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GENETIC VARIATION OF SOME COLLECTED PURSLANE (*Portulaca oleracea* L.) GENOTYPES REGARDING MORPHOLOGIC TRAITS

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ABSTRACT*. This experiment aimed to investigate the morphological diversity among twenty purslane genotypes from various areas of Iran. A high coefficient of variation was observed for the number of flowers per branch, the number of flowers per plant per branch, the dry-to-fresh weight ratio, and the number of capsules per branch. Cluster analysis based on morphological traits grouped the genotypes into four distinct clusters, with no apparent association to their geographical origins. Clusters I, II, and III contained high-yielding genotypes, whereas Cluster IV included two genotypes with superior reproductive and quality traits but lower overall yield performance. This suggests that cluster-specific traits can guide parental selection for hybridization based on breeding objectives such as yield enhancement or quality improvement. Additionally, trait-based dendrogram analysis divided the measured traits into four functional groups: seed and length characteristics, leaf and capsule traits, flower and ratio traits, and yield and yield components. This classification offers further insight into the interrelationships of traits and their contributions to plant performance. The considerable morphological variation observed across these genotypes suggests significant potential for selective breeding aimed at improving specific characteristics, such as fresh and dry yield, seed production, and plant architecture, thereby enhancing both the release of cultivars and a resource for genetic improvement in future breeding programs.*

KEYWORDS: *clustering, cutoff line, genetic diversity, yield performance*

INTRODUCTION

Purslane (*Portulaca oleracea* L.) is an annual herb known for its dual role as both a leafy vegetable and a medicinal herb, with origins traced to the Mediterranean region. It has since spread globally, thriving in diverse climates and conditions. In some areas, it is considered a weed due to its ability to produce a vast number of seeds, even in harsh environments (Carrascosa et al. 2023). Purslane is a nutrient-dense plant, rich in omega-3 fatty acids (especially alpha-linolenic acid), vitamins A, C, and E, magnesium, potassium, and iron. Its high antioxidant content supports dietary health, making it a functional food for addressing micronutrient deficiencies. Traditionally used in herbal medicine, it exhibits anti-inflammatory, antioxidant, antibacterial, and antidiabetic properties. Bioactive compounds, such as flavonoids, alkaloids, and betalains, contribute to its therapeutic potential. Drought-tolerant and able to thrive in poor soils, purslane requires minimal inputs, making it ideal for arid and marginal lands. It grows rapidly and can be cultivated as a low-maintenance leafy vegetable or used as ground cover to prevent soil erosion and suppress weeds. Due to its resilience to heat and water stress, purslane can help diversify crops and enhance food security under climate change. Its ability to grow in urban gardens and vertical farming systems adds to its versatility in modern sustainable agriculture. Common purslane varieties typically bear yellow flowers at the nodes, while ornamental types display a wider range of vibrant colors. The plant produces numerous small black seeds, known for their long-term viability in the soil (Mohebodini et al. 2024). What sets purslane apart from other leafy vegetables is its impressive nutritional content. Beyond its nutritional appeal, it offers valuable medicinal benefits (Fathi et al. 2021). Compounds such as alkaloids, flavonoids, and terpenoids contribute to its antibacterial properties, and it has also been found to promote wound healing (Budiawan et al. 2023). Additionally, purslane exhibits allelopathic effects, which makes it beneficial in organic farming as a natural herbicide or plant growth enhancer. It contains vital minerals such as magnesium and potassium, and provides significant amounts of essential vitamins (Srivastava et al. 2023). With its strong antioxidant activity and broad medicinal potential, purslane distinguishes itself from other plants in both the vegetable and medicinal categories (Gallo et al. 2017). Its resilience and nutrient density have led some researchers to view it as a valuable food source for the future, potentially playing a crucial role in addressing global nutritional needs in the years to come. A cluster analysis of some purslane genotypes categorized the populations into three distinct groups, with the two main components capturing two-thirds of the total variability. Similarly, the cluster analysis categorized the populations into three distinct groups (El-Bakatoushi et al. 2013). The study also found significant morphological similarities among populations from different regions, with seed characteristics playing a key role in identifying mixed populations. Another study identified one genotype with particularly high yield performance and potassium content, making it a promising candidate for cultivar development, which highlighted considerable variation in target traits both within and between genotypes, suggesting strong potential for genetic improvement programs focused on producing high-quality cultivars (Egea-Gilabert et al. 2014). Similarly, Sdouga et al. (2020) compared the morphological variation of three wild purslane genotypes with a common cultivar. They found significant heterogeneity, both within and between the genotypes, likely due to their diverse geographical origins. In addition to morphological analysis, cluster analysis is an effective method for examining genetic variation in purslane genotypes. Alam et al. (2015) employed techniques such as ISSR markers and multivariate statistical models to identify significant genetic variation within purslane populations. Talei et al. (2020) conducted cluster analysis on Iranian purslane populations, grouping them into distinct clusters based on traits such as leaf size, stem length, and seed characteristics. This type of analysis is invaluable for identifying genetically diverse populations and prioritizing them for breeding programs aimed at stress tolerance and higher yields. Cluster analysis also helps pinpoint traits contributing most to genetic divergence, such as branch number and leaf width, making it easier for breeders to select high-performing genotypes for future cultivar development. Genetic progress in any breeding program fundamentally depends on the genetic variation available within the plant materials. Selection of favorable individuals is directly tied to this diversity (Louwaars 2018). This evaluation plays a crucial role in identifying valuable genetic resources, including morphological traits such as leaf size, plant architecture, growth rate, and drought tolerance, which are key indicators of adaptive potential and agronomic performance. Assessing these traits across diverse accessions helps in recognizing genotypes with superior characteristics suitable for cultivation under specific environmental conditions. Understanding the range of morphological variation allows breeders to select parent lines with desirable traits (e.g., higher yield, better nutritional content, stress resistance). It provides a baseline for hybridization and selection strategies, ensuring that genetic diversity is conserved and optimally used. Morphological evaluation is a cost-effective, field-based approach that can be used in conjunction with molecular tools for a comprehensive understanding of genetic diversity. It enables the development of improved cultivars that are not only productive but also resilient to climate-induced stresses. Although morphological markers are frequently used to estimate genetic variation, they are often influenced by environmental factors that can reduce heritability. Nevertheless, morphological evaluation remains an essential preliminary step in categorizing plant materials for optimal breeding outcomes. Such evaluations are easy to record and widely adopted due to their efficiency in analyzing genetic diversity across crops. To estimate the structure of genetic variation and examine relationships between genotypes and traits, multivariate statistical models are often employed (Zhu & Zhou 2020). However, evaluating numerous traits simultaneously can be challenging, especially when there are complex interactions between the target trait and others. Despite the recognized potential of purslane as a nutrient-rich and climate-resilient crop, a significant lack of systematic data remains on its morphological diversity. This gap poses several challenges, like limited characterization of genotypes, constraints on breeding and selection, and underutilization of genetic resources. Although various purslane genotypes have been collected worldwide, most have not been systematically evaluated or cataloged based on their morphological traits. As a result, the extent and structure of genetic variation within the species remain poorly understood. The absence of detailed morphological profiles hampers the identification of superior genotypes for specific traits such as drought tolerance, biomass yield, or nutrient content. This restricts breeders' ability to develop targeted crop improvement strategies, slowing progress toward the development of improved cultivars. Without comprehensive phenotypic data, many potentially valuable landraces and wild accessions are underutilized or overlooked in breeding programs. The lack of standardized evaluation protocols also limits the comparability of results across studies and regions. The primary objectives of this study were to analyze the genetic variability among purslane genotypes based on morphological descriptors and to identify high-performing genotypes with potential for cultivar development.

MATERIALS AND METHODS

Materials

This study evaluated 20 native genotypes of *Portulaca oleracea* L., collected from diverse ecological regions across Iran (details provided in Table 1). For cultivation, a soil mixture composed of clay, sand, and organic manure in a 2:1:1 ratio was used. Thirty seeds per genotype were sown in 50 cm diameter pots. The experiment followed a completely randomized design with four replications, and all plants were grown under controlled greenhouse conditions. Irrigation was adapted to the developmental stage of the plants; initially, it was applied frequently and gently to ensure uniform germination, then gradually reduced in frequency but increased in volume as the plants established. Standardized growth conditions enabled accurate comparative assessment of morphological traits across genotypes.

The traits measured included the, number of branches per main stem (BMS); number of lateral branches (NLB); main stem length (MSL); length of longest lateral branch (LLL); length of lateral branch (LLB); third internode diameter (TID); chlorophyll content (CC); total soluble solids (TSS); leaf length (LL); leaf width (LW); length/width ratio (LWR); leaf area (LA); number of flowers per plant (NFP); number of flowers per branch (NFB); number of flowers plant/branch (FPB); dry shoot weight (DSW); fresh shoot weight (FSW); dry/fresh weight ratio (DFR); number of capsules per branch (NCB); and number of seeds per capsule (NSC). For data collection, different methods were employed to ensure accuracy and precision.

The number of branches, flowers, and capsules was counted manually. Length measurements, including the main stem and leaf lengths, were taken using a stainless-steel ruler (SHINWA, Japan), while leaf width was precisely estimated with a digital caliper (INSIZE, China). Fresh and dry shoot weights were recorded using a high-precision laboratory scale (Gram Lite EH, UK).

Statistical analysis

To ensure the reliability of the collected data, the Anderson-Darling normality test, as implemented in Minitab software version 14.0 (Minitab Inc., USA), was applied to assess the distribution of the data for each trait. This step was crucial to determine whether parametric statistical methods could be used for further analysis. To classify the genotypes and traits, Agglomerative Hierarchical Cluster Analysis was employed, utilizing standardized squared Euclidean distances derived from the dataset. The merging of these distances was accomplished using Ward's method (Sabaghnia 2012), which minimizes the variance within clusters. The resulting dendrograms provided a graphical representation of the relationships among genotypes and traits, generated using the Mult/Exploratory statement in Statistica software version 14.0 (TIBCO Inc., USA).

Table 1. Name, coordinates, and elevation were collected for purslane genotypes.

Code	Location	Coordinates	Elevation (m)
AR	Ardabil	38°15′N 48°17′E	1,351
BA	Bandar-Abbas	27°11′N 56°17′E	9
BE	Behbahan	30°35′N 50°14′E	326
BU	Bushehr	28°55′N 50°51′E	18
EQ	Eqlid	30°53′N 52°41′E	2,244
ES	Esfahan	32°39′N 51°40′E	1,574
HA	Hamadan	34°47′N 48°30′E	1,830
KA	Karaj	35°49′N 50°56′E	1,274
MA	Maragheh	37°23′N 46°14′E	1,510
MSH	Mashhad	36°19′N 59°32′E	995
NE	Nehbandan	31°32′N 60°02′E	1,187
NO	Nourabad	30°06′N 51°32′E	998
PA	Parsabad	39°38′N 47°54′E	75
QA	Qazvin	36°17′N 50°00′E	1,278
SHA	ShahreKord	32°19′N 50°51′E	2,063
SHI	Shiraz	29°36′N 52°32′E	1,500
SI	Sirjan	29°26′N 55°41′E	1,760
TE	Tehran	35°41′N 51°23′E	1,148
YA	Yasouj	30°40′N 51°34′E	1,837
ZA	Zanjan	36°41′N 48°29′E	1,810

To confirm the number of clusters and identify significant partitions illustrated in the dendrograms, Multivariate Analysis of Variance was conducted. This analysis utilized several statistical tests to determine the significance of Wilks' Lambda, Hotelling's T-squared statistic, Pillai's Trace, and Roy's Maximum Root. These tests were performed on the original dataset of all measured chickpea traits using the Multivariate statement in SPSS application version 17.0 (SPSS Inc., USA). The significance of these statistics helped define the cutoff points for clusters, ensuring that the identified groups are statistically robust.

RESULTS

Table 2 presents various descriptive indices, including the coefficient of variation (CV) for the measured traits in purslane genotypes. The CV values indicate the level of genetic variability among the traits evaluated: high CV (> 40%) was observed for several characteristics, including NFB, FPB, DFR, and NCB; moderate CV (20% < CV < 40%) was noted for traits such as NLB, TSS, NFP, and DSW; and low CV (< 20%) values were recorded for the remaining characteristics of purslane.

Table 2. Descriptive indices of measured traits of purslane genotypes.

	Mean	Minimum	Maximum	CV†
BMS‡	18.57	11.00	41.50	18.54
NLB	53.78	27.50	74.00	20.13
MSL	51.22	30.75	59.38	11.66
LLL	57.24	35.16	66.50	12.47
LLB	12.14	7.83	17.33	19.72
TID	12.97	4.54	14.74	15.49
CC	33.69	28.90	40.50	6.11
TSS	2.52	1.00	4.40	32.10
LL	60.61	20.75	73.00	17.08
LW	30.85	9.94	38.83	18.08
LWR	1.94	0.25	2.41	11.79
LA	34.32	13.78	52.90	17.25
NFP	4.78	2.50	7.00	21.19
NFB	10.78	5.00	44.80	63.18
FPB	2.49	0.87	16.29	88.26
DSW	11.28	6.13	15.94	20.53
FSW	18.28	9.78	23.93	14.69
DFR	2.89	1.18	7.82	41.93
NCB	29.00	13.50	86.00	51.00
NSC	88.09	65.00	106.00	11.73

†CV, coefficient of variation; ‡Traits are: number of branches per main stem (BMS); number of lateral branches (NLB); main stem length (MSL); length of longest lateral branch (LLL); length of lateral branch (LLB); third internode diameter (TID); chlorophyll content (CC); total soluble solids (TSS); leaf length (LL); leaf width (LW); length/width ratio (LWR); leaf area (LA); number of flowers per plant (NFP); number of flowers per branch (NFB); number of flowers plant/branch (FPB); dry shoot weight (DSW); fresh shoot weight (FSW); dry/fresh weight ratio (DFR); number of capsules per branch (NCB); and number of seeds per capsule (NSC).

These findings suggest a significant level of genetic variation among purslane genotypes, which could be leveraged to develop favorable trait combinations. The fresh shoot weight (FSW) varied from 9.78 to 23.93 g, while the dry shoot weight (DSW) varied from 6.13 to 15.94 g, demonstrating good variability among the collected purslane genotypes (Table 2). Alam et al. (2014) reported a high fresh weight of 56 g among 45 purslane accessions, indicating significant variability among all genotypes and measured morphological traits.

The CV values provide a metric for assessing the variability of the measured traits, highlighting a substantial diversity within these purslane genotypes. This considerable genetic variation in most morphological traits is advantageous for breeding programs. Understanding the patterns of genetic variation in crop resources is crucial for preserving germplasm and exploring practical variations within gene banks (Anglin et al. 2018).

The dendrogram (Fig. 1) was constructed to detect grouping patterns among purslane genotypes, with the cutoff point validated through significant results from Wilks' lambda, Hotelling's T-squared, Pillai's trace, and Roy's maximum root (Results are not shown). This cutoff point divided the purslane genotypes into four distinct clusters, with the average values of the traits in each cluster summarized in Table 3, highlighting the characteristics of the identified clusters. Cluster I contains three genotypes ('Zanjan', 'Hamadan', and 'Behbahan'), exhibiting the high yield performance, and Cluster II contains ten genotypes ('Bandar-Abbas', 'Eqlid', 'Karaj', 'Maragheh', 'Nehbandan', 'Parsabad', 'Qazvin', 'ShahreKord', 'Shiraz', and 'Tehran'), exhibiting the high yield performance (Table 3). Also, Cluster-III, comprising five genotypes ('Mashhad', 'Bushehr', 'Yasouj', 'Nourabad', and 'Esfahan'), shows high yield performance, while Cluster-IV contains two genotypes ('Ardabil' and 'Sirjan') with low yield performance. The categorization of purslane genotypes into four distinct clusters does not correspond to their geographical origins. Ebrahimi et al. (2023) reported that clustering 81 genotypes of *Carthamus tinctorius* based on morphological traits did not result in geographical separation according to their origins. Regarding adaptation within an area, breeding involves the incorporation of gene combinations that cause beneficial characteristics. The uniform genotypes resulting from the selection process are based on a foundation of genetic variation (Ribeiro et al., 2021). Phenotypic diversity among purslane genotypes may not reflect their overall genetic similarity or dissimilarity.

However, the genotypes of Cluster-I indicated high values for all traits except LLB, CC, TSS, NFP, NFB, FPB, DFR, and NCB, which were moderate or low in the recent traits (Table 3). The behavior of Cluster-II was relatively similar to that of Cluster-I, but this cluster showed high magnitudes for the number of flowers per plant (NFP).

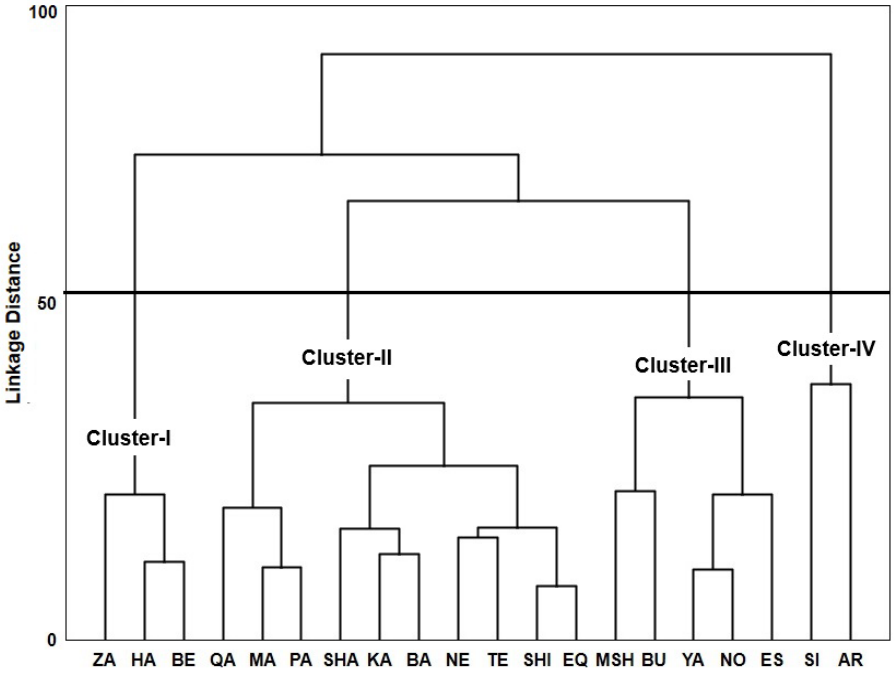

Figure 1. Dendrogram for clustering of 20 purslane genotypes (Codes of purslane genotypes are: AR, 'Ardabil'; BA, 'Bandar-Abbas'; BE, 'Behbahan'; BU, 'Bushehr'; EQ, 'Eqlid'; ES, 'Esfahan'; HA, 'Hamadan'; KA, 'Karaj'; MA, 'Maragheh'; MSH, 'Mashhad'; NE, 'Nehbandan'; NO, 'Nourabad'; PA, 'Parsabad'; QA, 'Qazvin'; SHA, 'ShahreKord'; SHI, 'Shiraz'; SI, 'Sirjan'; TE, 'Tehran'; YA, 'Yasouj'; and ZA, 'Zanjan')

Additionally, the performance of genotypes in Cluster-III was similar to that in the first cluster; however, this cluster exhibited high magnitudes for total soluble solids (TSS). Finally, Cluster-IV showed high values only for CC, TSS, LWR, NFB, FPB, DFR, and NCB; therefore, these genotypes are good candidates for improving quality characters or reproductive traits. Thus, all the detected clusters are beneficial for various purposes, and they can be utilized as parents in cross-breeding programs. Plant breeders seeking to cross adaptable genotypes with acceptable genetic diversity can benefit from understanding the structures of genetic variations in a plant, which requires a pedigree of all genotypes and the original ancestors of the related gene pool (Schreiber et al. 2024).

Table 3. Means of measured traits of purslane genotypes across four identified clusters.

	Cluster-I	Cluster-II	Cluster-III	Cluster-IV
BMS†	19.25	19.14	18.80	14.13
NLB	67.94	54.24	45.69	55.19
MSL	54.21	52.97	52.17	35.62
LLL	61.23	59.05	59.07	37.65
LLB	11.31	11.92	11.75	14.45
TID	13.61	13.64	13.39	7.58
CC	34.04	33.27	33.88	34.84
TSS	2.55	2.41	2.67	2.60
LL	63.03	63.53	64.07	33.78
LW	31.86	32.36	32.67	17.27
LWR	1.98	1.92	1.97	1.97
LA	35.81	36.36	35.20	19.66
NFP	4.75	5.04	4.42	4.47
NFB	9.25	9.36	7.42	30.14
FPB	1.97	1.90	1.89	7.92
DSW	11.81	12.04	11.00	7.37
FSW	18.47	19.59	17.55	13.31
DFR	2.67	2.88	2.80	3.48
NCB	23.67	25.83	24.25	68.04
NSC	91.08	90.63	84.77	79.50

†Traits are: number of branches per main stem (BMS); number of lateral branches (NLB); main stem length (MSL); length of longest lateral branch (LLL); length of lateral branch (LLB); third internode diameter (TID); chlorophyll content (CC); total soluble solids (TSS); leaf length (LL); leaf width (LW); length/width ratio (LWR); leaf area (LA); number of flowers per plant (NFP); number of flowers per branch (NFB); number of flowers plant/branch (FPB); dry shoot weight (DSW); fresh shoot weight (FSW); dry/fresh weight ratio (DFR); number of capsules per branch (NCB); and number of seeds per capsule (NSC).

Our results indicated remarkable variation among purslane genotypes, which can be leveraged to enhance fresh and dry yield performance, yield components, and other traits, such as chlorophyll content or total soluble solids. The clustering of similar genotypes into one group, based on morphological diversity and distances among them, is utilized in many crops (Shaygan et al. 2021, Sabaghnia et al. 2024). The cluster analysis indicated genetic variation among the genotypes, which is linked to the selection pressures experienced during breeding programs. This research offers a deeper understanding of purslane genotypes through their morphological traits and demonstrates the effectiveness of statistical tools, such as cluster analysis, in identifying the most variable traits within purslane, which may aid future genetic improvement initiatives. Each genotype appears to exhibit a similar degree of genetic variation, suggesting that the distances among genotypes may be limited (Chang et al. 2022). Nevertheless, notable genetic variation exists within the purslane genotypes, making hybridization a viable strategy for developing new breeding sources. The relationships among traits support the notion that only a few heritable traits are necessary to explain the genetic variation within the purslane germplasm, which can assist plant breeders in effective germplasm management and evaluation.

The dendrogram (Fig. 2) was generated to examine the relationships among the traits of purslane, with the cutoff point validated through four indices of multivariate analysis of variance (Results are not shown). The significant results from Wilks' lambda, Hotelling's T-squared, Pillai's trace, and Roy's maximum root confirmed the appropriate cutoff point within the dendrogram. The purslane traits were organized into four distinct groups: Group I was dedicated to NSC, LL, LLL, MSL, and NLB, so can be named as seed and length characteristics, while Group II comprised several traits, including NCB, LA, LW, and CC, so can be called as leaf and capsule properties. Group-III contains NFP, FPB, DFR, LWR, and TSS, thus can be identified as flower and ratio properties, while all remaining traits (NFB, DSW, TID, LLB, FSW, and BMS) were grouped into Group-IV (Fig. 2), and can be confirmed as yield and some yield components group. For a perfect genotype, variations in yield performance are attributed to changes in growth rates. The number of flowers per branch, the diameter of the third internode, the length of the lateral branch, and the number of branches per main stem are all associated with yield performance (Alam et al. 2014). The yield does not have a linear relationship with the other yield components (number of lateral branches, main stem length, leaf length, leaf width); therefore, it is categorized separately.

DISCUSSION

The morphological evaluation and cluster analysis of *Portulaca oleracea* genotypes in this study provide meaningful insights into the extent of genetic variation and the relationships among key traits. Recognizing patterns of variation among genotypes and traits helps clarify the genetic structure of crops, offering practical guidance for breeding programs (Sabaghnia et al. 2024). The dendrogram revealed substantial differences among genotypes, particularly in traits such as fresh and dry shoot weight, the number of flowers per plant, and chlorophyll content. High CV values for several yield-related and reproductive traits suggest a wide range of genetic diversity that can be used in breeding.

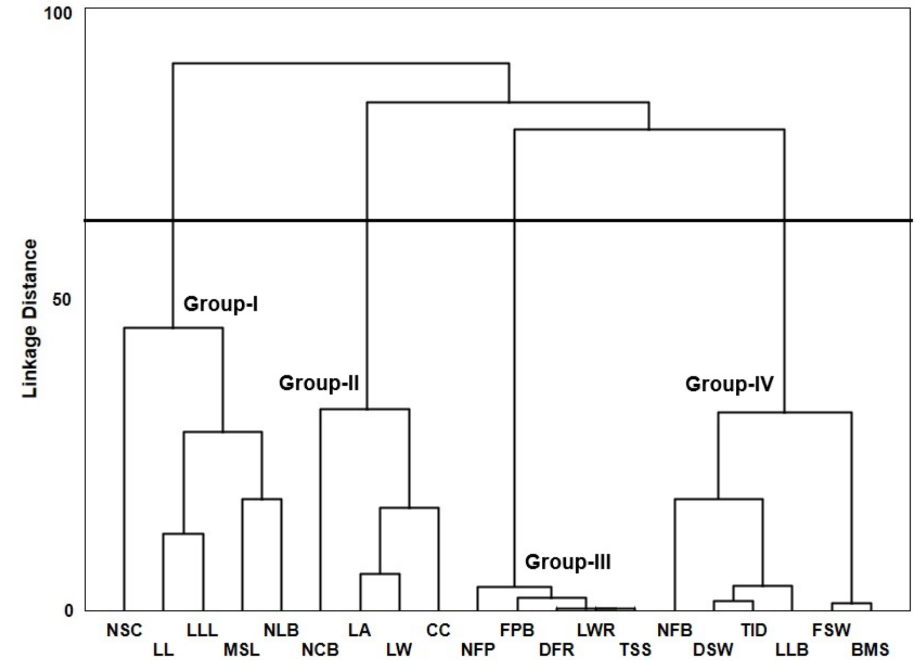

Figure 2. Dendrogram for clustering of 20 measured traits of purslane genotypes (Traits are: number of branches per main stem (BMS); number of lateral branches (NLB); main stem length (MSL); length of longest lateral branch (LLL); length of lateral branch (LLB); third internode diameter (TID); chlorophyll content (CC); total soluble solids (TSS); leaf length (LL); leaf width (LW); length/width ratio (LWR); leaf area (LA); number of flowers per plant (NFP); number of flowers per branch (NFB); number of flowers plant/branch (FPB); dry shoot weight (DSW); fresh shoot weight (FSW); dry/fresh weight ratio (DFR); number of capsules per branch (NCB); and number of seeds per capsule (NSC).)

This observation aligns with earlier research in other crops, where such variability has been crucial for enhancing specific characteristics (Fathi et al. 2021). With this diversity, breeders can select parent genotypes that complement each other in key traits, increasing the chances of producing improved offspring. For example, genotypes with high biomass can be used to enhance productivity, while those with high chlorophyll content and total soluble solids can contribute to better nutritional quality. Cluster analysis grouped the 20 genotypes into four distinct clusters, each defined by specific combinations of traits. Clusters I, II, and III mainly included high-yielding genotypes, though they differed in trait focus; Cluster II showed more flowers per plant, while Cluster III had higher TSS. In contrast, Cluster IV contained genotypes with lower yields but higher values in chlorophyll content, TSS, and reproductive traits, such as flower buds and fruits per branch. This variation in trait profiles allows breeders to make informed selections based on their goals. For instance, combining high-yielding genotypes from Cluster I with those in Cluster IV could result in hybrids that carry both strong yield and improved reproductive or quality traits. Additionally, the lack of a clear link between genotype clusters and their geographic origins suggests that genetic differences are not solely driven by environmental adaptation. This highlights the importance of selecting genotypes based on observable traits rather than geographic location, as also supported by previous studies (Lasky et al. 2023).

The trait dendrogram classified the morphological characteristics of Portulaca oleracea into four functionally meaningful groups, offering a valuable framework for trait-based selection in breeding. This grouping allows breeders to align trait selection with specific objectives. For instance, traits in Group I, such as seed count and shoot length, are particularly relevant for improving seedling vigor and early plant establishment. In contrast, enhancing biomass or marketable yield would require focusing on Group IV traits, such as FSW, DSW, and BMS. A notable outcome of the analysis was the observed non-linear relationship between certain morphological traits, such as LL, LW, and MSL, and yield. This suggests that simply increasing these traits may not translate into yield improvements, and therefore, they may not be ideal for direct selection (Fischer & Rebetzke 2018). Instead, traits with a more direct association to yield, such as NFB, TID, and FPB, may be more effective targets in breeding for yield enhancement.

Additionally, crossing genotypes from genetically distinct clusters, especially those combining high biomass producers (Cluster I) with genotypes exhibiting strong reproductive and nutritional traits (Cluster IV), may result in transgressive segregation, increasing the likelihood of developing superior offspring. This strategy maximizes genetic recombination and supports the identification of elite lines with enhanced overall performance. Moreover, creating a selection index that integrates traits from multiple functional groups could further optimize breeding outcomes. For example, an index that includes FSW, DSW, and BMS from Group IV along with NFP and TSS from Group III can help balance yield potential with nutritional quality. Such a multivariate approach offers a more holistic and effective alternative to single-trait selection, which may inadvertently lead to unfavorable trade-offs (Marulanda et al. 2021).

The absence of geographic structuring among the identified clusters suggests that the region of origin does not limit genetic diversity in purslane. This indicates that conservation strategies should prioritize the preservation of phenotypically diverse genotypes, regardless of their geographic provenance (Coates et al. 2018). Notably, although Cluster-IV genotypes exhibit lower yield performance, they may harbor rare alleles associated with stress tolerance or improved nutritional quality. As such, they represent valuable genetic resources and should be included in germplasm conservation efforts. The broad phenotypic variation observed across the collection also supports the use of recurrent selection as a breeding strategy. By establishing base populations with high variability, particularly from genetically diverse and high-performing genotypes in Clusters I and III, breeders can implement cyclical selection for traits such as DSW, NFP, and CC. This approach enables the gradual accumulation of genetic gains across successive cycles while maintaining overall genetic diversity within the breeding population.

Furthermore, the clustering of traits like TSS and CC alongside reproductive and yield-related traits suggests that simultaneous improvement of quality and yield is achievable without significant trade-offs. This is particularly promising for the development of dual-purpose cultivars that meet both productivity and nutritional goals. In addition, phenotypic variation in traits such as NSC and LWR offers opportunities for niche breeding objectives. For instance, selecting for lower LWR, associated with thicker, more succulent leaves, may enhance the appeal of cultivars for fresh consumption. At the same time, higher NSC values could be beneficial for genotypes aimed at seed production.

Ultimately, the identification of distinct trait groupings and genotype clusters provides a clear path for designing targeted breeding strategies. These strategies can focus on specific goals, whether they be yield, nutritional quality, or adaptability. The substantial genetic diversity uncovered in this study can be efficiently leveraged through informed parent selection and trait-based indices, paving the way for the development of improved purslane cultivars. Such efforts will support the crop's broader use as a nutritious, resilient, and economically viable component of sustainable food systems (Varshney et al. 2021).

CONCLUSIONS

This study revealed significant genetic diversity among purslane genotypes, particularly in yield-related and morphological traits. Cluster analysis effectively classified genotypes and traits into distinct groups, supporting targeted breeding strategies. The three desirable genotypic clusters (Cluster I, Cluster II, and Cluster III) identified are strong candidates for further evaluation to facilitate the next commercial release of purslane cultivars, as well as to serve as functional plant materials in breeding projects. They have performed exceptionally well, showcasing high levels of most target traits, making them suitable for cultivation in the cool, upland rainfed conditions of semi-arid environments.

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