MORPHOLOGICAL CHARACTERIZATION OF SOME COLLECTED NATIVE PURSLANE (*PORTULACA OLERACEA* L.) GENOTYPES

Mehdi MOHEBODINI[1], *Iman KHALILI-BASERI*[1], *Karim FARMANPOUR-KALALAGH*[2],
Naser SABAGHNIA[3]

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

[2] Department of Horticultural Science, Faculty of Agriculture, Tarbiat Modares University,
3119752619, Tehran, Iran

[3] Department of Plant Production and Genetics, Faculty of Agriculture, University of Maragheh,
5518779842, Maragheh, Iran

e-mail: mohebodini@uma.ac.ir

Abstract: Purslane (*Portulaca oleracea* L.), an annual herb commonly found across various regions of the world, is often considered either a weed or a valuable vegetable crop. This study aimed to evaluate the morphological variation among ten purslane genotypes collected from different regions of Iran. The trial was conducted in a greenhouse environment via a completely randomized scheme with four replicates, during which eleven traits were assessed. The genotype × trait interaction biplot model accounted for 90% of the observed variability, revealing four distinct genotypic groups. Notably, the Mashhad genotype exhibited the highest values for the flower number per branch, dry shoot weight, fresh shoot weight, branch number of the main stem, and the number of seeds per capsule. A positive correlation was observed among the flower number per plant, capsule number per branch, and flower number per branch, while these traits were negatively associated with main stem length, leaf length, and leaf width. The Mashhad genotype, along with those from Bandar-Abbas and Parsabad, demonstrated superior performance and distinctiveness, with the number of seeds per capsule and the number of branches on the main stem showing the highest discriminative potential. When evaluating dry shoot weight, the Mashhad genotype, followed by those from Parsabad and Bandar-Abbas, emerged as the most desirable, whereas the genotypes from Ardabil and Sirjan were the least desirable in this characteristic. The significant diversity identified among these purslane genotypes could be instrumental in enhancing the breeding of this crop for specific target traits.

Keywords: distinction ability, dry shoot weight, discriminative potential, perfect position

Introduction

Purslane (*Portulaca oleracea* L.) is an annual herbaceous plant, widely recognized either as a leafy green vegetable or a medicinal herb, with its origins traced back to the Mediterranean region. It has since spread across the globe, thriving in various climates [17]. In some areas, it is regarded as a weed due to its ability to produce abundant seeds, even under adverse conditions. The most common varieties of purslane have yellow flowers at the nodes, while ornamental

types boast flowers in a range of colors. The plant produces numerous tiny black seeds that can remain viable for many years [2]. Purslane stands out among leafy vegetables for its exceptional nutritional profile, particularly its high levels of omega-3 fatty acids, β-carotene, and α-tocopherol. Beyond its nutritional benefits, purslane also exhibits antibacterial and wound-healing properties, thanks to its rich content of alkaloids, flavonoids, and terpenoids. Additionally, its extract demonstrates allelopathic properties, making it useful in organic farming as a natural herbicide or plant extract. This nutrient-rich vegetable is a good source of essential minerals like potassium and magnesium, as well as vitamins A, B, and C [10]. Purslane's strong antioxidant capacity and medicinal potential further distinguish it from other vegetables and medicinal plants. These qualities have led some researchers to consider purslane a promising food source for the future, potentially playing a crucial role in human nutrition in the coming decades.

In a study from 2013, El-Bakatoushi et al. [7] conducted a PCA (principal components analysis) on traits from 16 purslane populations based on morphological characters, revealing that the first two components accounted for about 74% of the variability, and grouped the individuals into three main clusters. The study found that seed characteristics of populations from different locations exhibited significant morphological similarities, so they cannot be used to differentiate between microspecies of *Portulaca oleracea* [7]. However, there are contradictory results on the topic, with earlier investigations [4-6] who indicated that *P. oleracea* is a patchily distributed polyploid complex that can be identified by seed coat morphology and divided into biologically separable subspecies by barriers of ploidy levels. In another study, the assessment of morphological traits variation as well as biochemical analysis in twelve purslane genotypes highlighted significant inter-genotype diversity and identified a genotype with high yield performance and potassium content, making it a strong candidate for successful cultivar development [5]. This research also reported considerable diversity in the target traits both within and among genotypes, suggesting a strong potential for genetic improvement programs aimed at producing high-quality cultivars. Similarly, Sdouga et al. [16] compared the variation among three wild purslane genotypes with a common cultivar, finding significant morphological heterogeneity within and between the studied genotypes, largely due to their different geographical origins. They also emphasized the importance of purslane as a valuable medicinal plant, rich in phenols and flavonoids, which contributes to its broad medicinal properties and strong antioxidant capacity.

Genetic progress in any breeding program relies heavily on the genetic variation present within the plant materials, and the selection of the most favorable individuals is directly influenced by the level of this genetic diversity. Although morphological markers are commonly used to estimate genetic variation within populations, their effectiveness is often limited by environmental factors that can reduce heritability [3]. Nevertheless, morphological evaluation remains a crucial initial step in assessing and categorizing plant materials to optimize their use in breeding programs. These evaluations are relatively easy and reliable to record, which is why they are favored in many projects, given their proven efficiency in analyzing genetic diversity

across various crops. Multivariate statistical models are widely used to estimate the structure of genetic variation and to explore interrelationships among genotypes and traits. However, breeders often encounter challenges when evaluating multiple characteristics, particularly in defining selection indices, especially when interactions occur between the target trait and other studied traits [14]. The genotype × trait interaction biplot model, proposed by Yan [21], is considered one of the most reliable methods for such evaluations. This model enables breeders to assess the overall two-way data pattern through a graph generated by the first two principal components. It serves as a statistical tool to evaluate genotypes according to multiple traits, to detect favorable genotypes, and to select candidates for use as parents in crossbreeding program. Additionally, this model facilitates the visual evaluation of correlations among traits and helps identify both the ideal genotype and the ideal trait [19].

The goals of the current study were to: (1) assess the extent of genetic variation in several Iranian native purslane genotypes using morphological characteristics based on the genotype × trait interaction biplot model; (2) identify the ideal genotype for morphological trait assessment in purslane; and (3) determine the ideal trait for comparing purslane genotypes. This knowledge will be instrumental in identifying the most favorable genotypes for use as new materials in genetic improvement programs or for the commercial release of new cultivars.

Materials and Methods

Trial protocol

In this study, seeds from ten wild genotypes of purslane native to Iran were collected and named after the locality of collection: Mashhad (MSH), Yasouj (YA), Bushehr (BU), Shiraz (SHI), Bandar-Abbas (BA), Qazvin (QA), Sirjan (SI), Ardabil (AR), Parsabad (PA), and Esfahan (ES). These seeds were stored at 4°C in the laboratory. The geographical details of the collection sites are provided in Table 1. The soil used for cultivation was prepared by mixing clay, sand, and organic manure in a 2:1:1 ratio. The placement of the pots (each containing seeds from the same genotypes of purslane) was done randomly within the greenhouse without any systematic arrangement or grouping. This type of design ensures that any variation in environmental factors within the greenhouse (like light, temperature, humidity) is equally likely to affect all pots, reducing the risk of confounding effects. In this study, there were four replicates of each genotype, and by randomly assigning these replicates in the greenhouse, we aimed to control for any variability in growing conditions. For each genotype, 4 pots were sown, each with 30 seeds, for a total of 120 individuals. In total, for the 10 genotypes, 120 individuals were grown. The surface of each pot was covered with a 3–4 cm layer of the prepared soil mixture. Due to the small size of the seeds, irrigation was initially done slowly using sprinklers during the first three weeks, with frequent watering (five times a day) but in small amounts. As the plants grew and established, the frequency of irrigation was gradually reduced to once per day, with an increase in the volume of water applied.

Measured traits

For trait measurement, ten random plants were selected from each pot. Eleven traits were measured: the number of branches on the main stem (BMS), main stem length (MSL), leaf

length (LL), leaf width (LW), number of flowers per plant (NFP), number of flowers per branch (NFB), number of flowers per plant/branch (FPB), dry shoot weight (DSW), fresh shoot weight (FSW), number of capsules per branch (NCB), and number of seeds per capsule (NSC). The FPB is computed as the ratio of NFP to NFB, and DSW was determined after drying shoots for 24 h in the electric oven. Data collection involved counting, length measurement using a stainless-steel ruler, width estimation with a digital caliper, and weighing with a laboratory scale.

Table 1: Geographical properties of locations which used to colleting purslane genotypes

Code	Location	Coordinates	Elevation (m)
AR	Ardabil	38°15′N 48°17′E	1,351
ES	Esfahan	32°39′N 51°40′E	1,574
BA	Bandar-Abbas	27°11′N 56°17′E	9
BU	Bushehr	28°55′N 50°51′E	18
PA	Parsabad	39°38′N 47°54′E	75
SI	Sirjan	29°26′N 55°41′E	1,760
SHI	Shiraz	29°36′N 52°32′E	1,500
QA	Qazvin	36°17′N 50°00′E	1,278
MSH	Mashhad	36°19′N 59°32′E	995
YA	Yasouj	30°40′N 51°34′E	1,837

Statistical analysis

Data normality was assessed using the Anderson-Darling normality test. Principal component (PC) analysis was performed using a genotype × trait interaction biplot model, and the target model was generated with the GGEbiplot application, following the equation (Yan et al. 2000):

$$\frac{a_{ij} - b_j}{S_j} = \sum_{n=1}^{2} \lambda_n \xi_{in} \eta_{jn} + \varepsilon_{ij}$$

where a_{ij} is the value of genotype i for character j, b_j is the mean of genotypes in character j, S_j is the square root of variance for character j, λ_n is the singular value for PCn, ξ_{in} and η_{in} are values for genotypes i and character j on PCn, respectively, and ε_{ij} is the error term. Eigenvalues have been adjusted (via vectors absorption) to make them more suitable for graphical representation. In PCA biplots, this is crucial because both genotypes (entries) and traits (testers) need to be displayed in the same plot with comparable scales. Without such adjustments, the biplot might distort the relationships between genotypes and traits, making interpretation difficult. The Scaling = 1 was applied for achieving the scaled data; the Centering = 2 was used to obtain the centered data, and the option singular value decomposition (SVP) = 2 was applied to calculate the singular scores. Also, the SVP = 1 was used for obtaining the singular scores which were suitable for visual interpretation of correlations among genotypes via perfect entry-view.

Results and Discussion

Model fitting

The genotype × trait interaction biplot model accounted for 90% of the variation (77% - PC1 and 13% - PC2) within the standardized two-way dataset (Fig. 1), revealing a substantial proportion of variation that highlights the direct associations among traits. To visualize these relationships, vectors were plotted from the origin of the graph to the traits, facilitating the interpretation of trait interactions. The model demonstrated both additive and crossover interactions, suggesting that genotype rankings across traits can shift. Sabaghnia et al. [15] emphasized the complexity of selecting genotypes without considering genotype × trait interactions. In our study, the fitted biplot model, as recommended by Yan et al. [20], proved effective for exploring and visualizing genotype-trait relationships. The genotype × trait interaction biplot model revealed a high level of variation (90%) and confirmed the presence of both simple and complex interactions among the genotypes and traits. Similar interaction patterns have been documented in other vegetable crops, such as spinach [15] and green beans [11].
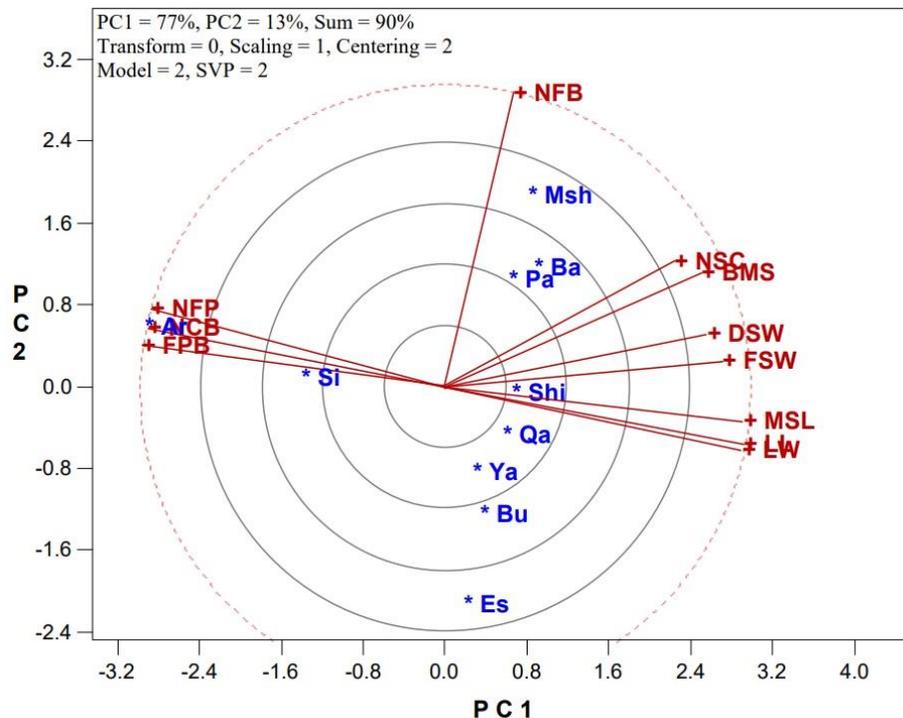

Fig. 1: The vector plot that indicates associations among traits

Traits' association

The biplot model captured a significant amount of variability, with trait associations determined by the cosine of their vectors, where cos0° = +1, cos90° = 0, and cos180° = -1. The

model displayed extensive variability through long vectors (Fig. 1). Notable associations included: (i) positive correlations between the number of flowers per plant (NFP), number of capsules per branch (NCB), and number of flowers per plant/branch (FPB); (ii) positive correlations between main stem length (MSL), leaf length (LL), and leaf width (LW); (iii) a positive relationship between dry shoot weight (DSW) and fresh shoot weight (FSW); and (iv) a positive link between the number of branches on the main stem (BMS) and number of seeds per capsule (NSC). Conversely, near-zero correlations were observed between the number of flowers per branch (NFB) and NFP, NCB, FPB, as well as with MSL, LL, and LW, as indicated by nearly perpendicular vectors (Fig. 1). Additionally, strong negative correlations were found between NFP, NCB, and FPB with MSL, LL, and LW, as demonstrated by obtuse angles (Fig. 1). It is interesting to notice that while the biplot method illustrates trait associations according the overall structure of the dataset, correlation coefficients measure the direct interrelationship of traits and may not always directly align with the biplot results. However, the results obtained confirmed pervious report [1] about the positive correlations between main stem length and leaf size, and between both fresh and dry shoot weight with the branch number on the main stem, main stem length, and leaf size. Most of the mentioned findings can be confirmed via the outcomes of Table 2, but some discrepancies between the model and the dataset were observed because the model described for less than whole of the variance (in current study, 90%) and not the whole variance.

Table 2: Correlation coefficients of morphological characteristics of purslane

	BMS†	MSL	LL	LW	NFB	NFP	FPB	DSW	FSW	NCB
MSL	0.81‡									
LL	0.76	0.95								
LW	0.74	0.94	0.99							
NFB	0.56	0.12	0.05	0.03						
NFP	-0.73	-0.97	-0.97	-0.97	0.02					
FPB	-0.78	-0.97	-0.98	-0.98	-0.10	0.98				
DSW	0.67	0.79	0.78	0.75	0.35	-0.73	-0.79			
FSW	0.68	0.86	0.84	0.82	0.24	-0.80	-0.85	0.95		
NCB	-0.76	-0.95	-0.98	-0.97	-0.05	0.98	0.98	-0.77	-0.83	
NSC	0.70	0.65	0.65	0.66	0.49	-0.62	-0.69	0.59	0.70	-0.64

†Traits are: MSL, main stem length (in mm); LL, leaf length (in mm); LW, leaf width (in mm); NFP, number of flowers per plant; NFB, number of flowers per branch; FPB, number of flowers plant / branch; DSW, dry shoot weight (in g); FSW, fresh shoot weight (in g); NCB, number of capsules per branch; and NSC, number of seeds per capsule.
‡ Critical values for correlation coefficients are 0.63 and 0.77 (degrees of freedom=8) at 0.05 and 0.01 probability level.

Polygon-view

Fig. 2 illustrates how the biplot model aids in comparing genotypes based on measured traits and identifies those that excel in specific areas, making them suitable candidates for breeding or commercial cultivation. A polygon was constructed with perpendicular lines to its

sides to facilitate comparisons among the vertex genotypes. Four key vertex genotypes were identified: Ardabil (AR), Mashhad (MSH), Bandar-Abbas (BA), and Esfahan (ES). Genotype Ardabil (AR) showed the highest values for the number of flowers per plant (NFP), number of capsules per branch (NCB), and number of flowers per plant/branch (FPB). Genotype Bandar-Abbas (BA) excelled in main stem length (MSL), leaf length (LL), and leaf width (LW). Genotype Mashhad (MSH) had the highest values for the number of flowers per branch (NFB), dry shoot weight (DSW), fresh shoot weight (FSW), number of branches on the main stem (BMS), and number of seeds per capsule (NSC). Conversely, genotype Esfahan (ES) did not show superior performance in any of the measured traits. The purslane genotypes were categorized into four main groups: Group I [Sirjan (SI) and Ardabil (AR)]; Group II [Mashhad (MSH)]; Group III [Shiraz (SHI), Bandar-Abbas (BA), and Parsabad (PA)]; and Group IV [Esfahan (ES), Yasouj (YA), Qazvin (QA), and Bushehr (BU)]. Among these, Mashhad (MSH) emerged as the top genotype for most traits, followed by the genotypes in Group III. Most of these findings can be verified via the means set out in Table 3, but some discrepancies between the model and the means were found because the model described for less than whole of the variance (in current study, 90%) and not the whole variance.
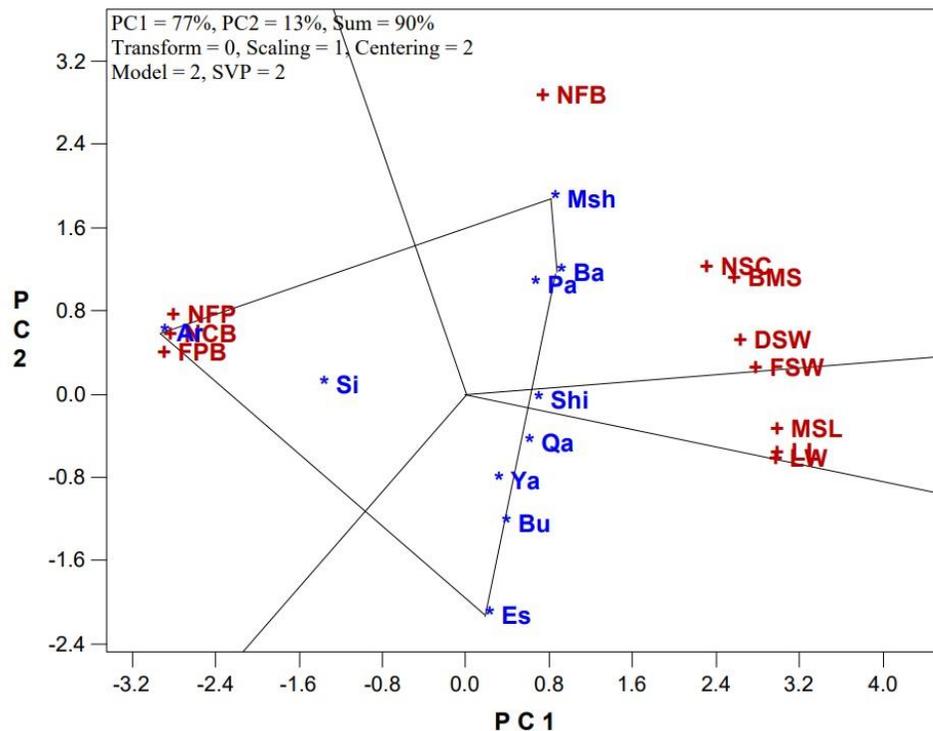

Fig. 2: The quadrilateral plot that indicates which genotype wins which trait

Table 3: Means and standard deviation values for morphological characteristics of purslane

	BMS	MSL	LL	LW	NFB	NFP
AR	13.3 ± 1.36	33.3 ± 4.31	22.8 ± 2.21	11.5 ± 2.07	4.6 ± 0.63	35.7 ± 5.47
ES	16.8 ± 1.76	50.3 ± 6.74	66.5 ± 5.50	34.6 ± 4.00	3.4 ± 0.48	6.6 ± 0.85
BA	19.4 ± 2.10	51.6 ± 7.22	62.9 ± 5.78	32.2 ± 4.19	5.4 ± 0.80	9.9 ± 1.34
BU	17.8 ± 1.83	52.9 ± 6.84	63.2 ± 5.08	31.4 ± 3.81	3.6 ± 0.49	6.5 ± 0.82
PA	18.8 ± 1.98	52.3 ± 7.00	63.6 ± 5.43	31.9 ± 4.02	5.6 ± 0.79	10.0 ± 1.30
SI	15.0 ± 1.63	37.9 ± 5.30	44.7 ± 4.20	23.0 ± 3.11	4.3 ± 0.63	24.6 ± 3.34
SHI	20.0 ± 2.06	54.5 ± 7.05	63.8 ± 5.24	33.4 ± 4.16	4.5 ± 0.61	8.3 ± 1.04
QA	19.0 ± 2.06	52.8 ± 7.39	64.5 ± 5.87	32.0 ± 4.14	4.4 ± 0.64	10.6 ± 1.44
MSH	23.8 ± 2.50	53.0 ± 7.10	65.2 ± 5.85	32.7 ± 4.57	6.2 ± 0.87	8.7 ± 1.13
YA	19.0 ± 1.96	52.6 ± 6.80	62.2 ± 5.08	31.7 ± 3.95	4.2 ± 0.58	8.1 ± 1.01
	FPB	DSW	FSW	NCB	NSC	
AR	9.80 ± 1.40	6.7 ± 0.78	12.0 ± 1.56	80.8 ± 9.17	74.0 ± 8.80	
ES	1.97 ± 0.29	10.3 ± 1.24	17.1 ± 2.30	21.6 ± 3.10	80.5 ± 9.92	
BA	1.89 ± 0.29	13.7 ± 1.73	21.3 ± 2.97	21.4 ± 3.20	92.8 ± 11.94	
BU	2.10 ± 0.30	11.0 ± 1.28	18.8 ± 2.43	30.8 ± 4.26	86.3 ± 10.27	
PA	1.83 ± 0.28	12.5 ± 1.51	19.7 ± 2.64	30.1 ± 4.32	90.0 ± 11.10	
SI	6.03 ± 0.92	8.0 ± 1.01	14.6 ± 2.04	55.3 ± 8.28	85.0 ± 10.94	
SHI	1.90 ± 0.28	10.1 ± 1.18	19.2 ± 2.49	23.5 ± 3.25	91.5 ± 10.89	
QA	2.30 ± 0.35	13.6 ± 1.71	21.0 ± 2.94	25.3 ± 3.78	81.5 ± 10.49	
MSH	1.74 ± 0.25	11.6 ± 1.40	18.2 ± 2.43	25.6 ± 3.67	89.3 ± 11.00	
YA	1.95 ± 0.28	10.1 ± 1.17	16.6 ± 2.15	21.3 ± 2.94	84.3 ± 10.04	

†Traits are: MSL, main stem length (in mm); LL, leaf length (in mm); LW, leaf width (in mm); NFP, number of flowers per plant; NFB, number of flowers per branch; FPB, number of flowers plant / branch; DSW, dry shoot weight (in g); FSW, fresh shoot weight (in g); NCB, number of capsules per branch; and NSC, number of seeds per capsule.

Perfect genotype

Fig. 3 shows the ideal position for a perfect genotype (near the center of the circles), with genotypes closest to this position being considered the best [21]. Genotypes Mashhad (MSH), Bandar-Abbas (BA), and Parsabad (PA) are nearest to this ideal position, indicating their superior performance. On the other hand, genotypes Sirjan (SI) and Ardabil (AR) are positioned farthest from this ideal, making them less desirable. The remaining genotypes ranked based on their proximity to the ideal genotype are Shiraz (SHI), Qazvin (QA), Yasouj (YA), Bushehr (BU), and Esfahan (ES). The identified ideal genotypes are crucial for a purslane genetic improvement program, especially since yield and quality characteristics often have low or even negative correlations in many vegetable crops. Therefore, employing multivariate statistical tools with graphical presentations is vital for determining ideal genotypes and enhancing purslane breeding strategies. Egea-Gilabert et al. [5] indicated high number of leaves per plant and long leaf blade characteristics for an ideal or ideotype genotype in purslane and we found relatively

such a similar association, so it can be recommended that for breeding new cultivars, emphasizing leaf properties will be more effective in genetic improvement programs.
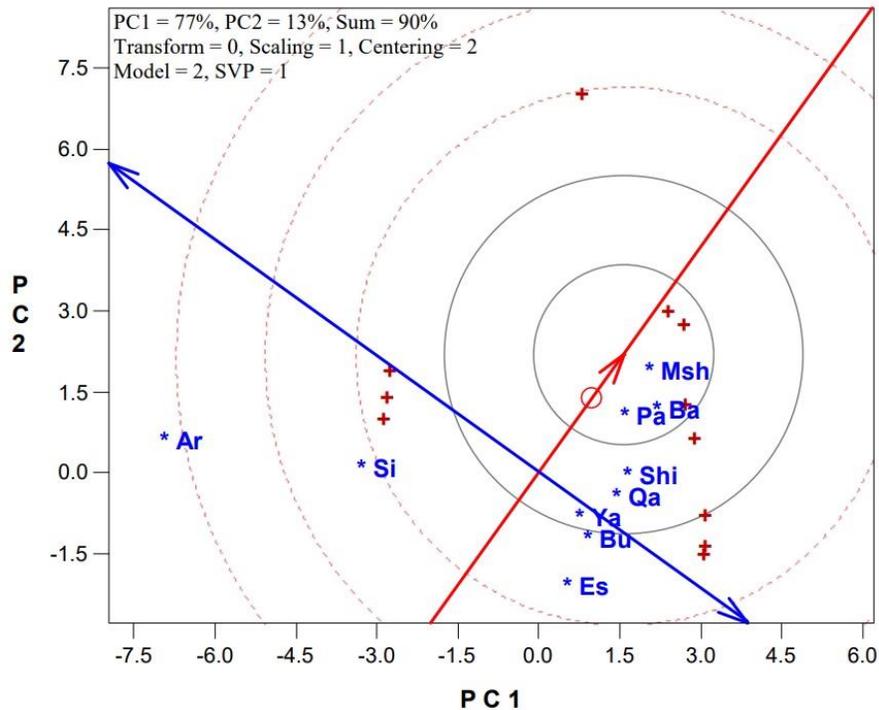

PC1 = 77%, PC2 = 13%, Sum = 90%
Transform = 0, Scaling = 1, Centering = 2
Model = 2, SVP = 1

Fig. 3: The perfect genotype plot that indicates the positions of genotypes

Perfect trait

The trait discriminative ability is determined by the magnitude of the standard deviation; a higher standard deviation indicates a greater potential for distinguishing among genotypes. This is illustrated in Fig. 4, where traits closer to the red line (ATA – average tester axis) are more discriminative, while those further away are less effective. Based on this model, the number of seeds per capsule (NSC) and the number of branches on the main stem (BMS) are identified as the most discriminative traits. In contrast, traits such as main stem length (MSL), leaf length (LL), leaf width (LW), dry shoot weight (DSW), fresh shoot weight (FSW), and number of flowers per branch (NFB) have a discriminative potential above average because they are above the red line is ATA (average tester axis), indicating they are effective at differentiating among purslane genotypes (Fig. 4). However, traits such as the number of flowers per plant (NFP), number of capsules per branch (NCB), and number of flowers per plant/branch (FPB) have low discriminative potential and are not recommended for future investigations. The typical potential of a trait, representing its symbolic importance, is assessed by the angle between the trait's vector and the axis of the average trait (average tester axis, ATA, red line in Fig. 4). Smaller angles denote greater typical potential. Therefore, the traits with the smallest angles, such as NSC and BMS, exhibit higher typical potential. In contrast, traits such as DSW, FSW, MSL, LL, LW, NFP, NCB, and FPB have moderate angles, indicating moderate typical potential

(Fig. 4). The number of flowers per branch (NFB) has a larger angle with the axis, reflecting its lower typical potential.
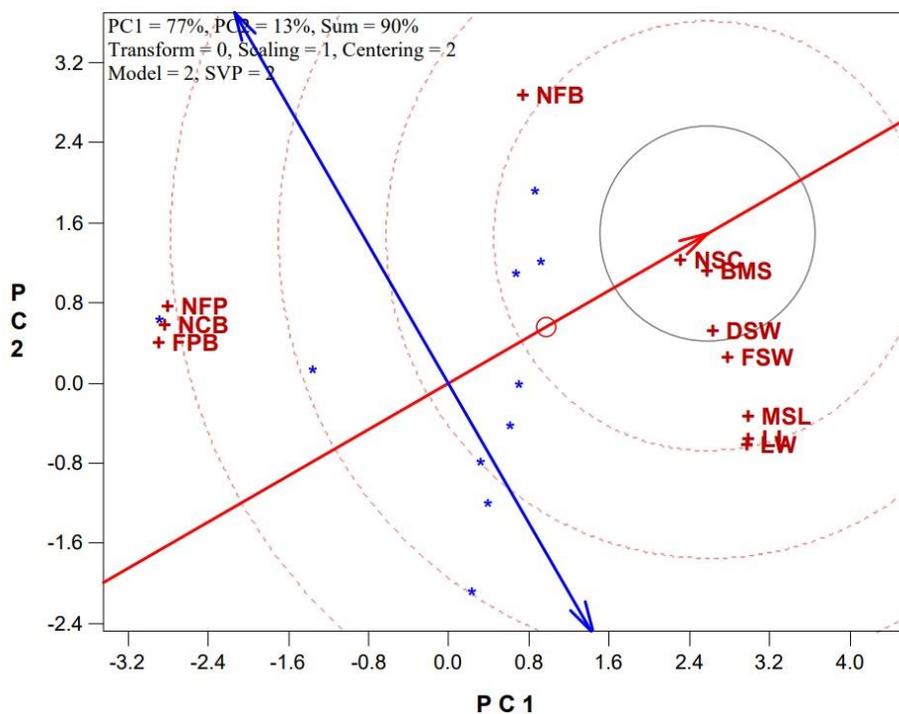

Fig. 4: The perfect trait plot that indicates the positions of traits

Examination of DSW

Fig. 5 examines the performance of purslane genotypes in terms of dry shoot weight (DSW), with the horizontal axis representing DSW and the arrow indicating its direction. Genotypes Mashhad (MSH), Parsabad (PA), and Bandar-Abbas (BA) are the most desirable for DSW performance, while genotypes Ardabil (AR) and Sirjan (SI) are the least favorable (Fig. 5). Genotypes Shiraz (SHI), Qazvin (QA), Yasouj (YA), and Bushehr (BU) also show above-average DSW performance as they lie above the average axis (blue line in Fig. 4). The distance of genotypes from the horizontal axis serves as an index of standard deviation; smaller distances indicate lower variability and are preferred for selection. Consequently, genotypes Shiraz (SHI) and Qazvin (QA), along with Parsabad (PA) and Bandar-Abbas (BA), are recommended due to their low variability. In contrast, genotype Esfahan (ES), which has low DSW performance and greater distance from the horizontal axis, exhibits high variability and is considered one of the least desirable genotypes. Evaluating purslane genotypes is crucial for preventing erosion in plant materials and effectively managing genetic improvement tasks. Our study observed substantial variation among purslane genotypes, which aligns with previous findings that report significant diversity in purslane [9, 13]. These interactions resulted in varying rankings of genotypes across traits, making it challenging to select the most superior genotypes. Ignoring these interaction effects complicates the selection process due to the interaction of the genotype × trait impact on genetic factors.

Comparison biplots

While genotype Mashhad (MSH) outperformed others in most traits, genotypes from Group III (Parsabad, Shiraz, and Bandar-Abbas) exhibited high yields and robust dry and fresh shoot weights, as well as favorable leaf characteristics. This suggests that these genotypes, being local and genetically diverse, have significant yield potential. Among the genotypes, those from Group II (Mashhad) and Group III (Parsabad, Shiraz, and Bandar-Abbas) displayed similar yield performance, but Shiraz, Parsabad, and Bandar-Abbas were closest to the ideal position on the horizontal axis, indicating their potential for commercial cultivar release. These genotypes should undergo multi-environmental trials to assess their adaptability and yield stability before final analysis. Our findings highlight that genotypes Mashhad, Parsabad, and Bandar-Abbas have high discriminative ability and symbolic potential for pursuing further investigations. These genotypes are suitable for exploring trait relationships in purslane. When the first principal component of the genotype × trait biplot model shows a significant association with genotype effects, it indicates that genotypes with higher values at the perfect position are likely to perform well. Low absolute values of the second principal component suggest reduced variability in reaction to the ideal position. The effectiveness of using the perfect position tool for identifying favorable genotypes based on multiple traits has been demonstrated in studies on spinach [15] and quince [13]. However, these findings are based on multi-environmental trials, and results may vary with different two-way datasets. To address this, an alternative model suggests replacing the first principal component with predictions from a linear regression model of tester-centered data on genotype effects, which makes the model more interpretable.
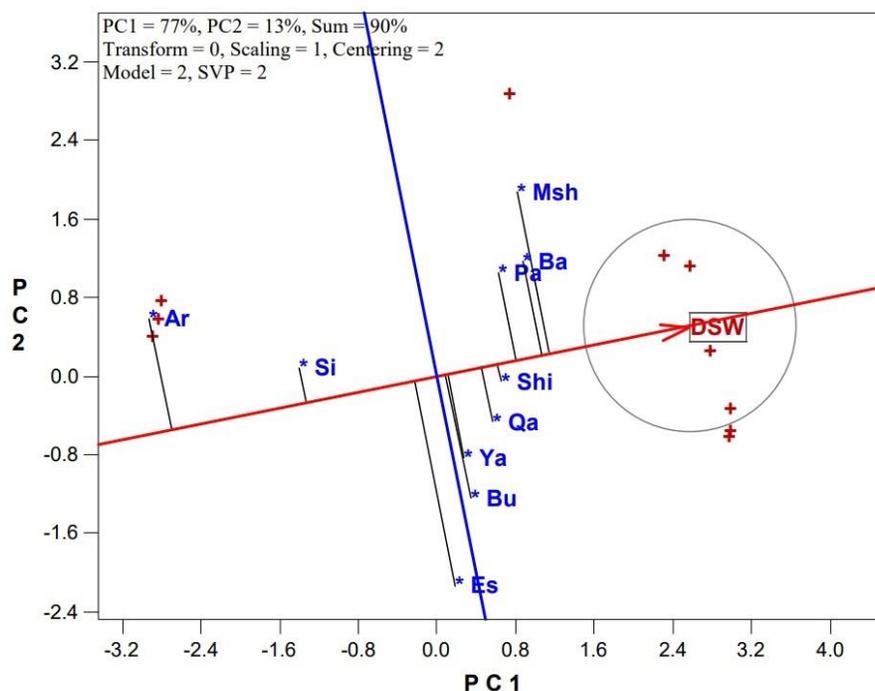

Fig. 5: Testing the performance of/at dry shoot weight (DSW) across ten genotypes

The seed number per capsule and the branch number of the main stem emerged as the most discriminative traits for distinguishing among purslane genotypes. These traits also demonstrated high typical potential for illustrating the symbolic characteristics of other traits. Evaluating purslane genotypes based on these traits yields more reliable findings and better detects variations among genotypes. Similar to identifying the perfect genotype, determining the perfect trait position highlights its discriminative and representative potential. High values indicate strong discriminative ability, while low absolute values of the second principal component reflect better representational potential. The effectiveness of using the perfect trait position tool for identifying favorable traits has been established in studies on sweet corn [18] and safflower [4]. This approach was applied to our genotype × trait dataset through regression adjustment of the primary biplot model.

Conclusions

In this study, among the nine of the eleven measured traits evaluated in purslane, dry and fresh shoot weight were found to be related to main stem length, branch number of the main stem, seed number per capsule and leaf length and width. These traits are valuable for selecting the most favorable genotypes. Based on discriminative and representative properties, the branch number of the main stem and the seed number per capsule were identified as the most effective traits. Evaluating these traits helps identify superior genotypes, which can assist breeders in developing new cultivars with higher yield performance. Genotypes Parsabad, Shiraz, and Bandar-Abbas were found to be the most favorable due to high measures of main stem length, leaf length, and leaf width, so they are recommended for cultivar release.

REFERENCES

1. Alam, A., Juraimi, A.S., Yusop, M.R., Hamid, A.A., Hakim, A., 2014, Morpho-physiological and mineral nutrient characterization of 45 collected Purslane (*Portulaca oleracea* L.) accessions, *Bragantia,* **73:** 426-437.
2. Amirul-Alam, M., Juraimi, A.S., Rafii, M.Y., Hamid, A.A., KamalUddin, M., Alam, M.Z., Latif, M.A., 2014, Genetic improvement of purslane (*Portulaca oleracea* L.) and its future prospects, *Molecular Biology Reports,* **41:** 7395-7411.
3. Chesnokov, Y.V., Kosolapov, V.M., Savchenko, I.V., 2020, Morphological genetic markers in plants, *Russian Journal of Genetics,* **56:** 1406-1415.
4. Danin, A., 1990, *Portulaca*. In: Castroviejo, S., et, al. (Eds.), *Flora Iberica*, vol. 2. Real Jardin Botanico C.S.I.C. Madrid, pp. 464–469.
5. Danin, A., Anderson, L.C., 1986, Distribution of *Portulaca oleracea* L. (Portulacaceae) subspecies in Florida, *SIDA Contributions to Botany*, **11:** 318–324.
6. Danin, A., Baker, I., Baker, H.G., 1978, Cytogeography and taxonomy of the *Portulaca oleracea* L. polyploidy complex, *Israel Journal of Botany*, **27:** 177–211.

7. Ebrahimi, H., Sabaghnia, N., Javanmard, A., Abbasi, A., 2023, Genotype by trait biplot analysis of trait relations in safflower, *Agrotechniques in Industrial Crops,* **3:** 67-73.

8. Egea-Gilabert, C., Ruiz-Hernández, M.V., Parra, M.Á., Fernández, J.A., 2014, Characterization of purslane (*Portulaca oleracea* L.) accessions: Suitability as ready-to-eat product, *Scientia Horticulturae,* **172:** 73-81.

9. El-Bakatoushi, R., Alframawy, A.M., 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: Morphology, Distribution, Functional Ecology of Plants*, **208:** 464-477.

10. Nemzer, B., Al-Taher, F., Abshiru, N., 2020, Phytochemical composition and nutritional value of different plant parts in two cultivated and wild purslane (*Portulaca oleracea* L.) genotypes, *Food Chemistry,* **320:** 126621.

11. Oliveira, T.R.A.D., Gravina, G.D.A., Oliveira, G.H.F.D., Araújo, K.C., Araújo, L.C.D., Daher, R.F., Cruz, D.P.D., 2018, The GT biplot analysis of green bean traits, *Ciência Rural,* **48:** e20170757.

12. Petropoulos, S., Karkanis, A., Martins, N., Ferreira, I.C., 2016, Phytochemical composition and bioactive compounds of common purslane (*Portulaca oleracea* L.) as affected by crop management practices, *Trends in Food Science and Technology,* **55:** 1-10.

13. Rahimi, M., Asadi-Gharneh, H.A., Sabaghnia, N., 2019, Evaluation of some traits in local Iranian quince (*Cydonia Oblonga* Miller) genotypes, *International Journal of Fruit Science,* **19:** 397-412.

14. Reynolds, M,, Chapman, S,, Crespo-Herrera, L,, Molero, G,, Mondal, S,, Pequeno, D,N,, Sukumaran, S,. 2020, Breeder friendly phenotyping, *Plant Science,* **295:** 110396.

15. Sabaghnia, N., Behtash, F., Janmohammadi, M., 2015, Graphic analysis of trait relations of spinach (*Spinacia oleracea* L.) landraces using the biplot method, *Acta Universitatis Agriculturae et Silviculturae Mendelianae Brunensis,* **63:** 1187-1194.

16. Sdouga, D., Branca, F., Kabtni, S., DiBella, M.C., 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.

17. Srivastava, R., Srivastava, V., Singh, A., 2023, Multipurpose benefits of an underexplored species purslane (*Portulaca oleracea* L.): A critical review, *Environmental Management,* **72:** 309-320. DOI:10.1007/s00267-021-01456-z

18. Stansluos, A.A.L., Öztürk, A., Niedbała, G., Türkoğlu, A., Haliloğlu, K., Szulc, P., Piekutowska, M., 2023, Genotype–trait (GT) biplot analysis for yield and quality stability in some sweet corn (*Zea mays* L. *saccharata* Sturt.) genotypes, *Agronomy,* **13:** 1538. DOI:10.3390/agronomy13061538

19. Yan, W., Frégeau-Reid, J., 2018, Genotype by yield* trait (GYT) biplot: a novel approach for genotype selection based on multiple traits, *Scientific Reports,* **8:** 8242.

20. Yan, W., Frégeau-Reid, J., Mountain, N., Kobler, J., 2019, Genotype and management evaluation based on Genotype by Yield*Trait (GYT) analysis, *Crop Breeding, Genetics and Genomics,* **1:** e190002

21. Yan, W., Rajcan, I., 2002, Biplot analysis of test sites and trait relations of soybean in Ontario, *Crop science*, **42(1):** 11-20.

CARACTERIZAREA MORFOLOGICĂ A UNOR GENOTIPURI NATIVE DE IARBĂ GRASĂ (*PORTULACA OLERACEA* L.)

(Rezumat)

Iarba grasă (*Portulaca oleracea* L.), o plantă anuală întâlnită frecvent în diferite regiuni ale lumii, este adesea considerată o buruiană sau o plantă cu valențe alimentare. Acest studiu şi-a propus să evalueze variația morfologică a zece genotipuri de iarbă grasă colectate din diferite regiuni ale Iranului. Studiul a fost realizat în seră,

printr-o schemă complet randomizată cu patru repetiții, în care au fost evaluate unsprezece caractere. Modelul dual de interacțiune genotip × trăsătură a reprezentat 90% din variabilitatea observată, evidențiind patru grupuri genotipice distincte. În mod special, genotipul Mashhad a prezentat cele mai mari valori pentru numărul de flori pe ramură, greutatea lăstarilor uscați, greutatea lăstarilor proaspeți, numărul de ramuri ale tulpinii principale și numărul de semințe per capsulă. S-a observat o corelație pozitivă între numărul de flori per plantă, numărul de capsule pe ramură și numărul de flori de pe ramură, în timp ce aceste trăsături au fost asociate negativ cu lungimea tulpinii principale, lungimea frunzei și lățimea frunzei. Genotipurile Mashhad, împreună cu Bandar-Abbas și Parsabad, au demonstrat performanțe și caractere distinctive superioare, astfel numărul de semințe per capsulă și numărul de ramuri de pe tulpina principală au avut cel mai mare potențial discriminativ. În ceea ce privește evaluarea greutății lăstarilor uscați, genotipul Mashhad, urmat de Parsabad și Bandar-Abbas, au fost cele mai evidente, în timp ce genotipurile Ardabil și Sirjan s-au situat pe ultimul loc, din acest punct de vedere. Diversitatea semnificativă identificată în cazul acestor genotipuri de iarbă grasă ar putea fi utilă în procesul de multiplicare a acestei plante cu scopul de a urmări caractere specifice.