The Pharma Innovation

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Exploring genetic variability and path analysis of common purslane (*Portulaca oleraceae* L.) for growth and yield contributing traits

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Abstract
Purslane (*Portulaca oleracea* L.), a nutrient-rich weed crop, holds promise for global agriculture. This study delves into its genetic characteristics using metrics like Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), heritability (h2), and Genetic Advance as a Percentage of Mean (GAM). Conducted with 15 accessions from Tamil Nadu, India, the research assessed 13 traits encompassing both biometrics and yield. The results of the Analysis of Variance (ANOVA) underscore significant diversity among accessions, crucial for subsequent crop improvement strategies. The consistently higher PCV than GCV values across traits suggest the influence of environmental factors. Heritability values ranging from 28.81 to 99.57 indicate varying degrees of genetic contribution to trait variability. Traits like plant height, number of branches, and yield exhibit high heritability and GAM, indicating the prevalence of additive gene effects. Genotypic correlations were generally stronger than phenotypic correlations, indicating genetic dominance in trait associations. Path analysis elucidated that plant height, fresh weight, and number of leaves play pivotal roles in directly influencing yield. Overall, this study enriches our understanding of trait variability, heritability, and selection prospects for enhancing purslane's agronomic potential.

Keywords: Common Purslane, genetic diversity, morphology of Purslane

Introduction
Purslane (*Portulaca oleracea* L.), a member of the Portulacaceae family, is recognized as a valuable weed crop in numerous global regions due to its nutritional richness. This herbaceous plant is consumed widely across the world and offers a substantial array of beneficial components, including minerals, fatty acids, proteins, phenols, flavonoids, vitamins, and other nutrients. These elements collectively or individually exhibit an array of health-promoting properties such as neuroprotection, antimicrobial action, antidiabetic effects, antioxidant capabilities, anti-inflammatory attributes, antiulcerogenic potential, anticancer properties, and inhibition of cholinesterase activity (Montoya-García *et al*., 2023) [6]. Notably, purslane stands out as a terrestrial source rich in omega-3 and omega-6 fatty acids, which play a crucial role in human health. Moreover, this ethnomedicinal herb holds significance within indigenous traditional healthcare systems. While previous research predominantly delved into purslane's ethnobotanical, phytochemical, pharmacological aspects, and stress tolerance mechanisms, factors influencing these traits have received less attention (Kumar *et al*., 2022; Kumar *et al*., 2021) [4, 5].

The importance of characterizing and differentiating various germplasms is a foundational step in advancing crop development endeavors (Egea-Gilabert *et al*., 2014) [2]. Enhancing plant traits through specialized techniques is central to crop development, aiming to achieve superior characteristics (Singh *et al*., 2020) [9]. Kumar *et al*. (2021) [5] underscored purslane's global significance as a traditional food crop that could contribute to long-term sustainable food security. However, the genetic resources of purslane remain relatively limited. Future initiatives should focus on expanding germplasm collections. To effectively enhance purslane, efforts should involve thorough characterization, phenotyping, and genotyping using diverse omics approaches. Amid the wide variability of purslane's component traits in Tamil Nadu, comprehensive and systematic research addressing this crop is lacking. Elevating the phytochemical content and yield potential of purslane necessitates a successful breeding program. However, such a program should be informed by research on the extent of variability within phytochemical and yield-related attributes.

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This study presents an investigation centered around 15 purslane accessions collected in Tamil Nadu.

Materials and Methods
Plant Material and Experimental Design
In the summer season of 2022, a study was conducted in the Namakkal district of Tamil Nadu. The study utilized 15 distinct accessions collected from various regions within Tamil Nadu. These accessions served as the basis for the experiment, which followed a completely randomized design and was carried out in a pot culture setup. To raise the crop, standard agronomic practices were implemented. For data collection, specific traits were observed in randomly selected, tagged plants from each accession. These traits included parameters like plant height, number of branches, number of internodes, stem girth, number of leaves, leaf area, leaf length, leaf breadth, leaf thickness, root length, fresh weight of the plant, and yield per plant.

Statistical Analysis
Statistical analysis was conducted using the mean data from the various accessions. For all the observed traits, analysis of variance (ANOVA) was performed, utilizing the means of the replications, following the approach recommended by Goulden (1939) [3]. Standard statistical methods were employed to calculate different genetic parameters. These parameters encompassed measures such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (h2), genetic advance as a percentage of the mean (GAM), as well as phenotypic and genotypic correlations. Furthermore, the study involved conducting a path analysis using genotypic correlations to explore relationships between traits. The statistical software R Studio was employed for these analyses.

Results and Discussion
The ANOVA results presented in Table 1 shed light on the 13 biometric and yield traits of the purslane accessions. These results unveil noteworthy variations among the accessions across all 13 traits, emphasizing the inherent diversity within the gene pool. This diversity holds immense importance for the ongoing pursuit of crop improvement, as it opens up avenues for the selection and enhancement of a wide array of traits through strategic breeding approaches. The study's outcomes offer valuable insights into the genetic variability, heritability, and potential avenues for trait selection within purslane accessions sourced from various regions in Tamil Nadu.

Genetic Variability, Heritability, and Genetic Advance
The study aimed to gain insights into the genetic characteristics of the gene pool using key metrics such as Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), heritability (h2), and Genetic Advance as a Percentage of Mean (GAM). These metrics hold significant value in formulating effective breeding strategies for crop enhancement. Across the traits examined, PCV values consistently surpassed corresponding GCV values, indicating the notable influence of environmental factors on trait expression. This observation underscores the existence of substantial genetic variability within the germplasm, with additive genes playing a pivotal role in shaping trait manifestation. Notably, an exception was observed in the case

of dry weight, where GCV exceeded PCV, signifying a more pronounced genetic influence on this trait. Most traits exhibited high GCV and PCV values, particularly attributes like plant height, number of branches, number of internodes, stem girth, number of leaves, leaf area, leaf breadth, leaf thickness, root length, and yield. Fresh weight of the plant showed moderate GCV and PCV, while leaf length displayed low GCV and high PCV. In contrast, dry weight displayed higher GCV and lower PCV, indicating a stronger genotype-based impact on phenotypic expression, with comparatively less influence from the environment. This underscores the importance of considering environmental factors in breeding programs, especially given that the observed variations in most traits can be attributed to environmental conditions.

Heritability values spanning from 28.81 to 99.57 were evident across all traits. Traits displaying substantial heritability and a noteworthy Genetic Advance as a Percentage of Mean (GAM) encompassed plant height, number of branches, number of internodes, stem girth, number of leaves, leaf breadth, leaf thickness, root length, fresh weight, and yield per plant. These high values suggest that these traits are strongly influenced by additive gene effects, rendering them well-suited for selection and subsequent improvement strategies. Traits like leaf area and leaf length exhibited moderate heritability alongside high GAM. Conversely, dry weight exhibited both low heritability and a limited GAM. The estimation of heritability (h2) provides a glimpse into the extent to which genetic factors contribute to the observed phenotypic variation. Traits characterized by elevated heritability values, such as plant height, number of branches, and yield per plant, are likely governed by additive gene effects, making them optimal candidates for targeted selection endeavors. Traits like leaf area and leaf length, displaying moderate heritability and substantial genetic advance, also present promising options for selection. However, it's important to note that dry weight exhibited low heritability and genetic advance, suggesting that this trait's variation may be more influenced by environmental factors.

Correlation Studies
Correlation coefficients were computed for diverse traits at both genotypic and phenotypic levels, as depicted in Table 3. Notably, genotypic correlation coefficients consistently surpassed phenotypic correlation coefficients, underscoring the dominant influence of genetic factors in shaping trait interrelationships. Recognizing the correlations between yield and its contributing attributes is critical due to the intricate nature of yield, which emerges from a complex interplay of various constituent traits and environmental factors. Correlation studies play an indispensable role in unveiling the connections between different traits. The greater magnitude of genotypic correlation coefficients in comparison to phenotypic correlation coefficients emphasizes the significant role of genetic factors in dictating the associations between traits. The robust positive correlations observed between yield per plant and growth traits underscore the potential influence of enhancing these growth-related attributes on augmenting yield capacity.

Path Coefficient Analysis
Utilizing the path coefficient analysis presented in Table 4, it became evident that plant height (0.91) exerted the most substantial direct influence on yield per plant, closely

followed by fresh weight (0.82) and number of leaves (0.24). In contrast, root length exhibited a notable negative direct effect (-0.69), while the number of branches also displayed a negative direct effect (-0.24). These findings indicate the potential of these specific traits for inclusion in the selection process aimed at enhancing purslane's characteristics. Moreover, indirect effects were observed, with leaf length (0.97), stem girth (0.83), and number of branches (0.68) demonstrating positive impacts on yield per plant through their interrelation with plant height. At the genotypic level, a residual effect of -0.02668 was observed. Path coefficient analysis provides valuable insights into both direct and indirect trait effects on yield per plant. The dominance of traits like plant height, fresh weight, and number of leaves in directly influencing yield per plant underscores their pivotal role in determining overall yield potential. This analytical approach serves as a valuable guide for breeders, directing their attention toward traits that hold the potential for substantial enhancements in yield.

Table 1: Mean sum of square of ANOVA for growth and yield attributes of purslane

S.No.	Characters	MSS of Genotypes	MSS of Error	F value	*p* value
1.	Plant height	110.01	2.32	47.513	<0.0001
2.	Number of branches	1.47	0.2	7.616	<0.0001
3.	Number of internodes	89.91	1.61	54.46	<0.0001
4.	Stem girth	0.06	0	22.23	<0.0001
5.	Number of leaves	3718.22	282.4	13.17	<0.0001
6.	Leaf area	0.43	0.1	3.48	0.00204
7.	Leaf length	0.48	0.17	2.96	0.00617
8.	Leaf breadth	0.33	0.11	3.006	0.00557
9.	Leaf thickness	0.12	0	88.433	<0.0001
10.	Root length	12.98	3.64	3.569	0.00168
11.	Fresh weight of the plant	1241.68	97.44	12.743	<0.0001
12.	Single plant yield	1052.27	63.733	16.51	<0.0001

p <0.05 indicates statistical significance

Table 2: Variation in genetic parameters for all the traits in the purslane

S.No	Traits	GCV	PCV	H^2	GAM
1.	Plant height	27.18	28.1	93.58	54.17
2.	Number of branches	25.04	30.38	67.96	42.53
3.	Number of internodes	31.19	32.03	94.8	62.55
4.	Stem grith	25.03	26.84	86.99	48.09
5.	Number of leaves	34.07	36.90	85.25	64.79
6.	Leaf area	36.28	50.84	50.91	53.32
7.	Leaf length	18.14	29.07	38.96	23.33
8.	Leaf breadth	30.87	34.18	81.67	57.48
9.	Leaf thickness	22.22	22.37	98.67	45.46
10.	Root length	30.34	31.46	93.05	60.30
11.	Fresh weight	14.78	14.82	99.51	30.38
12.	Dry weight	32.9	1.14	28.809	<0.0001
13.	Yield per plant	23.84	23.89	99.57	49.01

Table 3: Phenotypic and genotypic coefficients of correlation among different traits in purslane

		HT	BR	IN	SG	NL	LA	LL	LB	LT	RL	FW	DW	YD
HT	G	1												
	P	1												
BR	G	0.749**	1											
	P	0.615**	1											
IN	G	0.079NS	0.563**	1										
	P	0.078NS	0.432**	1										
SG	G	0.912**	0.907**	0.169NS	1									
	P	0.799**	0.734**	0.167NS	1									
NL	G	0.058NS	0.611**	0.933**	0.196NS	1								
	P	0.063NS	0.466**	0.817**	0.111NS	1								
LA	G	0.710**	0.316*	-0.228NS	0.823**	-0.421**	1							
	P	0.491**	0.278NS	-0.217NS	0.560**	-0.213NS	1							
LL	G	1.063**	0.622**	-0.483**	0.962**	-0.391**	0.971**	1						
	P	0.582**	0.238NS	-0.300*	0.535**	-0.297*	0.444*	1						
LB	G	0.639**	0.438**	-0.171NS	0.773**	-0.195NS	1.056**	0.959**	1					
	P	0.536**	0.318*	-0.147NS	0.632**	-0.185NS	0.617**	0.515**	1					
LT	G	-0.142NS	-0.349*	-0.504**	-0.071NS	-0.368*	-0.065NS	0.097NS	-0.124NS	1				
	P	-0.138NS	-0.276NS	-0.479**	-0.068NS	-0.342*	-0.024NS	0.070NS	-0.105NS	1				
RL	G	0.720**	0.726**	0.419**	0.728**	0.404**	0.432**	0.596**	0.415**	-0.235NS	1			
	P	0.649**	0.529**	0.410**	0.653**	0.375*	0.269NS	0.294*	0.408**	-0.232NS	1			

		HT	BR	IN	SG	NL	LA	LL	LB	LT	RL	FW	DW	YD
FW	G	0.614**	0.616**	0.147NS	0.806**	0.043NS	0.798**	0.579**	0.559**	0.153NS	0.385**	1		
	P	0.590**	0.500**	0.147NS	0.749**	0.032NS	0.556**	0.350*	0.513**	0.151NS	0.377*	1		
DW	G	0.619**	0.687**	0.623**	0.703**	0.489**	0.597**	0.272NS	0.375*	-0.248NS	0.739**	0.711**	1	
	P	0.588**	0.552**	0.609**	0.655**	0.447**	0.406**	0.154NS	0.347*	-0.247NS	0.728**	0.710**	1	
YD	G	0.697**	0.541**	-0.061NS	0.739**	-0.130NS	0.774**	0.753**	0.549**	0.132NS	0.136NS	0.874**	0.476**	1
	P	0.670**	0.446**	-0.059NS	0.691**	-0.126NS	0.539**	0.459**	0.503**	0.129NS	0.132NS	0.873**	0.475**	1

HT – Plant height, BR -Number of branches, IN – Number of internodes, SG – Stem girth, NL – Number of leaves, LA – Leaf area, LL – Leaf length, LB – Leaf breadth, LT – Leaf thickness, RL – Root length, FW – Fresh weight, DW – Dry weight, YD – Single plant yield, *-significance at 5%, **-significance at 1%, NS-non-significant, G-genotypic correlation and P-phenotypic correlation

Table 4: Estimates of direct and indirect effects of different traits on yield of purslane

	HT	BR	IN	SG	NL	LA	LL	LB	LT	RL	FW	DW
HT	0.91	-0.18	-0.01	0.004	0.01	-0.07	0.02	0.02	0.01	-0.50	0.51	-0.02
BR	0.68	-0.24	-0.04	0.004	0.15	-0.03	0.01	0.01	0.03	-0.51	0.51	-0.03
IN	0.07	-0.14	-0.07	0.001	0.23	0.02	-0.01	-0.01	0.04	-0.29	0.12	-0.02
SG	0.83	-0.22	-0.01	0.004	0.05	-0.08	0.02	0.02	0.01	-0.51	0.66	-0.03
NL	0.05	-0.15	-0.07	0.001	0.24	0.04	-0.01	-0.01	0.03	-0.28	0.04	-0.02
LA	0.65	-0.08	0.02	0.003	-0.10	-0.10	0.02	0.03	0.00	-0.30	0.66	-0.02
LL	0.97	-0.15	0.04	0.004	-0.09	-0.10	0.02	0.03	-0.01	-0.42	0.48	-0.01
LB	0.58	-0.11	0.01	0.003	-0.05	-0.11	0.02	0.03	0.01	-0.29	0.46	-0.01
LT	-0.13	0.09	0.04	0.000	-0.09	0.01	0.00	0.00	-0.08	0.16	0.13	0.01
RL	0.66	-0.18	-0.03	0.003	0.10	-0.04	0.01	0.01	0.02	-0.70	0.32	-0.03
FW	0.56	-0.15	-0.01	0.003	0.01	-0.08	0.01	0.02	-0.01	-0.27	0.82	-0.03
DW	0.56	-0.17	-0.05	0.003	0.12	-0.06	0.00	0.01	0.02	-0.52	0.59	-0.04

Residual effect –0.02668

Numeric in diagonals are direct effect and others are indirect effect.

Conclusion

The study underscores the substantial genetic variability within the examined genotypes across various traits. Leaf area recorded the highest PCV (36.28) and GCV (50.84), while yield per plant exhibited the highest heritability estimate (99.57). Notably, number of leaves displayed the highest Genetic Advance as a Percentage of Mean (64.79), indicating its potential for selection and improvement under additive gene effects. Positive correlations were observed between yield per plant and growth traits. Path coefficient analysis emphasized the direct influence of plant height and fresh weight on yield per plant. These findings suggest that targeted selection for yield enhancement in purslane should be considered.

Declaration

All authors declared that they have no conflicts of interest.

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