PLANT SCIENCE TODAY
ISSN 2348-1900 (online)
Vol x(x): xx–xx
https://doi.org/10.14719/pst.6119

HORIZON
e-Publishing Group

RESEARCH ARTICLE

Morphological diversity and genetic potential of *Aloe barbadensis* Mill. accessions from diverse agro-climatic regions of Tamil Nadu, India

C Abinaya[1*], J Suresh[2], ST Bini Sundar[3], E Kokiladevi[4], D Uma[5] & N Bharathi[6]

[1]Department of Spices, Plantation, Medicinal & Aromatic Crops, Tamil Nadu Agricultural University, Coimbatore 641 003, Tamil Nadu, India

[2]Horticulture College and Research Institute University for Women, Trichy 620 009, Tamil Nadu, India

[3]Department of Medicinal and Aromatic Crops, Tamil Nadu Agricultural University, Coimbatore 641 003, Tamil Nadu, India

[4]Department of Biotechnology, Tamil Nadu Agricultural University, Coimbatore 641 003, Tamil Nadu, India

[5]Department of Biochemistry, Tamil Nadu Agricultural University, Coimbatore 641 003, Tamil Nadu, India

[6]Department of Bioinformatics, Tamil Nadu Agricultural University, Coimbatore 641 003, Tamil Nadu, India

*Email: abi.abinaya177@gmail.com

ARTICLE HISTORY
Received: 24 October 2024
Accepted: 20 December 2024
Available online
Version 1.0 : 30 January 2025

Additional information

Peer review: Publisher thanks Sectional Editor and the other anonymous reviewers for their contribution to the peer review of this work.

Reprints & permissions information is available at https://horizonepublishing.com/journals/index.php/PST/open_access_policy

Publisher's Note: Horizon e-Publishing Group remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Indexing: Plant Science Today, published by Horizon e-Publishing Group, is covered by Scopus, Web of Science, BIOSIS Previews, Clarivate Analytics, NAAS, UGC Care, etc
See https://horizonepublishing.com/journals/index.php/PST/indexing_abstracting

CITE THIS ARTICLE
Abinaya C, Suresh J, Sundar STB, Kokiladevi E, Uma D, Bharathi N. Morphological diversity and genetic potential of *Aloe barbadensis* Mill. accessions from diverse agro-climatic regions of Tamil Nadu, India. Plant Science Today (Early Access). https://doi.org/10.14719/pst.6119

Abstract

Aloe barbadensis Mill. is a medicinal plant of great importance, widely cultivated for its therapeutic properties. However, limited research has been conducted on the morphological diversity of *Aloe vera* germplasm in India. This study assessed the morphological diversity of 40 *A. vera* accessions collected from different agro-climatic regions in Tamil Nadu, India. Eight quantitative morphological descriptors were evaluated. Significant variations were observed for all the studied traits, indicating substantial morphological diversity among the accessions. Principal component analysis revealed that the first three principal components (PC's) accounted for 72.90% of the total variation. Cluster analysis grouped the accessions into three main clusters based on morphological similarity. Associations were found between several traits, with correlation analysis showing significant positive correlations between plant size, leaf dimensions and yield-related traits. High broad-sense heritability estimates were observed for several characteristics, suggesting the potential for genetic improvement through selection. The findings highlight the morphological diversity in Tamil Nadu *A. vera* germplasm, which can be exploited for the genetic improvement and development of effective conservation strategies for this valuable medicinal plant. The morphological diversity observed in this study can be attributed to the diverse agro-climatic conditions and geographical locations from which the accessions were collected.

Keywords

Aloe barbadensis Mill.; cluster analysis; correlation; genetic resources; morphological diversity; principal component analysis

Introduction

Aloe barbadensis Mill., commonly known as *Aloe vera*, is a perennial succulent of the family Asphodelaceae, renowned for its extensive medicinal and therapeutic applications. Its gel, extracted from fleshy leaves, is widely used in the pharmaceutical, cosmetic and nutraceutical industries due to its anti-inflammatory, antimicrobial and antioxidant properties (1, 2). *Aloe vera* is often referred to as a "miracle plant" for its diverse applications, ranging from skincare products to alternative medicine (3). Globally, *Aloe vera* cultivation is concentrated in arid and semi-arid regions due to its ability to thrive in water-limited environments.

In India, *Aloe vera* is cultivated extensively across states like Rajasthan, Gujarat, Maharashtra, Tamil Nadu and Uttar Pradesh. The country's diverse agro-climatic zones provide an ideal environment for cultivating *Aloe vera*, resulting in significant morphological and genetic variability among accessions (4, 5). This variability holds immense potential for the development of improved cultivars suited to specific climatic and economic requirements. However, the genetic resources of *Aloe vera* in India remain underutilized due to limited studies on its morphological and genetic diversity.

Morphological characterization serves as the cornerstone for germplasm evaluation, providing critical insights into genetic diversity, conservation strategies and breeding programs (6). For effective germplasm management, morphological descriptors should be precise, stable across environments and easily measurable. Despite advances in molecular tools, morphological traits remain a cost-effective and practical approach for initial germplasm assessment. Studies on *Aloe vera* genetic resources have highlighted the importance of integrating morphological data with molecular markers for comprehensive diversity analysis (7).

The Arabian Peninsula is considered the primary center of origin for *Aloe vera*, with significant genetic diversity reported in this region. However, studies have demonstrated that accessions cultivated in India exhibit unique morphological and adaptive traits influenced by local agro-climatic conditions (8, 9). Despite this, systematic characterization of *Aloe vera* germplasm in India has been limited, often focusing on regional collections without integrating broader genetic or morphological data.

This study aimed to bridge this gap by characterizing 40 *Aloe vera* accessions collected from diverse agro-climatic regions of Tamil Nadu. Using a combination of morphological descriptors, this work assesses variability and identifies promising accessions for conservation and breeding. The findings provide a foundation for the sustainable utilization of *Aloe vera* genetic resources, which is critical in light of the increasing global demand for natural bioactive compounds.

Materials and Methods

Experimental site and plant material

The study was conducted at the Department of Medicinal and Aromatic Crops, Horticulture College and Research Institute, Tamil Nadu Agricultural University, Coimbatore, India. Forty *Aloe vera* accessions were collected from diverse agro-climatic regions of Tamil Nadu, representing a range of environmental conditions. These accessions were maintained under uniform cultural practices to ensure accurate and unbiased evaluation of morphological traits.

Experimental design

The experiment was arranged in a Randomized Block Design (RBD) with three replications. Each accession was planted in plots measuring 2 m × 2 m, with a spacing of 60 cm × 60 cm between plants. Standard agronomic practices such as irrigation, weeding and pest management were followed uniformly across the experimental field to minimize environmental variation and promote optimal plant growth.

Observations recorded

Eight quantitative morphological traits were selected based on their agronomic and economic importance, following the descriptors for *Aloe vera* developed by the International Plant Genetic Resources Institute (IPGRI). The traits evaluated were:

Plant height (cm): Measured from the base to the tip of the longest leaf.

Plant width (cm): Calculated as the average of two perpendicular canopy measurements.

Number of suckers: Total number of offshoots per plant.

Number of leaves: Counted as the total number of mature leaves per plant.

Leaf length (cm): Measured from the base to the tip of the longest leaf.

Leaf width (cm): Measured at the broadest part of the longest leaf.

Leaf ratio: Computed as the ratio of leaf length to leaf width.

Yield (kg/plant): Measured as the total fresh weight of leaves per plant.

Observations were recorded on three randomly selected plants per accession within each replication at 12 months after planting to ensure representativeness.

Data analysis

Statistical analyses were performed to evaluate variability, relationships among traits and morphological diversity among accessions.

Analysis of variance (ANOVA):

ANOVA was conducted to test the significance of differences among accessions for each trait. It partitioned total variability into components attributable to genetic and environmental factors.

Genotypic and phenotypic coefficients of variation (GCV and PCV):

GCV and PCV were calculated using the following formulae:

$$\text{GCV (\%)} = (\sqrt{\text{Genotypic variance}} / \text{Mean}) \times 100$$

$$\text{PCV (\%)} = (\sqrt{\text{Phenotypic variance}} / \text{Mean}) \times 100$$

These metrics quantified the extent of genetic and phenotypic variability. Higher GCV values relative to PCV indicated greater genetic control of the traits.

Broad-sense heritability (H^2):

Broad-sense heritability was computed as:

$$H^2 \text{ (\%)} = (\text{Genotypic variance} / \text{Phenotypic variance}) \times 100$$

This parameter estimated the proportion of phenotypic variance attributable to genetic factors, guiding the selection efficiency in breeding programs.

Genetic advance (GA):

GA was calculated to predict the expected improvement in a trait under selection pressure, using the formula:

$$\text{GA} = H^2 \times \text{Phenotypic standard deviation} \times \text{Selection intensity}$$

Correlation analysis:

Pearson’s correlation coefficients were computed to assess the relationships among traits, using the ‘corrplot’ package in R software (version 4.0.3). This helped identify traits that could indirectly improve others through correlated selection.

Principal component analysis (PCA):

PCA was conducted to identify key traits contributing to morphological variation. Principal components with eigenvalues greater than one were used for interpretation, capturing the maximum variation with fewer dimensions.

Cluster analysis:

Hierarchical cluster analysis was performed using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) based on Gower's distance. UPGMA grouped accessions into clusters reflecting their morphological similarity and the resulting dendrogram was compared to traditional classification schemes based on morphology and geographical origins.

Results

Morphological variation and descriptive statistics

The analysis of variance (ANOVA) revealed highly significant differences ($P < 0.001$) among the 40 *A. vera* accessions for all studied morphological traits. This result indicates substantial genetic variability within the collected germplasm, crucial for effective breeding programs (11). The coefficient of variation (CV) ranged from 13.63% for leaf ratio to 66.08% for number of suckers (Table 1), demonstrating varying levels of trait variability. The high CV for number of suckers (66.08%) and yield (32.04%) suggests these traits are exceptionally diverse and may be more responsive to selection pressures (12). The wide range observed for most traits, such as plant height (19.33 - 59.13 cm) and leaf length (4.7 - 56.1 cm), further corroborates the significant morphological diversity within the collection. This diversity is comparable to and in some cases exceeds, that reported in previous studies on *A. vera* (13, 14), indicating the potential value of this germplasm for breeding and conservation efforts.

Principal component analysis (PCA)

Principal Component Analysis (PCA) was employed to understand the multidimensional patterns of variation among the accessions. The first three principal components (PCs) accounted for 72.03% of the total variation (Table 2), which is considered a robust representation of the overall diversity (15). PC1, explaining 39.02% of the variation, was primarily associated with vegetative traits such as leaf width, plant height and plant width. This finding aligns with previous studies on aloe species, where vegetative characteristics often dominate the primary axis of variation (16, 17). The strong influence of vegetative traits on PC1 suggests that these characteristics are the primary differentiators among accessions. This information is valuable for developing core collections and streamlining future characterization efforts, as researchers can focus on these key traits to efficiently capture most morphological variation (18). The cumulative variation explained by the first three PCs (72.03%) is slightly lower than some reported values in other *A. vera* studies (19, 20), which might indicate a more complex pattern of trait relationships in this particular collection. This complexity could be advantageous for breeding programs, as it suggests diverse trait combinations.

Table 2. Eigenvalues, proportion of variation and cumulative variation explained by the first three principal components (PCs) in 40 *A. vera* accessions

Principal Component	Eigen value	Percentage of Variance	Cumulative Percentage of Variance
PC1	3.122	39.023	39.023
PC2	1.499	18.741	57.764
PC3	1.141	14.261	72.026
PC4	0.843	10.537	82.562
PC5	0.652	8.145	90.707
PC6	0.495	6.185	96.893
PC7	0.244	3.048	99.941
PC8	0.005	0.059	100.000

Cluster analysis

Hierarchical cluster analysis using Ward's method grouped the 40 *A. vera* accessions into three main clusters (Fig. 1). This clustering provides insights into the patterns of similarity and difference among accessions, which is crucial for selecting diverse parental lines in breeding programs (21). Cluster I, comprising 14 accessions, was characterized by high plant height, large leaves and high yield. Cluster II, the largest group with 18 accessions, showed moderate values for most traits. Cluster III, containing eight accessions, was distinguished by low plant height, small leaves and low yield. The clear differentiation between these clusters suggests distinct morphotypes within the collection, possibly reflecting different adaptive strategies or selection histories (22). The clustering pattern partially aligned with geographical origins, with Cluster I containing more accessions from semi-arid regions and Cluster II from coastal areas. However, this correspondence was not absolute, as indicated by the weak but significant Mantel test result ($r = 0.18$, $P < 0.05$). This partial geographic structuring of morphological diversity is consistent with findings in other plant species (23, 24). It suggests a complex interplay between environmental adaptation and human-mediated selection in shaping *A. vera* diversity.

Table 1. Descriptive statistics for the morphological traits in 40 *A. vera* accessions

Variable	Range	Mean	SD	CV (%)	p-value*
Plant height	19.33 - 59.13	41.14	7.83	19.03	<0.0001*
Plant width	18.67 - 67.47	44.55	9.35	20.97	<0.0001*
Number of suckers	0.0 - 12.0	2.57	1.70	66.08	<0.0001*
Number of leaves	4.0 - 15.67	12.30	1.96	15.96	<0.0001*
Leaf length	4.7 - 56.1	34.21	6.05	17.68	<0.0001*
Leaf width	3.98 - 9.18	6.21	0.96	15.44	<0.0001*
Leaf ratio	1.0 - 7.53	5.57	0.76	13.63	<0.0001*
Yield	1.52 - 6.5588	3.49	1.12	32.04	<0.0001*

SD- Standard deviation; CV- Coefficient of variation

*p-values from two-tailed one-sample t-test against a mean of 0. Significant at $\alpha = 0.05$.

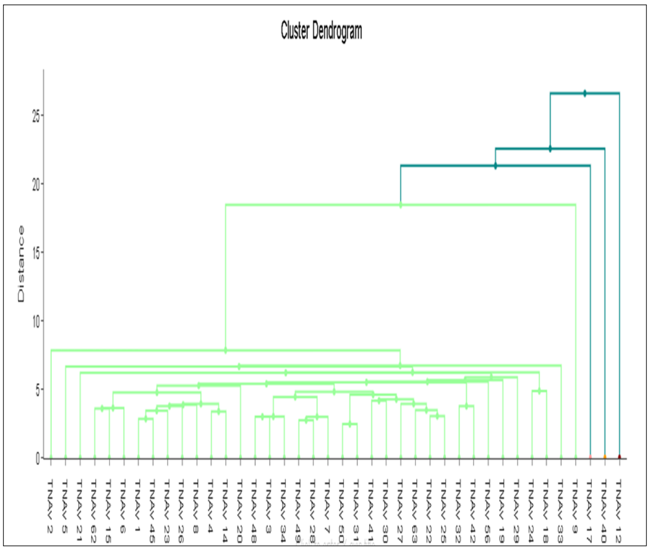

Fig. 1. Dendrogram showing the clustering of 40 *A. vera* accessions based on morphological traits using Ward's method.

Correlation analysis

The correlation analysis revealed several significant relationships among morphological traits (Fig. 2). The strong positive correlation between plant height and width (r = 0.78, P < 0.001) suggests these traits may be controlled by similar genetic factors or respond similarly to environmental conditions. This relationship could be leveraged in breeding programs, as selection for one trait will likely result in a correlated response in the other (25). Yield showed moderate to strong positive correlations with plant height (r = 0.59, P < 0.001), plant width (r = 0.52, P < 0.001) and leaf width (r = 0.58, P < 0.001). These correlations indicate that larger plants with wider leaves tend to yield higher, which aligns with the general expectation that increased photosynthetic capacity leads to higher biomass production (26). Interestingly, the number of suckers showed weaker correlations with other traits, suggesting a degree of independence in the genetic control of this characteristic. This relative independence could be valuable in breeding programs aimed at developing varieties with specific architectural characteristics, as it might be possible to select for sucker number without dramatically affecting other plant size traits (27).

Genetic parameters

The analysis of genetic parameters provided crucial insights into the genetic control of morphological traits in the studied *A. vera* population. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were highest for number of suckers (GCV: 66.08%, PCV: 76.99%), indicating substantial genetic variability for this trait (Table 3). This high variability suggests considerable potential for altering plant architecture through selection on sucker number (28).

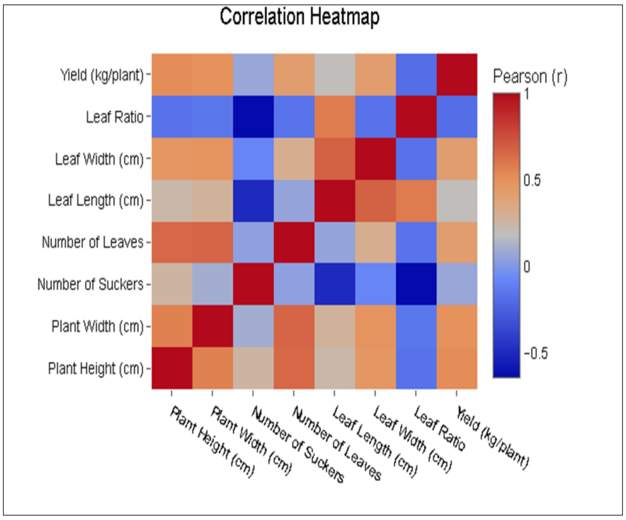

Fig. 2. Heatmap of Pearson's correlation coefficients among morphological traits in 40 *A. vera* accessions.

Broad-sense heritability estimates were high for several key traits, including plant height (74.48%), plant width (73.08%), leaf length (69.92%), leaf width (74.60%) and yield (72.07%). These high heritability values indicate that a large proportion of the observed phenotypic variation is due to genetic factors rather than environmental influences (29). The consistency of high heritability across multiple traits is particularly encouraging from a breeding perspective, as it suggests that phenotypic selection should be highly effective in improving these characteristics (30).

The genetic advance, when considered alongside heritability, provides an indication of the expected genetic gain under selection. The relatively high genetic advance values for traits like plant height (7.92) and plant width (9.19) suggest that these traits could respond well to selection pressure. The combination of high heritability and genetic advance for yield (heritability: 72.07%, genetic advance: 1.09) is particularly promising for developing higher-yielding *A. vera* varieties (31).

Conclusion

The morphological characterization of 40 *A. vera* accessions from Tamil Nadu, India, revealed substantial diversity for important traits. The findings suggest the potential for developing improved *A. vera* varieties through selection and breeding and contribute to the development of effective conservation and utilization strategies for *A. vera* genetic resources in India. Further studies using molecular markers can complement the morphological characterization and provide a comprehensive understanding of the genetic diversity and population structure of *A. vera* in India.

Table 3. Estimates of genetic parameters for morphological traits in 40 *A. vera* accessions

Character	Mean	Range	S.E.	GCV (%)	PCV (%)	H^2	G.A.
Plant height	41.14	19.33 - 59.13	2.80	19.03	22.03	74.48	7.92
Plant width	44.55	18.67 - 67.47	3.34	20.97	24.53	73.08	9.19
Number of suckers	2.57	0.0 - 12.0	0.60	66.08	76.99	73.72	1.72
Number of leaves	12.30	4.0 - 15.67	0.68	15.96	19.48	67.10	1.88
Leaf length	34.21	4.7 - 56.1	2.16	17.68	21.12	69.92	5.90
Leaf width	6.21	3.98 - 9.18	0.34	15.44	17.89	74.60	0.94
Leaf ratio	5.57	1.0 - 7.53	0.27	13.63	15.49	77.32	0.77
Yield	3.49	1.52 - 6.55	0.40	32.04	37.70	72.07	1.09

S.E.-Standard error; GCV- Genotypic coefficient of variation; PCV- Phenotypic coefficient of variation; H^2- Heritability; G.A.- Genetic advance

Acknowledgements

The authors would like to extend their sincere gratitude to the Department of Medicinal and Aromatic Crops, Horticulture College and Research Institute, Tamil Nadu Agricultural University, Coimbatore for providing with planting materials and experimental field required for the study.

Authors' contributions

JS contributed to conceptualised and supervised the research design and experimental planning. CA carried out the experiment, data collection and analysis. BS contributed by imposing the experiment, EK, DU and NB helped in article reviewing, correction and statistical analysis.

Compliance with ethical standards

Conflict of Interest: The authors have no conflict of interest.

Ethical issues: None

References

1. Surjushe A, Vasani R, Saple D. *Aloe vera*: a short review. Indian J Dermatol. 2008. 1;53(4):163-66. https://dx.doi.org/10.4103%2F0019-5154.44785
2. Eshun K, He Q. *Aloe vera:* a valuable ingredient for the food, pharmaceutical and cosmetic industries-a review. Crit Rev Food Sci Nutr 2004. 1;44(2):91-6. https://doi.org/10.1080/10408690490424694
3. Nayanakantha NM, Singh BR, Gupta AK. Assessment of genetic diversity in *Aloe* germplasm accessions from India using RAPD and morphological markers. Cey J Sci (Bio. Sci.). 2010. 39 (1): 1-9. https://doi.org/10.4038/cjsbs.v39i1.2315
4. Govindaraj M, Vetriventhan M, Srinivasan M. Importance of genetic diversity assessment in crop plants and its recent advances: an overview of its analytical perspectives. Genet Res Int. 2015. 2015 (1):431487. https://doi.org/10.1155/2015/431487
5. IPGRI. Descriptors for *Aloe* (*Aloe spp.*). International Plant Genetic Resources Institute. 2001.
6. Medrano M, Herrera CM. Geographical structuring of genetic diversity across the whole distribution range of *Narcissus longispathus*, a habitat-specialist, Mediterranean narrow endemic. Ann Bot. 2008. 1;102(2):183-94. https://doi.org/10.1093/aob/mcn086
7. Hill WG, Mulder HA. Genetic analysis of environmental variation. Genet Res. 2010;92(5-6):381-95. https://doi.org/10.1017/S0016672310000546
8. Nejatzadeh-Barandozi F, Naghavi MR, Enferadi ST, Mousavi A, Mostofi Y, Hassani ME. Genetic diversity of accessions of Iranian *Aloe vera* based on horticultural traits and RAPD markers. Ind Crop Prod. 2012. 1;37(1):347-51. https://doi.org/10.1016/j.indcrop.2011.12.013
9. Team RC. RA language and environment for statistical computing, R Foundation for Statistical. Computing. 2020.
10. Kumar R, Salar RK, Naik PK, Yadav M, Kumar A, Kumar A, et al. Elucidation of genetic diversity and population structure of sixty genotypes of *Aloe vera* using AFLP markers. S Afr J Bot. 2022. 1;147:1146-55. https://doi.org/10.1016/j.sajb.2021.06.008
11. Lagunes-Domínguez A, Pérez-Vázquez A, Hernández-Salinas G, Acosta-Osorio AA, Castillo-Zamudio RI. Agro-morphological characterization in *Aloe vera* genotypes in two states of Mexico. Rev Mexicana Scienc agric. 2024;15(3). https://doi.org/10.29312/remexca.v15i3.3659
12. Kumar S, Yadav M, Yadav A, Yadav JP. Molecular assessment of genetic diversity in Indian accessions of *Aloe vera* using SSR marker. Int J Pharm Pharm Sci. 2015;7(12):149-54.
13. Sharma P, Kharkwal AC, Kharkwal H, Abdin MZ, Varma A. A review on pharmacological properties of *Aloe vera*. Int J Pharm Sci Rev Res. 2014. 29(2):31-7.
14. Kruger EL, Volin JC. Reexamining the empirical relation between plant growth and leaf photosynthesis. Funct Plant Biol. 2006. 2;33(5):421-9. https://doi.org/10.1071/FP05310
15. Sánchez-Machado DI, López-Cervantes J, Sendón R, Sanches-Silva A. *Aloe vera*: Ancient knowledge with new frontiers. Trends Food Sci Technol. 2017. 1; 61:94-102. https://doi.org/10.1016/j.tifs.2016.12.005
16. Oboh BO. Multivariate analysis of the diversity among some Nigerian accessions of Amaranthus hybridus. IJPBG. 2007. 1(2):89-94. https://doi.org/10.3923/ijpbg.2007.89.94
17. Kumar R, Salar RK, Naik PK, Yadav M, Kumar A, Kumar A, *et al*. Elucidation of genetic diversity and population structure of sixty genotypes of *Aloe vera* using AFLP markers. S Afr J Bot. 2022. 1;147: 1146-55. https://doi.org/10.1016/j.sajb.2021.06.008
18. Kumar S, Yadav A, Yadav M, Yadav JP. Effect of climate change on phytochemical diversity, total phenolic content and in vitro antioxidant activity of *Aloe vera* (L.) Burm. f. BMC Res Notes. 2017.10:1-2. https://doi.org/10.1186/s13104-017-2385-3
19. Venugopal S, Padma M, Raj Kumar M, Seenivasan N, Saidaiah P, Sathish G. Genetic variability studies in ashwagandha (*Withania somnifera* L.) for yield and quality traits. Pharm Innov. J. 2021. 10:188-92. https://doi.org/10.1016/j.indcrop.2022.115696
20. Ghrab M, Zribi F, Mimoun MB, Rhouma A. Morphological investigation of genetic diversity of pistachio (*Pistacia vera*) germplasm in arid land of Tunisia. Plant Ecol Evol. 2012. 1;145(3):363-72. https://doi.org/10.5091/plecevo.2012.614
21. Tripathi N, Saini N, Tiwari S. Assessment of genetic diversity among *Aloe vera* accessions using amplified fragment length polymorphism. Int J Med Arom Plants. 2011. 1:115-21.
22. Khadivi-Khub A, Etemadi-Khah A. Phenotypic diversity and relationships between morphological traits in selected almond (*Prunus amygdalus*) germplasm. Agrofor Syst. 2015. 89:205-16. https://doi.org/10.1007/s10457-014-9754-x
23. Bisht Y, Sharma H, Jugran AK, Singh AV, Mishra PK, Pareek N. Assessment of genetic diversity and population structure of Indian common bean accessions using microsatellite markers. Plant Genetic Resources. 2023. 21(2):182-93. https://doi.org/10.1017/S1479262123000606
24. Arteaga S, Yabor L, Torres J, Solbes E, Muñoz E, Díez MJ, *et al*. Morphological and agronomic characterization of Spanish landraces of *Phaseolus vulgaris* L. Agriculture. 2019. 9;9(7):149. https://doi.org/10.3390/agriculture9070149
25. Eckert CG, Samis KE, Lougheed SC. Genetic variation across species' geographical ranges: the central-marginal hypothesis and beyond. Mol Ecol. 2008. 17(5):1170-88. https://doi.org/10.1111/j.1365-294X.2007.03659.x
26. Mamo T, Asheesh S, Mahama AA. Participatory plant breeding and participatory variety selection [Chapter 7]. In: Suza, W.P. (et al. (eds.) Crop Improvement. Ames, Iowa (USA): Iowa State University Digital Press.2023.161- 71.
27. Nyine M, Uwimana B, Swennen R, Batte M, Brown A, Christelová P, *et al*. Trait variation and genetic diversity in a banana genomic selection training population. PLoS One. 2017. 6;12(6): e0178734. https://doi.org/10.1371/journal.pone.0178734
28. Saljooghianpour M. Genetic diversity in different accessions of *Aloe sp*. using Morphological and AFLP markers. Indian J Agric Sci. 2013. 1;83(12).
29. Alatalo RV, Gustafsson L, Lundberg A. Phenotypic selection on heritable size traits: environmental variance and genetic response. Am Nat. 1990. 1;135(3):464-71. https://doi.org/10.1086/285056
30. Resende MD, Resende Jr MF, Sansaloni CP, Petroli CD, Missiaggia AA, Aguiar AM, *et al*. Genomic selection for growth and wood quality in Eucalyptus: capturing the missing heritability and accelerating breeding for complex traits in forest trees. New Phytol. 2012. 194 (1):116-28. https://doi.org/10.1111/j.1469-8137.2011.04038.x
31. Foulkes MJ, Snape JW, Shearman VJ, Reynolds MP, Gaju O, Sylvester-Bradley R. Genetic progress in yield potential in wheat: recent advances and future prospects. J Agric Sci. 2007. 1;145(1):17. https://doi.org/10.1017/S0021859607006740