academicJournals

Vol. 12(2), pp. 125-132, 12 January, 2017
DOI: 10.5897/AJAR2016.11873
Article Number: 7ECAD7162366
ISSN 1991-637X
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http://www.academicjournals.org/AJAR

African Journal of Agricultural Research

Full Length Research Paper

Mathematical models to estimate leaf area of citrus genotypes

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Received 26 October, 2016; Accepted 21 November, 2016

Mathematical models were developed, using 22 different genotypes of citrus, to estimate leaf area. The information of the relationship between leaf length and width $(L/W)^2$ for simple leaf blade form (eliptic, ovate, obovate, lanceolate); and length of the three folioles $(L_2 + L_3)/L_1$ for a compound leaf (trifoliate leaves), was used with the purpose to separate group of similarities of leaf blade form and promote high accuracy of estimate. The best models presented an excellent precision with errors varying from 1.2 to 6.2 (%) and r^2 higher than 0.95 for the majority of the models tested. Considering a single leaf blade, the linear model ($Y = \beta \cdot L \cdot W$) presented the lower mean deviation and lower square deviation. For the compound leaves, the potential models are simple to use, since use only the information of length of central foliole L_1 ($Y = \beta\ L_1^{\mu}$), although the use of linear models gave the best precision, as observed by using the model $Y = \beta\ .\ L_1\ .\ W_1$. Furthermore the model might be used as a single model independent of the relation $(L_2+L_3)/L_1$: $\{Y=\beta\cdot(L_1\cdot W_1 + L2\cdot W_2 + L_3\cdot W_3),\ r^2 = 0.98\}$.

Key words: *Citrus*, compound leaf, hybrids, leaf area modeling.

INTRODUCTION

Leaf area is a variable of extreme importance to physiological and agronomic studies, such as vegetable growing, interception of light, remote sensing, photosynthetic efficiency, absorption of carbon, evapotranspiration, absorption of agrochemicals by the leaves, assessment of pest attack and irrigation management (Coelho Filho et al., 2004, 2012; Guimarães et al., 2013; Griffith et al., 2011; Lopes and Pinto, 2005; Oliveira et al., 2013; Pereira et al., 2009; Silva et al., 2008; Stuckens et al., 2009).

Among the methods to estimate leaf area, mathematical models based on measures of biometric variables (leaf width and length) are widely used for various species of plants (Serdar and Demirsoy, 2006) and can be applied in studies of many types (Ramirez and Zullo Júnior, 2010; Bu et al., 2013; Coelho Filho et al., 2013; Padrón et al., 2016; Silva et al., 2008; Yi et al., 2010). However, due to the genetic variability for such characteristics, further studies and specific equations for each genotype are needed within a given species (Malagi

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Table 1. Genotypes used for leaf area estimation according to the leaf blade form.

	Single leaf (elliptical, ovate, obovate and lanceolate)	Compound leaves (trifoliate)
Genotype	'Sour' orange (SO)	TH-051
	'Sunki' mandarin (SM)	TH-127
	'Sunki Tropical' mandarin (STM)	'Swingle' citrumelo (SWCT)
	'Rangpur' lime (RL): Aluminum selection 01 (RL Al. 01)	LRF × (RL × TR) - 004
	'Rangpur' lime (RL): Aluminum selection 02 (RL Al. 02)	LRF × (RL × TR) - 005
	'Rangpur Santa Cruz' lime (RLSTC)	SM × TRFD - 007
	RL × SRT-034	SM × SWCT - 041
	SMFL × CWEB-004	SM × (RL × TR) - 016
	SMFL × CTC 13 – 012	SM × CTTR - 002
	SMFL × CTARG-044	SM × CTARG - 020
	VL 71164	SM × CTQT 1434 - 001

*CWEB, Citrus webberi; VL, 'Volkamer' lemon; TH, trifoliate hybrid; TRFD, Trifoliate 'Flying Dragon'; TR, trifoliate; CTARG, 'Argentina' citrange; SMFL, 'Sunki Florida' mandarin; LRF, 'Florida Rough' lemon; CTTR, 'Troyer' citrange; CTC, 'Carrizo' citrumelo; CTQT, 'Thomasville' citrangequat.

et al., 2010). Instruments such as portable scanners and optical laser are designed for measurements of leaf area index (LAI). However, many times, they are very expensive and complex for basic studies (Serdar and Demirsoy, 2006) and involve destructive measures, what makes the sequential readings inviable (Cristofori et al., 2008).

Citrus breeding programs have generated several hybrids, which should be evaluated for tolerance to abiotic and biotic stress and the leaf area is constantly assessed and correlated with most of others physiological traits. Thus, the present study aimed to develop an accurate mathematical model to estimate single blade leaf area, easily applicable and adaptable to any hybrid of *Citrus*.

MATERIALS AND METHODS

Genotypes used and growing conditions

This study was conducted with 22 genotypes of Genetic Breeding Program of citrus (GBP Citrus) of the Embrapa Cassava and Fruits, being classified into two groups according to the leaf types: Simple and compound (Table 1). The leaves of each genotype were collected in five plants of each genotype cultivated in greenhouse during a year, in pots of 40 L.

Modeling and statistics of the results

From each genotype, 22 to 49 leaves were randomly collected sampling the maximum range of scope as possible. The leaf area of each leaf was determined using the methodology of Marshall (1968).

For the simple leaves, the maximum length of the leaf (L) and the maximum width of the leaf (W); for the compound leaves, the maximum lengths of the central folioles (L_1) and lateral (L_2 and L_3) and the maximum widths of the central folioles (W_1) and lateral (W_2 and W_3) were considered. Through the software Table curve, the biometric measurements were treated as independent variables and the leaf area as the dependent variable. The best models were selected based on the coefficient of determination (r^2) (Table 2).

To increase the accuracy of the models for each type of leaf (simple and compound), they were separated into groups according to the form of the leaf blade. In the case of genotypes with single leaves, the criterion used was the relationship between the leaf length by its width (L/W) raised to the second power $(L/W)^2$, obtaining the groups: Group 1: $3 \leq (L/W)^2 \geq 4$; Group 2: $4.1 \leq (L/W)^2 \geq 4.7$, and Group 3: $4.8 \leq (L/W)^2 \geq 6$ (Table 3). For genotypes with compound leaves, was used the ratio between the sum of the length of lateral folioles and the length of the central folioles $(L_2+L_3)/L_1$, with the formation of the following groups: Group 1: $0.8 \leq (L_2+L_3)/L_1 \geq 0.89$; Group 2: $0.9 \leq (L_2+L_3)/L_1 \geq 1$; Group 3: $1.1 \leq (L_2+L_3)/L_1 \geq 1.3$ (Tables 4 and 5).

In order to compare the models proposed, besides the correlations analysis, we calculated the total errors of the estimate of the leaf area and their relative errors. The total error of the estimate for each model generated was calculated by means of Equation (1):

$$E = \sum_1^n Am - \sum_1^n Ar \qquad (1)$$

In which E is the total error of estimate of leaf area (cm²); Am is the estimated leaf area (cm²); and Ar is the leaf area measurement (cm²).

The relative error was calculated by the ratio between the difference of the sum of the estimated leaf area ($\sum_1^n Am$) and the corresponding measured value (($\sum_1^n Ar$) by the sum of the real leaf area ($\sum_1^n Ar$) (Equation 2):

$$RE = \left| \frac{\sum_1^n Am - \sum_1^n Ar}{\sum_1^n Ar} \right| \qquad (2)$$

In which RE is the relative error (%); ($\sum_1^n \mathrm{Am}$) the sum of leaf area, of all the leaves in a genotype, estimated by the proposed model (cm²) and ($\sum_1^n \mathrm{Ar}$) the sum of leaf area, considering all the leaves in a genotype (cm²).

RESULTS AND DISCUSSION

Adjusted models

The mathematical models presented the best adjustments

Table 2. Description of models obtained, where β and μ are constants estimated by the software table curve.

Model	Leaves form	
	Simple	Compound
1	$Y = \beta \cdot L \cdot W$	$Y = \beta \cdot (L_1 \cdot W_1)$
2	$Y = \beta \cdot (L \cdot W)^{\mu}$	$Y = \beta \cdot (L_1 \cdot W_1 + L_2 \cdot W_2 + L_3 \cdot W_3)$
3	$Y = \beta \cdot L^{\mu}$	$Y = \beta \cdot [(L_1 + L_2 + L_3) \cdot W_1]$
4		$Y = \beta \cdot (L_1 \cdot L_2 \cdot L_3)^{\mu}$
5		$Y = \beta \cdot (L_1 + L_2 + L_3)^{\mu}$
6		$Y = \beta \cdot {L_1}^{\mu}$

L, Maximum length of the leaf; W, maximum width of the leaf; L_1, maximum length of the central foliole; L_2 and L_3, maximum length of lateral folioles; W_1, maximum width of the central foliole; W_2 and W_3, maximum width of the lateral folioles.

Table 3. Number of leaves (NL) and total leaf area (TLA- cm^2) of genotypes, Constants β and μ of models; coefficients of determination (r^2); ratio of the length and width raised to the second power (L/W)^2 and grouping of genotypes (single leaves).

Genotype	NL	TLA	Model 1		Model 2			Model 3			(L/W)^2	G
			β	r^2	β	μ	r^2	β	μ	r^2		
STM	45	530	0.709	0.988	0.769	0.974	0.992	0.503	1.819	0.964	3.69	1
SO	26	741	0.687	0.983	0.794	0.964	0.992	0.388	1.970	0.917	3.73	1
RL × LRF -034	29	665	0.693	0.979	0.654	1.016	0.989	0.265	2.133	0.926	3.96	1
SMFL × CWEB-004	37	578	0.692	0.976	0.771	0.968	0.989	0.354	2.049	0.953	3.30	1
SM	41	732	0.713	0.989	0.797	0.969	0.994	0.377	2.020	0.958	3.41	1
VL 71164	27	735	0.723	0.993	0.697	1.010	0.998	0.224	2.231	0.979	3.95	1
RLSTC	43	614	0.675	0.997	0.667	1.000	0.992	0.496	1.756	0.954	4.30	2
SM × CTARG - 044	49	339	0.667	0.986	0.78	0.964	0.967	0.424	1.802	0.952	4.66	2
SMFL × CTC 13-012	40	305	0.670	0.994	0.811	0.935	0.990	0.398	1.913	0.964	4.03	2
RL Al. 02	29	637	0.739	0.994	0.748	0.996	0.997	0.295	0.38	0.988	4.85	3
RL Al. 01	32	696	0.729	0.996	0.758	0.990	0.996	0.429	1.862	0.995	5.50	3
β average			0.700		0.746			0.378				

* ME, Mean absolute and relative error; E, error (if positive; the model overestimated and if negative; the model underestimated the leaf area); R.E., Relative error (represents the percentage of over or underestimate of the model); Model 1: $Y = \beta \cdot (L \cdot W)$; Model 2: $Y = \beta \cdot (L \cdot W)^{\mu}$; Model 3: $Y = \beta \cdot (L)^{\mu}$.

were linear and potential, so they were selected for more detailed analysis. For genotypes with single leaves, three models were chosen: one linear and two potentials; for genotype with compound leaves, six were chosen: three linear and three potential (Table 2).

Models for genotypes with single leaves

All equations of the models individually generated for the genotypes possessing single leaves presented r^2 above 0.9 (Table 3). The constant μ of Model 2 (simple leaf blade) tended to unity, showing that, regardless of the format of the leaf, leaf area is approximately 70% of the area of the rectangle (L.W), with no gains in accuracy with the use of the potential model. When only the length of the midribs as independent variable is used (model 3), the lowest value for constant μ was approximately 1.8, being characterized as potential (Table 3).

As shown in Figure 1, the adjusted models considering the three leaf groups (simple leaf), explained very well the variation of the data presenting excellent adjustment to mathematical models $r^2 \geq 0.99$. It was noticed a proximity to responses of the models when analyzing range in the abscissa axis corresponding to small leaves (L·W ≤ 30 cm, L ≤ 5 cm) (Figure 1A to C). Consequently, the procedure of grouping, expressed by the ratio (L/W)^2, promotes gains in estimates of LA, especially for larger leaves, range in which there is a greater dispersion of the models, regardless of the genotype tested. When considering the leaves grouping based on the relation (L/W)^2, it was possible even the distinction of the access selected from a genotype, as the case of Rangpur lime (RL), in which the selections Aluminum 01 and 02 (group 3) belonged to distinct groups of Santa Cruz (RLSTC) (Group 2) (Table 3).

Table 4. Sum of the errors of the estimation of leaf area (E) of genotypes of single leaves, relative errors (RE) and coefficient of determination (r^2).

Genotype	E (cm^2)	Model 1		Model 2			Model 3			G
		RE (%)	r^2	E (cm^2)	RE (%)	r^2	E (cm^2)	RE (%)	r^2	
STM	-6.19	1.23	0.99	-0.66	0.13	0.99	9.97	1.99	0.95	1
SO	13.26	1.78	0.98	7.91	1.07	0.98	0.38	0.05	0.88	1
RL x LRF -034	11.22	1.69	0.98	9.91	1.49	0.98	32.91	4.94	0.88	1
SMFL x CWEB-004	7.09	1.23	0.98	9.98	1.73	0.98	-22.93	3.97	0.94	1
SM	-11.81	1.61	0.99	-9.50	1.30	0.99	-38.72	5.29	0.92	1
VL 71164	-20.86	2.84	0.99	-26.46	3.60	0.99	-22.07	3.00	0.97	1
RLSTC	15.34	4.78	0.99	17.92	5.59	0.99	60.36	18.83	0.98	2
SM x CTARG – 044	-2.63	0.78	0.99	20.01	5.91	0.99	70.20	20.73	0.95	2
SMFL x CTC 13-012	16.21	5.31	0.99	19.22	6.31	0.99	21.65	7.09	0.95	2
RL Al. 02	-3.95	0.62	0.99	-31.24	4.90	0.99	88.31	13.81	0.98	3
RL Al. 01	4.81	0.69	0.99	-24.77	3.56	0.99	106.80	15.27	0.97	3
*ME.	10.12	1.23		16.21	1.90		39.84	6.20		

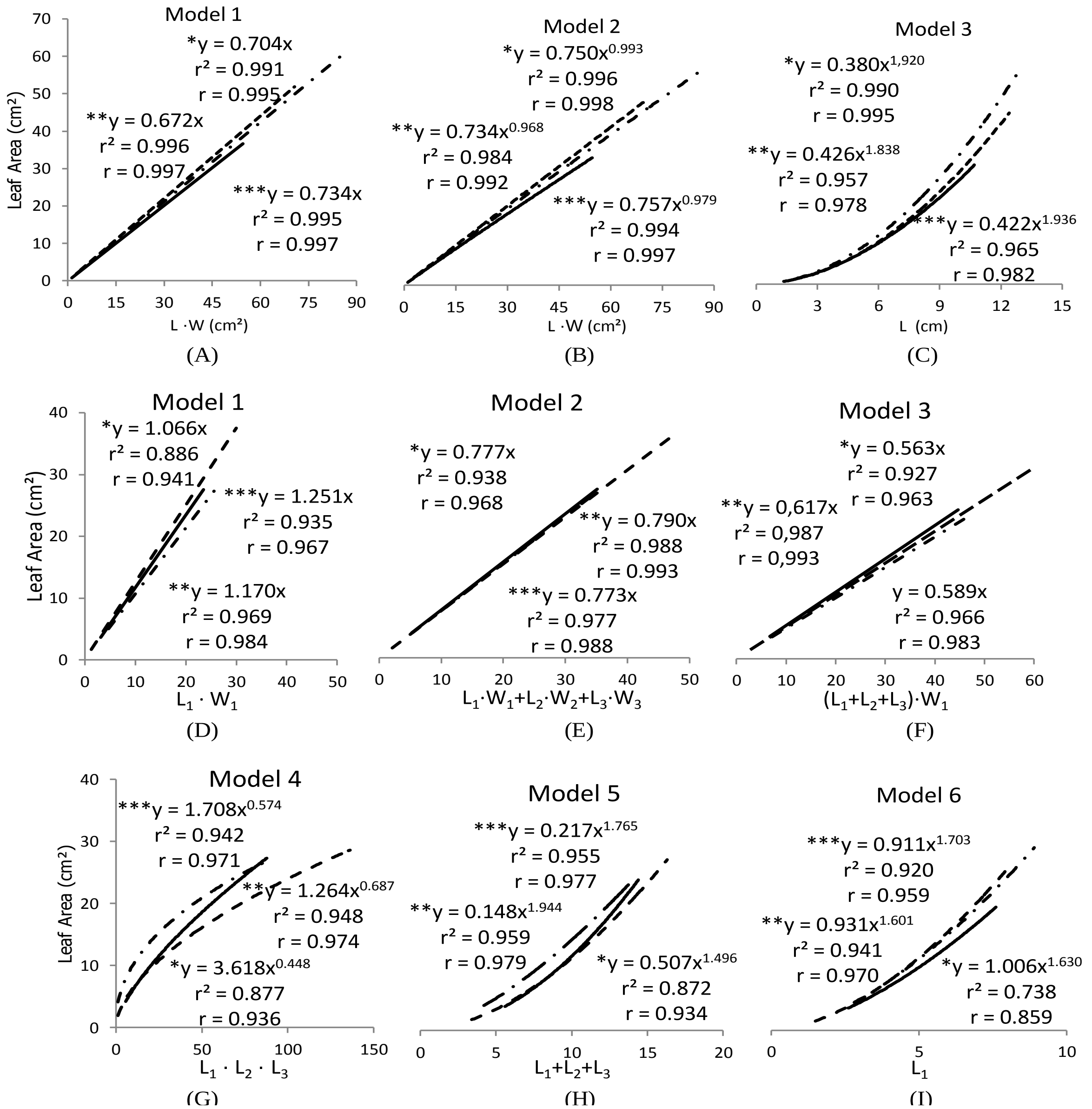
The estimates were based on the models proposed for each group presented in Figure 1.* ME, Mean absolute and relative error; E, Error (if positive, the model overestimated and if negative, the model underestimated the leaf area); R.E., Relative error (represents the percentage of over or underestimate of the model); Model 1: $Y = \beta \cdot (L \cdot W)$, Model 2: $Y = \beta \cdot (L \cdot W)^{\mu}$, Model 3: $Y = \beta \cdot (L)^{\mu}$.

Table 5. Number of leaves (NL), total leaf area (TLA -cm^2).

Genotype	NL	TLA	Model 1		Model2		Model 3		L: $(L_2+L_3)/L_1$	G
			β	r^2	β	r^2	β	r^2		
SM x (RL x TR) - 016	31	495	1.051	0.86	0.731	0.84	0.560	0.93	0.857	1
SM x CTTR - 002	38	492	1.046	0.86	0.779	0.96	0.559	0.96	0.808	1
TH - 051	26	330	1.170	0.97	0.790	0.99	0.617	0.99	0.985	2
SWCT	22	431	1.229	0.94	0.768	0.99	0.590	0.99	1.120	3
TH - 127	22	340	1.263	0.90	0.777	0.98	0.602	0.96	1.100	3
SM x SWCT - 041	28	466	1.273	0.85	0.802	0.97	0.598	0.95	1.132	3
LRF x (RL x TR) - 004	29	432	1.266	0.90	0.773	0.94	0.599	0.93	0.159	3
SM x TRFD – 007	30	349	1.230	0.92	0.752	0.98	0.579	0.96	1.121	3
LFR x (RL x TR) - 005	31	409	1.287	0.89	0.784	0.97	0.596	0.93	1.187	3
SM x CTQT 1431 - 001	38	294	1.254	0.87	0.788	0.97	0.587	0.95	1.197	3
SM x CTARG - 020	35	384	1.205	0.93	0.745	0.97	0.562	0.95	1.130	3
β average			1.207		0.771		0.586			

Constant β used on linear models and respective coefficients of determination; average of the sum of the lateral lengths divided by the central and grouping of genotypes (compound leaves). Model 1: $Y = \beta \cdot (L_1 \cdot W_1)$, Model 2: $Y = \beta \cdot (L_1 \cdot W_1 + L_2 \cdot W_2 + L_3 \cdot W_3)$, Model 3: $Y = \beta \cdot [(L_1 + L_2 + L_3) \cdot W_1]$.

The estimate errors for each genotype, from the use of the adjusted models for each group (Figure 1), are presented in Table 4. In the case of the linear model (Y = β. (L.W)) they were lower in relation to the two powers (Models 2 and 3), with ER ranging from 0.62% to aluminum RL 02 to 5.31% for SMFL x CTC 13-012; and the average deviation the lowest among the three models tested (Table 4). The third model, in which it was used only the length (L) as the independent variable, proved to be comparatively less precise, especially for the genotypes belonging to groups 2 and 3. That result indicates the need of use of all the variables L and W in the estimates of single leaves for a greater precision regardless of the group. Considering that there were different responses depending on the genotype evaluated, with relative error (RE) minimum of 0.05% for SO and maximum of 20.73% for SM x CTARG - 044, proportionally different from the models which used L.W as input variable □ 6.31%. Among the models for simple leaf format, the most appropriate was the linear (Y = β. (L.W)). The advantages are by the high precision on the estimates and ease of practical application, confirming



(A) (B) (C)

(D) (E) (F)

(G) (H) (I)

Figure 1. Regressions fitted for grouped genotypes (A to C - single leaves and D to I - compound leaves) and their coefficients of determination (-··Group 1* - Group 2**, - - -Group 3***, L- maximum length of the leaf, W - maximum width of the leaf, L_1 - maximum length of the central foliole, L_2 and L_3 - maximum length of lateral folioles, W_1 - maximum width of the central foliole, W_2 and W_3 - maximum width of the lateral folioles; axis Y of same scale for the graphics from A to C and D to I).

and justifying its widespread use in the estimate of leaf area in different plant species (Blanco and Folegatti, 2005; Coelho Filho et al., 2005, 2012, Cristofori et al., 2007; Malagi et al., 2010; Sousa et al., 2014; Souza and Amaral, 2015).

Models for compound leaves genotypes

The mathematical models tested fitted well for all genotypes, by the values of $r^2 \geq 0.84$ (Tables 4 and 5). The choice of mathematics ratio $(L_2+L_3)/L_1$, originally based on visual observations of variability, was attested by the high correlation with the constant β, model 1 (Table 5), Spearman's correlation coefficient of 0.98 (figure not shown).

Considering only the linear models (Table 5), there was less variation in the amplitude of the values of the constant β in the third model proposed; therefore, the model was sensitive to changes in the shape of leaves. In a converse way, variations were greater for the first model. Such results probably reflect the number of variables used in each model.

Analyzing the estimates of leaf area within each

Table 6. Number of leaves (NL), total leaf area (TLA-cm²).

Genotype	NL	TLA	Model 4			Model 5			Model 6			G
			β	μ	r^2	β	μ	r^2	β	μ	r^2	
SM × (RL × TR) - 016	31	495	3.458	0.48	0.94	0.321	1.73	0.93	0.764	1.84	0.86	1
SM × CTTR - 002	38	492	3.510	0.42	0.91	0.543	1.42	0.93	0.991	1.58	0.86	1
TH - 051	26	330	1.264	0.69	0.95	0.148	1.94	0.96	0.931	1.60	0.94	2
SWCT	22	431	1.705	0.61	0.92	0.169	1.92	0.94	0.703	1.92	0.87	3
TH - 127	22	340	1.418	0.62	0.92	0.114	2.01	0.95	0.535	2.01	0.84	3
SM × SWCT - 041	28	466	2.368	0.50	0.94	0.337	1.60	0.95	0.866	1.75	0.88	3
LRF × (RL × TR) - 004	29	432	1.981	0.54	0.92	0.291	1.65	0.94	1.260	1.51	0.94	3
SM × TRFD - 007	30	349	1.958	0.52	0.93	0.265	1.66	0.95	0.852	1.71	0.89	3
LFR × (RL × TR) - 005	31	409	1.834	0.55	0.96	0.281	1.65	0.97	1.192	1.54	0.95	3
SM × CTQT 1431 - 001	38	294	1.827	0.51	0.94	0.294	1.58	0.96	1.072	1.53	0.94	3
SM × CTARG - 020	35	384	1.842	0.54	0.97	0.251	1.69	0.97	0.969	1.63	0.88	3
β and μ averages			2.106	0.55		0.274	1.71		0.921	1.70		

Constant β and μ used on models and their respective coefficients of determination, and grouping of genotypes (compound leaves). Model 4: $Y = \beta \cdot (L_1 \cdot L_2 \cdot L_3)^{\mu}$, Model 5: $Y = \beta \cdot (L_1 + L_2 + L_3)^{\mu}$, Model 6: $Y = \beta \cdot (L_1)^{\mu}$

Table 7. Sum of errors, relative errors, coefficient of correlation between the area of each leaf and the estimated area to the linear models of genotypes of compound leaves estimates based on the specific model for each group presented in Figure 1.

Genotype	Model 1			Model 2			Model 3		
	E (cm²)	RE (%)	r²	E (cm²)	RE (%)	r²	E (cm²)	RE (%)	r²
SM × RL × TR) - 016	0.00	0.00	0.93	19.99	4.04	0.93	-4.55	0.92	0.97
SM × CTTR - 002	3.78	0.77	0.93	-6.40	1.30	0.98	2.95	0.60	0.98
TH - 051	-5.92	1.79	0.99	-3.07	0.93	1.00	-2.52	0.76	0.99
SWCT	2.42	0.56	0.97	-0.27	0.06	0.99	0.61	0.14	0.99
TH - 127	-10.19	3.00	0.96	-4.22	1.24	0.99	-11.56	3.40	0.99
SM × SWCT - 041	-10.04	2.15	0.93	-15.62	3.35	0.98	-5.97	1.28	0.97
LRF × (RL × TR) - 004	0.57	0.13	0.97	17.30	4.00	0.98	4.13	0.96	0.98
SM × TRFD - 007	-0.32	0.09	0.97	5.71	1.64	0.99	-0.36	0.10	0.98
LFR × (RL × TR) - 005	-25.03	6.11	0.96	-13.93	3.40	0.99	-16.79	4.10	0.97
SM × CTQT 1431 - 001	-12.71	4.32	0.96	-10.89	3.70	0.99	-5.84	1.98	0.99
SM × CTARG - 020	5.88	1.53	0.97	7.28	1.90	0.99	7.60	1.98	0.98
*ME	7.35	1.48		9.43	1.25		4.97	1.01	

*ME, Mean absolute and relative error, E, Error (if positive, the model overestimated and if negative, the model underestimated the leaf area); R.E., Relative Error (represents the percentage of over or underestimate of the model); Model 1: $Y = \beta \cdot (L_1 \cdot W_1)$, Model 2: $Y = \beta \cdot (L_1 \cdot W_1 + L_2 \cdot W_2 + L_3 \cdot W_3)$, Model 3: $Y = \beta \cdot [(L_1 + L_2 + L_3) \cdot W_1]$.

genotype, based on the adjusted models from each group (Figure 1), it was observed that the largest number of independent variables used in Model 2 reflected the higher values for the coefficient of determination, except in SM x (RL x TR) genotype - 016, in which it was noticed the best fit when using the third model (Table 5). Possibly the greatest number of independent variables of the model 2 increased its sensitivity, regardless of the leaf groups (1, 2 and 3), expressed by the proximity of the angular coefficients obtained (Figure 1E). That result suggested the feasibility of using an average value, regardless of grouping.

Considering that observation, a single regression with the data of 11 genotypes of compound leaves based on that model ($Y = \beta \cdot (L_1 \cdot W_1 + L_2 \cdot W_2 + L_3 \cdot W_3)$ was performed. The value of β is equal to 0.776 and the model explained very well to the values observed by the coefficient of determination of 0.976 (figure not shown). In that case, in function of response independent of the genotype, the lack of concerning with groupings is a positive point. However, there is a need for a greater number of independent variables, which can restrict its use in practice, when the goal is to perform a large number of measures.

The proximity of the results with the use of linear models (Table 7) (average deviation of the relative error

Table 8. Sum of errors, relative errors, coefficient of determination between the average area of each leaf and the estimated area for the potential models of genotypes of compound leaves.

Genotype	Model 4			Model 5			Model 6		
	E (cm^2)	RE (%)	r^2	E (cm^2)	RE (%)	r^2	E (cm^2)	RE (%)	r^2
SM x (RL x TR) - 016	56.29	11.38	0.92	56.07	11.33	0.93	-6.70	1.35	0.84
SM x CTTR – 002	-35.95	7.30	0.97	-44.59	9.06	0.97	-96.44	19.59	0.78
TH – 051	-1.44	0.44	0.97	-1.45	0.44	0.97	-2.30	0.70	0.96
SWCT	-63.63	14.78	0.94	-58.40	13.56	0.95	-56.96	13.23	0.91
TH – 127	-5.46	1.61	0.95	-2.78	0.82	0.97	-0.05	0.01	0.91
SM x SWCT – 041	-13.07	2.80	0.93	-11.43	2.45	0.94	-18.84	4.04	0.89
LRF x (RL x TR) – 004	12.82	2.97	0.95	15.78	3.65	0.96	8.66	2.00	0.95
SM x TRFD – 007	14.18	4.07	0.95	15.05	4.32	0.96	16.44	4.71	0.94
LFR x (RL x TR) – 005	7.59	1.86	0.96	4.98	1.22	0.96	-9.47	2.31	0.96
SM x CTQT 1431 – 001	31.96	10.86	0.94	26.17	8.89	0.96	17.44	5.93	0.96
SM x CTARG – 020	8.91	2.32	0.97	8.53	2.22	0.97	10.04	2.62	0.94
*ME	22.74	4.07		22.23	3.96		24.46	4.24	

Estimates based on model specific to each group presented in Figure 1. *ME, Mean absolute and relative error; E, Error (if positive, the model overestimated and if negative, the model underestimated the leaf area), R.E., Relative error (represents the percentage of over or underestimate of the model); Model 4: $Y = \beta \cdot (L_1 \cdot L_2 \cdot L_3)^{\mu}$, Model 5: $Y = \beta \cdot (L_1 + L_2 + L_3)^{\mu}$, Model 6: $Y = \beta \cdot (L_1)^{\mu}$.

(RE) ranging from 1.01 to 1.48; and average deviation of error (E) ranging from 4.97 to 9.43), justifies the use of the Model 1 $Y = \beta \cdot (L_1 \cdot W_1)$, due to its greater simplicity and practicality, confirming one more time the widespread use by different authors.

Analyzing the potential models, it was found that the constant μ for groups in the leaf model 4 ($Y = \beta \cdot (L_1 \cdot L_2 \cdot L_3)^{\mu}$ were lower than one (Table 6), suggesting a reduction in the estimate rate of leaf area according to the increase of leaf length (Figure 1 G), what can cause major errors in the estimate of the area of leaves with high length. On fifth and sixth models, once the exponents are larger than the unit (Table 6), the angular coefficient of the tangent lines to the curve increases with the elevation of the value of the input variable, the opposite of what happened in the fourth model (Figure 1G to I).

Despite the high accuracy of the estimates obtained individually for the genotypes, in relation to the potential models 4, 5 and 6, according to the coefficients of determination (Table 8), when analyzing the statistical parameters 'average error' and 'standard error', there is a greater precision and accuracy when used with the linear models (Tables 7 and 8).

In a general way, the estimates of leaf area for all genotypes using the six models proposed resulted in high coefficients of determination (>0.88). Exception for SM x CTTR - 002 and SM x (RL x TR) - 016, with respective values of 0.78 and 0.84; both for the sixth model. When compared only the potential models, the fifth model presented the best adjustment, lower errors of estimate (E and ER) and a higher r^2 (Table 8). Among the linear models, due to the proximity of the errors and high values of r^2, the model Y = β. L.W is very interesting for the greater ease of practical determination, favoring the largest sample in studies of plant growth. Earnings comparatively small in accuracy can be obtained with the use of the linear models 2 and 3 ($Y = \beta \cdot (L_1 \cdot W_1 + L_2 \cdot W_2 + L_3 \cdot W_3)$, Model 3: $Y = \beta \cdot [(L_1 + L_2 + L_3) \cdot W_1]$, despite the larger number of variables to be measured. Compared to the linear, it can provide errors of estimates higher than the linear, for some genotypes. Different types of mathematical models have been generated for different plant species and leaf type. However, the models are developed for specific species and are usually restricted to few varieties or form of leaf, as performed by Coelho Filho et al. (2005, 2012); Malagi et al. (2010); Souza and Amaral (2015) and Toebe et al. (2012). In the present study different mathematical models of leaf area estimate with different levels of accuracy were developed, with advantages of being applicable to any genotype of citrus just requiring the knowledge of biometric relations that differentiate the leaf shape.

Conclusions

The greater precision of estimates is achieved when using specific models for each type (simple and compound leaves) and separating these types in homogeneous groups in relation to leaf dimensions and folioles. For simple and compound leaves, the respective linear models (Y = β. L. W; Y = β.L_1.W) showed the best statistical performance, besides being easy to use. The potential models Y= β L^{μ} and Y= β L1$^{\mu}$, respectively for simple and compound leaves, require only one input biometric variable, which in a practical way, allow an increase in the number of repetitions, but provide errors of estimates higher than linear models. The model $Y = \beta (L_1 \cdot W_1 + L_2 \cdot W_2 + L_3 \cdot W_3)$ has been sensitive in the estimates of leaf area, independent of the grouping of compound leaves genotypes, for a $\beta = 0.7755$.

Conflict of interests

The authors have not declared any conflict of interests

ACKNOWLEDGMENTS

AGVP student scholarship was funded by Macroprograma/EMBRAPA. The work was supported by the CNPq (grant/research 305307/2012-6; coordinated by MACF).

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