 860 g m−2 and dry leaf mass of 200 g m−2. These values

provide a descriptive benchmark for interpreting the accession collection. Formal tests of differences between individual accessions and the check require the original plot-level data.

3.4. Trait association and multivariate analyses

Principal component analysis was performed to assess phenotypic variation among 110 Crotalaria juncea L. entries, including 109 Genebank accessions and the reference cultivar Mo‘jiza-73. The first two principal components explained 73.97% of the total variation, with PC1 accounting for 51.91% and PC2 for 22.07% (Figure 1). The PCA biplot demonstrated differences among accessions based on seed yield, plant height, seeds per pod, dry stem mass, and dry leaf mass. Accession K10 showed a distinct position and recorded the highest seed yield (4,900 g m^{-2}). Other high-yielding accessions, including K28, K37, K46, and K32, also exhibited distinct multivariate profiles. These findings identify promising candidates for further agronomic evaluation and breeding programmes.

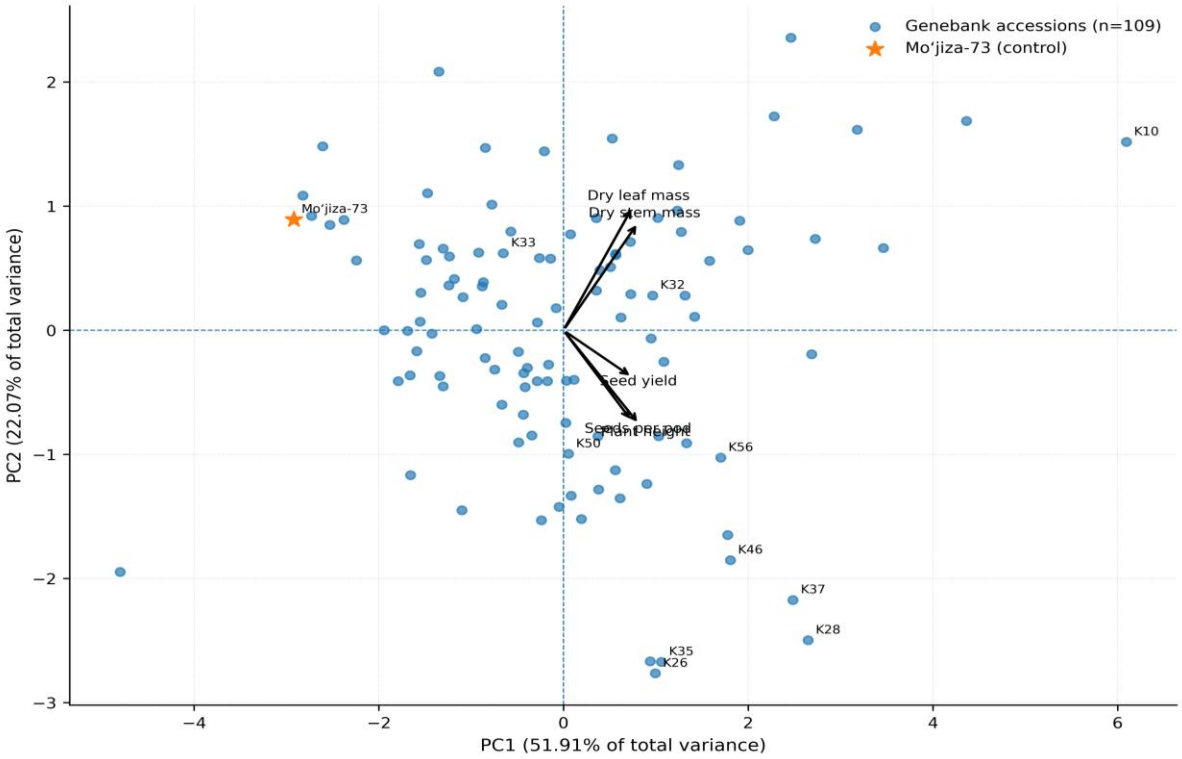


Figure 1. Principal component analysis (PCA) biplot of 110 Crotalaria juncea L. entries based on five quantitative agro-morphological traits.

4. Discussion

The present evaluation provides a first quantitative overview of 109 sunn hemp accessions maintained in the Uzbek genebank and grown under the field conditions of Qibray District in 2025. The observed range in seed yield and biomass-related traits indicates that the collection contains phenotypic variation that may be useful for selecting material for further agronomic testing. The broad seed-yield range is particularly relevant because seed production is necessary for maintaining accessions, supplying planting material and supporting breeding activities. At the same time, dry stem

and leaf mass represent distinct components of above-ground biomass and may be relevant where sunn hemp is considered for fibre, green manure or cover-crop purposes.

The results are consistent with the broader rationale of Crotalaria germplasm characterization. Muli et al. (2021) showed that phenomic evaluation combined with multivariate analyses can reveal useful variation within Crotalaria collections and assist the identification of accessions for crop improvement. Maruthi et al. (2019) documented diversity among Indian sunn hemp accessions and demonstrated the value of systematic characterization for diversified uses. Desai et al. (2023) further emphasized genetic divergence as a basis for selecting contrasting parental material, while Maruthi et al. (2024) focused on biomass and fibre-related diversity. Together, these studies support the importance of evaluating sunn hemp collections across multiple agronomic traits rather than relying on a single yield measure.

The inclusion of Mo‘jiza-73 as a reference cultivar is useful because it provides a familiar benchmark against which the range of accession means can be viewed. However, the present spreadsheet does not contain replicate-level observations, so the differences between the check and individual accessions cannot be interpreted as statistically significant. The accessions with the highest recorded seed yield should therefore be treated as preliminary candidates, not as confirmed superior genotypes. Their performance needs to be validated using plot-level data and, preferably, in additional seasons or locations.

Multivariate approaches can strengthen the interpretation of this type of dataset. Studies in lentil, wheat, chickpea, mungbean and other crops have used PCA and clustering to summarize correlated agronomic traits, identify groups of similar accessions and select promising material for breeding (Tripathi et al., 2022; Singh et al., 2023; Irfan et al., 2025). For the present collection, correlation analysis may help clarify whether high seed yield is associated with plant stature or biomass accumulation. PCA may identify the combinations of traits that explain the largest share of variation, while hierarchical clustering may provide a practical grouping of accessions with similar phenotypic profiles. These methods describe multivariate phenotypic patterns and should not be described as proof of molecular genetic relationships.

A further consideration is the environmental specificity of the evaluation. Sunn hemp is grown across diverse production systems, and genotype performance can vary with photoperiod, temperature, soil properties, water availability and management. Research on C. juncea biomass accumulation under contrasting climatic settings has highlighted the importance of environment when interpreting growth and biomass outcomes. Therefore, the Qibray results should be considered a location- and season-specific assessment. Multi-location and multi-year trials would be required to identify stable accessions and to estimate genotype-by-environment interaction.

Overall, the study establishes a useful baseline for the characterization of Uzbek sunn hemp germplasm. The next stage should combine the accession-level phenotypic data with the original three-replication observations, additional qualitative descriptors, seed quality measurements and, where feasible, molecular marker data. Such an integrated approach would support more robust selection decisions and improve the utilization of conserved C. juncea resources in local breeding programmes.

5. Conclusion

The evaluation of 109 Crotalaria juncea L. germplasm accessions and the reference cultivar Mo‘jiza-73 under the field conditions of Qibray District, Uzbekistan, in 2025 revealed considerable variation in seed yield and other important agro-morphological traits. Among the evaluated entries, K10 demonstrated the highest seed yield (4,900 g m^{-2}), indicating its potential value for future breeding programmes. PCA further confirmed the diversity of phenotypic characteristics, with the first two components explaining 73.97% of the total variation. The identified promising accessions may serve as valuable genetic resources for further selection, multi-location evaluation and sunn hemp improvement in Uzbekistan.Data availability

The accession-level dataset used for this draft was supplied by the authors. The complete catalogue, including K codes and NC identifiers, should be provided as supplementary material after institutional verification.

References

1. Desai, T. B., Bala, M., & Patel, R. K. (2023). Genetic divergence in sunnhemp [Crotalaria juncea (L.)]. Legume Research, 46(4), 413–416. https://doi.org/10.18805/LR-4397
2. Irfan, M., Bhat, M. A., et al. (2025). Genetic diversity assessment and morpho-agronomic characterization of mungbean (Vigna radiata (L.) Walp.) germplasm using multivariate analysis. BMC Plant Biology, 25, 1514. https://doi.org/10.1186/s12870-025-07561-z
3. Kumar, A., Singh, A., Arya, M., Kumar, V., Singh, Y., & Chaturvedi, S. K. (2025). Estimation of genetic diversity using principal component analysis and cluster analysis in chickpea (Cicer arietinum L.) germplasm based on agro-morphological traits. Journal of Experimental Biology and Agricultural Sciences, 13(3), 380–388. https://doi.org/10.18006/2025.13(3).380.388
4. Kumar, S., Kumar, B., & Sheera, A. (2024). Characterization and principal component analysis of rice germplasm (Oryza sativa L.) under sub-tropical ecology of Jammu region of India. Plant Archives, 24(2), 1782–1791. https://doi.org/10.51470/PLANTARCHIVES.2024.v24.no.2.256
5. Kumar, A., Kumar, H., Singh, C. M., Kumar, M., Sharma, V., Kumar, S., & Panwar, G. S. (2025). Multivariate analysis for elucidating genetic diversity of chickpea (Cicer arietinum L.) germplasm using agro-morphological traits. Legume Research, 48(4), 590–596. https://doi.org/10.18805/LR-4956
6. Maruthi, R. T., Kumar, A. A., Choudhary, S. B., Sharma, H. K., & Mitra, J. (2019). DIVA-GIS based insight into geographical distribution and diversity spectrum of Indian sunnhemp (Crotalaria juncea L.) accessions suitable for diversified applications. Legume Research, 43(6), 749–756. https://doi.org/10.18805/LR-4055
7. Maruthi, R. T., Kumar, A. A., Choudhary, S. B., Sharma, H. K., & Mitra, J. (2024). Diversity assessment of Indian sunnhemp (Crotalaria juncea L.) accessions for enhanced biomass and fibre yield using geographic information system approach. Legume Research, 47(3), 391–396. https://doi.org/10.18805/LR-4510
8. Muli, J. K., Neondo, J. O., Kamau, P. K., Odari, E., Budambula, N., et al. (2021). Phenomic characterization of Crotalaria germplasm for crop improvement. CABI Agriculture and Bioscience, 2, 10. https://doi.org/10.1186/s43170-021-00031-0
9. Nair, R. M., et al. (2022). [Sunn hemp-related fibre/genetic resource study; bibliographic details must be confirmed before submission]. https://doi.org/10.1080/15440478.2022.2139327

10. Singh, G., Singh, G. P., et al. (2023). Diversity in Indian wheat (Triticum aestivum L.) germplasm for various agro-morphological traits. Plant Genetic Resources, 21(1), 81–89. https://doi.org/10.1017/S1479262123000461
11. Singh, J., Kumar, D., Sood, S., Bhardwaj, V., et al. (2025). Morpho-physiological characterization and principal component analysis for agronomic traits in tetraploid potato germplasm. Discover Applied Sciences, 7, 1149. https://doi.org/10.1007/s42452-025-07216-6
12. Saha, D., & Datta, S. (2026). Complete chloroplast genome of Crotalaria juncea, a bast fibre crop with late-acting self-incompatibility, reveals evolutionary insights and phylogenetic relationships within Fabaceae. BMC Plant Biology, 26, 847. https://doi.org/10.1186/s12870-026-08702-8
13. Squarisi, J. M. M., Ferreira, M. R., Malaquias, J. V., Ramos, A. K. B., Karia, C. T., Braga, G. J., & Carvalho, M. (2026). Phenomic characterization of Crotalaria germplasm in Embrapa's genebank, Brazil. Genetic Resources, DOI record. https://doi.org/10.46265/genresj.WHMW8903
14. Tripathi, K., Kumari, J., Gore, P. G., Mishra, D. C., Singh, A. K., et al. (2022). Agro-morphological characterization of lentil germplasm of Indian National Genebank and development of a core set for efficient utilization in lentil improvement programs. Frontiers in Plant Science, 12, 751429. https://doi.org/10.3389/fpls.2021.751429
15. Zhang (2024). Crotalaria juncea genotype biomass accumulation in northern semi-arid and humid-continental climates. Agronomy, 14(10), 2334. https://doi.org/10.3390/agronomy14102334