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Allometric modelling to estimate the leaf area of purslane (*Portulaca umbraticola* Kunth.)

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Abstract: *Portulaca umbraticola* is a species that has several uses, including ornamental. Among the variables measured in ornamental plants are the biometric data of the leaves, which can be obtained through image analysis, using indirect method, which is simple, accurate and economically viable. This work aimed to propose equations obtained by mathematical models to estimate the leaf area of *P. umbraticola*. The study was conducted at the Universidade Federal Rural do Semi-Árido, Mossoró, RN, Brazil. Three hundred leaves of each of the five genotypes of *P. umbraticola* were evaluated for length, width, product between length and width, and leaf area. Determination and correlation coefficients, Akaike information criterion, Willmott agreement index, coefficient of variation, normality using the Shapiro-Wilk test, principal components and Student's t-test were used to systematize the data. Descriptive measurements obtained from the leaf blades of *P. umbraticola* showed variability between genotypes, demonstrating that the sample was representative for the population analyzed. The regression models obtained were linear and potential. Allometric equations can be used to estimate leaf area in *P. umbraticola*, and the recommended equations are $\hat{y} = 0.356*L$ ($R^2 = 0.91$) for length, $\hat{y} = 1.665*W$ ($R^2 = 0.90$) for width and $\hat{y} = 0.016 \times 0.0711*LW$ ($R^2 = 0.99$), $\hat{y} = 0.715*LW$ ($R^2 = 0.99$) and $\hat{y} = 0.724*LW$ ($R^2 = 0.99$) for the relationship between leaf length and width. The equations to estimate the leaf area of *P. umbraticola* showed excellent data fits, with values of $R^2 = 0.993$ and little dispersion of the data.

Keywords: ‘Beldroega’, leaf length, leaf width, biometrics, non-destructive method, allometric equations.
Abbreviations: PANC - Unconventional Food Plant; UFERSA - Federal Rural University of the Semi-Arid Region; PCA - Principal component analysis.

Introduction

Portulaca umbraticola Kunth., popularly known as ‘beldroega’ or ‘caruru’, is considered an Unconventional Food Plant (PANC), of the Portulacaceae family, which encompasses more than 120 species of succulent herbs and shrubs (Erkan, 2012; Zhou et al., 2015). This species has several potentialities of use; in addition to being used as PANC (Biondo et al., 2018), it is also used for ornamental purposes (Montero et al., 2022), in animal feed (Silva et al., 2015), and has nutritional, medicinal, pharmacological and phyto-remediation properties (Srivastava et al., 2021).

The species exhibits phenotypic variability for anthocyanin pigmentation in the stem and plant size (Beltran et al., 2021). The leaves have morphological and anatomical aspects and distinct amounts between genotypes (Santos et al., 2023). There is also variation for size and hue of the flowers, which potentiates its use for ornamental purposes (Souza et al., 2022).

Leaves are responsible for harboring the photosynthetic apparatus in their specialized cells and are directly and indirectly involved in plants' vegetative and reproductive development (Krupek and Gonçalves, 2022).

Due to the importance of leaves, leaf area is considered by many researchers as the parameter of greatest importance for studies involving the growth, development and physiology of plants. Numerous methods can determine this parameter, classified as direct and indirect, destructive and non-destructive (Zhang, 2020). Direct methods are accurate, but require high-cost equipment and more time in labor in the analyses. In addition, direct methods destroy the sample, making its use unfeasible throughout the life cycle of the plants. On the other hand, indirect methods are simple, precise and economically viable, and regression models with allometric relationships can be used, considering the dimensions of the leaves (length and width) (Santos et al., 2021).

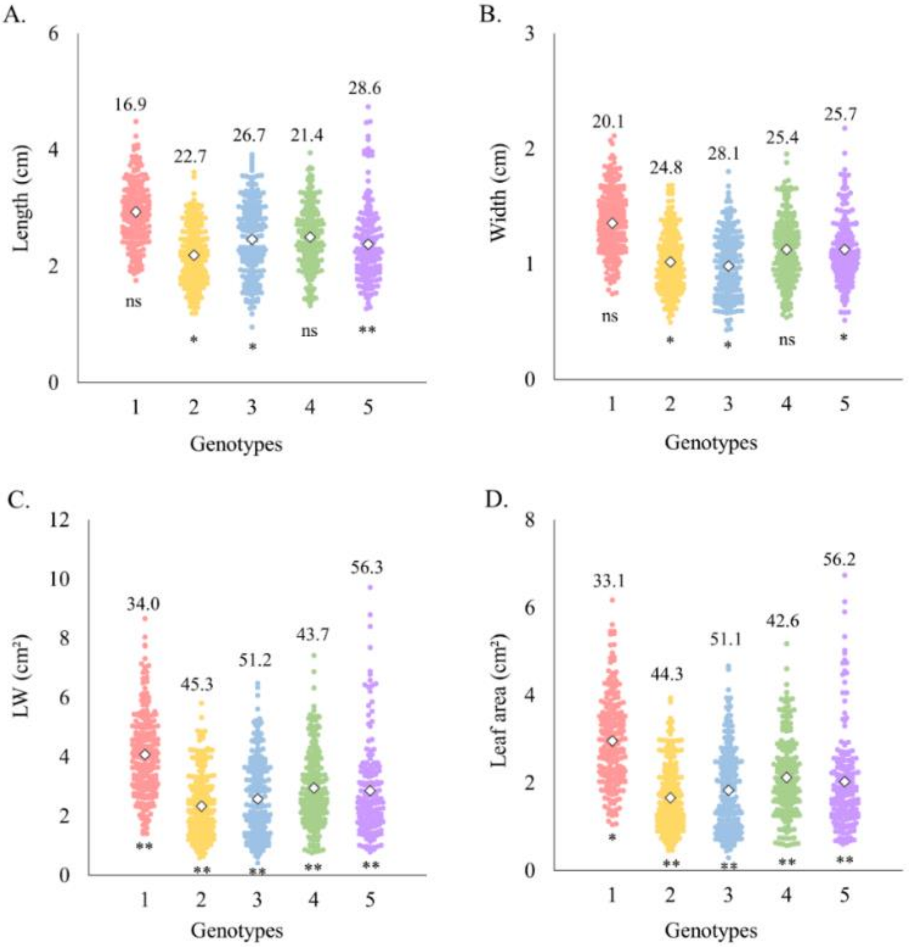

Figure 1. Descriptive analysis of length (A), width (B), product between length and width (C) and leaf area (D) for *P. umbraticola* genotypes. The distribution of upper and lower points represents the data set's extreme values (maximum and minimum). The symbol (□) within the data distribution represents the means in each genotype. The numbers above the points refer to the coefficients of variation. The significance below the points refers to the Shapiro-Wilk normality test. **: significant at 1% probability; *: significant at 5% probability; ^{ns}: Not significant. Genotypes: 1 - RN-013; 2 - RN-011; 3 - RN-010; 4 - RN-008; 5 - RN-009.

Regression models for leaf area prediction have been proposed in other studies with agricultural and forest species (Salazar et al., 2018; Ribeiro et al., 2019; Ribeiro et al., 2020; Hernandéz-Fernandez et al., 2021), but not with *P. umbraticola*. In this context, these studies will collaborate with the study of the growth and physiology of the species. Thus, the objective of this work was to propose equations obtained by mathematical models to estimate the leaf area of the species *P. umbraticola* Kunth.

Results and Discussion

Descriptive statistics

The analysis of the descriptive measurements obtained from the leaf blades of *P. umbraticola* from different parts of the plant showed variability between genotypes based on the evaluated characters (leaf length, leaf width, product between length and width, and leaf area) (Figure 1). This indicates that the leaves had different sizes, which is of interest for the prediction analysis proposed in this work. Other authors have also reported data variability (Ribeiro et al., 2020; Tognere et al., 2021) in the estimation of leaf area, demonstrating that the sample was representative of the population analyzed, in *Mesosphaerum suaveolens* and *Trema micrantha*. This inhomogeneity between genotypes makes it possible to use this type of analysis to characterize leaves in genotypes of this species.

High values of the coefficient of variation were observed (Figure 1). The genotypes RN-010 and RN-009 had the highest dispersion values for leaf length (26.7 and 28.6), leaf width (28.1 and 35.7), the product between length and width (51.2 and 56.3) and leaf area (51.1 and 56.2). These results are significant in studies involving leaf data estimation since the more fantastic the dispersion of the data, the better the representativeness of the regression models for the species under study, and this methodology may be used in future studies with the species. Cargnelutti Filho et al. (2015) and Lessa et al. (2018) reported that wide variability is essential in modelling and, consequently, in the representativeness of the models.

The regression equations allow us to accurately estimate the area of the leaves in a simple, fast way and without the need for their destruction (Oliveira et al., 2020). In this same aspect, Ribeiro et al. (2020) reported that the variation of the data is a positive aspect in the estimation of leaf area data through images, which will allow the use in different plant phenological stages.

The genotypes evaluated were significant for the normality of the data, based on the characters evaluated (Figure 1), except for the genotypes RN-013 (1) and RN-008 (4) for leaf length

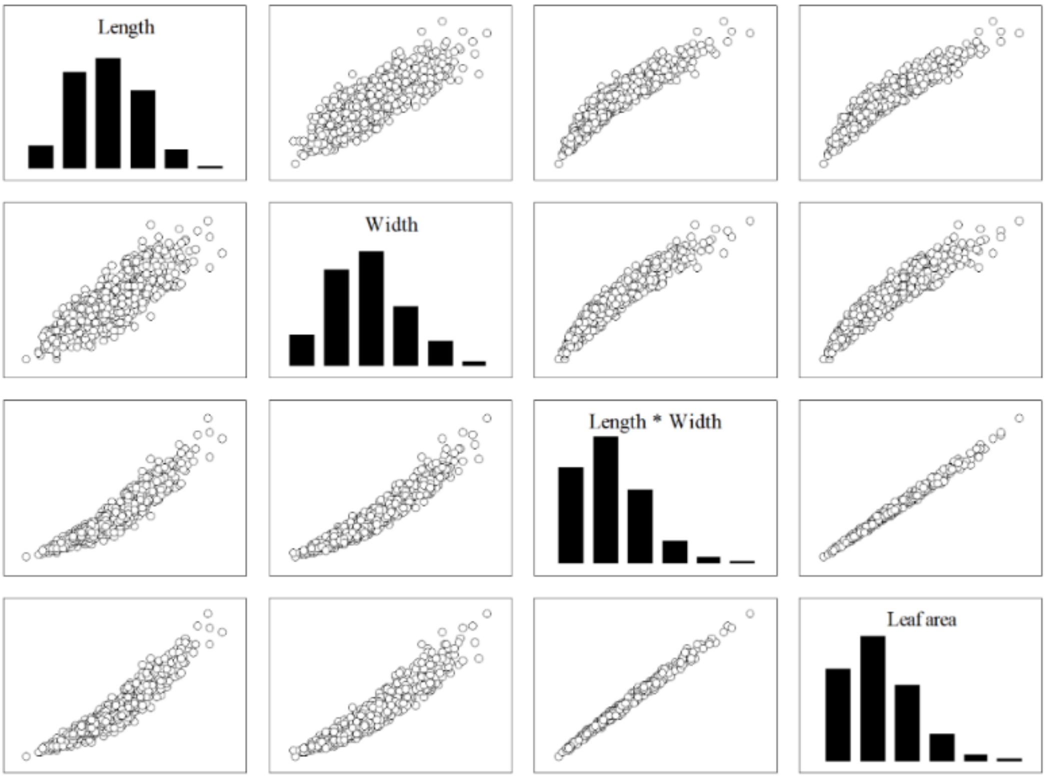

Figure 2. Matrix with histograms (diagonal) and scatterplots between length, width, the product between length and width, and leaf area of 1,100 leaves used to generate models to estimate the leaf area of *P. umbraticola* genotypes.

and width. The assumption of normality in a set of data is to evaluate their behavior, based on the comparison between the parametric values in the normal distribution and the values estimated in the experimental sample (Santos and Ferreira, 2003). Martin et al. (2013) reported that the absence of normality might occur for the estimated data in the leaf area index, as observed in some genotypes.

The scatterplots between the variables length, width, the relationship between length and width, and leaf area showed patterns in the data that suggest the fit of linear and nonlinear models, depending on the variables (Figure 2). For the length, the width of the leaf blade and leaf area showed more distance from normality, characterized mainly by the skewed asymmetry to the right. It is considered that nonnormality occurs when any of the variables that describe a phenomenon follows any probability distribution other than average (Pino, 2014), as observed in this study.

The fit of linear and nonlinear models has also been verified in other studies using the same leaf analysis methodology but with different species, such as *Erythrina velutina* Willd. (Ribeiro et al., 2022), *Eustoma grandiflorum* (Dias et al., 2022) and *Manilkara zapota* L. (Ribeiro et al., 2023), so it is necessary to investigate, through statistical models, the models that best fit the data.

Equations for estimating leaf area

The coefficient of determination (R^2) of the equations to model the leaf area in *P. umbraticola* genotypes, determined by digital photos as a function of the characteristics evaluated individually and jointly, indicated that the data were described by the linear and power models (Table 1). These models showed an adjusted coefficient of determination (R^2) higher than 80%, indicating a reasonable estimate of leaf area in *P. umbraticola*. The highest determination coefficients were obtained in the RN-010 genotype, with values higher than 90%, demonstrating that the equations could accurately estimate this species' leaf area.

The Willmott index (*d*) values were higher than 0.90 for the individual genotypes and for the joint analysis of both (Table 1). When the Willmott index has high values, as observed in this study, it indicates that the models can reproduce the observed values accurately (Cardozo et al., 2014) because there is a high proximity between the real and estimated values.

The equations selected to estimate the leaf area had low values of the root mean squared error (Table 1), indicating that the equations described are adequate to estimate the leaf area of *P. umbraticola* genotypes as a function of the leaf dimensions, because they have high values of the coefficient of determination, combined with the low values of the mean square.

Pearson's correlation coefficients between the variables analyzed were positive, with values higher than 90% for most observations, indicating the existence of an association between the variables. A positive correlation indicates that the correlated characters vary in the same direction (Pessoa et al., 2023), and values close to 1 evidence a more significant association between the characteristics since the correlation ranges from -1 to 1 (Silva et al., 2014).

The equations proposed to estimate the leaf area of *P. umbraticola* had excellent fits ($R^2 = 0.9986$) of the data, corresponding to more than 99% of the relationship between length and width of the leaf area, with little dispersion of the data (Figure 3). These results indicate that the linear regression model for the length estimates with leaf width was adequate to reproduce the data accurately.

The estimates of leaf area in *P. umbraticola* genotypes using image analysis proved to be an adequate alternative in the search for the best regression functions. When the regression equation meets the statistical criteria evaluated, it can be

Table 1. Statistical models, regression coefficients (β_0 and β_1), coefficient of determination (R^2), Pearson's linear correlation coefficient (r), Akaike information criterion (AIC), Willmott agreement index (d), root mean squared error (RMSE), and equations for estimating leaf area of *P. umbraticola* genotypes as a function of leaf dimensions.

Equation code	Model	Coefficients		R^2	r	*d*	RMSE	Estimator of LA ($\hat{y}$)
		β_0	β_1					
				Genotype RN-013				
1	$\hat{y} = \beta_0 + \beta_1 * L + \varepsilon_i$	-2.43	1.83	0.86	0.93	0.96	0.35	$\hat{y} = -2.43 + 1.83 * L$
2	$\hat{y} = \beta_0 + \beta_1 * W + \varepsilon_i$	-1.45	3.25	0.81	0.90	0.94	0.41	$\hat{y} = -1.45 + 3.25 * W$
3	$\hat{y} = \beta_0 + \beta_1 * LW + \varepsilon_i$	0.09	0.70	0.98	0.99	0.99	0.11	$\hat{y} = 0.09 + 0.70 * LW$
4	$\hat{y} = \beta_1 * LW + \varepsilon_i$	----	0.72	0.99	0.99	0.99	0.12	$\hat{y} = 0.72 * LW$
5	$\hat{y} = \beta_0 * L^{\beta_1} + \varepsilon_i$	0.39	1.84	0.87	0.93	0.96	0.35	$\hat{y} = 0.39 * L^{1.84}$
6	$\hat{y} = \beta_0 * W^{\beta_1} + \varepsilon_i$	1.85	1.49	0.82	0.90	0.94	0.41	$\hat{y} = 1.85 * W^{1.49}$
7	$\hat{y} = \beta_0 * LW^{\beta_1} + \varepsilon_i$	0.76	0.96	0.98	0.99	0.99	0.11	$\hat{y} = 0.76 * LW^{0.96}$
8	$\hat{y} = \beta_0 * {\beta_1}^{L} + \varepsilon_i$	0.52	1.77	0.85	0.92	0.95	0.37	$\hat{y} = 0.52 * 1.77^{L}$
9	$\hat{y} = \beta_0 * {\beta_1}^{W} + \varepsilon_i$	0.71	2.76	0.80	0.89	0.94	0.43	$\hat{y} = 0.71 * 2.76^{W}$
10	$\hat{y} = \beta_0 * {\beta_1}^{LW} + \varepsilon_i$	1.25	1.22	0.89	0.80	0.94	0.43	$\hat{y} = 1.25 * 1.22^{LW}$
				Genotype RN-011				
1	$\hat{y} = \beta_0 + \beta_1 * L + \varepsilon_i$	-1.39	1.39	0.89	0.94	0.97	0.24	$\hat{y} = -1.396 + 1.396 * L$
2	$\hat{y} = \beta_0 + \beta_1 * W + \varepsilon_i$	-1.16	2.77	0.91	0.95	0.97	0.21	$\hat{y} = -1.169 + 2.775 * W$
3	$\hat{y} = \beta_0 + \beta_1 * LW + \varepsilon_i$	0.04	0.69	0.99	0.99	0.99	0.05	$\hat{y} = 0.041 + 0.692 * LW$
4	$\hat{y} = \beta_1 * LW + \varepsilon_i$	----	0.70	0.99	0.99	0.99	0.05	$\hat{y} = 0.707 * LW$
5	$\hat{y} = \beta_0 * L^{\beta_1} + \varepsilon_i$	0.36	1.87	0.90	0.95	0.97	0.22	$\hat{y} = 0.366 * L^{1.876}$
6	$\hat{y} = \beta_0 * W^{\beta_1} + \varepsilon_i$	1.55	1.70	0.91	0.95	0.97	0.20	$\hat{y} = 1.550 * W^{1.707}$
7	$\hat{y} = \beta_0 * LW^{\beta_1} + \varepsilon_i$	0.72	0.97	0.99	0.99	0.99	0.05	$\hat{y} = 0.727 * LW^{0.974}$
8	$\hat{y} = \beta_0 * {\beta_1}^{L} + \varepsilon_i$	0.28	2.15	0.88	0.94	0.96	0.24	$\hat{y} = 0.288 * 2.155^{L}$
9	$\hat{y} = \beta_0 * {\beta_1}^{W} + \varepsilon_i$	0.34	4.33	0.89	0.94	0.97	0.23	$\hat{y} = 0.347 * 4.339^{W}$
10	$\hat{y} = \beta_0 * {\beta_1}^{LW} + \varepsilon_i$	0.71	1.39	0.89	0.94	0.97	0.23	$\hat{y} = 0.713 * 1.398^{LW}$
				Genotype RN-010				
1	$\hat{y} = \beta_0 + \beta_1 * L + \varepsilon_i$	-1.50	1.35	0.90	0.95	0.97	0.28	$\hat{y} = -1.502 + 1.356 * L$
2	$\hat{y} = \beta_0 + \beta_1 * W + \varepsilon_i$	-1.37	3.25	0.92	0.96	0.98	0.25	$\hat{y} = -1.370 + 3.253 * W$
3	$\hat{y} = \beta_0 + \beta_1 * LW + \varepsilon_i$	0.01	0.70	0.99	0.99	0.99	0.06	$\hat{y} = 0.010 + 0.706 * LW$
4	$\hat{y} = \beta_1 * LW + \varepsilon_i$	----	0.70	0.99	0.99	0.99	0.06	$\hat{y} = 0.709 * LW$
5	$\hat{y} = \beta_0 * L^{\beta_1} + \varepsilon_i$	0.28	1.98	0.93	0.96	0.98	0.24	$\hat{y} = 0.287 * L^{1.983}$
6	$\hat{y} = \beta_0 * W^{\beta_1} + \varepsilon_i$	1.79	1.76	0.93	0.96	0.98	0.24	$\hat{y} = 1.792 * W^{1.767}$
7	$\hat{y} = \beta_0 * LW^{\beta_1} + \varepsilon_i$	0.71	0.99	0.99	0.99	0.99	0.06	$\hat{y} = 0.713 * LW^{0.995}$
8	$\hat{y} = \beta_0 * {\beta_1}^{L} + \varepsilon_i$	0.27	2.07	0.92	0.96	0.97	0.25	$\hat{y} = 0.274 * 2.071^{L}$
9	$\hat{y} = \beta_0 * {\beta_1}^{W} + \varepsilon_i$	0.37	4.63	0.90	0.94	0.97	0.29	$\hat{y} = 0.372 * 4.634^{W}$
10	$\hat{y} = \beta_0 * {\beta_1}^{LW} + \varepsilon_i$	0.76	1.36	0.90	0.94	0.97	0.29	$\hat{y} = 0.767 * 1.360^{LW}$
				Genotype RN-008				
1	$\hat{y} = \beta_0 + \beta_1 * L + \varepsilon_i$	-1.85	1.59	0.88	0.94	0.96	0.30	$\hat{y} = -1.854 + 1.590 * L$
2	$\hat{y} = \beta_0 + \beta_1 * W + \varepsilon_i$	-1.28	3.01	0.91	0.95	0.97	0.26	$\hat{y} = -1.281 + 3.019 * W$
3	$\hat{y} = \beta_0 + \beta_1 * LW + \varepsilon_i$	0.06	0.69	0.99	0.99	0.99	0.07	$\hat{y} = 0.060 + 0.699 * LW$
4	$\hat{y} = \beta_1 * LW + \varepsilon_i$	----	0.71	0.99	0.99	0.99	0.07	$\hat{y} = 0.716 * LW$
5	$\hat{y} = \beta_0 * L^{\beta_1} + \varepsilon_i$	0.34	1.92	0.89	0.94	0.97	0.29	$\hat{y} = 0.348 * L^{1.928}$
6	$\hat{y} = \beta_0 * W^{\beta_1} + \varepsilon_i$	1.69	1.62	0.91	0.95	0.97	0.25	$\hat{y} = 1.692 * W^{1.625}$
7	$\hat{y} = \beta_0 * LW^{\beta_1} + \varepsilon_i$	0.74	0.96	0.99	0.99	0.99	0.07	$\hat{y} = 0.747 * LW^{0.967}$
8	$\hat{y} = \beta_0 * {\beta_1}^{L} + \varepsilon_i$	0.34	2.00	0.87	0.93	0.96	0.31	$\hat{y} = 0.347 * 2.008^{L}$
9	$\hat{y} = \beta_0 * {\beta_1}^{W} + \varepsilon_i$	0.47	3.56	0.89	0.94	0.97	0.29	$\hat{y} = 0.476 * 3.561^{W}$
10	$\hat{y} = \beta_0 * {\beta_1}^{LW} + \varepsilon_i$	0.93	1.29	0.97	0.94	0.89	0.29	$\hat{y} = 0.936 * 1.297^{LW}$
				Genotype RN-009				
1	$\hat{y} = \beta_0 + \beta_1 * L + \varepsilon_i$	-1.82	1.62	0.93	0.96	0.98	0.28	$\hat{y} = -1.828 + 1.622 * L$
2	$\hat{y} = \beta_0 + \beta_1 * W + \varepsilon_i$	-2.14	3.70	0.88	0.94	0.96	0.38	$\hat{y} = -2.148 + 3.707 * W$
3	$\hat{y} = \beta_0 + \beta_1 * LW + \varepsilon_i$	0.01	0.70	0.99	0.99	0.99	0.08	$\hat{y} = 0.010 + 0.710 * LW$
4	$\hat{y} = \beta_1 * LW + \varepsilon_i$	----	0.71	0.99	0.99	0.99	0.08	$\hat{y} = 0.710 * LW$
5	$\hat{y} = \beta_0 * L^{\beta_1} + \varepsilon_i$	0.41	1.77	0.95	0.97	0.98	0.25	$\hat{y} = 0.412 * L^{1.777}$
6	$\hat{y} = \beta_0 * W^{\beta_1} + \varepsilon_i$	1.48	2.02	0.92	0.96	0.97	0.31	$\hat{y} = 1.487 * W^{2.029}$
7	$\hat{y} = \beta_0 * LW^{\beta_1} + \varepsilon_i$	0.71	0.99	0.99	0.99	0.99	0.08	$\hat{y} = 0.715 * LW^{0.995}$
8	$\hat{y} = \beta_0 * {\beta_1}^{L} + \varepsilon_i$	0.47	1.78	0.92	0.96	0.97	0.31	$\hat{y} = 0.473 * 1.783^{L}$
9	$\hat{y} = \beta_0 * {\beta_1}^{W} + \varepsilon_i$	0.37	4.16	0.90	0.95	0.97	0.35	$\hat{y} = 0.373 * 4.169^{W}$
10	$\hat{y} = \beta_0 * {\beta_1}^{LW} + \varepsilon_i$	1.03	1.24	0.90	0.95	0.97	0.35	$\hat{y} = 1.033 * 1.242^{LW}$
				Pooled group				
1	$\hat{y} = \beta_0 + \beta_1 * L + \varepsilon_i$	-1.81	1.57	0.89	0.94	0.97	0.34	$\hat{y} = -1.814 + 1.578 * L$
2	$\hat{y} = \beta_0 + \beta_1 * W + \varepsilon_i$	-1.50	3.23	0.89	0.94	0.97	0.34	$\hat{y} = -1.507 + 3.234 * W$

3	$\hat{y} = \beta_0 + \beta_1 * LW + \varepsilon_i$	0.01	0.71	0.99	0.99	0.99	0.08	$\hat{y} = 0.016 + 0.711 * LW$
4	$\hat{y} = \beta_1 * LW + \varepsilon_i$	----	0.71	0.99	0.99	0.99	0.08	$\hat{y} = 0.715 * LW$
5	$\hat{y} = \beta_0 * L^{\beta_1} + \varepsilon_i$	0.35	1.89	0.91	0.95	0.97	0.31	$\hat{y} = 0.356 * L^{1.893}$
6	$\hat{y} = \beta_0 * W^{\beta_1} + \varepsilon_i$	1.66	1.72	0.90	0.94	0.97	0.32	$\hat{y} = 1.665 * W^{1.724}$
7	$\hat{y} = \beta_0 * LW^{\beta_1} + \varepsilon_i$	0.72	0.99	0.99	0.99	0.99	0.08	$\hat{y} = 0.724 * LW^{0.991}$
8	$\hat{y} = \beta_0 * {\beta_1}^{L} + \varepsilon_i$	0.39	1.90	0.88	0.94	0.96	0.35	$\hat{y} = 0.396 * 1.902^{L}$
9	$\hat{y} = \beta_0 * {\beta_1}^{W} + \varepsilon_i$	0.46	3.65	0.87	0.93	0.96	0.37	$\hat{y} = 0.460 * 3.654^{W}$
10	$\hat{y} = \beta_0 * {\beta_1}^{LW} + \varepsilon_i$	0.99	1.26	0.87	0.93	0.96	0.37	$\hat{y} = 0.994 * 1.269^{LW}$

used accurately in the estimation of leaf area according to the species under analysis, assisting in future studies, without the need for leaf destruction nor the use of exclusive equipment for length and width measurements (Oliveira et al., 2019).

Principal components

The analyses showed that the first two principal components allowed explaining 96.00% of the variance contained in the original variables (Figures 4A and 4B). The principal component PC1 and the principal component PC2 contributed with 85.87% and 10.13%, respectively. This analysis allowed us to group the genotypes according to their variation in only one group. Determining the proximity between genotypes demonstrates that phenotypic characterization using leaf imaging efficiently estimates parameters related to the biometric area in *P. umbraticola*, regardless of the genotype evaluated.

The variables had similar contributions to PC1, showing a vector of the same length (Figure 4B). The principal component analysis aims to group individuals according to the variation of their characteristics (Hongyu et al., 2015), so the results were similar between genotypes.

Relationship between observed leaf area and estimated leaf area

It was verified that the equations proposed to estimate the *Portulaca umbraticola* leaf area had excellent fits, with values of $R^2 = 0.993$ and little dispersion of the data (Figure 5A). The leaf area observed and estimated showed no significant difference in Student's t-test (Figure 5 B), indicating that the leaf area of this species can be estimated using the proposed model, with precision and accuracy.

The accurate estimation of leaf area using an equation indicates that obtaining the allometric relationship between length and width is of paramount importance because it is a growth variable and recognized for its importance in plant productivity, as photosynthesis depends on the interception of light made by the canopy for the production of chemical energy (Goergen et al., 2021). Zhang et al. (2023) also reported the efficiency between real and estimated leaf areas in *Nicotiana tabacum* L. as observed in this study.

Materials and Methods

Experimental site and plant material

The study was conducted in the didactic garden of the Center for Agricultural Sciences of the Federal Rural University of the Semi-Arid Region, Mossoró, Rio Grande do Norte, Brazil (5°11'S, 37°20'W). The climate is classified as BSh, considered dry and very hot, with dry season and summer rains (Alvares et al., 2013). The region's average temperature is approximately 28 °C and the annual rainfall is around 695 mm. According to the Brazilian soil classification system, the soil of the area was classified as Ultisol (United States, 2014), corresponding to the *Argissolo Vermelho Eutrófico* (EMBRAPA, 2018).

Five genotypes of *P. umbraticola* were used: RN-008, RN-009, RN-010, RN-011 and RN-013, selected based on their phenotypic variability, mainly for flower color (Figure 6). In each genotype, 220 expanded leaves of different parts of the plant were collected, without damage caused by biotic/abiotic factors, from plants grown in the field and coming from vegetative propagation.

Obtaining images and extracting data

The selected leaves had different shapes and sizes to test the model's generality and seek greater variability of sample data (Figure 7). Immediately after collection, the samples were packed in plastic bags and taken for analysis in a controlled environment, with a temperature of 24 ºC to keep the leaves turgid.

The leaves were photographed using a cell phone camera (Redmi 10c®) with 8165 x 6124 pixels, and the images were processed, contrasted and analyzed individually with the ImageJ® software (National Institute of Health, USA), according to the methodology described by Ribeiro et al. (2018). During the digitization of the images, rulers graduated in centimeters were included as indicators of the reference scale for the analyses on each leaf.

The length (L) - distance between the insertion end of the petiole and the opposite distance from the midrib (Figure 2), width (W) - measurement perpendicular to the midrib, at the widest point, and actual leaf area (LA, cm²) were calculated individually for each leaf. Next, the product between length and width (LW) (cm²) was calculated.

Statistical analysis

Descriptive analysis was used to calculate the data's maximum, minimum and mean values. The coefficient of variation was calculated and normality was verified by the Shapiro-Wilk test.

The criteria for choosing the best equations to estimate leaf area in individual and joint analysis of *P. umbraticola* genotypes were: coefficient of determination (R²), Pearson's linear correlation coefficient (r), Akaike's information criterion (AIC), Willmott agreement index (d) and root mean squared error (RMSE). Principal component analysis (PCA) was also performed.

The leaf area observed and leaf area estimated by the proposed model were compared by Student's t test for paired samples ($p < 0.01$). Data analysis was performed using the software R v.4.1.2 (R® Core Team 2022).

Conclusion

Allometric equations based on biometric dimensions can estimate leaf area in *Portulaca umbraticola* Kunth. The recommended equations are $\hat{y} = 0.356*L$ ($R^2 = 0.91$) for

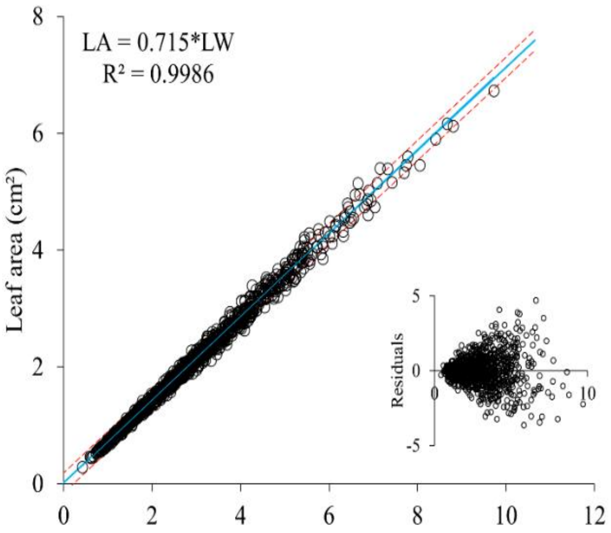

Figure 3. Relationship between the observed leaf area and the product between length and width of the leaves of *P. umbraticola* genotypes (grouped data), from the model LA = 0.715*LW. The analysis of the dispersion pattern of the residuals is presented in the insertion.

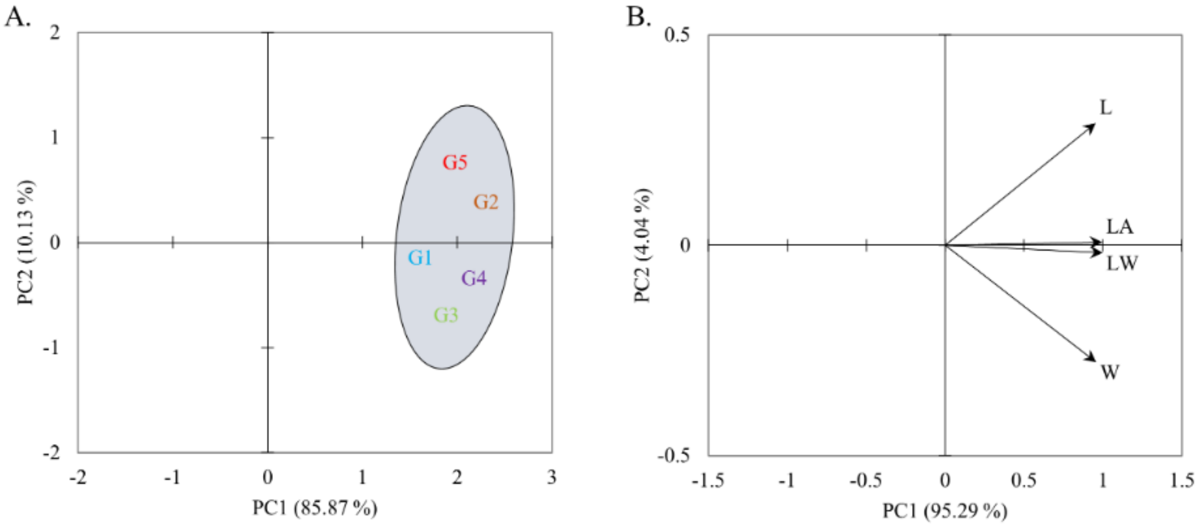

Figure 4. A=Principal component analysis (PCA) of leaf parameters of five genotypes of *Portulaca umbraticola* Kunth. The large circle represents the grouping formed by the Euclidean distance of dissimilarity. B= Loading plot between length, width, the product between length and width, and leaf area of *P. umbraticola* genotypes. Genotypes: G1: RN-013; G2: RN-011; G3: RN-010; G4: RN-008 and G5: RN-009.

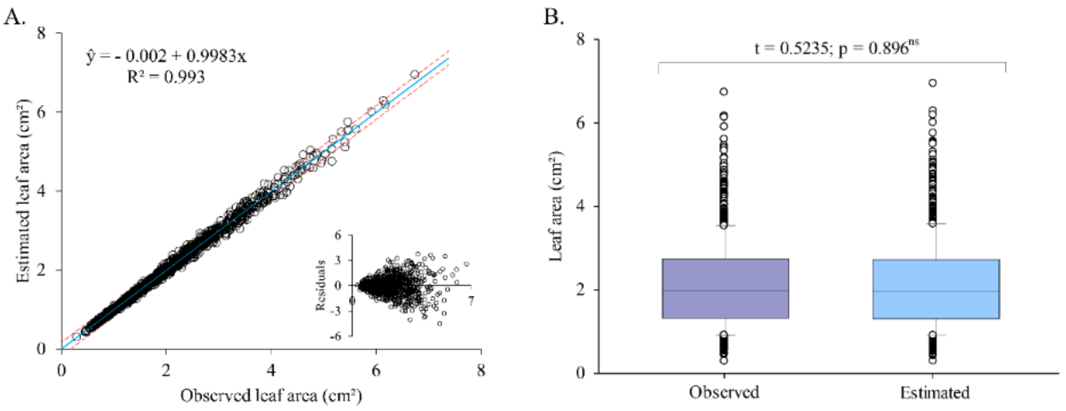

Figure 5. A. Relationship between the observed leaf area and leaf area estimated by the model LA = 0.715*LW as a function of the product between length and width. A = Analysis of the dispersion pattern of the residuals is presented in the insertion. B = Observed and estimated leaf area compared with each other by Student's t-test ($p < 0.01$).

Figure 6. Genotypes of *P. umbraticola* Kunth. a - RN-013; b - RN-011; c - RN-010; d - RN-008; and e - RN-009.

Figure 7. Linear dimensions of the leaves [length (L) and width (W)] of *P. umbraticola*.

length, $\hat{y} = 1.665*W$ ($R^2 = 0.90$) for width, and $\hat{y} = 0.016 \times 0.0711*LW$ ($R^2 = 0.99$), $\hat{y} = 0.715*LW$ ($R^2 = 0.99$) and $\hat{y} = 0.724*LW$ ($R^2 = 0.99$) for the relationship between leaf length and width in leaves in *P. umbraticola*. The equations to estimate the leaf area of *P. umbraticola* showed excellent data fits, with values of $R^2 = 0.993$ and little dispersion of the data.

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