

Journal of Plant Physiology and Breeding

Print ISSN: 2008-5168 Online ISSN: 2821-0174

2025, 15(2): 65-78

Factor analysis of genetic diversity in some Iranian purslane accessions using agromorphological traits

Mehdi Mohebodini¹, Iman Khalili-Baseri¹, Mohsen Janmohammadi¹, and Naser Sabaghnia¹,

¹Department of Horticultural Science, Faculty of Agricultural Science and Natural Resources, University of Mohaghegh Ardabili, 7218759612, Ardabil, Iran.

²Department of Plant Production and Genetics, Faculty of Agriculture, University of Maragheh, 5518779842, Maragheh, Iran.

Article Info

Article type: Research article

Article history:

Received: May 12, 2025 Revised: July 9, 2025 Accepted: August 6, 2025 Published online: December 12,

Keywords:

2025

Biomass, Factor analysis, Genetic variation, Purslane

Abstract

Objective: As a highly nutritious vegetable crop, purslane (*Portulaca oleracea* L.) is recognized for its dual role as both a leafy vegetable and a medicinal herb. This study aimed to assess the genetic diversity of 20 Iranian purslane accessions using selected agro-morphological traits.

Methods: Seeds from local purslane accessions were collected from different regions of Iran. The experiment was conducted under controlled greenhouse conditions, using a randomized complete block design with four replications. A total of 16 agro-morphological traits were measured. Phenotypic coefficient of variation was calculated for all traits to verify the existence of variability among the collected accessions. To group the accessions, factor analysis was performed to uncover a pattern of variability among the studied accessions. Only factors with eigenvalues greater than unity were retained and used.

Results: The results revealed considerable genetic variation among the genotypes, with the phenotypic coefficient of variation ranging from 11.66% (main stem length) to 51.00% (number of capsules per branch). High variability in traits such as total soluble solids and dry/fresh weight ratio, and relatively high variability for number of flowers per plant, dry shoot weight, number of lateral branches, number of branches per main stem, leaf width, leaf area, and leaf length, was observed, highlighting their potential value for future breeding efforts. Factor analysis identified five main factors accounting for 90.1% of the observed variability, with the first factor describing 48.6% of the variability and associated with plant biomass potential. The next factors emphasized the number of flowers and branches, leaf properties, the number of lateral branches, and total soluble solids, respectively. The accessions were categorized into three distinct categories, and Group A contained accessions with better biomass and some yield-related traits.

Conclusion: This research provided an understanding of genetic diversity in purslane, offering information for selecting favorable genotypes for breeding programs aimed at enhancing biomass and yield performance. Accessions from Group A, such as those from Bushehr, Isfahan, and Maragheh areas, Iran, were

^{*}Corresponding author; sabaghnia@maragheh.ac.ir

recommended for further evaluation and potential cultivar release for rainfed, semiarid conditions.

Cite this article: Mohebodini M, Khalili-Baseri I, Janmohammadi M, Naser Sabaghnia. 2025. Factor analysis of genetic diversity in some Iranian purslane accessions using agro-morphological traits. J Plant Physiol Breed. 15(2): 65-78. https://doi.org/10.22034/jppb.2025.67279.1367



© The Author(S)

Publisher: University of Tabriz

Disclaimer/Publisher's Note: The statements, opinions, and data contained in the article are solely those of the individual author(s) and not of the *Journal of Plant Physiology and Breeding* and/or the editor(s). *Journal of Plant Physiology and Breeding* and/or the editor(s) disclaim responsibility for any injury to persons or property resulting from any ideas, methods, instructions, or products referred to in the content.

Introduction

Purslane (Portulaca oleracea L.) is an annual leafy vegetable crop used as potherb and traditional medicine (Fathi et al. 2019). Native to the Mediterranean region, it has since achieved a global distribution, adapting well to a variety of climatic and environmental conditions (Srivastava et al. 2023). In certain contexts, purslane is regarded as a weed due to its prolific seed production and capacity to thrive even under adverse conditions. The purslane varieties feature yellow flowers at the nodes, whereas ornamental cultivars exhibit a broader spectrum of vibrant floral colors (Amirul-Alam et al. 2014). The plant produces numerous small, black seeds noted for their longevity and persistence in the soil seed bank. The nutritional profile of purslane distinguishes it from other leafy vegetable crops. In addition to its dietary value, it also possesses notable medicinal properties and bioactive compounds such as alkaloids, flavonoids, and terpenoids, which contribute to its antimicrobial effects and its role in promoting wound healing (Kumar et al. 2022). Also, purslane is a rich source of some minerals, such as magnesium and potassium, and some vitamins. With its high antioxidant capacity and diverse pharmacological potential, purslane stands out among both vegetable crops and medicinal plants. Its sustainable characteristics and nutrient value have led to growing interest in its role as a future food resource, with the potential to contribute significantly to global nutritional security (Petropoulos et al. 2019).

Egea-Gilabert *et al.* (2014) evaluated some purslane genotypes using morphological traits, reporting high diversity among genotypes, and demonstrated superior yield performance and high potassium content, indicating their potential for cultivar development. They found considerable variation in key traits within and among genotypes, underscoring the suitability of this crop for breeding initiatives aimed at developing the most favorable varieties. Also, Sdouga *et al.* (2020) examined the morphological traits of three landraces of purslane in comparison with a cultivated variety, and reported significant heterogeneity within and between genotypes, likely reflecting the

influence of their diverse geographical origins. Moreover, the above study reaffirmed the medicinal value of purslane, attributing its extensive therapeutic potential and strong antioxidant activity to its high levels of phenolic compounds and flavonoids. Naeem *et al.* (2022) investigated the morphological characteristics of 25 purslane accessions and found significant variation in traits such as plant height and fresh weight of both roots and shoots among three accessions. Their study highlighted the potential of purslane as a rich source of bioactive compounds and emphasized the considerable diversity in both its morphological and biochemical traits. This variability presents opportunities for selecting superior accessions for breeding programs focused on improving specific plant attributes, such as growth performance and bioactive content.

Morphologic traits are often influenced by environmental factors, which can limit their heritability (Yang et al. 2019). However, morphological evaluation remains a critical preliminary step in the classification of plant materials for breeding purposes, as such traits are easy to observe, costeffective to record, and widely utilized for assessing genetic diversity in various crops. However, analyzing numerous traits simultaneously can pose challenges, particularly due to complex interactions among target traits. To better understand the pattern of genetic diversity and find relationships among traits and genotypes, multivariate statistical models, such as factor analysis, are employed (Coulibaly et al. 2024). El-Bakatoushi et al. (2013) used factor analysis to classify different genotypes of purslane based on their morphological traits and found that stem length, leaf dimensions, and seed characteristics were effective in categorizing genotypes. Thus, factor analysis is beneficial to grasp the genetic diversity of different genotypes and to have a better understanding of the significant morphological characteristics that could influence selection for breeding purposes. The present study aimed to investigate genetic diversity among some native purslane accessions of Iran via morphological traits using factor analysis. Also, the study wants to explore interrelationships among the most important traits in the purslane accessions.

Materials and Methods

Seeds from 20 local purslane accessions were collected from diverse geographical regions across Iran (Table 1). A standardized soil mixture composed of sand, clay, and organic substances (1:2:1 ratio) was prepared to provide uniform growth conditions. Experimental units consisted of pots with a diameter of 0.5 meters, each filled with the prepared soil mixture. The experiment was conducted in a greenhouse under controlled environmental conditions and arranged in a randomized complete block scheme with four replications. Each pot was sown with 30 seeds (which were thinned later to 20 plants), and was subsequently protected with a thin soil layer to ensure uniform germination. Due

Table 1. Code, name, geographic coordinates, and altitude of purslane accessions.

Code	Location	Coordinates	Altitude (m)
A1	Ardabil	38°15′N 48°17′E	1351
A2	BandarAbbas	27°11′N 56°17′E	9
A3	Behbahan	30°35′N 50°14′E	326
A4	Bushehr	28°55′N 50°51′E	18
A5	Eqlid	30°53′N 52°41′E	2244
A6	Esfahan	32°39′N 51°40′E	1574
A7	Hamadan	34°47′N 48°30′E	1830
A8	Karaj	35°49′N 50°56′E	1274
A9	Maragheh	37°23′N 46°14′E	1510
A10	Mashhad	36°19′N 59°32′E	995
A11	Nehbandan	31°32′N 60°02′E	1187
A12	Nourabad	30°06′N 51°32′E	998
A13	Parsabad	39°38′N 47°54′E	75
A14	Qazvin	36°17′N 50°00′E	1278
A15	ShahrKord	32°19′N 50°51′E	2063
A16	Shiraz	29°36′N 52°32′E	1500
A17	Sirjan	29°26′N 55°41′E	1760
A18	Tehran	35°41′N 51°23′E	1148
A19	Yasouj	30°40′N 51°34′E	1837
A20	Zanjan	36°41′N 48°29′E	1810

to the small size and delicate nature of purslane seeds, special attention was given to the initial irrigation process. For the first three weeks, gentle sprinkler irrigation was applied five times daily in small volumes to maintain consistent moisture levels without displacing the seeds. As seedlings established their root systems, the irrigation frequency was gradually reduced to once per day, while the volume of water per application was increased to support vegetative growth. The traits included the number of branches per main stem, number of lateral branches, main stem length, length of longest lateral branch, third internode diameter, total soluble solids, leaf area, leaf length, leaf width, number of flowers per plant, dry shoot weight, number of capsules per branch, fresh shoot weight, length/width ratio, dry/fresh weight ratio, and number of seeds per capsule. Length measurements, like the main stem and leaf lengths, were taken via a lab ruler, while leaf width was precisely

measured using a lab caliper. Fresh and dry shoot weights were recorded using a high-precision laboratory scale.

To verify the reliability of the collected data and the suitability of parametric statistical methods, the Anderson–Darling normality test was applied using Minitab software version 14.0 (Minitab Inc., USA). Then, some descriptive statistics, including the phenotypic coefficient of variation, were calculated. Factor analysis was performed to uncover patterns of interrelationships among the accessions and among the measured traits. This multivariate technique is particularly valuable for reducing many associated variables into a small set of unassociated factors, thus simplifying the interpretation of complex traits. The factor analysis employed varimax rotation to enhance the interpretability of the factor structure. Only factors with eigenvalues greater than one were retained and used in grouping the accessions. This analysis was conducted using Statistica software version 14.0 (TIBCO Inc., USA). Although the number of genotypes was not five times the number of traits for the computation of communalities, the calculated communalities were relatively high, so they were reported. Communalities were computed to assess the proportion of variance in each trait explained by the extracted factors, thereby highlighting traits that contribute most significantly to the observed variability among genotypes.

Results and Discussion

According to the descriptive statistics presented in Table 2, the phenotypic coefficient of variation (PCV) among the measured traits ranged from 11.66% for the main stem length to 51.00% for the number of capsules per branch across the evaluated purslane genotypes. These PCVs reflect the extent of genetic variability among the traits, with the main stem length, dry-to-fresh weight ratio, and total soluble solids exhibiting particularly high levels of variation. Also, traits such as number of flowers per plant, dry shoot weight, number of lateral branches, number of branches per main stem, leaf width, leaf area, and leaf length showed relatively high PCV. In contrast, the remaining traits showed moderate levels of variability. The observed variability can be utilized in breeding programs of purslane to develop improved cultivars. Notably, the relatively high PCV for dry shoot weight, number of lateral branches, number of branches per main stem, leaf width, leaf area, and leaf length suggests considerable diversity in biomass production among the purslane accessions (Table 2). These PCVs underscore the substantial phenotypic diversity present in the current collection of purslane accessions. In our research, the average dry shoot weight per plant was 11.28, which was almost twofold higher than that reported by Alam *et al.* (2014), who reported an average plant dry weight of 5.8 g in a separate set of purslane accessions. This difference can be attributed to the

Table 2. Some descriptive measures of traits of purslane (*Portulaca oleracea* L.) accessions that were evaluated in this study.

Traits	Mean	Median	SD†	PCV‡
Number of branches per main stem	18.57	18.50	3.44	18.54
Number of lateral branches	53.78	55.50	10.83	20.13
Main stem length	51.22	52.63	5.97	11.66
Length of the longest lateral branch	57.24	59.00	7.14	12.47
Third internode diameter	12.97	13.61	2.01	15.49
Total soluble solids	2.52	2.40	0.81	32.10
Leaf length	60.61	63.15	10.35	17.08
Leaf width	30.85	32.38	5.58	18.08
Leaf length/Leaf width ratio	1.94	1.96	0.23	11.79
Leaf area	34.32	35.16	5.92	17.25
Number of flowers per plant	4.78	4.75	1.01	21.19
Dry shoot weight	11.28	11.47	2.32	20.53
Fresh shoot weight	18.28	18.52	2.69	14.69
Dry/fresh shoot weight ratio	2.89	2.65	1.21	41.93
Number of capsules per branch	29.00	25.00	14.79	51.00
Number of seeds per capsule	88.09	89.00	10.33	11.73

SD: Standard deviation; PCV: Phenotypic coefficient of variation.

differences in the accessions assessed and in the environmental conditions. Investigating the structure of genetic diversity in vegetable crops such as purslane is not only vital for the conservation of plant germplasm but also essential for identifying useful genetic variations within germplasm collections (Salgotra and Chauhan 2023).

The factor analysis identified five factors with eigenvalues greater than one, collectively accounting for 90.1% of the total phenotypic variance among the evaluated purslane accessions (Table 3). The communalities of the traits ranged from 0.712 for the dry/fresh shoot weight ratio to 0.974 for the leaf length, with the majority exceeding 0.80, indicating a high proportion of the trait variance was explained by the five extracted factors (Table 3). These high communality values underscored the robustness of the factor analysis in summarizing the variability among purslane traits and highlighted its effectiveness in revealing the underlying structure of trait interrelationships in the studied accessions of this plant.

The first factor described 48.6% of the variability and was primarily determined by the traits related to biomass production. These included main stem length, length of the longest lateral branch,

Table 3. The rotated values of the extracted factors for the measured traits of purslane (*Portulaca oleracea* L.) accessions.

Traits	F1	F2	F3	F4	F5	Communality
Number of branches per main stem	0.243	0.711	0.034	-0.012	0.046	0.760
Number of lateral branches	0.013	0.077	-0.026	0.974	0.020	0.955
Main stem length	0.972	0.105	-0.050	0.045	-0.012	0.961
Length of the longest lateral branch	0.949	0.114	-0.075	-0.010	0.007	0.920
Third internode diameter	0.977	0.064	-0.094	0.053	-0.002	0.970
Total soluble solids	0.009	-0.002	-0.022	0.022	0.966	0.934
Leaf length	0.979	0.007	-0.102	-0.019	0.065	0.974
Leaf width	0.974	-0.016	-0.091	-0.023	0.098	0.967
Leaf length/Leaf width ratio	-0.051	0.210	0.855	-0.012	0.083	0.785
Leaf area	0.967	0.147	-0.042	0.021	-0.006	0.959
Number of flowers per plant	0.074	0.955	0.043	0.112	-0.020	0.932
Dry shoot weight	0.747	0.330	-0.464	0.156	-0.071	0.912
Fresh shoot weight	0.813	0.208	-0.244	0.181	-0.246	0.857
Dry/fresh shoot weight ratio	-0.283	-0.372	0.651	0.037	-0.261	0.712
Number of capsules per branch	-0.972	0.010	0.100	-0.050	-0.074	0.964
Number of seeds per capsule	0.655	0.318	0.355	0.435	0.001	0.845
λ	7.37	3.63	1.45	1.23	1.10	
%	48.6	20.2	8.4	6.9	6.0	
Cumulative	48.6	68.8	77.2	84.1	90.1	

F: Factor

leaf width, third internode diameter, leaf length, fresh shoot weight, leaf area, dry shoot weight, and number of seeds per capsule. The second factor accounted for 20.2% of the variance and was correlated with the number of flowers per plant and the number of branches per main stem, emphasizing traits related to branching and reproductive output. The third factor contributed 8.4% of the total variance and was defined by high loadings for the leaf length-to-width ratio and the dry-to-fresh weight ratio, leading to its interpretation as a leaf-shape and weight-efficiency factor. This provides breeders with insight into how leaf morphology and leaf weight ratios may influence plant growth. Leaf shape is important for optimizing light interception and photosynthesis, which affects biomass accumulation and plant performance (He *et al.* 2023). Similarly, the dry-to-fresh weight ratio is indicative of plant water usage efficiency, a critical trait for breeding purslane cultivars that can tolerate abiotic stresses while maintaining high productivity. The fourth factor, explaining 6.9% of

the variance, was primarily associated with the number of lateral branches and was thus interpreted as the lateral branching factor. The lateral branching is essential for improving plant architecture and optimizing space utilization in agricultural settings. A higher number of lateral branches can lead to increased plant density, which can result in improved yield (Mulry *et al.* 2015). The fifth factor, which accounted for 6.0% of the variance, showed a strong relationship with total soluble solids and was labeled as the soluble solids factor. Sdouga *et al.* (2020) used principal component analysis to evaluate purslane morphological traits. They reported that the first principal component, related to leaf and stem biomass traits, contributed 32% to the total variance, while the second component, associated with branching and fruiting traits, accounted for 18% of the total variation.

A two-dimensional diagram based on the two first factors (Figure 1) effectively illustrated the associations among the measured traits. The visualization allowed for the interpretation of trait relationships and patterns, given the acceptable explanatory power of these two first factors. The first factor separated groups I and II from groups III, IV, and V, while the second factor distinguished Group IV from Group V, and also Group I from Group II. The number of capsules per branch and the dry/fresh weight ratio were categorized as distinct characteristics in Group IV and Group V, respectively. However, the traits within groups I, II, and III were related to each other. A similar strategy has been used in other crops like Carthamus tinctorius (Sabaghnia et al. 2024) and Secale cereale (Sabaghnia and Janmohammdi 2025). Group I included the number of branches per main stem and the number of flowers per plant. This result is reasonable because as the number of branches per main stem increases, this affects the number of flowers per plant positively. Group II comprised leaf length-to-width ratio, total soluble solids, and number of lateral branches. Group III contained traits primarily associated with biomass, yield-related traits, and morphological performance, expressed by dry shoot weight, fresh shoot weight, number of seeds per capsule, leaf area, main stem length, length of longest lateral branch, third internode diameter, leaf length, and leaf width. Two traits, the number of capsules per branch and the dry/fresh weight ratio, were grouped individually into Group IV and Group V, respectively. These results are consistent with those of Mohebodini et al. (2024), who reported significant correlations among leaf characteristics and biomass traits in various Iranian purslane landraces. The identification of these underlying factors offers valuable insights into the genetic architecture of purslane, allowing breeders to focus on the most influential traits for selection. Also, the trait associations within these factors can help streamline breeding efforts by guiding the selection of accessions with superior performance in specific areas, such as biomass production or seed yield (Singh et al. 2020).

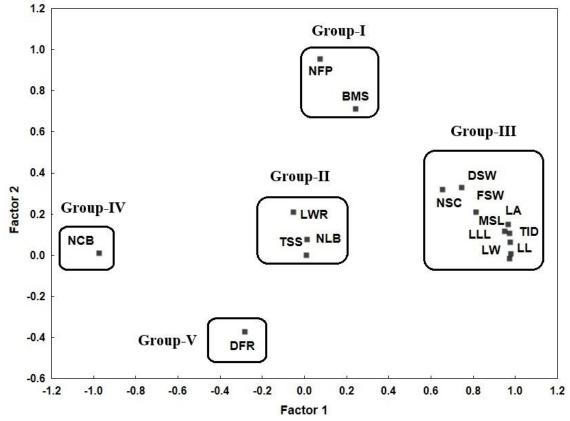


Figure 1. Two-dimensional plot of first two factors for classifying traits in purslane (*Portulaca oleracea* L.) accessions; BMS: Number of branches per main stem; NLB: Number of lateral branches; MSL: Main stem length; LLL: Length of longest lateral branch; TID: Third internode diameter; TSS: Total soluble solids; LL: Leaf length; LW: Leaf width; LWR: Leaf length/Leaf width ratio; LA: Leaf area; NFP: Number of flowers per plant; DSW: Dry shoot weight; FSW: Fresh shoot weight; DFR: Dry/fresh shoot weight ratio; NCB: Number of capsules per branch; NSC: Number of seeds per capsule.

The two-dimensional diagram of purslane accessions based on the first two factors (Figure 2) revealed three distinct genotypic clusters. Group A consisted of 11 accessions (A4, A6, A7, A8, A9, A11, A12, A14, A15, A16, and A18); Group B included seven accessions (A2, A3, A5, A13, A17, A19, and A20), and Group C comprised two accessions (A1 and A10). The trait means for each group are presented in Table 4. Accessions in Group A exhibited superior performance for the majority of traits, particularly those associated with biomass production, leaf and stem development, and reproductive output. However, this group showed relatively lower or moderate values for total soluble solids, number of capsules per branch, and dry/fresh shoot weight ratio. These findings suggest that while these genotypes have a good potential for improving biomass and overall growth, further refinement of their reproductive traits, particularly capsule production per branch, may be necessary. The Group B accessions also showed generally high values for most traits, though they recorded lower than average values for the number of lateral branches, leaf length/leaf width ratio, number of flowers per plant, dry/fresh shoot weight ratio, and number of capsules per branch. These moderate

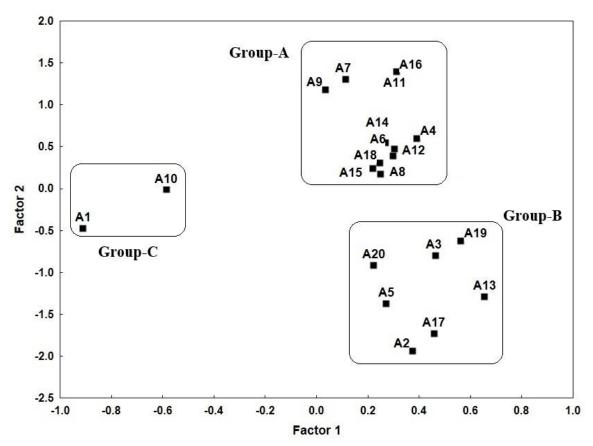


Figure 2. Two-dimensional plot of the first two factors for classifying purslane (*Portulaca oleracea* L.) accessions; A1-A20: Codes of accessions were described in Table 1.

trait values could be offset by relatively high performance in other yield-related components, such as the number of seeds per capsule. These accessions could serve as candidates for breeding programs focused on improving reproductive characteristics, as they exhibit relatively high biomass and leaf area (Carrascosa *et al.* 2023). However, further breeding is needed to improve branching and flower production, which could result in higher seed yields. The Group C accessions displayed the lowest values for most traits. However, this group exhibited favorable characteristics in traits such as number of lateral branches, total soluble solids, leaf length/leaf width ratio, dry/fresh shoot weight ratio, and, most importantly, number of capsules per branch, indicating their potential utility in breeding programs targeting increased capsule production and grain yield. Thus, they could be useful in breeding programs aimed at improving drought-stress tolerance and in developing cultivars that can thrive in harsh environments.

Based on overall trait performance, the accessions in Group A, specifically, A4 (Bushehr, from south of Iran), A6 (Esfahan, from the Center), A7 (Hamadan, from the West), A8 (Karaj, from the Center), A9 (Maragheh, from the Northwest), A11 (Nehbandan, from the Southeast), A12 (Nourabad,

Table 4. The mean values of traits in three identified groups from factor analysis in the purslane (*Portulaca oleracea* L.) accessions.

Traits	Group A	Group B	Group C
Number of branches per main stem	19.59	18.23	14.13
Number of lateral branches	56.24	50.86	55.19
Main stem length	53.15	52.66	35.62
Length of the longest lateral branch	59.32	59.58	37.65
Third internode diameter	13.63	13.47	7.58
Total soluble solids	2.43	2.63	2.60
Leaf length	63.49	63.77	33.78
Leaf width	32.24	32.56	17.27
Leaf length/Leaf width ratio	1.97	1.90	1.97
Leaf area	36.44	35.17	19.66
Number of flowers per plant	5.23	4.18	4.47
Dry shoot weight	11.84	11.51	7.37
Fresh shoot weight	19.32	18.07	13.31
Dry/fresh shoot weight ratio	2.90	2.70	3.48
Number of capsules per branch	25.47	24.34	68.04
Number of seeds per capsule	91.48	85.30	79.50

from the West), A14 (Qazvin, from the Northwest), A15 (ShahrKord, from the Center), A16 (Shiraz, from the South), and A18 (Tehran, from the Center), are considered the promising candidates for the cultivar development. These genotypes are recommended for further evaluation through multi-environmental trials, particularly under rainfed conditions in cool upland semi-arid regions. However, other groups have some merits that should be used in crossing blocks in the breeding programs to produce desirable varieties.

Purslane is regarded for its nutritional and medicinal properties, and the findings revealed significant genotypic variation in several morphological traits, including biomass and yield-related traits such as fresh and dry shoot weight, leaf and stem characteristics, and reproductive traits. This variation is advantageous for breeding, as it provides a wide range of traits to select from for improving specific characteristics, such as yield potential, drought tolerance, or nutrient content (Borsai *et al.* 2018), particularly in areas with semi-arid and rainfed conditions.

Conclusion

This study highlights the significant genetic diversity within purslane genotypes, offering valuable insights for breeding programs aimed at improving biomass yield. Factor analysis identified plant biomass, number of branches and flowers, leaf length-to-width and dry-to-fresh weight ratios, number of lateral branches, and total soluble solids as the main influencing factors. Also, the identification of distinct genotypic groups based on key morphological traits, like Group A, provided a good foundation for selecting superior accessions for cultivar development. By focusing on genotypes with high biomass and yield-related traits, future breeding efforts can enhance the potential of purslane as a sustainable crop, meeting both nutritional and market demands.

Ethical Considerations

The authors avoided data fabrication and falsification.

Funding

This research received no specific grant from funding agencies in the public or commercial sectors.

Conflict of Interest

The authors declare that they have no conflict of interest with any organization concerning the subject of the manuscript.

References

- Alam A, Juraimi AS, Yusop MR, Hamid AA, Hakim A. 2014. Morpho-physiological and mineral nutrient characterization of 45 collected purslane (*Portulaca oleracea* L.) accessions. Bragantia 73(4): 426-437. https://doi.org/10.1590/1678-4499.253
- Amirul Alam M, Juraimi AS, Rafii MY, Hamid AA, Kamal Uddin M, Alam MZ, Latif MA. 2014. Genetic improvement of purslane (*Portulaca oleracea* L.) and its future prospects. Mol Biol Rep. 41: 7395-7411. https://doi.org/10.1007/s11033-014-3628-1
- Borsai O, Al Hassan M, Boscaiu M, Sestras RE, Vicente O. 2018. The genus *Portulaca* as a suitable model to study the mechanisms of plant tolerance to drought and salinity. EuroBiotech J. 2(2): 104-113. https://doi.org/10.2478/ebtj-2018-0014
- Carrascosa A, Pascual JA, Ros M, Petropoulos SA, Alguacil MDM. 2023. Agronomical practices and management for commercial cultivation of *Portulaca oleracea* as a crop: a review. Plants. 12(6): 1246. https://doi.org/10.3390/plants12061246

- Coulibaly M, Bodjrenou G, Fassinou Hotègni NV, Akohoue F, Agossou CA, Azon CF, Matro X, Bello S, Adjé COA, Sanou J, *et al.* 2024. Genotype by environment interaction and stability analysis of three agronomic traits in Kersting's groundnut (*Macrotyloma geocarpum*) using factor analytic modeling and environmental covariates. Crop Sci. 64(4): 2095-2115. https://doi.org/10.1002/csc2.21249
- Egea-Gilabert C, Ruiz-Hernández MV, Parra MÁ, Fernández JA. 2014. Characterization of purslane (*Portulaca oleracea* L.) accessions: suitability as ready-to-eat product. Sci Hortic. 172: 73-81. https://doi.org/10.1016/j.scienta.2014.03.051
- El-Bakatoushi R, Alframawy AM, Samer M, El-Sadek L, Botros W. 2013. Evolution of the *Portulaca oleracea* L. aggregate in Egypt on molecular and phenotypic levels revealed by morphology, inter-simple sequence repeat (ISSR) and 18S rDNA gene sequence markers. Flora: Morphol Distrib Funct Ecol Plants. 208(7): 464-477. https://doi.org/10.1016/j.flora.2013.07.008
- Fathi S, Kharazmi M, Najafian S. 2019. Effects of salicylic acid foliar application on morphophysiological traits of purslane (*Portulaca olaracea* L.) under salinity stress conditions. J Plant Physiol Breed. 9(2): 1-9. https://doi.org/10.22034/jppb.2019.10439
- He J, Gan JH, S, Qin L. 2023. Productivity, photosynthetic light-use efficiency, nitrogen metabolism and nutritional quality of C4 halophyte *Portulaca oleracea* L. grown indoors under different light intensities and durations. Front Plant Sci. 14: 1106394. https://doi.org/10.3389/fpls.2023.1106394
- Kumar A, Sreedharan S, Kashyap AK, Singh P, Ramchiary N. 2022. A review on bioactive phytochemicals and ethnopharmacological potential of purslane (*Portulaca oleracea* L.). Heliyon 8(1): 1e08669. https://doi.org/10.1016/j.heliyon.2021.e08669
- Mohebodini M, Khalili-Baseri I, Farmanpour-Kalalagh K, Sabaghnia N. 2024. Morphological characterization of some collected native purslane (*Portulaca oleracea* L.) genotypes. Contrib Bot. 59: 7-20. https://doi.org/10.24193/Contrib.Bot.59.1
- Mulry KR, Hanson BA, Dudle DA. 2015. Alternative strategies in response to saline stress in two varieties of *Portulaca oleracea* (purslane). PloS One 10(9): e0138723. https://doi.org/10.1371/journal.pone.0138723
- Naeem MY, Jabran K, Özden M, Bakhsh A. 2022. Assessment of morphological and biochemical characteristics of common purslane (*Portulaca oleracea* L.) accessions. Pak J Agric Sci. 59(6): 1017-1028. https://doi.org/10.21162/PAKJAS/22.101
- Petropoulos SA, Fernandes Â, Dias MI, Vasilakoglou IB, Petrotos K, Barros L, Ferreira ICFR. 2019. Nutritional value, chemical composition and cytotoxic properties of common purslane

(*Portulaca oleracea* L.) in relation to harvesting stage and plant part. Antioxidants. 8(8): 293. https://doi.org/10.3390/antiox8080293

- Sabaghnia N, Janmohammdi M. 2025. Genetic diversity in rye (*Secale cereale* L.) landraces based on agro-morphological traits under the semi-arid conditions of Iran. Genet Res Crop Evol. 72(5): 5127-5138. https://doi.org/10.1007/s10722-024-02188-9
- Sabaghnia N, Ahadnezhad A, Janmohammadi M. 2024. Genetic diversity in safflower (*Carthamus tinctorius* L.) germplasm for vegetative and agronomic characteristics in semi-arid regions. Plant Genet Res. 22(4): 241-250. https://doi.org/10.1017/S1479262124000200
- Salgotra RK, Chauhan BS. 2023. Genetic diversity, conservation, and utilization of plant genetic resources. Genes. 14(1): 174. https://doi.org/10.3390/genes14010174
- Sdouga D, Branca F, Kabtni S, Di Bella MC, Trifi-Farah N, Marghali S. 2020. Morphological traits and phenolic compounds in Tunisian wild populations and cultivated varieties of *Portulaca oleracea* L. Agronomy. 10: 948. https://doi.org/10.3390/agronomy10070948
- Singh RK, Prasad A, Muthamilarasan M, Parida SK, Prasad M. 2020. Breeding and biotechnological interventions for trait improvement: status and prospects. Planta. 252: 54. https://doi.org/10.1007/s00425-020-03465-4
- Srivastava R, Srivastava V, Singh A. 2023. Multipurpose benefits of an underexplored species purslane (*Portulaca oleracea* L.): a critical review. Environ Manage. 72(2): 309-320. https://doi.org/10.1007/s00267-021-01456-z
- Yang X, Li J, Zhao T, Mo L, Zhang J, Ren H, Gao Y. 2019. Variation and heritability of morphological and physiological traits among *Leymus chinensis* genotypes under different environmental conditions. J Arid Land. 11: 66-74. https://doi.org/10.1007/s40333-018-0018-x