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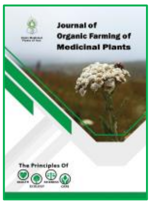

Original Article

Path analysis of key morphological traits influencing dry shoot biomass in purslane (*Portulaca oleracea*)

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ABSTRACT

The current investigation aimed to evaluate the relationships between various morphological traits and dry shoot weight (DSW) in purslane (*Portulaca oleracea*), using path analysis to quantify both direct and indirect effects. A total of 20 local landraces of purslane were collected from different geographical regions across Iran. These plants were cultivated under controlled greenhouse conditions using a completely randomized design with four replications. A comprehensive set of morphological traits was measured, including leaf length (LL), main stem length (MSL), third internode diameter (TID), leaf area (LA), number of seeds per capsule (NSC), and leaf width (LW), among others. Correlation analysis showed significant positive relationships between DSW and several morphological traits, such as MSL, TID, LL, LW, LA, and NSC. Further path analysis identified leaf length (LL) and the length of the longest lateral branch (LLL) as the main determinants of DSW, with LL exerting the strongest positive direct effect. The indirect effect of LL through LLL was also significant. Notably, traits such as leaf width (LW) and main stem length (MSL) influenced DSW indirectly through their effects on LL and LLL, respectively. Multiple regression analysis supported the importance of these traits, identifying LL and LLL as the primary contributors to variation in DSW. These findings underscore the key role of morphological traits in biomass accumulation in purslane. The strong correlations and direct effects observed between these traits and DSW suggest that leaf characteristics and stem morphology are critical factors for improving purslane yield.

1. Introduction

As both a vegetable crop and medicinal plant, purslane (*Portulaca oleracea* L.) is a hardy, fast-growing species commonly found in fields and among vegetable crops. It thrives under direct sunlight, uses the C4 photosynthetic pathway to fix carbon, and can switch to the CAM system under extreme stress conditions (Ferrari et al. 2020). This plant is highly adaptable to different soil types, successfully establishing itself across a wide range of environments. Purslane is particularly known for its abundant seed production, even under suboptimal growing conditions. It produces small yellow flowers, either singly or in clusters, at each node and at the tips of its stems. Ornamental varieties may exhibit flowers in a variety of colors (Zhang et al. 2024). Although the flowers of common purslane are short-lived, they produce capsules filled with small, black seeds that can remain viable in a dormant state for extended periods. A succulent annual herb, purslane is native to South Asia and is widely distributed across diverse ecosystems. In many cultures, it is consumed as a leafy vegetable or salad ingredient, with a taste similar to spinach. Purslane can be eaten raw in salads, cooked on its own, or mixed with other vegetables (Petropoulos et al. 2016). It is also added to soups and stews, where its slightly mucilaginous texture helps thicken the broth. In some areas, its thick stems are pickled. For centuries, purslane has been an integral part of traditional diets in many regions. Beyond its culinary appeal, purslane is valued for its high nutritional content and strong antioxidant properties. Rich in both macro- and micronutrients, it provides significant amounts of potassium, magnesium, and vitamins. Notably, purslane is one of the few plant-based sources of omega-3 fatty acids, which are typically scarce in vegetables. This trait has led to increasing interest in cultivating purslane as a nutritious and sustainable crop (Carrascosa et al. 2023). Its ability to adapt to a wide range of environmental conditions further enhances its appeal for agricultural production.

Correlation and path analysis of yield components are essential tools for identifying promising genotypes in plant breeding. Trait correlations are particularly significant because they reveal the strength and direction of relationships among different characteristics. Understanding these correlations, especially between yield and its contributing components, provides breeders with valuable insights into the cause-and-effect mechanisms underlying yield performance (Sabaghnia and Janmohammadi, 2024). This understanding enables the selection of the most advantageous combinations of traits that contribute to improved yield. While simple linear correlation coefficients offer useful information about the relationships between traits, they do not account for the underlying causal relationships. This is where path analysis becomes critical. Path analysis allows for the decomposition of correlation coefficients to distinguish between the direct and indirect effects of various traits on yield, offering a more comprehensive understanding of how specific characteristics influence performance (Sabaghnia et al. 2025). Given its crucial role in uncovering the structure of trait interactions related to yield improvement, path analysis serves as a powerful method for identifying the traits that exert the most significant direct and indirect influences on yield. Consequently, many plant breeders rely on this approach to prioritize and select the most impactful traits for optimizing crop productivity.

Yield, as a quantitative trait, is influenced by a wide range of genetic and environmental factors. Consequently, selection for yield is a fundamental objective in breeding programs, with plant traits playing a vital role in determining performance. However, direct selection based solely on yield is often inefficient, whereas indirect selection through traits with high heritability tends to produce more reliable and practical outcomes (Fischer and Rebetzke, 2018). The complexity of yield performance is largely due to its association with multiple other traits. While correlation coefficients provide valuable insights into the linear relationships among traits, they do not fully explain the nature of these relationships. In contrast, path analysis offers a more detailed understanding by partitioning correlations into direct and indirect effects, thereby clarifying the individual contribution of each trait to yield. By identifying both the direct and indirect influences of morphological characteristics on yield, path analysis supports breeders in prioritizing the most impactful traits for selection. The objective of the present study was to explore the relationships between yield performance and morphological traits in purslane genotypes using correlation and path analysis. This approach aimed to uncover the pathways through which various traits influence yield, thereby providing a basis for effective indirect selection in purslane breeding programs.

2. Materials and Methods

2.1 Experiment

To determine the relationships between dry shoot weight (DSW) and its contributing traits, path analysis was conducted using 20 local purslane landraces collected from various regions of Iran (Table 1).

Table 1. The geographical coordinates of purslane genotypes.

Location	Coordinates	Location	Coordinates
Ardabil	38°15′N 48°17′E	Nehbandan	31°32′N 60°02′E
Bandar-Abbas	27°11′N 56°17′E	Nourabad	30°06′N 51°32′E
Behbahan	30°35′N 50°14′E	Parsabad	39°38′N 47°54′E
Bushehr	28°55′N 50°51′E	Qazvin	36°17′N 50°00′E
Eqlid	30°53′N 52°41′E	ShahreKord	32°19′N 50°51′E
Esfahan	32°39′N 51°40′E	Shiraz	29°36′N 52°32′E
Hamadan	34°47′N 48°30′E	Sirjan	29°26′N 55°41′E
Karaj	35°49′N 50°56′E	Tehran	35°41′N 51°23′E
Maragheh	37°23′N 46°14′E	Yasouj	30°40′N 51°34′E
Mashhad	36°19′N 59°32′E	Zanjan	36°41′N 48°29′E

The plants were cultivated in pots measuring 50 cm in diameter, filled with a soil mixture composed of clay, sand, and organic manure in a 2:1:1 ratio. The experiment was arranged in a completely randomized design with four replications and was carried out under controlled greenhouse conditions. Each pot was sown with 30 seeds, which were then covered with a 3–4 cm layer of the prepared soil mix. During the first three weeks, irrigation was applied gently using sprinklers, five times daily in small amounts to maintain optimal moisture levels. As the plants grew and their root systems became more established, the frequency of irrigation was reduced to once daily, while the volume of water was increased to support further development. A wide range of morphological and physiological traits were evaluated, including the number of branches per main stem (BMS), number of lateral branches (NLB), leaf width (LW), main stem length (MSL), length of the longest lateral branch (LLL), leaf length (LL), lateral branch length (LLB), diameter of the third internode (TID), chlorophyll content (CC), total soluble solids (TSS), leaf length-to-width ratio (LWR), number of flowers per plant (NFP), leaf area (LA), number of flowers per branch (NFB), flowers per plant-to-branch ratio (FPB), dry shoot weight (DSW), number of capsules per branch (NCB), and number of seeds per capsule (NSC). The number of branches, flowers, and capsules was recorded manually, while measurements of main stem and leaf lengths were taken using a ruler. Leaf width was measured with a digital caliper, and dry shoot weight was determined using a highly accurate laboratory scales.

2.2 Path analysis

The normality of the residuals data for various traits was evaluated using the Ryan-Joiner statistic with Minitab 14.0 (Minitab Inc., PA, USA). Although, this normality test is only good for small sample sizes, but it is poor for large sample sizes except normal distribution, so it is suitable for current dataset. However, the results of the Ryan-Joiner statistic (Table 2), indicated normal distribution shape for all measured traits.

Table 2. The statistic of Ryan-Joiner test and their p-values for measured traits of purslane genotypes.

Traits†	RJ‡	p-value	Traits	RJ	p-value
BMS	0.954	0.06	LWR	0.985	0.10
NLB	0.981	0.10	LA	0.969	0.07
MSL	0.968	0.07	NFP	0.981	0.09
LLL	0.974	0.09	NFB	0.987	0.10
LLB	0.988	0.10	FPB	0.984	0.10
TID	0.981	0.10	DSW	0.976	0.09
CC	0.987	0.10	DFR	0.988	0.10
TSS	0.983	0.10	NCB	0.984	0.10
LL	0.971	0.07	NSC	0.981	0.09
LW	0.981	0.10			

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

‡ Ryan-Joiner test

Homoscedasticity of variances was tested using Levene's test. Pairwise simple correlations between traits were calculated using SPSS version 23.0 (IBM Inc., IL, USA). To gain a more comprehensive understanding of the relationships among traits and to identify those with the greatest influence on dry shoot weight (DSW), path coefficient analysis was conducted. Initially, a linear stepwise regression analysis was performed, with DSW as the dependent variable and the remaining traits as independent variables. This method allowed for the identification of the most significant variables contributing to the variation in DSW, providing a basis for the subsequent path analysis. Subsequently, path analysis was applied to calculate the directly and indirectly impacts of the selected traits on the dependent variable in the initial step, and on intermediary traits like branching pattern in the following steps. Stepwise regression was used for exploratory variable selection, despite risks of overfitting, due to its utility in identifying dominant predictors. Bootstrapping assessed the stability of path coefficients, with 1000 resamples generating bias-adjusted estimates and 95% confidence intervals. This enabled the comparison of bootstrapping results with those obtained through conventional methods. Additionally, to address potential multicollinearity, tolerance as well as variance inflation factor (VIF) was computed. The used thresholds for these collinearity diagnostics were assumed as Tolerance > 0.2 and variance inflation factor (VIF) < 5, for confirmation of minimal multicollinearity. All statistical analyses were conducted using SPSS, and path diagrams were visualized using AMOS 14.0 (IBM Inc., IL, USA).

3. Results

3.1 Correlations

The correlations in Table 3 revealed significant (p-value<0.05) positive associations between dry shoot weight (DSW) and several morphological traits, including main stem length (MSL), third internode diameter (TID), leaf length (LL), leaf width (LW), leaf area (LA), and number of seeds per capsule (NSC). Conversely, DSW showed a negative correlation with chlorophyll content (CC), number of flowers per branch (NFB), number of flowers per plant/branch (FPB), and number of capsules per branch (NCB). Additionally, LA exhibited a strong positive correlation (p-value<0.05) with several traits, including number of branches per main stem (BMS), main stem length (MSL), length of the longest lateral branch (LLL), TID, LL, LW, and NSC. In contrast, LA was negatively correlated with NFB, FPB, and NCB. These observations align with Alam et al. (2014), who also found a positive relationship between leaf area, plant height, and dry shoot weight. Interestingly, no significant (p-value<0.05) positive associations were detected between morphological traits and CC or total soluble solids (TSS). These findings suggest that morphological attributes contribute more directly to biomass accumulation than physiological traits such as chlorophyll content. Given the strong correlations observed, these morphological traits may serve as reliable indicators in breeding programs focused on enhancing DSW in purslane. To further elucidate the complex interrelationships among these traits and to quantify their direct and indirect effects on DSW, conducting a path analysis is essential. This statistical approach will provide a clearer understanding of how each trait impacts biomass accumulation, enabling more strategic selection in purslane breeding for improved yield and stress resilience.

Table 3. Association coefficients between traits of purslane genotypes.

	BMS†	*NLB*	*MSL*	*LLL*	*LLB*	*TID*	*CC*	*TSS*	*LL*	*LW*	*LWR*	*LA*	*NFP*	*NFB*	*FPB*	*DSW*	*DFR*	*NCB*
NLB	*0.05‡*																	
MSL	*0.76*	*0.09*																
LLL	*0.72*	*0.04*	*0.98*															
LLB	*-0.49*	*-0.06*	*-0.51*	*-0.46*														
TID	*0.73*	*0.08*	*0.96*	*0.94*	*-0.44*													
CC	*-0.62*	*0.01*	*-0.32*	*-0.23*	*0.26*	*-0.39*												
TSS	*0.07*	*0.01*	*-0.01*	*-0.02*	*-0.07*	*0.01*	*0.22*											
LL	*0.70*	*0.00*	*0.94*	*0.91*	*-0.41*	*0.97*	*-0.41*	*0.07*										
LW	*0.68*	*0.00*	*0.92*	*0.90*	*-0.45*	*0.97*	*-0.38*	*0.09*	*0.99*									
LWR	*-0.04*	*0.02*	*-0.07*	*-0.03*	*-0.09*	*-0.12*	*0.20*	*-0.01*	*-0.12*	*-0.11*								
LA	*0.76*	*0.05*	*0.97*	*0.94*	*-0.40*	*0.96*	*-0.35*	*0.01*	*0.95*	*0.94*	*-0.09*							
NFP	*0.50*	*0.18*	*0.17*	*0.15*	*-0.02*	*0.16*	*-0.31*	*0.02*	*0.08*	*0.06*	*0.17*	*0.24*						
NFB	*-0.67*	*0.06*	*-0.95*	*-0.94*	*0.46*	*-0.96*	*0.29*	*-0.04*	*-0.97*	*-0.97*	*0.05*	*-0.93*	*-0.02*					
FPB	*-0.72*	*-0.04*	*-0.96*	*-0.94*	*0.44*	*-0.99*	*0.35*	*-0.05*	*-0.98*	*-0.98*	*0.06*	*-0.97*	*-0.17*	*0.98*				
DSW	*0.42*	*0.11*	*0.52*	*0.43*	*-0.18*	*0.64*	*-0.61*	*-0.01*	*0.66*	*0.66*	*-0.15*	*0.61*	*0.01*	*-0.57*	*-0.61*			
DFR	*-0.27*	*-0.05*	*-0.35*	*-0.44*	*0.03*	*-0.34*	*-0.07*	*-0.14*	*-0.37*	*-0.37*	*0.27*	*-0.33*	*-0.24*	*0.38*	*0.39*	*0.12*		
NCB	*-0.69*	*-0.09*	*-0.95*	*-0.93*	*0.43*	*-0.97*	*0.32*	*-0.06*	*-0.97*	*-0.97*	*0.11*	*-0.95*	*-0.07*	*0.97*	*0.97*	*-0.58*	*0.38*	
NSC	*0.63*	*0.38*	*0.64*	*0.60*	*-0.17*	*0.61*	*-0.31*	*0.02*	*0.59*	*0.59*	*0.28*	*0.67*	*0.38*	*-0.55*	*-0.62*	*0.52*	*-0.08*	*-0.59*

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

‡Critical amounts P>0.05 and P>0.01 (with 18 degrees of freedom) are 0.44 and 0.56, respectively.

3.2 Path coefficients

To evaluate the significance of various purslane traits in relation to dry shoot weight, a multiple regression model was utilized while accounting for multicollinearity indices (Table 4). All traits were initially treated as primary-order variables, with DSW designated as the dependent variable. A stepwise regression model was subsequently applied to extract the direct effects of these traits. Notably, this approach resulted in a substantial reduction in multicollinearity indices (Table 5). The corrected coefficient of determination (R^2 adj) identified LL and LLL as the primary contributors to variation in DSW (Table 5). Among the evaluated traits, LL exhibited the strongest positive direct effect on DSW (1.59), exceeding the impact of the LLL. However, the indirect effect of LL through LLL was negative (−0.93), whereas LLL influenced DSW indirectly through LL with a substantial positive effect (1.45). To visually represent these relationships, a path analysis diagram was developed (Figure 1). Similar patterns, where leaf traits significantly ($\alpha > 0.05$) affect biomass accumulation, have been reported in previous studies on mutant lines of purslane (Feizi-Kelasi and Fotokian, 2020). When analyzing primary-order traits and considering LL and LLL as key target variables, it was observed that LW had a positive influence on LL, while MSL positively affected LLL. (Table 5). These two traits accounted for 98% and 94% of the variability in LL and LLL, respectively. The critical roles of LW and MSL in promoting purslane growth and biomass accumulation have been previously highlighted by Karkanis and Petropoulos (2017) and Mohebodini et al. (2024). To identify tertiary-order traits, the secondary-order variables (LW and MSL) were examined as target traits in separate analyses. The results showed that FPB had a strong negative influence on LW, explaining 95% of its variation with a substantial direct effect (-0.98) (Table 5). In contrast, LA exhibited a significant positive effect (0.91, p-value<0.01) on MSL, accounting for approximately 93% of its variation. Additionally, TID negatively influenced FPB (-0.55), with an explanatory power of 97%, while it positively affected LA (0.96), explaining 91% of its variation. These findings are consistent with the results of Alam et al. (2014), who reported the significant role of leaf area in enhancing dry shoot weight in purslane. This comprehensive analysis effectively classified traits into primary, secondary, and tertiary orders, thereby revealing their hierarchical influence on DSW. Based on the results, LL, LW, FPB, and TID can be considered key morphological indicators for improving yield performance in purslane breeding programs.

3.3 Bootstrapping

Plant breeders frequently utilize both point estimates and confidence intervals to enhance the reliability and robustness of their statistical analyses. In this context, resampling techniques like bootstrapping play a critical role by providing reliable estimates of standard errors and bias for direct effects. Using a thousand resampling iterations (Table 6), the exceptionally low standard error and bias values reinforce the statistical strength and reliability of the path analysis results. These findings suggest that path analysis is an effective tool for mitigating potential multicollinearity issues, especially among highly correlated traits. One of the major advantages of integrating a stepwise multiple regression model within path analysis lies in its capacity to minimize the impact of multicollinearity. A key assumption in multiple regression is the independence of predictor variables at each step of the analysis. However, in practical applications, many traits are strongly interrelated, leading to concerns about multicollinearity. To overcome this challenge, traits were systematically classified into primary, secondary, and tertiary orders, which helped reduce redundancy and enhance the accuracy of the analytical framework. This hierarchical trait classification strategy has been successfully applied in various plant breeding studies, including those by Zavoshti et al. (2023) on Onobrychis viciifolia, Sabaghnia and Janmohammadi (2024) on Cicer arietinum, and Sabaghnia et al. (2025) on Nigella sativa. By structuring traits into different levels of influence, this approach provides a more comprehensive understanding of trait interrelationships, ultimately enhancing the reliability and interpretability of path analysis results.

3.4 Comparison of models

In this study, path analysis, integrating multiple regression and correlation analysis, was performed using the mean values of replicates. However, an important methodological consideration arises regarding the most appropriate dataset for correlation and regression analysis. While using mean values instead of raw data can help reduce experimental error, the decision between the two approaches depends on the specific analytical objective. When a variable functions as an independent variable in regression analysis or as one of the paired variables in correlation analysis, where genotype effects can be accurately captured, it is generally preferable to use the mean value for each genotype (Kumar et al. 2022). Conversely, when the independent variables in regression analysis or the paired variables in correlation analysis are traits influenced by different genotypes, using replicate-level data may be more appropriate for path analysis. This approach allows for a more comprehensive evaluation of trait interrelationships while accounting for genetic

Table 4. Multiple regression coefficients and direct effects (β) of path analysis for dry shoot weight (DSW) and independent traits.

Traits	b	SD	B	t	Sig.	Tol.	VIF
BMS	-0.11	0.53	-0.14	-0.20	0.87	0.06	15.82
NLB	0.11	0.10	0.51	1.09	0.47	0.13	7.45
MSL	-2.29	1.30	-7.72	-1.76	0.33	0.00	643.17
LLL	0.90	0.70	3.79	1.28	0.42	0.20	7.67
LLB	-0.58	0.56	-0.60	-1.05	0.49	0.09	11.05
TID	1.44	1.86	1.72	0.77	0.58	0.01	165.24
CC	-0.55	0.67	-0.42	-0.81	0.57	0.12	8.68
TSS	0.30	0.57	0.13	0.53	0.69	0.47	2.15
LL	0.44	0.65	2.69	0.68	0.62	0.11	9.06
LW	-0.54	1.14	-1.66	-0.47	0.72	0.00	420.44
LWR	-6.24	8.77	-0.39	-0.71	0.61	0.10	9.89
LA	0.92	0.53	3.01	1.74	0.33	0.01	100.08
NFP	-0.48	2.38	-0.21	-0.20	0.87	0.03	37.37
NFB	-0.41	1.41	-1.76	-0.29	0.82	0.00	1201.50
FPB	1.06	5.84	1.27	0.18	0.89	0.00	1635.70
DFR	1.62	1.97	0.45	0.82	0.56	0.10	9.96
NCB	0.24	0.16	2.12	1.53	0.37	0.02	64.55
NSC	0.15	0.18	0.48	0.79	0.57	0.08	12.36

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

Table 5. Coefficient of determination (R^2), direct effects (β) and multicollinearity indices of path analysis.

Y	R^2	X	β	Tol.	VIF
DSW	0.57	LL	1.59	0.17	5.77
		LLL	-1.02	0.17	5.77
LL	0.98	LW	0.86	1.00	1.00
LLL	0.94	MSL	0.95	1.00	1.00
LW	0.95	FPB	-0.98	1.00	1.00
MSL	0.93	LA	0.91	1.00	1.00
FPB	0.97	TID	-0.55	1.00	1.00
LA	0.91	TID	0.96	1.00	1.00

X, dependent item; Y, independent item; Tol., tolerance; variance inflection factor (VIF). Traits are: MSL, main stem length; LLL, length of longest lateral branch; TID, third internode diameter; LL, leaf length; LW, leaf width; LA, leaf area; FPB, number of flowers plant / branch; dry shoot weight (DSW).

Table 6. Bootstrapping indices for path analysis for dry shoot weight (DSW) and independent traits

Y	X	Mean	Bias	SD†	Sig.	Lower‡	Upper
DSW	LL	1.59	-0.25	0.74	0.02	-0.79	2.35
	LLL	-1.02	-0.10	0.54	0.01	-2.51	-0.26
LL	LW	0.85	-0.04	0.12	0.00	0.57	1.03
LLL	MSL	0.96	-0.03	0.13	0.00	0.55	1.12
LW	FPB	-0.98	0.13	0.31	0.01	-1.02	0.10
MSL	LA	0.92	-0.04	0.20	0.00	0.35	1.19
FPB	TID	-0.56	0.11	0.27	0.00	-1.02	-0.06
LA	TID	0.96	-0.10	0.34	0.01	-0.30	1.06

†SD, standard deviation; ‡ interval estimates of means for direct effects. Traits are: MSL, main stem length; LLL, length of longest lateral branch; TID, third internode diameter; LL, leaf length; LW, leaf width; LA, leaf area; FPB, number of flowers plant / branch; dry shoot weight (DSW).

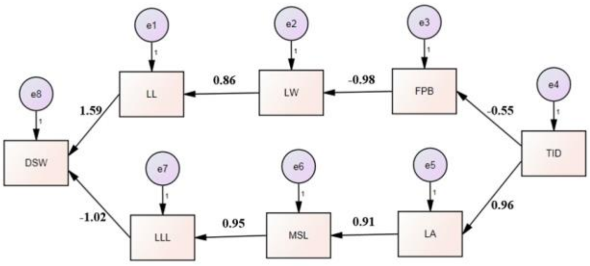

Fig. 1. Path diagram of measured traits of twenty purslane genotypes which indicating the possible paths.
Traits are: MSL, main stem length; LLL, length of longest lateral branch; TID, third internode diameter; LL, leaf length; LW, leaf width; LA, leaf area; FPB, number of flowers plant / branch; dry shoot weight (DSW).

variability among genotypes. The analysis of genetic variation in vegetable crops based on morphological characteristics is influenced by both genetic and environmental factors. The observed diversity in the morphological traits of purslane suggests that this variation may, in part, be attributed to geographical conditions. Morphological variation among genotypes is crucial for selecting superior parental material for future genetic improvement programs, particularly given purslane's high nutritional value, including its rich content of essential minerals (Srivastava et al. 2023). The findings of this study revealed significant differences among purslane genotypes in terms of agronomic traits and yield potential. Similarly, Ren et al. (2011) reported considerable genetic diversity among purslane accessions collected from different geographical regions. The widespread distribution of purslane across the Mediterranean region, combined with its ability to adapt to diverse microclimatic conditions, has contributed to the development of a rich genetic reservoir. This genetic diversity holds substantial potential for future breeding initiatives. Evaluating purslane genotypes is valuable not only for consumers, due to its nutritional benefits, but also for producers, as ease of cultivation is essential. Moreover, commercialization is necessary to enhance its market potential. Therefore, plant breeders must take these factors into account when designing comprehensive breeding programs for purslane improvement.

4. Discussion

Morphological traits play a critical role in determining plant biomass and productivity in purslane, such as plant height, number of branches, leaf area, and fresh shoot weight, influence dry shoot weight. Taller plants generally accumulate more biomass due to enhanced photosynthetic capacity and resource allocation. Studies have shown that plant height significantly (p-value<0.05) correlates with dry shoot weight in leafy vegetables, as it affects light interception efficiency and biomass distribution (Alam et al. 2016). A high number of branches increases a plant's capacity to produce more leaves, thereby enhancing photosynthetic activity and ultimately contributing to greater biomass production. Under drought-stressed conditions, genotypes with a higher number of branches tend to maintain better productivity (Jin et al. 2015). In the present study, DSW showed negative correlations with CC, NFB, FPB, and NCB. This finding is in agreement with the results of Naeem et al. (2022), who reported a positive relationship between leaf characteristics, plant height, and biomass accumulation. LA is a critical trait influencing light interception, transpiration, and carbon fixation. Plants with larger leaf areas generally demonstrate higher photosynthetic efficiency, which contributes to increased shoot biomass. Previous studies on purslane and other leafy vegetables have confirmed that larger leaves are associated with greater dry matter accumulation (Carrascosa et al. 2023). Moreover, fresh shoot weight is considered a strong predictor of dry shoot weight, as it directly reflects the vegetative growth potential of the plant. A positive correlation between fresh and dry biomass has been documented in purslane, underscoring the importance of shoot growth in determining overall productivity. (Inanloofar et al. 2013). While primarily a below-ground trait, root dry weight impacts shoot biomass by improving water and nutrient uptake. A well-developed root system plays a crucial role in supporting above-ground growth, especially under drought stress conditions, and is therefore a key factor in dry matter accumulation (Hosseinzadeh et al. 2020). These morphological traits collectively influence overall plant vigor and adaptability under diverse environmental conditions. Understanding their contributions to dry shoot weight through statistical methods such as path analysis offers valuable insights for developing effective breeding strategies and agronomic practices aimed at enhancing purslane productivity.

Path analysis, a statistical method integrating multiple regression and correlation analysis, plays a critical role in understanding the relationships between morphological traits in purslane. Given its potential as a nutrient-rich and drought-tolerant crop, identifying the key traits that influence dry shoot weight is crucial for enhancing yield and improving stress resilience (Mohamed et al. 2024). This study employed path analysis to disentangle the direct and indirect effects of morphological traits on DSW, utilizing either mean values or replicate-level data to ensure statistical robustness. Purslane exhibits considerable morphological diversity, making it an ideal candidate for trait-based selection in breeding programs. The findings revealed that LL, LLL, LW, FPB, and TID significantly (p-value<0.05) contribute to variations in DSW. Among these, LL exhibited the strongest positive direct effect, whereas LLL influenced DSW indirectly through its effect on LL. The identification of these key traits highlights the effectiveness of path analysis in quantifying the individual contributions of morphological characteristics to biomass accumulation. A major advantage of path analysis is its ability to partition the direct and indirect impacts of variables, thereby addressing the multicollinearity problem often encountered in multiple regression models (Janmohammadi et al. 2014). By categorizing traits into primary, secondary, and tertiary orders, the study minimized confounding effects, enabling a clearer understanding of trait interactions.

The identification of key morphological traits influencing DSW has direct implications for purslane breeding programs. Since leaf-related traits, such as LL, LW, and LA, showed strong associations with biomass accumulation, selecting for these features can contribute to improved yield performance. Moreover, the findings from path analysis highlight the contrasting roles of TID and FPB in determining DSW. While TID was positively associated with biomass production, FPB negatively impacted LW and overall biomass allocation. These observations are consistent with earlier studies emphasizing the importance of leaf area in promoting biomass accumulation in purslane (Alam et al. 2014). Given the nutritional value of purslane as a food crop, optimizing morphological traits related to DSW can also enhance nutrient yield (Petropoulos et al. 2019). One of the major challenges in path analysis is multicollinearity, which can mask the true relationships among traits. In this study, the application of a stepwise multiple regression model helped to address this issue by ensuring the inclusion of only non-redundant, independent traits in the analysis. Additionally, the classification of traits into primary, secondary, and tertiary orders further reduced redundancy and improved interpretability. Future research on genetic improvement in purslane could benefit from expanding this analytical framework by integrating molecular markers alongside morphological evaluations, thereby enhancing the precision and effectiveness of trait selection.

While this study successfully identified key morphological determinants of DSW in purslane, further research is necessary to investigate the physiological and biochemical interactions underlying these relationships. Exploring the genetic diversity of purslane accessions using molecular markers may also help validate trait-marker associations, thereby improving selection efficiency (Jia et al. 2017). This study underscores the utility of path analysis in pinpointing critical morphological traits that influence DSW. By employing both mean values and replicate-level data, the analysis ensured robust statistical inferences and minimized the effects of multicollinearity, offering valuable insights for purslane breeding programs. The results indicate that leaf-related traits, namely LL, LW, and LA, are strong predictors of biomass accumulation. Additionally, traits such as TID and FPB play important, yet opposing, roles in influencing DSW. Looking ahead, the integration of physiological and molecular approaches with morphological trait analysis will enhance the effectiveness of breeding efforts, ultimately contributing to the genetic improvement of purslane for increased yield and stress tolerance. The methodological framework established in this study provides a solid foundation for future research focused on optimizing both the productivity and nutritional quality of purslane.

5. Conclusion

The analysis revealed significant correlations between dry shoot weight and a range of morphological traits, emphasizing the critical roles of leaf characteristics, main stem length, and internode diameter in biomass accumulation. Stepwise regression and path analysis further identified leaf length and the length of the longest lateral branch as key contributors to dry shoot weight, with both traits exerting direct and indirect effects on plant growth and productivity. These findings emphasize the critical role of morphological traits in improving purslane yield. Incorporating these traits into breeding programs could enhance dry shoot weight and improve stress resilience, ultimately contributing to more efficient and sustainable purslane cultivation.

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