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FACTOR ANALYSIS OF GENETIC VARIATION IN MORPHOLOGICAL TRAITS OF IRANIAN SUMMER SAVORY (*SATUREJA HORTENSIS* L.) LANDRACES

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Abstract: Summer savory (*Satureja hortensis* L.), a member of the Lamiaceae family, is an important vegetable crop and medicinal plant, widely used both as food and as an herbal remedy. In the present study, the phenotypic diversity of 29 Iranian landraces was evaluated based on plant height, stem length, root length, internode length, number of leaflets per main stem, leaf area of leaves on the main stem and lateral branches, fresh weight of stem, root and whole plant, dry weight of stem, root and whole plant, and essential oil content. Factor analysis revealed that 89% of the observed variation could be explained by the first five factors, which were characterized based on varimax-rotated scores as biomass, dwarfism and leaflet traits, leaf area, low essential oil content, and reduced root length. A plot of the first two factors, accounting for 62% of the total variation, distinguished five genotypic groups. Notably, Group C genotypes - G6 (Sistan), G15 (Hamadan), G23 (Arak), and G27 (Tonkabon-A) - exhibited high biomass and essential oil content, making them promising candidates for cultivar development and future breeding programs. To classify the traits, a two-dimensional plot based on the first two factors was generated. This analysis showed that internode length, plant height, stem length, and the leaf area were grouped together. Similarly, root length, number of leaflets per main stem, and essential oil content were clustered together, while the remaining traits constituted a separate cluster. Overall, this study revealed considerable genetic diversity among Iranian summer savory landraces based on morphological traits, providing valuable information for germplasm conservation and efficient selection in breeding programs.

Keywords: phenotypic diversity, plant dry weight, selection, varimax rotation

Introduction

Summer savory (*Satureja hortensis* L.) is an annual aromatic and medicinal plant native to Mediterranean regions, including the Balkans, Anatolia, and western Asia. Currently, summer savory is widely cultivated in several European countries. In Iran, it occurs in several regions, particularly in the central, western, and southwestern parts of the country. This plant is characterized by its erect stems and bisexual flowers, and it exhibits a diploid chromosome number of 2n = 48 [12]. Summer savory is valued for its medicinal properties and is traditionally employed as a carminative, stomachic, expectorant, stimulant, antispasmodic, and aphrodisiac.

The essential oil of this species is dominated by carvacrol and thymol, accompanied by phenolic derivatives, β-caryophyllene, linalool, and additional terpenoid compounds [22, 24]. It is utilized in the form of oleoresin, volatile oils, tinctures, and herbal extracts for its seasoning qualities, antioxidant activity, and antimicrobial effects.

In light of the growing global demand for medicinal plants, the development of standardized commercial cultivars with consistent quality traits has become crucial. Over the past few decades, breeding programs have resulted in the registration of new cultivars of various medicinal plants in several countries [24]. The primary goals in breeding medicinal plants, including summer savory, are to improve agronomic traits, enhance yield performance, and increase the content of bioactive compounds.

To develop new, high-yielding cultivars that are well adapted to target environments and resilient to climate change challenges, it is essential to establish breeding programs grounded in comprehensive characterization and rigorous selection processes. Agronomic traits can be used to identify differences among accessions, and the selection of specific breeding lines or their combination scan be guided by traits aligned with each breeding objective [2]. Exploring genetic variation within germplasm collections is a crucial step in genetic improvement programs. Several studies have investigated morphological and agronomic diversity, with a focus on yield potential and major pharmaceutical properties of summer savory, thus contributing to the development of commercial cultivars [14, 20]. The evaluation of morphological traits is a straightforward and rapid approach for identifying and characterizing plant materials through phenotypic measurements, offering insights into variation in key morphological features. Among multivariate analysis techniques, factor analysis is widely used to characterize crop germplasm. When applied to descriptive datasets, it can effectively categorize various accessions within genetic resource collections and support the selection of promising genotypes [19].

Hadian et al. [5] studied 28 Iranian landraces of summer savory and reported significant differences in agronomic traits among the landraces, highlighting the potential for selection based on three main genotypic groups identified through cluster analysis. In a subsequent study, Hadian et al. [6] assessed morphological diversity among 30 Iranian accessions and identified three accessions (Isfahan, Maraghe, and Yasooj) as having the highest yield performance (53, 41, and 40 g plant^{-1}, respectively). They also found that the major essential oil components were carvacrol (average 63%), γ-terpinene (average 15%), and p-cymene (average 9%). Khadivi-Khub et al. [9] evaluated 57 individuals of *Satureja bachtiarica* and reported that seven principal components accounted for 75.91% of the observed variation, with high contributions from traits including stem biomass, stem diameter and weight, sepal length, petal size, leaf and flower weight, sepal diameter, and bract size. Similarly, Vozhdehnazari et al. [23] reported significant variation in morphological traits and essential oil profiles among 30 *Satureja* populations (from 10 species) using permutational multivariate analysis of variance (PERMANOVA), and identified seven traits associated with essential oil quality, including number of main branches and leaf width. In our previous factor-analytic study of Iranian summer savory accessions, we identified eight independent factors that together explained 87.705% of the total variance. The first, a “weight” factor comprising biomass-related traits; accounted for 22.033%; the second, a "stem-length" factor, explained 17.411%; and the third, a "leaf-size" factor (leaf length and width), accounted for 13.279%. The remaining factors captured variation in other morphological traits, including lateral leaf dimensions [15]. Morphological traits have also proven to be reliable tools for assessing genetic variation in various vegetable and medicinal crops, including *Carthamus tinctorius* L. [1], *Portulaca oleracea* L. [13], and *Nigella sativa* L. [20].

The aim of this research was to assess genetic variation among summer savory landraces collected from diverse regions of Iran using agronomic traits, with the goal of supporting future breeding programs.

Materials and Methods

A total of 29 summer savory accessions were collected from different regions of Iran (Table 1). The experiment was conducted in a randomized complete block design (RCBD) with three replications. Each experimental unit consisted of four rows, with 20×20 cm spacing within and between rows. All recommended local agronomic practices were applied throughout the growing season. Morphological traits were evaluated at the flowering stage using five randomly selected plants from each plot. The recorded traits included internode length (IL), plant height (PH), number of leaflets per main stem (LMS), stem length (SL), leaf area of the main stem leaves (LAMS), root length (RL), and leaf area of lateral branch leaves (LALB). Yield-related traits - including stem fresh weight (SFW), plant fresh weight (PFW), and root fresh weight (RFW) - were measured by harvesting the two central rows of each plot. After drying the samples in a forced-air oven, stem dry weight (SDW), plant dry weight (PDW), and root dry weight (RDW) were recorded. Weighting was performed using an electronic balance with 0.1 g accuracy. Essential oil (EO) content was determined from 50 g samples from each plot subjected to hydrodistillation with 500 ml distilled water for 4 hours using a Clevenger apparatus. The extracted essential oil was dehydrated with sodium sulfate to remove residual water and obtain purified essential oil.

Table 1: Geographical area, region, and coordinates of *Satureja hortensis* L. landraces.

No.	Area	Region	Coordinates	No.	Area	Region	Coordinates
G1	Shush	Khuzestan	32°11′N 48°15′E	G16	Tabriz-B	E.Azarbaijan	38°06′N 46°16′E
G2	Tabriz-A	E.Azarbaijan	38°06′N 46°16′E	G17	Isfahan	Isfahan	32°39′N 51°39′E
G3	Ardabil	Ardabil	38°15′N 48°17′E	G18	Qazvin	Qazvin	36°16′N 49°59′E
G4	Razan-A	Isfahan	35°23′N 49°02′E	G19	Tuserkan-A	Hamadan	34°33′N 48°27′E
G5	Mashhad	R.Khorasan	36°15′N 59°36′E	G20	Ilam	Ilam	33°38′N 46°22′E
G6	Sistan	Sistan	27°35′N 60°35′E	G21	Borujerd	Lorestan	34°01′N 48°44′E
G7	Tonkabon-B	Mazandaran	36°48′N 50°52′E	G22	Kelachay	Gilan	37°05′N 50°21′E
G8	Shiraz	Fars	29°35′N 52°34′E	G23	Arak	Markazi	34°05′N 49°42′E
G9	Qom	Qom	34°38′N 50°52′E	G24	Dezful	Khuzestan	32°23′N 48°25′E
G10	Kermanshah	Kermanshah	34°19′N 47°04′E	G25	Razan-B	Isfahan	35°23′N 49°02′E
G11	Sanandaj	Kurdistan	35°19′N 46°58′E	G26	Tehran	Tehran	35°41′N 51°23′E
G12	Parsabad	Ardabil	39°37′N 47°54′E	G27	Tonkabon-A	Mazandaran	36°48′N 50°52′E
G13	Sardasht	W.Azarbaijan	36°09′N 45°28′E	G28	Sarab	E.Azarbaijan	37°56′N 47°32′E
G14	Tuserkan-B	Hamadan	34°33′N 48°27′E	G29	Qeshm	Hormozgan	26°48′N 55°53′E
G15	Hamedan	Hamadan	34°48′N 48°30′E				

Data normality and the homogeneity of residuals were evaluated using the Kolmogorov-Smirnov and Levene's tests in Minitab 17.0 (Minitab Inc., State College, PA, USA). To manage the complexity of the dataset and assess interrelationships among traits and genotypes, factor analysis was employed to reduce multiple correlated traits to a smaller set of independent factors. Varimax rotation was applied, and factor loadings were obtained for components with eigenvalues > 1, enabling the identification of the most influential factors. This analysis was carried out in Statistica 15.0 (TIBCO Software Inc., Palo Alto, CA, USA). The Kaiser-Meyer-Olkin (KMO) statistic was used to measure sampling adequacy and the Bartlett’s test sphericity was applied to evaluate the suitability of the data for factor analysis. In addition, communalities, representing the proportion of each trait’s variance explained by the common factors, were calculated to determine the contribution of each trait to the total variation.

Results and Discussion

The suitability dataset for factor analysis (Table 2) was confirmed by a Kaiser-Meyer-Olkin (KMO) value of 0.71, exceeding the minimum threshold of 0.50. This indicated that interrelationships among traits were adequate for reliable factor analysis. Bartlett’s test of sphericity (Table 2) was also significant, further supporting the KMO result and confirming sufficient associations among traits. Thus, the dataset was considered suitable for factor analysis. The results showed that the first five eigenvalues were greater than 1 and together explained 89% of the total variance (Table 3). The first factor alone accounted for 38% of the variance and was primarily associated with plant fresh weight (PFW), stem fresh weight (SFW), root fresh weight (RFW), plant dry weight (PDW), stem dry weight (SDW), and root dry weight (RDW). Therefore, the first factor was designated as biomass. Similarly, Fathi et al. [4] applied factor analysis to local cultivars of summer savory and reported that the dry weights of shoots, flowers, and leaves were grouped as the first, fourth, and fifth factors, explaining 14.849%, 8.213%, and 7.993% of the total variance, respectively.

Table 2: Assessment of dataset suitability for factor analysis.

Test	Index	Value
KMO†	KMO Statistic	0.71
Bartlett‡	Chi-Square	611.41
	Degrees of freedom	91
	Significance (p)	<0.001

†KMO = Kaiser-Meyer-Olkin measure of sampling adequacy

‡Bartlett’s test = test of sphericity

The second factor was characterized by high negative loadings for plant height (PH), stem length (SL), and internode length (IL), along with a high positive loading for number of leaflets per main stem (LMS), accounting for 24% of the observed variation. This factor was therefore designated as dwarfism and leaflet traits (Table 3). Plant height is a crucial trait in medicinal plant breeding, particularly for facilitating mechanical harvesting [24]. The observed association among PH, SL, and IL suggests that these traits are influenced by shared genetic components regulating their expression.

The third factor, explaining 10% of the variability, included the leaf area of the main stem leaves (LAMS) and the leaf area of lateral branch leaves (LALB), and was designated as leaf area (Table 3). As leaves are the primary organs for capturing sunlight and conducting photosynthesis, larger leaf area enhances the production of photoassimilates, ultimately supporting greater synthesis of secondary metabolites [7].

Table 3: Varimax-rotated factor loadings and communalities (Comm).

Traits	Factor1	Factor2	Factor3	Factor4	Factor5	Comm.
PFW	0.986	0.079	0.023	0.063	-0.040	0.977
SFW	0.983	0.093	0.031	0.088	0.004	0.982
RFW	0.816	0.321	-0.028	0.022	-0.243	0.885
PH	-0.025	-0.985	0.086	-0.005	0.015	0.966
SL	-0.072	-0.928	0.162	0.058	0.260	0.989
RL	0.223	0.339	-0.058	-0.135	-0.892	0.974
IL	-0.136	-0.825	0.285	0.163	0.288	0.904
LMS	0.198	0.568	-0.443	-0.385	-0.106	0.907
PDW	0.968	-0.073	0.054	-0.027	-0.147	0.963
SDW	0.989	-0.093	0.030	0.010	-0.005	0.980
RDW	0.803	0.351	-0.022	-0.037	-0.189	0.876
EO	-0.099	0.090	-0.126	-0.972	-0.103	0.980
LAMS	0.104	-0.316	0.897	0.139	0.043	0.887
LALB	0.188	-0.308	0.390	0.176	0.163	0.855
Variance	5.33	3.41	1.31	1.20	1.11	
% Var	38.0	24.0	10.0	9.0	8.0	

Traits: plant fresh weight (PFW), stem fresh weight (SFW), root fresh weight (RFW), plant height (PH), stem length (SL), root length (RL), internode length (IL), number of leaflets per main stem (LMS), plant dry weight (PDW), stem dry weight (SDW), root dry weight (RDW), essential oil content (EO), leaf area of main stem leaves (LAMS), and leaf area of lateral branch leaves (LALB).

The fourth factor accounted for 9% of the variation and was characterized by a negative loading for essential oil (EO), thus termed low essential oil content.

The fifth factor, explaining 8% of the variance, was associated with root length (RL) and showed negative loadings, leading to its designation as reduced root length. Nikrouz-Gharamaleki et al. [15] evaluated 29 Iranian landraces of summer savory and extracted eight factors accounting for 88% of the total variation, which they categorized as biological yield, plant height, internode characteristics, and leaf-related traits such as leaf length, small leaf size, and leaf width. Based on the values of communalities (Table 3), all measured traits demonstrated high reliability, indicating strong genetic relationships among the traits.

Similar to the KMO index and Bartlett's test, communalities are considered a useful criterion for determining the appropriate number of factors to retain [11]. In this study, all extracted communalities were high (86-99%), confirming that the selected factors adequately explained trait variability. The consistently high values indicated that the five retained factors were appropriate and accounted for most of the observed variance. Similarly, Fathi et al. [3] identified six factors -plant dry weight, shoot dry weight, leaf dry weight, branch number, 100-seed weight, flavonoids, and pigments - which together explained 86% of the total variance in 20 summer savory genotypes. In the present study, several of these previously reported factors were also identified, along with additional characteristics related to essential oil content, root length, and dwarfism combined with leaflet traits.

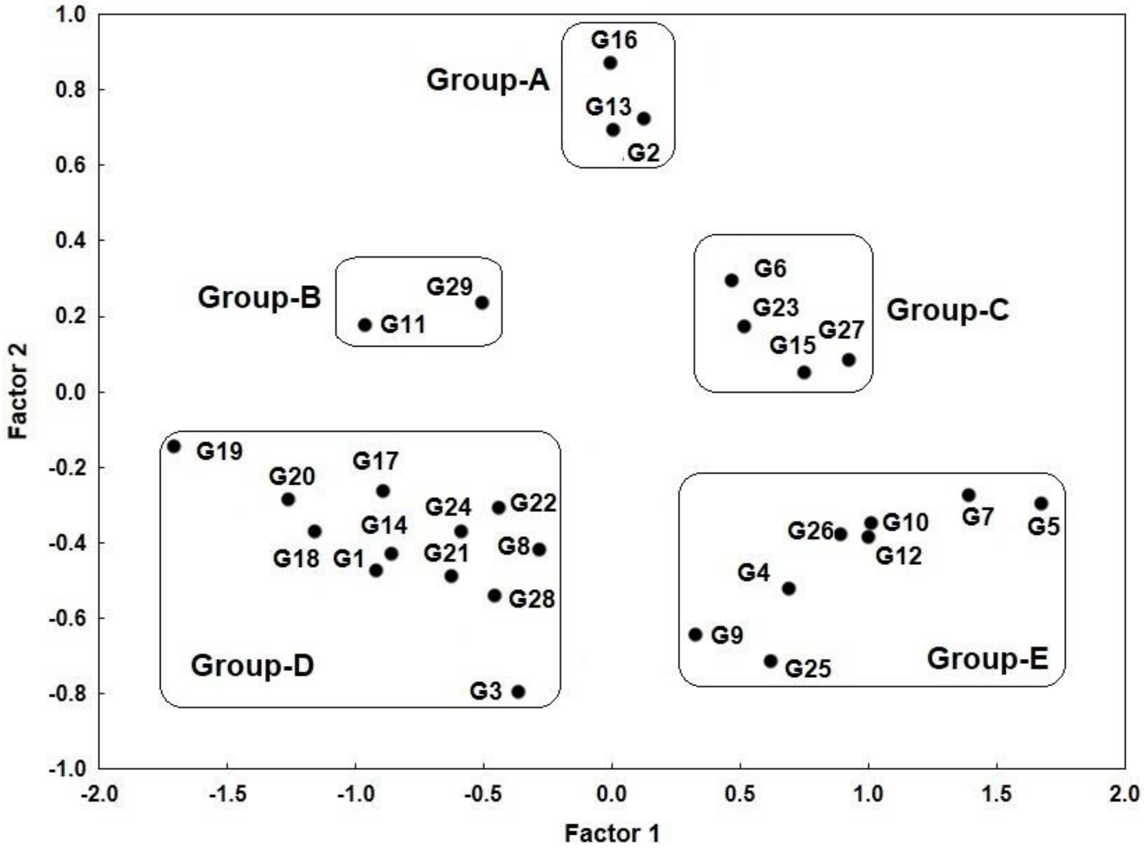

Fig. 1: Distribution of 29 *Satureja hortensis* L. genotypes based on the first two factors.

To classify and visualize relationships among the genotypes, a two-dimensional plot was generated (Figure 1), in which the first two factors together accounted for 62% of the total variation. This strong genotype-by-trait interaction indicates the presence of both linear and crossover effects in the summer savory dataset, reflecting differences in trait rankings across genotypes. This observation is consistent with previous findings in summer savory [8], as well as in other crops such as Moldavian balm [17] and safflower [18], which highlight the difficulty of achieving consistent indirect selection responses without accounting for genotype-by-trait interactions. Based on the two-dimensional factor plot five genotypic groups were identified: Group A (G2, G13, and G16); Group B (G11 and G29); Group C (G6, G15, G23, and G27); Group D (G1, G3, G8, G14, G17, G18, G19, G20, G21, G22, G24, and G28), and Group E (G4, G5, G7, G9, G10, G12, G25, and G26).

Table 4 presents the mean values of the summer savory traits for each of the five identified groups. Genotypes in Group A exhibited high values for PH, SL, IL, LAMS, and LALB; moderate values for PFW, PDW, SFW, and SDW; and low values for RFW, RL, LMS, RDW, and EO.

Genotypes in Group B demonstrated low values for all measured traits, except for higher LMS and EO, while those in Group C exhibited high values for PFW, SFW, RL, LMS, PDW, SDW, and EO; moderate values for RFW, RDW, LAMS, and LALB; and low values for PH, SL, and IL (Table 4).

Table 4: Mean trait values for the five genotypic groups identified by factor analysis.

Traits	Group-A	Group-B	Group-C	Group-D	Group-E
PFW	53.84	48.10	66.78	44.87	69.11
SFW	52.12	48.21	64.60	43.55	66.99
RFW	1.52	1.56	1.87	1.62	2.50
PH	69.63	60.33	61.08	58.79	58.50
SL	56.08	45.83	44.58	42.09	41.09
RL	14.53	13.95	16.50	16.70	17.59
IL	4.76	3.72	3.34	3.34	3.24
LMS	6.09	29.36	28.67	26.42	29.26
PDW	9.05	6.34	10.14	7.13	10.54
SDW	8.70	7.36	9.61	6.68	9.94
RDW	0.39	0.43	0.52	0.44	0.60
EO	2.12	2.43	2.54	2.50	2.35
LAMS	1.70	1.40	1.45	1.27	1.31
LALB	1.51	1.25	1.32	1.18	1.21

Traits: plant fresh weight (PFW), stem fresh weight (SFW), root fresh weight (RFW), plant height (PH), stem length (SL), root length (RL), internode length (IL), leaflets per main stem (LMS), plant dry weight (PDW), stem dry weight (SDW), root dry weight (RDW), essential oil content (EO), leaf area of main stem leaves (LAMS), and leaf area of lateral branch leaves (LALB).

Additionally, genotypes in Group D generally showed low values for all traits except for higher RL, LMS, and EO, whereas genotypes in Group E displayed high values for most traits, except for moderate EO content and low values for PH, SL, IL, LAMS, and LALB.

Based on these findings, Group A is characterized by high leaf area and plant height; Groups B and D are notable for higher numbers of leaflets per main stem and greater essential oil production; Group C stands out for its high biomass and essential oil content; and Group E is valuable for its high biomass and strong root characteristics. These findings are consistent with the report of Nikrouz-Gharamaleki et al. [15], who observed considerable morphological diversity among Iranian landraces of summer savory and a positive relationship between essential oil content and plant dry weight.

From a practical standpoint, the genotypes in Group C can be considered promising candidates for cultivar release and for use in future breeding programs. Their high biomass and essential oil content make them particularly valuable for breeders aiming to develop high-yielding cultivars with enhanced essential-oil profiles, in line with current breeding targets and consistent with previous studies by Svoboda and Greenaway [21] and Rezaei-Chiyaneh and

Jamali [16]. Group C genotypes originate from geographically distinct regions of Iran; G6 (Sistan, SE Iran), G15 (Hamadan, W Iran), G23 (Arak, central Iran), and G27 (Tonkabon-A, N Iran), reflecting substantial genetic diversity among local Iranian landraces of summer savory. Although summer savory is native to the Balkans and Anatolia [10], it has been cultivated in Iran for centuries [3], underscoring the need to investigate its local adaptation traits within the country.

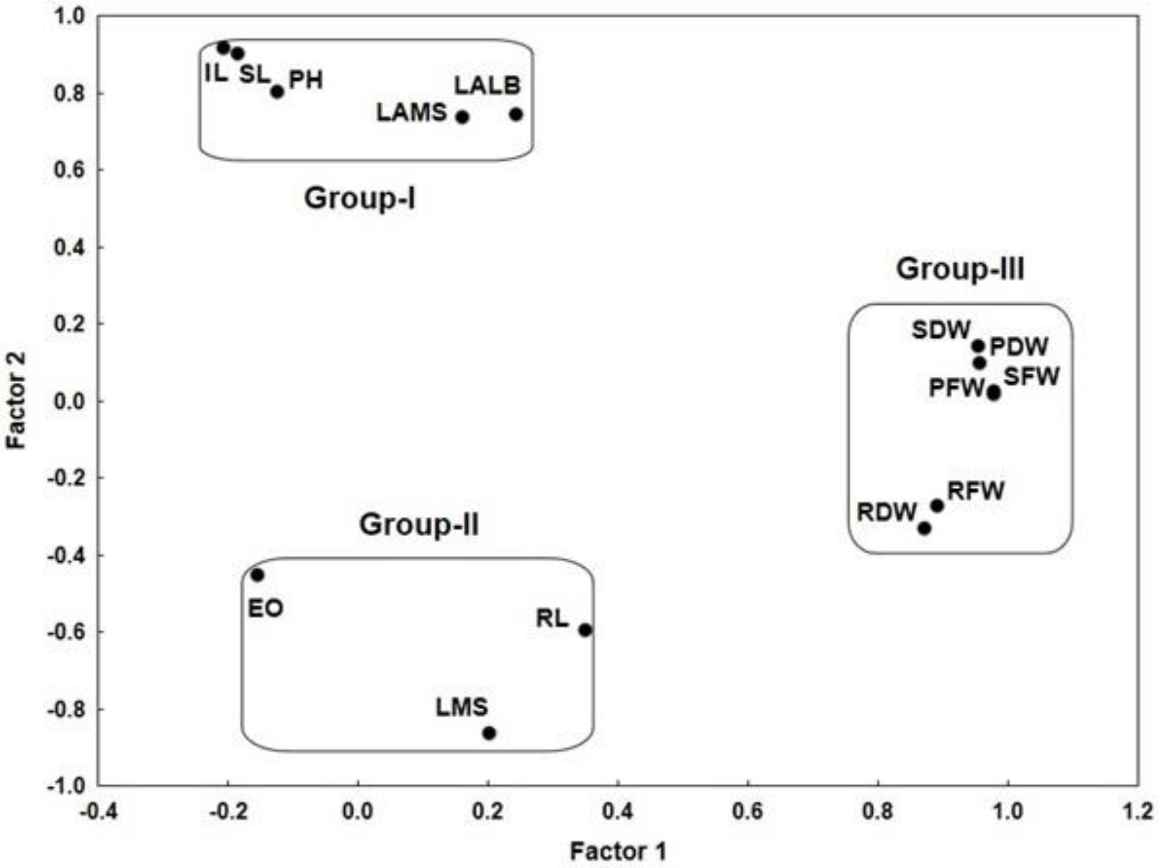

Fig. 2: Distribution of fourteen summer savory traits based on the first two factors.

To categorize the measured traits and interpret their relationships a two-dimensional plot (Figure 2). Traits such as SL, IL, PH, LAMS, and LALB were clustered into Group I. Similarly, Hadian et al. [4] reported positive correlations among plant height, internode length, and leaf size when evaluating 30 Iranian accessions of summer savory. In addition, PFW, SFW, RFW, PDW, SDW, and RDW clustered into Group II, whereas RL, LMS, and EO formed Group III (Figure 2). The results suggest that taller summer savory plants tend to have larger leaf areas, while genotypes with longer root systems possess a greater number of leaflets per main stem and higher essential oil content. Moreover, fresh and dry biomass traits - such as shoot, root, and total plant weight - were associated, indicating that increases in one of these traits are likely accompanied by increases in the others. Hadian et al. [5] also found significant associations between plant fresh and dry weight in 28 accessions of summer savory, although they did not report any significant correlations between essential oil content and morphological traits.

The relatively high explanatory power of factor analysis suggests that the chosen traits effectively captured the underlying genetic structure of the studied germplasm. The first factor, associated with biomass traits, confirms the importance of biomass-related traits as primary selection criteria in summer savory breeding programs.

Traits related to plant height, internode length, and leaf area were strongly associated, suggesting that selection for taller plants may simultaneously enhance photosynthetic capacity through increased leaf area. In contrast, essential oil content was associated with longer root systems and a greater number of leaflets per main stem, implying a potential indirect selection strategy for enhancing oil yield by targeting these morphological attributes.

From a breeding perspective, the identification of genotypic groups with distinct trait combinations offers practical pathways for cultivar development. For instance, Group-C genotypes, with high biomass and essential oil content, represent prime candidates for direct cultivar release or as parents in crossing programs. In addition, genotypes in Groups-B and D, characterized by high essential oil content but lower biomass, could be exploited in breeding programs focused on improving oil yield without significantly altering plant size.

This study successfully employed factor analysis as a multivariate approach to dissect the genetic structure of agronomic traits in summer savory, providing a framework for efficient utilization of its genetic resources. Similar studies, such as that of Vozhdehnazari et al. [23], have demonstrated that multivariate approaches can guide breeders toward cultivars with enhanced levels of active compounds and improved morphological characteristics, ultimately facilitating the development of superior varieties.

Factor analysis identified biomass-related traits as the strongest drivers of phenotypic variation in Iranian summer savory, consistent with Nikrouz-Gharamaleki et al. [15], with fresh and dry weights of shoots, roots, and whole plants loading most heavily on the first factor. In our dataset, this factor explained a larger share of variance, highlighting biomass as the primary determinant of accession-level differences. In contrast to Nikrouz-Gharamaleki et al. [15], who separated stem length and leaf dimensions as separate factors, our results point to a single factor integrating plant height, internode length, and the number of leaflets per main stem; evidence of stronger interdependencies among growth traits in the evaluated accessions. Leaf attributes were captured as total leaf area rather than individual dimensions, emphasizing traits with direct functional relevance to photosynthesis and biomass accumulation. Essential oil content and root length emerged as independent factors, highlighting the breeding value of quality and belowground traits. Factor-score–based clustering revealed distinct groups; accessions with high biomass and essential oil, high essential oil but moderate biomass, and high biomass with strong root systems; corroborating substantial genetic diversity among Iranian landraces. Associations between essential oil content, root length, and leaf number per main stem suggest indirect selection avenues for enhancing secondary metabolite yield via morphological proxies. Overall, while our results corroborate the primary conclusions of Nikrouz-Gharamaleki et al. [15], they also emphasize integrating quality traits (e.g., essential oil content) and demonstrate the utility of a simplified, highly explanatory factor structure to guide selection and cultivar development. Finally, the current findings underline the necessity of considering genotype-by-trait interactions, as suggested by the significant variation explained by the first two factors. Ignoring these interactions could lead to suboptimal selection outcomes, particularly in species such as summer savory, where both biomass and secondary metabolite production are economically important traits. The present study confirmed that Iranian summer savory germplasm harbors substantial genetic diversity for agronomic and quality traits. These findings suggest practical breeding opportunities, including the potential for simultaneous improvement of biomass and essential oil yield by carefully selecting genotypes that combine favorable traits. Future studies should integrate molecular markers with morpho-agronomic traits to refine the selection process and uncover the genetic basis of key traits.

Conclusions

The present study identified five factors, namely biomass, dwarfism and leaflet number, leaf area, low essential oil content, and reduced root length. Significant genetic variability was observed among Iranian summer savory landraces based on agronomic traits and essential oil content. Genotypes in Group-C (G6, G15, G23, and G27) exhibited superior performance in both biomass production and essential oil content, making them promising candidates for direct cultivar development or as valuable parents in breeding programs. These findings provide practical strategies for breeders aiming to improve summer savory, particularly for developing high-yielding cultivars with enhanced essential oil profile.

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ANALIZA FACTORIALĂ A VARIAȚIEI GENETICE A CARACTERELOR MORFOLOGICE ALE SOIURILOR DE VARĂ LOCALE (IRANIENE) DE CIMBRU (*SATUREJA HORTENSIS* L.)

(Rezumat)

Cimbrul (*Satureja hortensis* L.), un membru al familiei Lamiaceae, este o importantă plantă legumicolă și medicinală, utilizată pe scară largă atât ca aliment, cât și ca remediu natural. În prezentul studiu, diversitatea fenotipică a 29 de varietăți locale iraniene a fost evaluată pe baza înălțimii plantei, lungimii tulpinii, lungimii rădăcinii, lungimii internodului, numărului de foliole pe tulpina principală, suprafeței foliare a frunzelor de pe tulpina principală și ramurile laterale, greutății proaspete a tulpinii, rădăcinii și a plantei întregi, greutății uscate a tulpinii, rădăcinii și a plantei întregi și conținutului de ulei esențial. Analiza factorială a arătat că 89% din variația observată ar putea fi explicată de primii cinci factori, care au fost caracterizați pe baza scorurilor rotative varimax ca și biomasă, nanism și trăsături ale foliolelor, suprafață foliară, conținut scăzut de ulei esențial și lungime redusă a rădăcinii. O reprezentare grafică a primilor doi factori, reprezentând 62% din variația totală, a distins cinci grupuri genotipice. În special, genotipurile din Grupa C - G6 (Sistan), G15 (Hamadan), G23 (Arak) și G27 (Tonkabon-A) - au prezentat un conținut ridicat de biomasă și uleiuri esențiale, ceea ce le face candidați promițători pentru dezvoltarea de noi soiuri și utili în implementarea viitoarelor programe de ameliorare. Pentru a clasifica trăsăturile, a fost generat un grafic bidimensional bazat pe primii doi factori. Această analiză a arătat că lungimea internodului, înălțimea plantei, lungimea tulpinii și suprafața frunzelor au fost grupate împreună. În mod similar, lungimea rădăcinii, numărul de foliole pe tulpina principală și conținutul de ulei esențial au fost grupate împreună, în timp ce restul trăsăturilor au constituit un grup separat. Per total, acest studiu a relevat o diversitate genetică considerabilă în rândul soiurilor locale (iraniene) de cimbru, pe baza trăsăturilor morfologice, oferind informații valoroase pentru conservarea germoplasmei și selecția eficientă în programele de ameliorare.

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