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Variability and heritability in morphological traits of *Polygonatum cirrhifolium* germplasm collected from Himachal Pradesh

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ABSTRACT

Polygonatum cirrhifolium (Mahameda) is an important medicinal plant of the Himalayan region facing pressure due to overexploitation. The present study evaluated genetic variability, heritability and genetic divergence among 23 germplasm sources collected from Himachal Pradesh. The experiment was conducted at the Field Research Station, Brundhar, Manali, district Kullu, Himachal Pradesh using a randomized block design with three replications. Significant variation was observed for all morphological traits, indicating substantial genetic variability. PCV values were higher than GCV for all traits, reflecting environmental influence; however, the narrow differences suggested strong genetic control. Heritability ranged from 38.78 to 75.20 per cent, with plant height and number of leaves per node showing high heritability and suitability for direct selection. Cluster analysis grouped the sources into two major clusters, while PCA identified plant height and leaf traits as key contributors to variability. The study highlights the potential for selecting superior genotypes for breeding and commercial cultivation.

Keywords: *Polygonatum cirrhifolium*; Genetic variability; Heritability; Germplasm; Morphological traits; PCA; Cluster analysis; Medicinal plant

INTRODUCTION

The species of genus *Polygonatum* have been extensively studied because they have been employed for centuries as drugs and have a broad spectrum of pharmacological properties. *Polygonatum cirrhifolium* is a vulnerable medicinal plant of Himalaya under the Astavarga group. It is also a major constituent in Chyavanprash (Suyal et al 2022). This is an erect, tall succulent herb occurring in small clumps over the northwestern Himalayas between 1,600-4,000 m amsl (Giri et al 2017). *P cirrhifolium* is commonly known as Mahameda or coiling leaf Solomon's seal and belongs to the family Asparagaceae under the tribe Polygonateae (Meng et al 2014). In many regions, young shoots get consumed in salads and people also make use of the wild leafy vegetable (Wujisguleng et al 2012). Its rhizome contains sugars (glucose, sucrose), steroidal saponins (sibiricoside A and B) and n-butanol extract constituents such as phenols, polysaccharides, tannins, steroidal terpenoids, along with compounds like α-L-rhamnopyranosyl, β-D-glucopyranoside, dauvosterol, β-sitosterol and fatty acids (Suyal et al 2022). It is a wild food source and traditional medicine for Vata, Pitta and Raktadoshas, sexual disorders, piles, intestinal disorders, wounds, asthma, inflammation and jaundices as well (Khan et al 2013). The plant is also rich in saponins, alkaloids, flavonoids, antioxidants and diosgenin (b-sitosterol) as major phytochemicals (Virk et al 2016).

P cirrhifolium rhizome is persistently overharvested from its natural habitats for its medicinal benefits. Due to overexploitation, it is under pressure to live in the wild and has been classified as threatened under the vulnerable category by the IUCN (Bhatt et al 2014, Saha et al 2015). Although the wild sources are considered as best in terms of medicinal value, but due to shrinkage of forest and shortage of these plants in the natural habitats, their cultivation close to the natural settings is considered as best alternative (Dajic-Stevanovic and Pljevljakusic 2015). Domestication and cultivation of wild medicinal plants without proper selection and field testing lead to reduction in yield.

Therefore, to promote the cultivation of this species there is need of selection and identification of genetically superior source to ensure high quality and better return to farming communities. Genetic variability is considered as the fundamental basis of evolution and the capability of a species to adopt adverse environmental conditions. It provides information about the use of germplasm in conservation and breeding strategies (Cipriano et al 2016). Thus the assessment of genetic variation and mode of inheritance of traits are considered as an essential step in crop improvement programme (Osei et al 2019). The heritability estimates provide information about the genetic control of a particular trait. Simply, it indicates about the proportion of variations in traits controlled by the genetic difference among the individuals of a population. Higher heritability means higher genetic control of a particular trait and greater the response to the selection.

Germplasm of *P cirrhifolium* was collected from its natural distribution range in Himachal Pradesh by the ICFRE – Himalayan Forest Research Institute, Shimla and subsequently established at the Field Research Station (FRS), Brundhar, Jagatsukh, Manali, Himachal Pradesh. Environmental variation is known to influence plant adaptation, which in turn affects the quality and efficacy of the final product (Suyal et al 2019). Therefore, the present study aimed to assess genetic variability and estimate heritability of various morphological traits in *P cirrhifolium* germplasms, with a view to supporting future breeding programmes and the development of improved varieties for commercial cultivation.

MATERIAL and METHODS

Study area: In 2023, the research work on genetic variability and heritability of morphological traits in *P cirrhifolium* (Wall) Royle was done at FRS, Brundhar, Jagatsukh, Manali, Himachal Pradesh. The research station is located at 32°112'49.583" N latitude and 77°122'15.403" E longitude with an altitude of 1,893 m amsl. The experiment was conducted in a nursery with 23 sources of *P cirrhifolium* arranged in randomized block design with three replications. The rhizomes were obtained from different locations of Himachal Pradesh with altitudinal ranges of 1,800-3,600 m amsl to include different ecological conditions (Table 1).

Table 1. Germplasm collection sites with location codes

Location	Location code	District
Ban Bihar (Manali)	BAN	Kullu
Yalinge-Nichar	YAL	Kinnaur
Kulta-Parvati	KUP	Kullu
Tower House (Nichar)	TWH	Kinnaur
Shakryala (Chattri Mani)	SHA	Mandi
Nagani (Nichar)	NAG	Kinnaur
Kanoi (Khakhanal)	KAN	Kullu
Dandibag-Khatnol	DNK	Shimla
Kasol-Parvati	KSP	Kullu
Lapah (GHNP)	LAP	Kullu
Jani-Tapri	JAT	Kinnaur
Kulang (Palchan)	KUG	Kullu
Shahdhar (Sarahan)	SHD	Shimla
Tosh-Parvati	TOP	Kullu
Cheog-Theog	CHT	Shimla
Yuchpago-Chhitkul	YUC	Kinnaur
Deha Chopal	DHC	Shimla
Barshaini-Parvati	BRP	Kullu
Manikaran-Parvati	MNP	Kullu
Katgaon	KTG	Kinnaur
Ded Sungra	DDS	Kinnaur
Kache (Bhabanagar)	KCH	Kinnaur
Odidhar (Jadun)	ODH	Shimla

Assessment of vegetative growth traits: Morphological observations were recorded at three and six months after planting to evaluate vegetative growth. The traits assessed included plant height, collar diameter, number of leaves per node, leaf length and leaf width.

Statistical analysis: The recorded data were subjected to statistical analysis to assess variation among germplasm sources collected from different locations. Analysis of variance (ANOVA) was performed using IBM SPSS Statistics (Version 29.0.0.0). Genetic parameters, including variability (Burton and DeVane 1953, Pillai and Sinha 1968) and heritability (Lush 1940), were estimated using the standard formulas described below:

Genotypic coefficient of variation (GCV):

$$\mathrm{GCV}(\%) = \frac{\sqrt{\text{Genotypic variance } (\sigma_g^2)}}{\text{Population mean of character } (\bar{x})} \times 100$$

Phenotypic coefficient of variation (PCV):

$$\mathrm{PCV}(\%) = \frac{\sqrt{\text{Phenotypic variance } (\sigma_p^2)}}{\text{Population mean of character } (\bar{x})} \times 100$$

Broad sense heritability (H_{BS}^2):

$$H_{BS}^2(\%) = \frac{\text{Genotypic variance } (\sigma_g^2)}{\text{Phenotypic variance } (\sigma_p^2)} \times 100$$

The estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were categorized as low (<10%), medium (10-20%) and high (>20%) following Sivasubramanian and Menon (1973). Heritability estimates were classified as low (<30%), medium (30-60%) and high (>60%) as per Robinson (1966). Hierarchical cluster analysis and principal component analysis (PCA) were performed and the dendrogram and biplot were generated using PAST software (Version 4.03).

RESULTS and DISCUSSION

Phenotypic variation

A significant variation was observed among the different sources for all the studied morphological traits, indicating the presence of substantial genetic variability within the germplasm (Table 2). Significant variability was observed among the evaluated sources for all growth and leaf traits, indicating a strong genetic base. Plant height was recorded the highest in BAN (36.18 cm) and KSP (31.22 cm) which were at par and lowest in YUC (14.58 cm), KAN (15.93 cm), YAL (16.59 cm), TWH (16.70 cm) and DNK (19.10 cm), the five being at par. Collar diameter was maximum in KSP (2.59 mm), KUG (2.57 mm), JAT (2.41 mm), KTG (2.34 mm), BAN (2.29 mm), NAG (2.24 mm), LAP (2.23 mm), DNK (2.19 mm), TOP (2.19 mm) and DDS (2.18 mm), all being statistically at par. It was minimum in YUC (1.59 mm), BRP (1.62 mm), KUP (1.64 mm), KAN (1.65 mm), MNP (1.89 mm), DHC (1.91 mm) and YAL (1.93 mm), which were at par. Number of leaves per node was highest in KUP (5.00) and lowest in CHT (3.00), DHC (3.00), BRP (3.00), MNP (3.00), NAG (3.00), KTG (3.00), KCH (3.00), TWH (3.33), DDS (3.33) and ODH (3.33), all being at par. Leaf length was the maximum in ODH (8.66 cm), KCH (8.05 cm), BAN (7.86 cm), KTG (7.59 cm) and MNP (7.53 cm), all being at par and minimum in KUP (4.71 cm), TWH (4.93 cm) and YUC (5.63 cm), the latter three being at par. Leaf width was noticed maximum in BAN (1.97 cm). It was minimum in all the locations (0.89-1.25 cm) except KSP (1.31 cm) and ODH (1.41 cm).

Variability in several growth traits has been reported in different crops and effectively utilized in selection processes for breeding programmes (Ulak et al 2022). Variation in leaf morphology is particularly important, as it directly influences photosynthetic efficiency, biomass accumulation and plant adaptability (Guet et al 2015, Dong et al 2020). The present findings are in agreement with earlier studies conducted in India on *P verticillatum*, which reported significant variability in growth and leaf-related traits, indicating a high level of genetic diversity (Suyal et al 2019). Morphological traits are key determinants of plant biomass and are closely associated with enhanced productivity (Mathan et al 2016). Therefore, the selection of superior genotypes with desirable characteristics is essential to achieve stable and higher yields under agricultural conditions. The coefficient of variation serves as an important statistical measure for assessing the extent of variability among different traits (Xu et al 2021).

Genotypic and phenotypic coefficient of variation

The estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) showed that PCV values were consistently higher than the corresponding GCV values for all the traits studied (Table 3), indicating the influence of

Table 2. Morphological traits among diverse sources of the studied germplasm

Location code (source)	Plant height (cm)	Collar diameter (mm)	Number of leaves/node	Leaf length (cm)	Leaf width (cm)
BAN	36.18	2.29	4.00	7.86	1.97
YAL	16.59	1.93	3.67	6.09	1.02
KUP	22.17	1.64	5.00	4.71	0.89
TWH	16.70	2.09	3.33	4.93	0.93
SHA	21.03	2.12	4.00	6.49	1.24
NAG	25.44	2.24	3.00	7.13	1.07
KAN	15.93	1.65	3.67	6.55	1.19
DNK	19.10	2.19	4.00	6.53	1.24
KSP	31.22	2.59	4.00	7.35	1.31
LAP	23.44	2.23	4.00	6.94	1.02
JAT	28.91	2.41	4.00	7.27	1.10
KUG	27.10	2.57	4.00	7.15	1.00
SHD	20.29	2.16	3.67	7.09	0.97
TOP	21.82	2.19	3.67	7.00	1.09
CHT	24.52	2.02	3.00	7.28	1.08
YUC	14.58	1.59	3.67	5.63	0.98
DHC	26.76	1.91	3.00	6.43	1.05
BRP	19.86	1.62	3.00	6.54	1.12
MNP	28.12	1.89	3.00	7.53	1.05
KTG	30.28	2.34	3.00	7.59	1.25
DDS	21.07	2.18	3.33	7.11	1.08
KCH	30.98	2.02	3.00	8.05	1.08
ODH	22.82	2.16	3.33	8.66	1.41
Average	23.69	2.09	3.58	6.87	1.14
$CD_{0.05}$	5.02	0.41	0.56	1.24	0.37
P-value	3.79E-11	7.98E-06	2.24E-08	5.94E-06	0.0012
SE	0.73	0.04	0.07	0.13	0.03

BAN: Ban Bihar (Manali), YAL: Yalinge-Nichar, KUP: Kulta-Parvati, TWH: Tower House (Nichar), SHA: Shakryala (Chattri Mani), NAG: Nagani (Nichar), KAN: Kanoi (Khakhanal), DNK: Dandibag-Khatnol, KSP: Kasol-Parvati, LAP: Lapah (GHNP), JAT: Jani-Tapri, KUG: Kulang (Palchan), SHD: Shahdhar (Sarahan), TOP: Tosh-Parvati, CHT: Cheog-Theog, YUC: Yuchpago-Chhitkul, DHC: Deha Chopal, BRP: Barshaini-Parvati, MNP: Manikaran-Parvati, KTG: Katgaon, DDS: Ded Sungra, KCH: Kache (Bhabanagar), ODH: Odidhar (Jadun)

environmental factors on trait expression. The difference between GCV and PCV was relatively small for plant height and number of leaves per node (around 3%) and slightly higher for collar diameter and leaf width (about 4.5%), suggesting moderate variability and good scope for effective selection. However, leaf width exhibited a comparatively larger difference (approximately 9.5%), reflecting a stronger environmental influence on this trait. In general, a narrow difference between GCV and PCV indicates minimal environmental interference and a greater role of genetic factors in the expression of traits (Johnson et al 1955). In the present study, most traits, including plant height, collar diameter, number of leaves per node and leaf length, showed relatively small differences between GCV and PCV, suggesting that these traits are largely governed by genetic factors and can be reliably used in selection programmes. These findings are in agreement with earlier reports in *Valeriana jatamansi* (Thakur et al 2018) and *Gloriosa superba* (Rajagopal and Kandhasamy 2009). Similar trends have also been observed in other medicinal and forest species, where higher PCV than GCV reflects the influence of environmental conditions on phenotypic expression (Terfa and Gurmu 2020).

Heritability

Heritability is an important parameter that indicates the extent to which traits are transmitted from parents to progeny. It is commonly classified as low (<30%), medium (30-60%) and high (>60%). Estimation of heritability helps plant breeders

Table 3. Genetic variability, coefficients of variation and heritability for morphological traits in *P cirrhifolium*

Parameter	Range	Mean ± SE	GCV (%)	PCV (%)	H²b (%)
Plant height (cm)	36.18-14.58	23.69 ± 0.73	22.460	25.900	75.20
Collar diameter (mm)	2.59-1.59	2.09 ± 0.04	13.085	17.804	54.02
Number of leaves/node	5-3	3.58 ± 0.07	13.285	16.340	66.11
Leaf length (cm)	8.66-4.71	6.87 ± 0.13	12.091	16.342	54.74
Leaf width (cm)	1.97-0.89	1.14 ± 0.03	15.791	25.356	38.78

identify traits that are most suitable for genetic improvement, with traits exhibiting moderate to high heritability generally considered more reliable for selection.

In the present study, most of the traits exhibited moderate to high heritability (Table 3), with values ranging from 38.78 to 75.20 per cent. Plant height showed the highest heritability (75.20%), followed by number of leaves per node (66.11%), indicating that these traits are predominantly governed by genetic factors and can be effectively improved through direct selection. Moderate heritability estimates were observed for collar diameter (54.02%) and leaf length (54.74%), suggesting the combined influence of genetic and environmental factors on their expression. In contrast, leaf width exhibited comparatively lower heritability (38.78%), reflecting a greater environmental influence and a relatively lower response to selection.

Overall, traits such as plant height and number of leaves per node, which fall under the high heritability category (>60%), are less influenced by environmental variation and, therefore, hold significant potential for use in selection programmes (Ravi et al 2021).

Genetic divergence

The UPGMA-based hierarchical clustering of 23 *P cirrhifolium* sources grouped them into two major clusters based on their morphological traits (Fig 1). Cluster I, the smaller group, comprised seven sources from Kullu, Kinnaur and Shimla (KSP, KTG, KCH, JAT, MNP, KUG and DHC). These accessions exhibited superior growth performance, with higher mean values for plant height and leaf length (Table 4), indicating close morphological similarity and a possible shared genetic background. Cluster II, the larger group, included the remaining 16 sources and was further divided into three sub-clusters. The first sub-cluster consisted of sources from Kullu and Kinnaur (YAL, KAN, TWH and YUC) collected from elevations ranging between 2,106 and 3,527 m. The second sub-cluster was further divided into two groups: one comprising only the high-altitude source KUP (3,053 m) and the other including SHA, TOP, DDS, DNK, SHD and BRP collected from elevations of 1,617-2,622 m. Although KUP and YUC originated from higher elevations and were placed in different sub-clusters, they were closely associated, indicating strong morphological resemblance. The third sub-cluster included NAG, CHT, LAP and ODH (1,956-2,310 m), which showed comparatively moderate to lower growth along with greater variability in leaf traits. Notably, sources from different geographic regions and altitudinal ranges were often grouped together, suggesting that morphological variation is influenced more by genetic factors than by geographic origin or elevation. This observation is in agreement with earlier diversity study (Yeshitila et al 2023).

Principal component analysis (PCA) was used to examine the relationships among the evaluated sources and their morphological traits (Fig 2). The analysis identified five principal components (PCs) with eigenvalues greater than one (Table 5). Among these, PC1 exhibited the highest eigenvalue ($\lambda_1 = 31.8057$), followed by PC2 (0.586426). Consequently, the PCA biplot based on PC1 and PC2 was used to interpret the results. The contribution of different traits to these components indicated that plant height and leaf-related characteristics played a major role in source differentiation. In PC1, plant height showed the highest loading (0.99386), followed by leaf length (0.10463) and collar diameter (0.028591).

In contrast, PC2 was predominantly influenced by leaf length (0.89012), with smaller contributions from leaf width (0.055382) and collar diameter (0.044979). The PCA biplot exhibited a clustering pattern consistent with the UPGMA analysis, indicating clear grouping among the sources. BAN was distinctly separated as an outlier, mainly due to its comparatively greater plant height. ODH showed the highest leaf

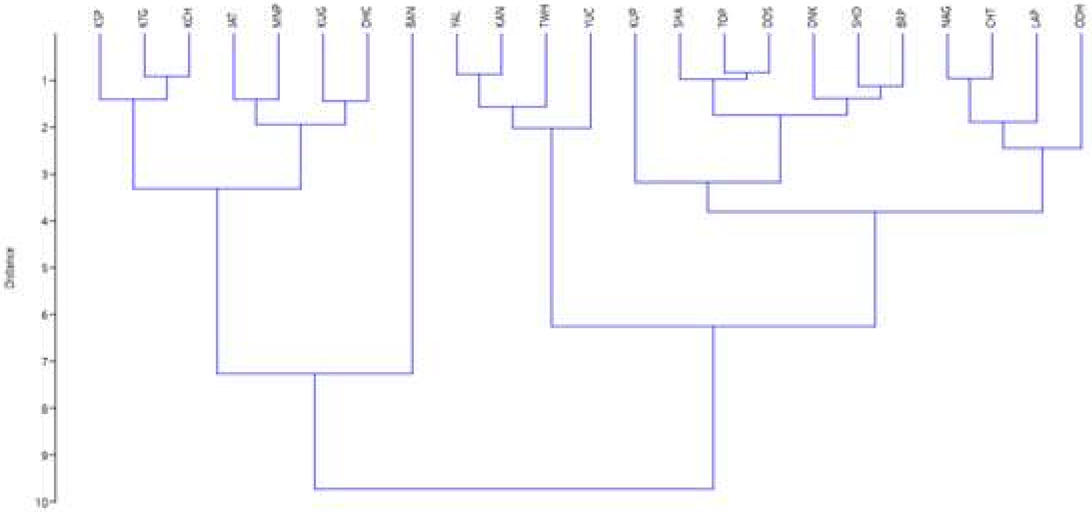

Fig 1. UPGMA-based dendrogram illustrating genetic relationships among 23 sources of *P cirrhifolium*

Table 4. Cluster-wise mean performance of morphological traits in *P cirrhifolium*

Cluster number	Plant height (cm)	Collar diameter (mm)	Number of leaves/node	Leaf length (cm)	Leaf width (cm)
1	29.94	2.25	3.50	7.40	1.23
2	20.36	2.00	3.62	6.58	1.09

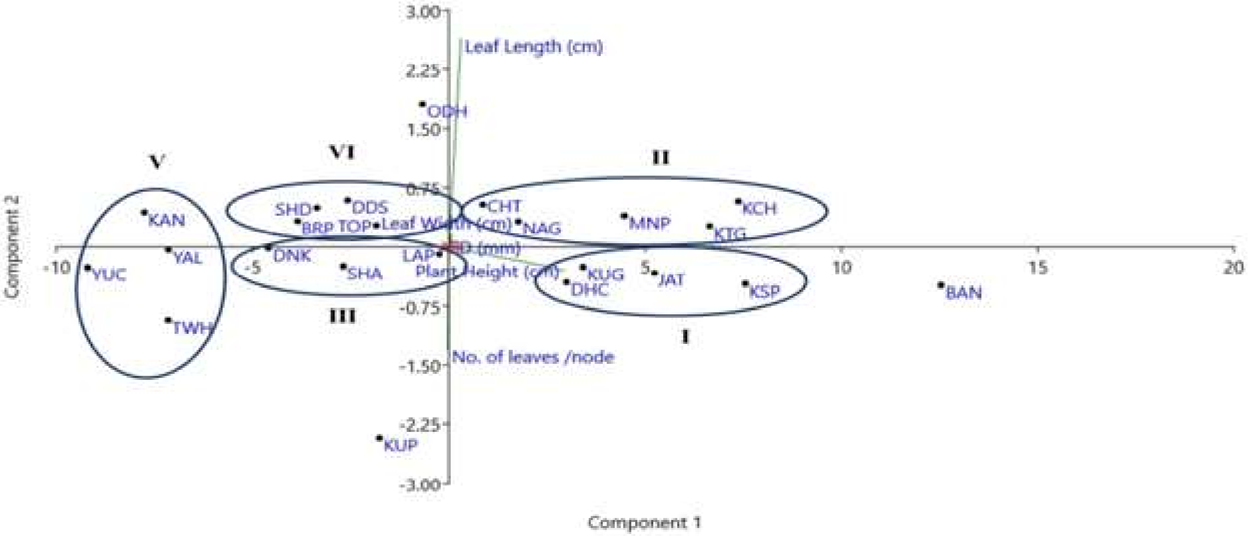

Fig 2. Principal component analysis (PCA) biplot showing distribution of germplasm sources and contribution of morphological traits in *P cirrhifolium*

length, with NAG also displaying a positive association with this trait. In terms of leaves per node, KUP recorded the maximum values. Conversely, YUC, KAN, YAL and TWH clustered together, reflecting their consistently lower performance across all studied traits. Overall, both hierarchical clustering and PCA clearly demonstrated that plant height and leaf traits are the most influential variables contributing to genetic divergence and grouping of Mahameda sources. Similar findings were reported by Suyal et al (2019), emphasizing the role of plant height and leaf traits in variability of *P verticillatum*.

Table 5. Principal component analysis (PCA) of morphological traits in *P cirrhifolium*

Parameter	Principal components				
	PC 1	PC 2	PC 3	PC 4	PC 5
Plant height (cm)	0.99386	–0.099544	–0.04566	–0.0096	–0.01255
Collar diameter (mm)	0.028591	0.044979	0.23659	0.90234	0.35631
Number of leaves/node	–0.0077031	–0.43897	0.86865	–0.13128	–0.1883
Leaf length (cm)	0.10463	0.89012	0.40121	–0.08645	–0.16823
Leaf width (cm)	0.020493	0.055382	0.16252	–0.40122	0.89951
Eigenvalue	31.8057	0.586426	0.196914	0.046238	0.025803
% variance	97.381	1.7955	0.6029	0.14157	0.079002

CONCLUSION

The present investigations revealed a significant level of genetic variability among the germplasm sources of *P cirrhifolium*, indicating good potential for selection and improvement. The higher values of PCV compared to GCV across all traits confirmed the influence of environmental factors; however, the relatively small differences between them for most traits suggested a predominant role of genetic components. Traits such as plant height and number of leaves per node exhibited high heritability, indicating their stability and effectiveness for direct selection in breeding programmes. Moderate heritability observed for other traits reflects the combined influence of genetic and environmental factors, while lower heritability in leaf width suggests limited response to selection. Both hierarchical clustering and principal component analysis demonstrated clear genetic divergence among the sources and highlighted the importance of plant height and leaf-related traits in determining variability. The study concludes that selection of superior sources based on these key traits can contribute to the development of high-yielding and quality planting material, thereby, supporting the conservation and commercial cultivation of this important medicinal species.

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