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Agro-morphological diversity of Salvia mirzayanii Rech. F. & Esfand. (Lamiaceae) populations grown wild in Iran: the first step in plant conservation and domestication

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ABSTRACT

The genus *Salvia* L. (Lamiaceae) comprises approximately 900 species distributed worldwide. Iran is home to 58 annual and perennial *Salvia* species, 17 of which—such as *Salvia mirzayanii* Rech. f. & Esfand—are endemic. This species predominantly grows in the southern regions of Iran, particularly in the Fars and Hormozgan provinces. Traditionally, *S. mirzayanii* has been used for treating gastrointestinal disorders including gastric irritation, diarrhea, abdominal pain, and poisoning, as well as for relieving headaches and promoting wound healing. In the present study, morphological diversity among seven populations of *S. mirzayanii* (*SMPs*), collected from various geographic regions—Bavanat (*SMP1*), Sarvestan (*SMP2*), Darab (*SMP3*), Lar (*SMP4*) Tange-Zagh (*SMP5*), Sarchahan (*SMP6*), and Sirmand (*SMP7*)—was assessed as a fundamental step for conservation, domestication, and breeding efforts. Eighteen qualitative and quantitative traits related to yield were evaluated. The Darab population (*SMP3*) exhibited the greatest leaf length and width, while the Sirmand population (*SMP7*) showed the highest values for peduncle length, internode length, and bract width. Factor analysis revealed that the first three factors accounted for 51.784% of the total variance. Key traits contributing to the observed variation among populations included corolla length, filament length, anther length, pistil length, bract length, and bract width. Cluster analysis based on morphological traits grouped the *SMPs* into two main clusters. The first cluster comprised the Sarchahan (*SMP6*), Sirmand (*SMP7*), Tange-Zagh (*SMP5*), Darab (*SMP3*), and Sarvestan (*SMP2*) populations, while the second cluster included the Bavanat (*SMP1*) and Lar (*SMP4*) populations. The findings of this study provide valuable insights for selecting superior genotypes suitable for in-situ and ex-situ conservation, as well as for future use in agricultural systems.

Keywords: *Salvia sp., Medicinal plant, Diversity, Conservation, Germplasm, Cluster analysis*

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Introduction

Medicinal and aromatic plants (MAPs) are among the most important natural resources due to their therapeutic properties and have been used for centuries (1). According to the World Health Organization (WHO), over 80% of the global population relies on these remedies, either through traditional or modern practices. Additionally, several semi-synthetic drugs have been developed by mimicking the chemical compounds found in plants (2, 3).

In recent years, pharmaceutical industries have primarily sourced plant raw materials from natural habitats. This practice has led to several critical issues, such as species extinction, heterogeneity in plant material, and a lack of sustainable supply (4, 5). Given the growing significance of MAPs in both the pharmaceutical and food industries, it is essential to protect plant habitats and genetic resources (6). Efforts should include domestication, the development of high-quality and homogeneous cultivars, and the cultivation of these species (7, 8). Furthermore, because wild-collected plant materials often possess unique secondary metabolites (SMs), it is important to conserve these populations as genetic models in plant, seed, or gene banks (9).

In response to the increasing demand from the pharmaceutical industry, there has been a growing trend toward the cultivation of MAPs. However, a key component of any breeding or large-scale cultivation initiative must be the protection of natural populations and gene pools (Venkatasubramanian et al., 2018). Genetic diversity within MAPs populations is vital, as it provides resilience and adaptability to environmental changes (10). MAPs often exhibit significant variability in both morphological and phytochemical traits across different climates and natural habitats (11).

Therefore, for effective pharmaceutical application and sustainable use, it is necessary to evaluate MAPs from genetic, chemical, and agronomic perspectives (12). Wild plant populations are considered among the most valuable genetic resources of a region, making their protection a top priority. In general, conserving plant species is far more efficient and cost-effective before they reach the brink of extinction (13). Initially, conservation should be implemented *in situ*, and if required, *ex situ*. Both approaches rely heavily on a comprehensive understanding of the morphological, phytochemical, and genetic diversity within and among plant populations (14).

Morphological traits are the earliest markers used in plant classification studies (Kakaei and Kahrizi, 2025). These traits are valuable for germplasm management, particularly for ensuring that offspring are true-to-type in homogeneous (inbred) lines (15). Morphological evaluation is simple, rapid, and cost-effective, especially when using identification keys. Historically, MAP classification has been based primarily on morphological characteristics (16). Some of these traits can serve as genetic markers in germplasm studies (17). However, polygenic morphological traits are often influenced by environmental interactions and exhibit low heritability, which complicates their use in taxonomy and increases the cost of analysis (18). Nevertheless, computer-based systems have enhanced the visualization and analysis of morphological data (19).

The genus *Salvia* L. (Lamiaceae) is one of the largest in the family, comprising over 900 species distributed worldwide (20). *Salvia* species are rich in secondary metabolites, including terpenoids and phenolic compounds (21). They are particularly valued for their pentacyclic triterpenoids, which have significant medicinal potential (22-24). Many *Salvia* species are also widely used as herbal teas, food flavorings, and in the cosmetics, perfumery, and pharmaceutical industries (24).

In Iran, 58 *Salvia* species have been documented, 17 of which, including *S. mirzayanii* Rech. f. & Esfand., are endemic (25, 26). Commonly known in Persian as

"*Mourtalkh*," *S. mirzayanii* is a small shrub (20–50 cm in height) with stalked, branched stems covered with glandular trichomes, particularly on the lower parts (27) (Ghasemi et al., 2023). It typically grows on rocky slopes in the Irano-Turanian region in southern Iran, particularly in the provinces of Sistan and Baluchestan, Kerman, Hormozgan, Fars, Bushehr, and Khuzestan (28, 29).

Traditionally, the aerial parts of *S. mirzayanii* have been used to treat digestive ailments such as heartburn, diarrhea, and abdominal pain, as well as poisonings, arthralgia, headaches, and to lower fat and blood glucose levels. It is also used for wound healing (30-32). Antioxidant, antimicrobial, and antiviral properties have been reported for this valuable plant (33). Due to its limited natural distribution, increasing human activity, habitat disturbance, overharvesting for medicinal use, and low natural propagation rate, *S. mirzayanii* is now considered at risk of extinction in its natural habitats in southern Iran (Ghasemi et al., 2023).

Although the phytochemical profile and biological activities of *S. mirzayanii* have been studied (34), and its antiglycation effect has recently been reported (35), previous research has primarily focused on ecological distribution and abundance (36), as well as genetic and molecular characterization in some *Salvia* species (37, 38). However, to the best of our knowledge, morphological diversity—which is crucial for breeding programs—has not yet been assessed in *S. mirzayanii*. The present study aims to evaluate the agro-morphological diversity among *S. mirzayanii* populations (*SMPs*) found in southern Iran. The outcomes of this study are expected to facilitate the identification of superior populations suitable for domestication, breeding, and commercial exploitation.

Materials and methods

Plant materials

Following several field expeditions to natural habitats, the aerial parts of ten individuals from each *S. mirzayanii* population were collected from seven distinct locations across Fars and Hormozgan provinces in southern Iran (Table 1, Fig. 1). The collected samples were taxonomically identified, and voucher specimens from each ecotype were deposited in the Herbarium of Medicinal Plants and Drugs Research Institute (MPH), Shahid Beheshti University, Tehran, Iran. The geographical and edaphological characteristics of each collection site were recorded using a digital Global Positioning System (GPS) device (Table 1).

Agro-morphological analysis

Seventeen quantitative phenotypic traits related to the vegetative yield and reproductive structures of *S. mirzayanii* were measured. These traits included leaf length, leaf width, petiole length, internode length, number of nodes, inflorescence length, internode length within the inflorescence, bract length, bract width, calyx length, calyx width, corolla length, peduncle length, filament length, anther length, and pistil length. Measurements were carried out using a digital caliper, and a microscope was employed for traits requiring higher precision.

Statistical analysis

Morphological trait data were subjected to one-way analysis of variance (ANOVA), and mean comparisons among populations were conducted using Duncan's multiple range test in IBM SPSS Statistics (version 23). Further statistical analyses, including variance analysis, factor analysis, and cluster analysis (CA) of morphological and phytochemical traits, were performed using SAS software (version 9.4). Principal component analysis (PCA) was conducted in Minitab to explore relationships among *S. mirzayanii* individuals. All graphs and path diagrams were generated using Microsoft Excel 2013 and R software, respectively.

Table 1. Geographic and climatic characteristics of the studied *Salvia mirzayanii* populations (SMPs) from Iran

Population name and code	Bavanat (*SMP1*)	Sarvestan (*SMP2*)	Darab (*SMP3*)	Lar (*SMP4*)	Tang-e-Zagh (*SMP5*)	Sarchahan (*SMP6*)	Sirmand (*SMP7*)
Location	Fars	Fars	Fars	Fars	Hormozgan	Hormozgan	Hormozgan
Latitude (N)	30° 44´	29° 12´	28° 46´	30° 42´	27° 24´	27° 26´	27° 55´
Longitude (E)	53° 42´	53° 35´	54° 55´	54° 12´	56° 11´	56° 18´	56° 17´
Altitude (m.a.s.l.)	1600	1830	1450	1680	1120	960	870
Mean annual temp. (°C)	10.5	18.0	22.0	23.0	20.5	25.3	20.3
Maximal mean annual temp. (°C)	22.5	28.1	31.0	34.0	34.6	33.4	37.0
Minimal mean annual temp. (°C)	6.0	8.0	11.0	14.0	12.0	17.3	14.2
Rainfall (mm/year)	270	220	230	203	210	226	205

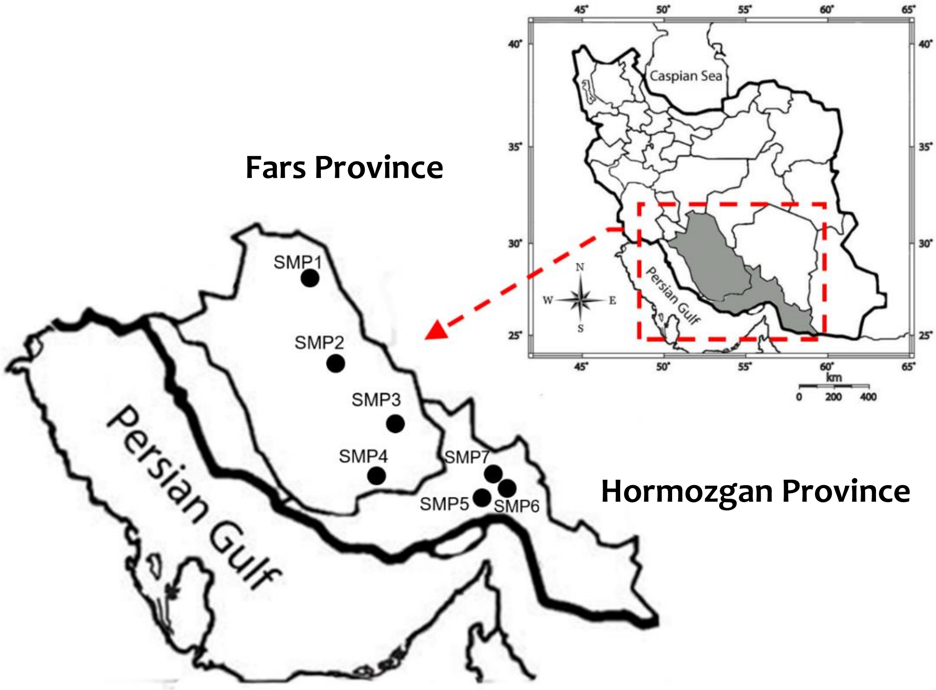

Fig. 1. Geographical distribution of the studied *Salvia mirzayanii* populations (SMPs). For detailed description of populations, cf. Table 1.

Results and discussion

Morphological variabilty

The analysis of morphological traits among the studied *SMPs* revealed a substantial degree of phenotypic variability (Table 2), with the highest coefficients of variation (CV) observed in petiole length, internode length, number of nodes, inflorescence length, and peduncle length. These traits represent key morphological indicators that can be leveraged in breeding, conservation, and domestication strategies, particularly due to their potential correlations with bioactive metabolite production. Notably, *SMP3* exhibited the highest leaf length and width, while the *SMP4* showed superiority in reproductive-related traits such as calyx length and width, filament length, anther length, and inflorescence-related parameters.

Table 2. Morphological variations in the studied *Salvia mirzayanii* populations (SMPs).

No.	Trait	Code	Measurement unit	Mean	Minimum	Maximum	CV
1	Leaf length	LL	mm	25.77	17.65	38.27	20.40
2	Leaf width	LW	mm	4.72	3.08	7.79	25.21
3	Petiole length	PETL	mm	3.83	2.10	7.24	34.37
4	Internode Length	INL	mm	21.35	9.63	40.00	42.72
5	Number Node	NN	-	8.1	4.00	14.00	36.34
6	Inflorescence length	INFL	mm	10.70	5.00	19.60	33.43
7	Inflorescence internode length	INFIL	mm	14.08	8.15	22.80	19.79
8	Bract length	BL	mm	11.28	3.08	16.07	21.59
9	Bract width	BW	mm	12.09	8.15	14.92	13.72
10	Calyx length	CL	mm	12.93	11.96	15.03	7.54
11	Calyx width	CW	mm	6.85	3.78	11.56	21.53
12	Corolla length	CRL	mm	16.64	12.61	21.30	18.17
13	Peduncle length	PL	mm	2.82	1.06	7.31	41.51
14	Stamen length	SL	mm	17.70	12.80	24.23	20.17
15	Anther length	AL	mm	1.49	0.98	2.08	23.14
16	Pistil length	PISL	mm	19.49	13.00	27.21	24.71

In contrast, the *SMP1* displayed the lowest mean values for leaf and reproductive structures, suggesting potential local environmental limitations or genetic constraints (Table 3). Comparable trends in morphological diversity have been reported in other aromatic and medicinal Lamiaceae species. For instance, in *Thymus daenensis* Celak., Heydari et al. (2019) documented significant variation in leaflet width, calyx diameter, and inflorescence internode length, supporting the role of ecological differentiation in shaping morphometric traits (39). Similarly, Luo et al. (2022) reported broad morphological and chemical diversity among *Morinda officinalis* How. populations, attributing such patterns to both genetic background and environmental gradients (17). In a recent study on *Colchicum luteum* Baker., an endangered medicinal species, Rather et al. (2022) emphasized the importance of morphological divergence as a tool for intraspecific classification and conservation prioritization (16).

Table 3. Morphological and reproductive trait means of *Salvia mirzayanii* populations (SMPs) studied across seven locations.

No.	Trait[a]	Bavnat (*SMP1*)	Sarvestan (*SMP2*)	Darab (*SMP3*)	Lar (*SMP4*)	Tang-e-hzagh (*SMP5*)	Sarchahan (*SMP6*)	Sirmand (*SMP7*)
1	LUSC[b]	Light green, olive,	light brown,	light green,	olive	olive	olive	olive
2	LLSC[c]	light green, biege	light green	light green,	biege	biege	Light	Light
3	LL	22.65± 2.2	28.61± 9.1	29.26± 2.1	22.88±	23.65± 6.7	28.69±	24.66±
4	LW	4.09± 0.8	5.22± 1.2	6.15± 1.5	3.72± 0.7	4.78± 1.5	4.49± 0.8	4.64± 0.5
5	PETL	2.51± 0.2	4.20± 0.8	4.20± 0.8	3.38± 1.8	3.18± 1.0	4.4± 0.6	4.71± 2.2
6	IL	11.56 ± 2.7	23.89± 4.3	26.04 ± 9.6	12.36±	24.74± 3	28.71±	32.20±
7	NN	12.67± 1.5	6.33± 1.5	5.67± 1.5	11± 1	5.67± 0.5	10± 1	6± 1
8	INFL	6.77± 2.6	8.97± 1.3	10.93± 4.2	14.63±	11.41± 0.5	11.17± 1	11.07±
9	INFIL	11.88± 3.5	16.26± 5.6	13.82± 0.3	16.27±0.0	13.40± 1.1	12.29±	14.65± 2
10	BL	7.85± 4.2	13.45± 2.5	10.94± 2.2	12.06±	11.71± 0.3	11.56±	11.42±
11	BW	11.2± 1.6	12.29± 3.2	10.60± 2.3	12.5± 1.1	12.64± 0.2	12.53±	12.94±
12	CL	13.12± 1.4	13.26± 0.3	12.76± 0.5	13.97±	12.43± 0.2	12.74±	12.1± 0.1
13	CW	7.88± 0.5	5.29± 1.3	6.30± 0.9	8.09± 3	7.01± 0.5	6.73± 0.8	6.69± 0.8
14	CRL	19.37± 0.8	18.71± 2.3	17.47± 3.3	19.61±	13.99± 0.7	13.12±	14.24±
15	PL	1.78± 0.1	2.58± 1	2.58± 1	4.68± 2.3	2.50± 3	2.62± 1.3	2.73± 0.5
16	SL	19.88± 1.2	19.61± 4.1	19.52± 4.7	20.89±	15.02± 1.3	13.49±	15.52±
17	AL	1.78± 0.1	1.94± 0.1	1.44± 0.2	1.51± 0.4	1.25± 0.1	1.08± 0.1	1.47± 0.2
18	PL	23.47± 1.1	24.60± 2.2	24.60± 2.2	23.06±	14.39± 1.7	13.86± 1	16.30±
19	OC[d]	1.12± 0.21	0.58± 0.11	1.09± 0.03	0.75±0.13	1.2± 0.2	1.8± 0.2	2.2± 0.2

[a] For a detailed code of quantitative traits (mm), cf. Table 2.

[b] LUSC, leaf upper surface color

[c] LLSC, leaf lower surface color

[d] OC, oil content

Such findings align with our observations in *S. mirzayanii*, where population-specific differences in both vegetative and reproductive traits suggest underlying genetic differentiation, potentially shaped by distinct microclimatic conditions across southern Iran. Moreover, Zhumaliyeva et al. (2023) highlighted the substantial phytochemical diversity within *Salvia* species, underlining the link between morphological traits and secondary metabolite variability (20). This is further supported by genetic profiling of *Salvia* spp. using molecular markers, where Zheng et al. (2021) demonstrated strong associations between morphological clustering and genetic distance. The observed pattern in *S. mirzayanii* also resonates with broader evolutionary and ecological findings within the genus (38). For instance, variation in floral and inflorescence architecture, as detected in the current study, may have adaptive significance related to pollinator attraction and reproductive efficiency. As such, traits with high CV—especially those related to floral dimensions—warrant further exploration for their ecological and pharmaceutical relevance. In summary, our findings highlight not only the considerable morphological variability among *SMPs* but also underscore the importance of integrating phenotypic assessments with phytochemical and molecular analyses to guide future conservation and breeding efforts. These results provide a solid foundation for selecting elite genotypes with desirable agro-morphological and medicinal traits, particularly from high-performing populations such as *SMP3* and *SMP4*.

3.2. Simple correlation coefficients of traits

Correlation analysis among the measured agro-morphological traits in *SMPs* is graphically presented in Fig. 2. The results revealed significant positive and negative correlations among several traits. Notably, calyx width (r = 0.440), corolla length (r = 0.501), peduncle length (r = 0.528), filament length (r = 0.528), and pistil length (r = 0.511) showed positive correlations with calyx length. These associations suggest that as the calyx elongates, other floral organs develop proportionally, possibly indicating reduced environmental stress. Previous studies on *Thymus daenensis* demonstrated that heat and drought stress decrease photosynthetic efficiency and alter primary metabolic pathways, shifting metabolism toward secondary metabolite production, such as phytochemical compounds including essential oils (39). Under such stress, plants tend to reduce the size of aerial organs, including flowers, while increasing trichome density to enhance survival. This may explain the higher phytochemical content observed in SMPs from warmer regions like *SMP7* and *SMP6*.

Moreover, internode length (r = 0.509) was positively correlated with phytochemical content, whereas corolla length (r = −0.628), filament length (r = −0.507), anther length (r = −0.446), and pistil length (r = −0.623) showed negative correlations. These findings suggest that longer internodes might improve light penetration and photosynthetic activity, thereby enhancing phytochemical biosynthesis (39). Research on *Satureja khuzistanica* Jamzad. reported positive correlations between rosmarinic acid content and leaf area, alongside negative correlations with peduncle length and leaf color (40). However, in contrast to the present findings, that study found a negative correlation between phytochemical content and internode length. Additionally, calyx width (r = 0.456), calyx length (r = 0.525), and inflorescence internode length (r = 0.437) showed strong positive correlations with peduncle length, further supporting the hypothesis that floral organ expansion occurs under less stressful environmental conditions. Anther length was negatively correlated with inflorescence length at a 1% significance level, suggesting a phenotypic trade-off between these traits in response to environmental factors. A recent study on Iranian populations of *Grammosciadium platycarpum* Boiss. & Hausskn., a rich source of (S)-(+)-linalool, demonstrated significant correlations between phenotypic traits related to yield—such as internode length and branch number—and dry fruit weight, the primary site of phytochemical production in this species. Furthermore, phytochemical content and composition were strongly associated with these phenotypic yield attributes, highlighting the importance of selecting key morphological traits for breeding programs aimed at enhancing medicinal metabolite production (Ghasemi et al., 2023). These findings are consistent with the current results, emphasizing the critical role of phenotypic traits in optimizing phytochemical yield and quality in medicinal plants.

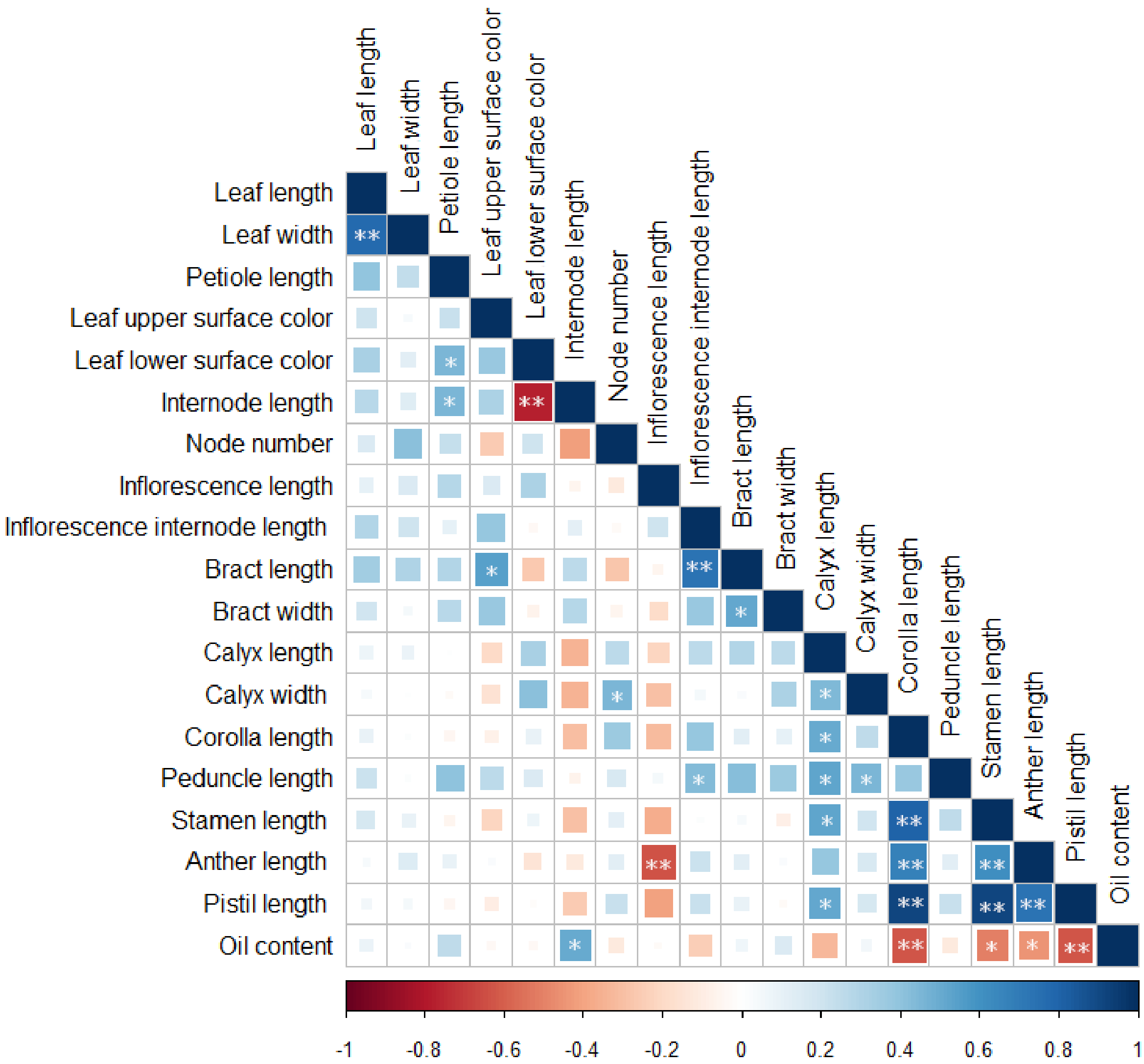

Fig. 2. Plot of correlation between different morphological traits among *Salvia mirzayanii* populations

Factor analysis

Factor analysis using the varimax rotation method in R identified five principal components that together explained 76.58% of the total variance among the 18 measured agro-morphological traits (Table 4). The importance of each factor is evident from its contribution to the overall variance, reflecting their role in differentiating populations. Key traits influencing these components were related to both vegetative and reproductive organs, including corolla length, filament length, anther length, pistil length, bract length, and bract width. Notably, the first two components alone explained 37.89% of the variance, underscoring their major contribution to phenotypic diversity among *SMPs*. This pattern aligns with previous studies on other medicinal and aromatic plants. For instance, Eghlima et al. (2025) reported that five principal components accounted for over 75% of morphological and chemical variability in *Grammosciadium platycarpum* populations, highlighting traits associated with essential oil biosynthesis and fruit yield as key differentiators among geographically distinct populations (41). Similarly, Heydari et al. (2019) found that floral organ traits dominated total variation in *Thymus daenensis*, emphasizing their sensitivity to environmental stresses and genetic divergence (39).

These findings emphasize the biological significance of the identified morphological traits in capturing variation among *SMPs*. Moreover, the consistency of these results with those of related Lamiaceae species supports the effectiveness of multivariate analyses in selecting promising genotypes for breeding and domestication efforts.

Table 4. Factor analysis of 18 agro-morphological traits in *Salvia mirzayanii* using varimax rotation method.

No.	Trait	Factor				
		1	2	3	4	5
1	Leaf upper surface color	–0.126	0.708	0.292	–0.203	–0.073
2	Leaf lower surface color	–0.072	–0.108	–0.812	0.42	–0.055
3	Leaf length	–0.035	0.214	0.236	0.049	0.825
4	Leaf width	0.026	0.03	0.045	–0.081	0.971
5	Petiol length	–0.038	0.188	0.683	0.167	0.289
6	Internode Length	–0.239	0.237	0.736	–0.331	0.07
7	Node number	0.184	–0.191	–0.166	0.534	–0.371
8	Inflorescence length	–0.508	0.343	–0.588	–0.289	–0.129
9	Inflorescence internode length	0.196	0.836	–0.127	0.018	0.188
10	Bract length	0.101	0.815	0.196	0.042	0.265
11	Bract width	–0.081	0.556	0.373	0.453	–0.054
12	Calyx length	0.493	0.202	–0.22	0.57	0.157
13	Calyx width	0.11	0.036	–0.073	0.874	–0.002
14	Corolla length	0.883	0.184	–0.132	0.002	–0.011
15	Peduncle length	0.16	0.564	0.006	0.588	0.079
16	Stamen length	0.899	–0.038	–0.093	0.089	–0.095
17	Anther length	0.842	–0.006	0.198	0.056	0.087
18	Pistil length	0.968	0.07	–0.054	0.055	–0.066
	Eigenvalue	3.943	2.878	2.005	2.429	2.035
	% of variance	21.907	15.987	13.889	13.494	11.308
	Cumulative	21.907	37.894	51.784	65.278	76.586

Cluster analysis

Based on 18 agro-morphological traits (Fig. 3, Fig. 4) effectively grouped the studied *SMPs* into two main clusters, reflecting the influence of genetic and environmental factors on morphological differentiation. Group A consisted *SMP2*, *SMP3*, *SMP4*, and *SMP1*, primarily located in Fars Province. These populations shared similarities in floral traits, especially corolla and filament lengths.

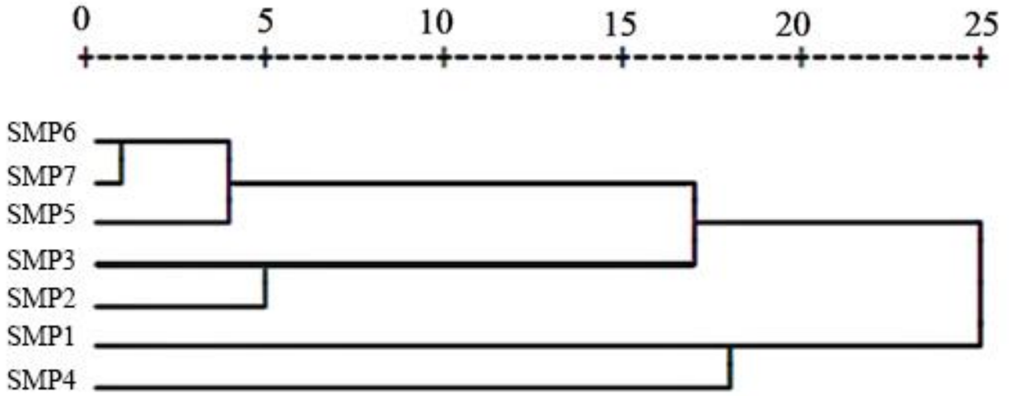

Fig. 3. Clustering of the seven populations of *Salvia mirzayanii* using eighteen quantitative and qualitative traits

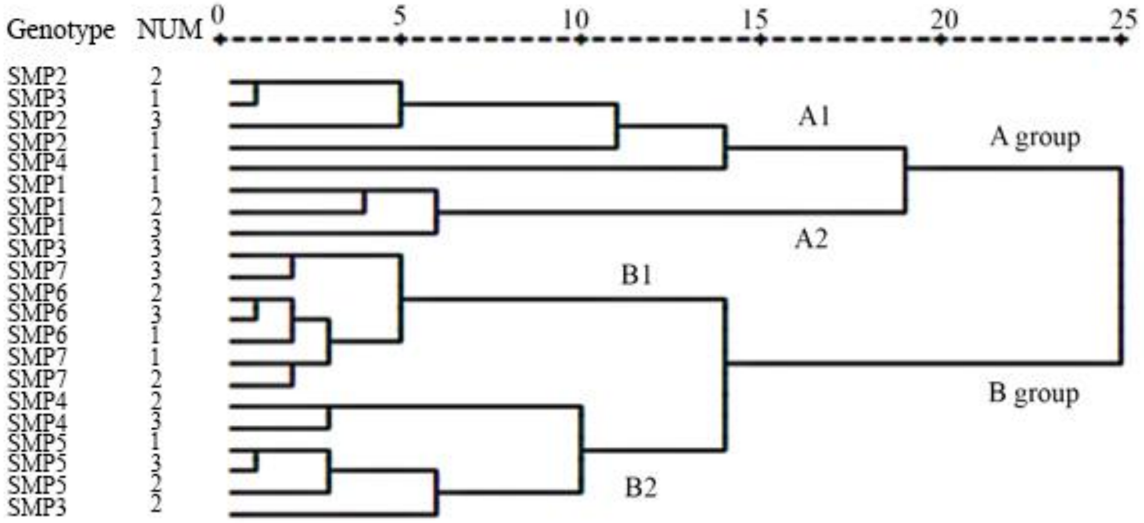

Fig. 4. Grouping of the studied individuals of *Salvia mirzayanii* populations based on the morphological traits

Within this group, subgroup A1 (*SMP2*, *SMP3* and *SMP4*) exhibited additional similarity in pistil length, while *SMP1* formed a distinct subgroup (A2), indicating a unique morphological profile across all measured traits. Group B included *SMP3*, *SMP4*, *SMP5*, *SMP7*, and *SMP6*, which showed closer resemblance in bract length, calyx length, and anther length. Subgroup B1 (*SMP3*, *SMP6*, and *SMP7*) was similar in calyx length and width, whereas subgroup B2 (*SMP3*, *SMP4*, and *SMP5*) aligned more closely in peduncle length and anther size. These clustering patterns suggest that environmental factors such as climate, elevation, and soil composition likely drive morphological divergence within and between regions. Interestingly, the *SMP3* and *SMP4* in both clusters may reflect morphological plasticity due to environmental heterogeneity or gene flow among geographically close populations.

Similar clustering patterns have been observed in other medicinal species. For example, Pouyanfar et al. (2018) reported that ecotypes of *Melissa officinalis* grouped according to their ecological origins, highlighting habitat-driven selection in shaping phenotypic diversity (42). Likewise, Eghlima et al. (2025) found that clusters of *Grammosciadium platycarpum* populations corresponded closely with both morphological traits and essential oil profiles, emphasizing the link between trait variation and ecological adaptation (41). These findings are particularly relevant for breeding and conservation strategies. Grouping populations with similar agro-morphological traits can facilitate the selection of superior genotypes for cultivation and pharmaceutical applications. Additionally, distinct populations such as *SMP1*, which diverge markedly from others, may represent unique genetic resources deserving conservation and further molecular investigation.

Overall, the robust clustering revealed by this analysis underscores the morphological diversity within *S. mirzayanii* and highlights the interplay between genotype and environment in shaping plant form. Future studies integrating genetic markers and metabolomic profiling would be valuable for validating these groupings and exploring their correlation with phytochemical compounds.

Conclusion

Among the studied populations, *SMP4* exhibited the highest values for several floral traits, including corolla length, inflorescence length and internode length, calyx length and width, peduncle length, and filament length. It is noteworthy that reductions in corolla, filament, and pistil lengths are often observed in tropical regions, likely due to heat stress. Cluster analysis grouped *SMP1* and *SMP4* distinctly from other populations, as they shared similar morphological traits such as leaf length and width, internode length, node number, and floral organ dimensions. Meanwhile, *SMP7* showed superior vegetative traits, including the greatest internode length, bract width, and petiole length, indicating its strong potential for future breeding and domestication efforts. Given that *S. mirzayanii* is an endangered species, conserving its genetic and morphological diversity is of paramount importance. The present findings provide valuable guidance for selecting key populations for conservation and breeding programs. Furthermore, future studies integrating molecular and phytochemical data are recommended to complement morphological assessments, thereby supporting sustainable cultivation and utilization of this species.

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Authors' Contributions

Abdolreza Nematollahi: Conceptualization, Investigation, Formal analysis, Writing-original draft. **Vahid Fozi:** Methodology, Data Curation, Formal analysis, Visualization, Writing-review and editing. **Fatemeh Poureshaghi:** Formal analysis, Visualization, Writing-review and editing. **Javad Hadian:** Conceptualization, Supervision, Resources, Funding acquisition, Project administration, Formal analysis, Writing-review and editing.

Declaration of Interest

The authors of this article declared no conflict of interest.

Ethical Considerations

All ethical principles were adheried in conducting and writing this article.

Transparency of Data

In accordance with the principles of transparency and open research, we declare that all data and materials used in this study are available upon request.

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