

EVALUATION OF NON-LINEAR TAPER EQUATIONS FOR PREDICTING THE DIAMETER OF EUCALYPTUS TREES¹

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ABSTRACT – This study aims to evaluate non-linear stem taper models for predicting the pre-commercial diameter of eucalyptus trees and to analyze the effect of genotype on stem taper. The treatments comprise three different genotypes of *Eucalyptus* sp. in a 3 × 3 m plantation spacing. Seventy sample trees aged 10 years were felled for each treatment. The outside bark diameter measurements were taken at 0.5 m; 1.0 m; 1.5 m; 2.0 m, and then at intervals of 2.0 m till the top of the stem. Four non-linear models were evaluated, namely, the sigmoid model of Garay (1979), the variable exponent model of Kozak (1988), the segmented model of Max and Burkhart (1976), and the compatible model of Demaerschalk (1972). The performance of the models was assessed using the following statistical validation methods: correlation coefficient, standard error of estimate, mean bias, bias variance, root mean squared error, and mean absolute deviation. Graphical analysis of residues was used to evaluate the accuracy and precision of the estimates. Compared with other models, the variable exponent model of Kozak (1988) best described the stem profile, and predicted the total volume of the trees. The identity test showed that the stem profile is affected by the genotype.

Keywords: *Regression analysis; Variable exponent model; Genotypes*

AVALIAÇÃO DE FUNÇÕES DE AFILAMENTO NÃO-LINEARES PARA ESTIMAÇÃO DE DIÂMETROS COMERCIAIS EM ÁRVORES DE EUCALIPTO

RESUMO – Este trabalho teve como objetivo a escolha de um modelo de afilamento para melhor estimar o perfil médio de árvores de diferentes clones de eucalipto, verificando se uma mesma função pode ser empregada para três genótipos distintos de eucalipto. Os tratamentos consistiram em diferentes clones de eucalipto plantados sob o espaçamento de 3 x 3 m. Para cada tratamento foram abatidas cerca de 70 árvores-amostra aos 10 anos de idade. Os diâmetros das seções ao longo do fuste foram medidos a partir da base em 0.5 m; 1.0 m; 1.5 m; 2.0 m e, a partir daí, em intervalos de 2.0 m. Foram testados quatro modelos não-lineares: Garay (1979), Kozak (1988), Max e Burkhart (1976) e Demaerschalk (1972). As estatísticas utilizadas para avaliar os ajustes foram: coeficiente de correlação entre diâmetros observados e estimados, erro-padrão residual, bias (média dos erros), variância do bias, raiz quadrada do erro quadrático médio e a média das diferenças absolutas. O modelo escolhido para representar os tratamentos, pela melhor performance de ajuste, foi o de Kozak (1988). Testes de identidade de modelo foram aplicados para verificar igualdade no formato do fuste entre os tratamentos. Com base nos resultados, a hipótese de igualdade na forma do fuste dos genótipos foi rejeitada, ao nível de 5% de significância. Assim, pôde-se concluir, que existe efeito do genótipo no afilamento do fuste de eucalipto.

Palavras-Chave: *Análise de Regressão; Equação expoente-forma; Genótipo.*



1. INTRODUCTION

The term ‘taper’ was defined by Husch et al. (1993) to describe the rate of diameter decrease in the stem of a tree. Taper equations or functions can predict the narrowing rate or diameter along the bole, which make them very useful techniques for wood assortments. Höjer (1903) conducted the first studies on tree taper. Thereafter, two noteworthy studies by Kozak et al. (1969) and Demaerschalk (1972) were published. Research on stem taper of trees in Brazil began in the early 1970s in *Pinus* and eucalyptus forest plantations (Silva, 1974; Campos and Ribeiro, 1982; Guimarães and Leite, 1992; Schneider et al., 1996).

Predicting the diameter along the base of the stem is one of the greatest challenges of taper functions given the presence of geometric distortions in this portion (Kozak, 2004; Souza et al., 2008). Based on the variation of geometrical shapes, Max and Burkhart (1976) proposed a model that divides the stem into three sections expressed using three separate sub-models, which together represent the global taper equation. The same basic concept introduced a range of segmented taper equations (Demaerschalk and Kozak, 1977; Parresol et al., 1987). Currently, there exist several models that describe the stem form of trees, and they are broadly categorized into two groups: segmented and non-segmented taper equations. Non-segmented taper equations are classified as polynomial, sigmoid, compatible, or incompatible (Lima, 1986; Pereira et al., 2005; Campos and Leite, 2013). They may also be defined using multivariate analysis (Guimarães and Leite, 1992).

Compatible models show consistency between their taper and volume predictions, where the taper equations are the first derivative of the volume equations. Segmented models consider the sectioning of the stem resulting in a more detailed form description (Lima, 1986; Garcia et al., 1993). The variable exponent (Kozak, 1988) and sigmoid models include inflection points that enable them to outline bole diameters that are near the ground more appropriately. The variable exponent model of Kozak (1988) assumes one inflection point (at 0.25 of the total height) and an exponential pattern of decreasing diameter sizes from the tree bottom to top. The sigmoid taper functions are based on biological growth models so that they can describe the natural shape of the tree trunks (Lima, 1986; Muhairwe, 1999).

Present studies have explored a range of taper functions having significant variation in their

performances and results when applied on empirical data. There exist unique functions that, for a particular genotype, outperform the different models, but these yield biased predictions in other instances (Morley and Little, 2012) and thus cannot be universally applied. Several taper functions can generate satisfactory results for most cases in terms of prediction accuracy (Andrade, 2014), which makes assessment a complex task.

Two desirable properties are required in a taper model: the diameter at the maximum height should be null, and the diameter at 1.3 m should be equal to the field measurements of the diameter at breast height (DBH) (Campos and Leite, 2013). Weiskittel et al. (2011) highlighted that comparative studies of taper functions based only on modeling performances are not justifiable, and a biological explanation for the phenomena is important in selecting the appropriate equation. The present study explored well-established taper models that could provide a biological explanation. Therefore, we aimed to compare the non-linear taper models in predicting the pre-commercial diameter of eucalyptus trees, and verify if the same taper model could be employed for three distinct eucalyptus genotypes.

2. MATERIAL AND METHODS

The dataset used in this study comprises trees sampled from eucalyptus stands located at the Bahia state in Brazil. Seventy sample trees (aged 10 years) of each genotype were harvested, constituting three treatments: genotype 1 (G1), genotype 2 (G2), and genotype 3 (G3). The plantation spacing was similar (3 × 3 m) for all treatments. The sampled trees presented a minimum and maximum DBH of 6 cm and 30 cm, respectively, and the total height ranged between 12–42 m.

The four non-linear taper models tested in each genotype were as follows: the sigmoid model of Garay (1979), the Kozak (1988) variable exponent model, the segmented model of Max and Burkhart (1976), and the compatible model of Demaerschalk (1972). These models are given below.

Garay (1979):

$$d = \text{DBH} \{ \beta_0 [1 + \beta_1 \ln(1 - \beta_2 h_1^{\beta_3} H - \beta_3)] \} + \varepsilon \quad \text{EQ1}$$

Kozak (1988):

$$d = \alpha_0 \text{DBH}^{\alpha_1} \alpha_2^{\text{DBH}} \left(\frac{1 - \sqrt{Z}}{1 - \sqrt{p}} \right)^{\beta_1 Z^2 + \beta_2 \ln(Z + 0,001) + \beta_3 \sqrt{Z} + \beta_4 e^Z + \beta_5 \text{DBH} \cdot H^{-1}} + \varepsilon \quad \text{EQ2}$$

Max and Burkhart (1976):EQ3

$$d = DBH \sqrt{\beta_1(Z-1) + \beta_2(Z^2-1) + \beta_3(\alpha_1-Z)^2 I_1 + \beta_4(\alpha_2-Z)^2 I_2} + \varepsilon$$

Demaerschalk (1972): EQ4

$$d = 10^{\beta_0} DBH^{\beta_1} H^{2\beta_2} (H-h)^{2\beta_3} + \varepsilon$$

Here, d denotes the estimated diameter (cm) at hi height; H denotes the total tree height (m); DBH denotes the diameter (cm) at 1,3 m; $\alpha_0, \alpha_1, \alpha_2, \beta_0, \beta_1, \beta_2, \beta_3, \beta_4, \beta_5$ denote the model parameters to be estimated; $Z = hi/H, p = 0.25, e$ denotes the Napier's constant; ε denotes the random error, which is $\varepsilon \sim N(0, \sigma^2)$; and I1 and I2 denote conditional variables where:

$$I1 = 1, \text{ if } \alpha_1 - Z \geq 0;$$

$$I1 = 0, \text{ if } \alpha_1 - Z < 0;$$

$$I2 = 1, \text{ if } \alpha_2 - Z \geq 0;$$

$$I2 = 0, \text{ if } \alpha_2 - Z < 0.$$

The models were fitted using the quasi-Newton optimization algorithm implemented in STATISTICA 12.0 (2014) software. For each fitted model, the following statistics were calculated: correlation coefficient between the observed and predicted values (r_{yy}), standard deviation (s_{yx}), bias, bias variance (s_{bias}^2), root mean squared error (RMSE), and mean absolute deviation (MAD) (Islam et al., 2009; Campos and Leite, 2013): EQ5

$$r_{\hat{Y}Y} = \frac{n^{-1} \sum_{i=1}^n (\hat{Y}_i - \hat{Y}_m)(Y_i - \bar{Y})}{\sqrt{[n^{-1} \sum_{i=1}^n (\hat{Y}_i - \hat{Y}_m)] [n^{-1} \sum_{i=1}^n (Y_i - \bar{Y})^2]}} \quad RMSE = \sqrt{n^{-1} \sum_{i=1}^n (Y_i - \hat{Y}_i)^2}$$

$$Bias = n^{-1} \sum_{i=1}^n (\hat{Y}_i - Y_i) \quad MAD = n^{-1} \sum_{i=1}^n |\hat{Y}_i - Y_i|$$

$$s_{yx} = \sqrt{(n-p)^{-1} \sum_{i=1}^n (Y_i - \hat{Y}_i)^2} \quad s_{bias}^2 = \frac{\sum [bias - (Y_i - \hat{Y}_i)]^2}{n-1}$$

Here, n denotes the number of observations; p denotes the number of coefficients or parameters; \hat{Y}_i denotes the i^{th} observed value; Y_i denotes the i^{th} estimated value; \bar{Y} denotes the mean of the observed values, and \hat{Y}_m denotes the mean of the estimate \hat{Y}_i .

The assessment of the fitted models compared their ability to estimate the diameter along the stem using fit statistics and graphical residual analysis. The models were further tested for their ability to predict individual tree volumes in different DBH classes.

Given that the parameters of the outperformed model were obtained for each genotype, they were compared based on the model identity test proposed by Regazzi and Silva (2004). This method verified if different non-linear regression lines could be combined based on the following definitions:EQ6

$$y = \sum_{i=1}^h D_i f(\theta_i; x) + \varepsilon \quad (\text{Complete Model})$$

$$y = f(\theta; x) + \varepsilon \quad (\text{Reduced Model})$$

Here, y denotes the d vector of the dependent or response variables; x denotes the vector of the explanatory variables of the complete and reduced models; f denotes the non-linear function; q_i denotes the vector of the unknown parameters to each i treatment; h represents the number of equations (comparative cases); $D_i = 1$ and $D_i = 0$, to each treatment $i = \{1, \dots, h\}, i' = \{1, \dots, h\}$ being $i \neq i'$; q denotes the vector of the unknown parameters of the reduced models (combined data) tested under the normality

$$F(H_0) = \frac{SQ_{R(H_0)} \cdot (pH-p)^{-1}}{SQ_{Res}(C) \cdot (n-pH)^{-1}}$$

$$SQ_{R(H_0)} = SQ_{Par}(R) - SQ_{Par}(C);$$

$$SQ_{Par}(C) = \sum y_i^2 - \sum \sum (y_h - w_h)^2$$

$$SQ_{Par}(R) = y_r^2 - \sum (y_r - w_r)^2$$

$$GL_{R(H_0)} = GL_C - GL_R$$

$$GL_{Res} = n - p.H$$

$$F_{tab} = F_{\alpha}(GL_{R(H_0)}; GL_{Res})$$

Here, $SQ_{R(H_0)}$ denotes the squared sum of reduction because of the null hypothesis (H_0); $SQ_{Par}(C)$ denotes the squared sum of parameters of the complete model; $SQ_{Par}(R)$ denotes the squared sum of parameters of the reduced model; $SQ_{Res}(C)$ denotes the squared sum of residues of the complete model; α denotes the significance level; $GL_{R(H_0)}$ denotes the degrees of freedom of reduction because of the H_0 hypothesis; and GL_{Res} denotes the degrees of freedom of residues. If $F \geq F_{tab}$, a significant difference exists among the stem form of the compared genotypes.

3.RESULTS

The model parameters were estimated at 5% significance level (Table 1). All models obtained acceptable fit statistics to the data of the different treatments, yielding r_{YY} values up to 0.9 and low standard errors (s_{yx}) ranging between 3–7% (Table 2).



Table 1 – Parameter estimates of four non-linear taper models for comparison with three eucalyptus genotypes.
Tabela 1 – Estimativa dos parâmetros dos quatro modelos de afilamento não-lineares ajustados para três genótipos de eucalipto.

Models	Parameters	Genotypes		
		G1	G2	G3
Garay (1979)	β_0	1.107340*	1.190890*	1.198089*
	β_1	0.414265*	0.296575*	0.246004*
	β_2	0.895645*	0.961870*	0.982824*
	β_3	0.525989*	0.275107*	0.232351*
Kozak (1988)	α_0	0.743504*	1.303963*	1.085063*
	α_1	1.079283*	0.781925*	0.888015*
	α_2	0.995487*	1.009075*	1.003484*
	β_1	-0.307557*	-0.388695*	-0.047764*
	β_2	-0.091382*	-0.028682*	-0.047157*
	β_3	0.741395*	-0.149235*	-0.037372*
	β_4	0.126891*	0.436131*	0.231334*
	β_5	-0.372076*	-0.092661*	0.032447*
Max and Burkhart (1976)	α_1	0.905747*	0.917845*	0.866042*
	α_2	0.026687*	0.063157*	0.069662*
	β_1	-4.245083*	-5.185282*	-4.18163*
	β_2	1.910249*	2.442356*	1.867851*
	β_3	-1.550061*	-2.074024*	-1.80369*
Demaerschalk (1972)	β_4	541.005660*	87.561162*	89.320141*
	β_0	0.030710*	0.081341*	0.034373*
	β_1	1.011851*	0.958780*	0.924798*
	β_2	-0.327240*	-0.673794*	-0.547186*
	β_3	0.632890*	0.658029*	0.592764*

Onde: * = Significant at 5% probability; β_k, α_k = Estimated Model Parameters.

Table 2 – Fit statistics of four non-linear models for three eucalyptus genotypes.
Tabela 2 – Estatísticas de Qualidade de Ajuste das quatro equações ajustadas para três genótipos de eucalipto.

Model	Genotype	Fit statistics					
		$r_{\hat{y}y}$	s_{yx} (%)	Bias (%)	Bias (cm)	s^2_{bias}	MAD (cm)
Garay (1979)	G1	0.995	4.577	0.080 ^{ns}	0.011 ^{ns}	0.396	0.462
	G2	0.995	4.890	-0.352*	0.043*	0.360	0.460
	G3	0.994	5.363	-0.349*	0.044*	0.447	0.513
Kozak (1988)	G1	0.997	3.934	0.017 ^{ns}	0.002 ^{ns}	0.293	0.395
	G2	0.996	4.551	0.018 ^{ns}	0.002 ^{ns}	0.313	0.417
	G3	0.994	4.995	0.037 ^{ns}	0.005 ^{ns}	0.389	0.460
Max and Burkhart (1976)	G1	0.996	4.195	0.092*	0.013*	0.333	0.424
	G2	0.995	4.883	-0.372*	0.046*	0.359	0.465
	G3	0.994	5.085	-0.356*	0.044*	0.402	0.487
Demaerschalk (1972)	G1	0.995	4.833	0.030 ^{ns}	0.004 ^{ns}	0.442	0.447
	G2	0.993	5.795	-0.097*	0.012*	0.508	0.504
	G3	0.992	6.143	0.001 ^{ns}	0.001 ^{ns}	0.589	0.520

Where, $r_{\hat{y}y}$ = correlation coefficient; s_{yx} = standard error of estimate; s^2_{bias} = bias variance; MAD = mean absolute deviation; * = significantly different from zero at 5% probability by one sample *t*-test; ^{ns} = significantly equal to zero at 5% probability by one sample *t*-test.

The Kozak (1988) model presented the highest correlation coefficient ($r_{\hat{y}y}$) values and the lowest values of bias, indicating the most accurate model to fit the data. The statistics in the precision of estimates, s_{yx} (%), did not show a large variation throughout the

assessment. However, the Kozak (1988) variable exponent model and the segmented model of Max and Burkhart (1976) showed the most precise results, whereas the compatible model of Demaerschalk (1972) presented the lowest precision for the three genotypes.

We tested bias using a one-sample *t*-test at 5% significance level to verify its equality from zero (Table 2). This test evaluates the significant difference between the calculated or resulted bias (mean error) and a mean value equal to 0 (null hypothesis), considering bias or error variance (s^2_{bias}) and repetitions of each case (Islam et al., 2009). This assessment resulted in non-significant values of bias for all treatments in Kozak (1988). In contrast, the bias in the segmented model of Max and Burkhart (1976) is statistically different from zero for all cases.

The bias consists in a good statistic for accuracy assessment, but it should be interpreted carefully. For example, the resulting predictions in a modeling process can overestimate certain regions of the dataset, whereas underestimation can occur in other sections. The resulting values of bias can move closer to zero given that opposite trends cancel each other. To overcome this impasse, Muhairwe (1999) suggested MAD for a more correct interpretation of prediction errors. In the present study, MAD values vary between 0.4 and 0.6 cm. For G1, the sigmoid model of Garay (1979) showed the highest MAD values. Similarly, the compatible model of Demaerschalk (1972) presented the highest values for G2 and G3. High values of these statistics indicate a broader range of error dispersion of estimates.

The analysis of residual dispersion of the models tested (Figure 1) showed errors along the different sections of the stem, given that the largest and smallest diameter can be found at the bottom and top of the stem, respectively. The compatible model of Demaerschalk (1972) presented the greatest dispersion of errors for all treatments. The sigmoid model of Garay (1979) presented the greatest diameter estimate error for G1, whereas good performances could be observed for G2 and G3. For all treatments relative to the compatible and sigmoid models, the segmented model of Max and Burkhart (1976) and the Kozak (1988) variable exponent model showed better potential for diameter prediction, especially for the largest diameter, and concentrating the errors closer to zero. The good fit of the two models can be observed in the graphical representation of case percentage per residue classes (Figure 1), where they presented the highest percentage of cases around the classes of 0%.

Despite the large number of errors in diameter prediction, the compatible model of Demaerschalk (1972) did not show the same inaccuracy in predicting the

total volume of trees for all genotypes (Table 3). The compatible model along with the Kozak (1988) variable exponent model showed the most accurate predictions for individual volume in all size classes. For G3 and G4, all models underestimated the small trees, and the most excessive negative bias is presented by the segmented model of Max and Burkhart (1976) and the sigmoid model of Garay (1979).

Given that the variable exponent taper equation had outperformed the estimation of diameters and individual volumes, and its operational convenience of fitting in the segmented models, the Kozak (1988) variable exponent model was chosen for further tests of treatment effects on the tree bole.

A model identity test was used to compare the stem profiles of the treatments estimated by Kozak (1988). Table 4 summarizes the comparison results. The effect of the genotype was observed among the treatments as shown in the resulting significant values.

The difference found in the stem form in all treatments suggests that a single model can be used in a management plan for wood assortments. However, the model parameters must be calculated for each treatment, i.e., for each genotype, a specific equation must be used.

4. DISCUSSION

The sigmoid model of Garay (1979) has shown satisfactory results, although not the best performance, for modeling tree stems of eucalyptus, *Pinus*, and teak plantations (Nogueira et al., 2008; Leite et al., 2011; Campos et al., 2014; Andrade, 2014). The sigmoid model of Biging (1984) was also highlighted in stem taper studies as shown in Soares et al. (2011) for natural forests in Brazil. The successful performances of sigmoid equations are attributed to their derivation from biological growth models, where the proposed taper equations attempt to establish the same relation on trunk narrowing from ground to the tree top.

The compatible model of Demaerschalk (1972), which is one of the most popular and widely used in Brazil (Andrade, 2014), showed low ability for estimating the diameter at the bottom of the stem in eucalyptus trees, but performed well in individual tree volume estimates. This result can be explained by the restrictions on the parameters of the model, which leads to an individual tree volume equation through integration

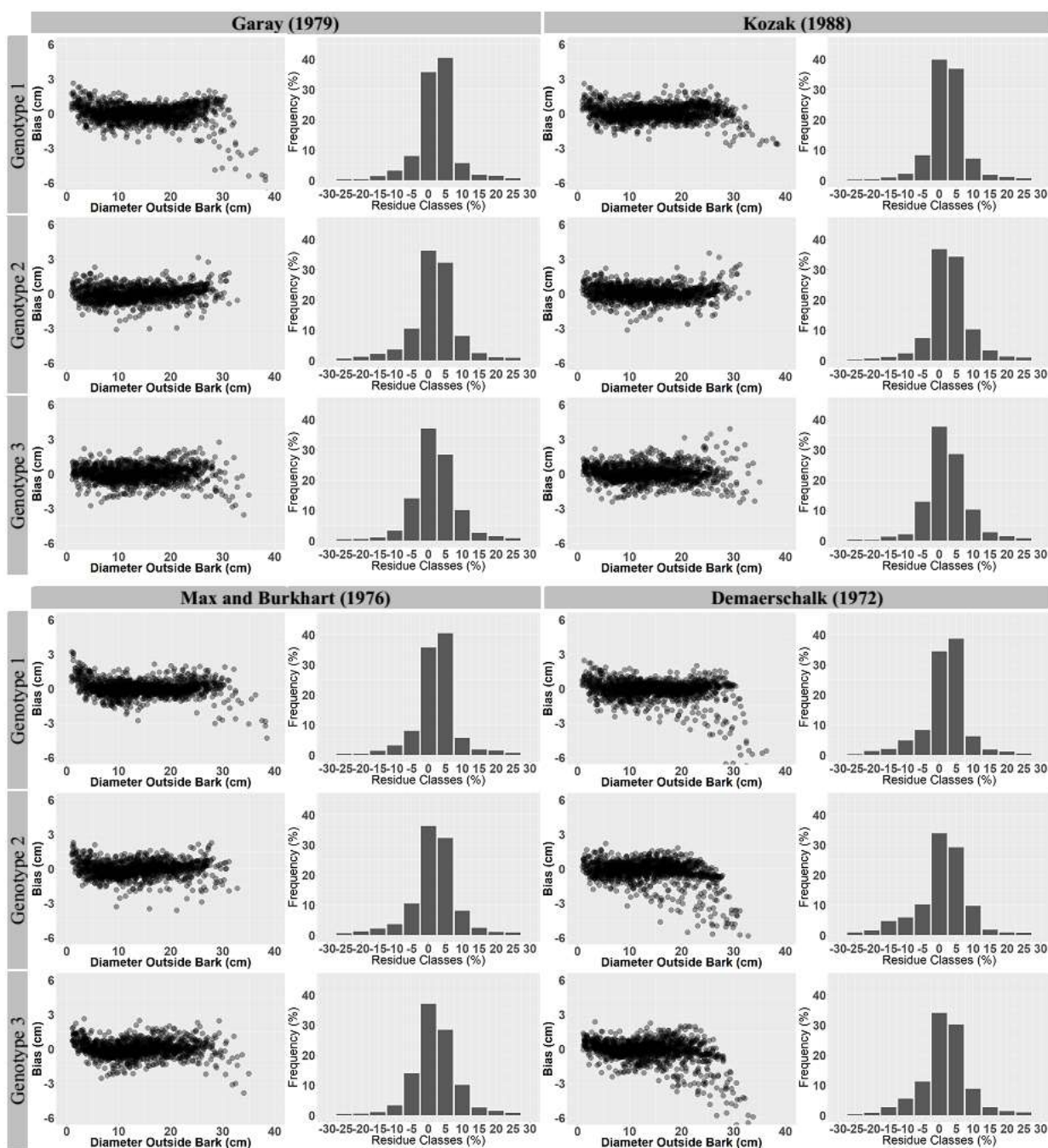


Figure 1 – Distribution of residues of diameter estimates (cm) as a function of the observed diameters, and cases percentage per residue classes of the estimated diameter for models of Garay (1979), Kozak (1988), Max and Burkhart (1976), and Demaerschalk (1972).

Figura 1 – Distribuição dos resíduos das estimativas de diâmetro, em cm, em função do diâmetro observado, e, percentagem de casos por erro percentual das estimativas de diâmetros dos modelos de Garay (1979), Kozak (1988), Max e Burkhart (1976) e Demaerschalk (1972), em árvores de eucalipto.

Table 3 – Validation statistics for individual tree volume (m³ per tree) by diameter at breast height classes.
Tabela 3 – Estatísticas de Validação para a estimativa do volume total (m³ por árvore) para cada classe de DBH.

Centro de Classe (DBH)	n	Garay (1979)		Kozak (1988)		Max and Burkhart (1976)		Demaerschalk (1972)	
		Bias	RMSE	Bias	RMSE	Bias	RMSE	Bias	RMSE
		(%)	(%)	(%)	(%)	(%)	(%)	(%)	(%)
G1:									
1	12	0.647	7.292	0.308	7.617	0.682	7.577	0.310	8.539
2	12	0.841	7.976	0.801	7.943	0.807	7.807	1.390	8.929
3	12	1.103	7.539	0.492	6.924	1.137	7.091	0.933	7.891
4	15	0.267	7.735	0.020	6.098	0.231	6.586	0.007	7.993
5	12	1.648	7.570	1.601	5.799	1.687	5.588	1.6930	8.419
6	7	1.868	9.011	1.462	7.855	1.828	8.020	1.941	9.888
G2:									
1	11	8.156	18.306	3.619	10.873	8.220	18.172	9.060	15.170
2	13	5.593	12.661	1.498	8.749	5.625	12.111	0.623	13.346
3	14	2.898	12.246	1.337	11.619	2.908	11.937	0.083	14.183
4	14	1.281	8.606	0.618	7.073	1.880	8.332	1.251	7.399
5	14	0.619	8.107	0.536	7.007	0.621	6.302	0.605	7.938
6	7	1.140	5.262	0.210	4.527	1.144	5.686	0.946	4.7470
G3:									
1	12	8.661	14.138	1.021	9.108	8.671	14.100	1.612	10.311
2	11	8.019	11.649	2.482	8.391	8.001	11.769	2.677	9.093
3	16	1.583	9.321	0.796	8.286	1.558	8.802	1.389	12.167
4	13	0.483	10.442	0.417	9.570	0.405	9.118	0.381	9.520
5	13	0.228	9.044	0.095	7.271	0.266	7.189	0.120	7.482
6	7	2.479	9.420	0.706	8.518	2.527	9.497	0.048	9.054

Where: n = number of sampled trees by DBH class; MAD = mean absolute deviation; RMSE = root mean square error (RMSE was used instead of s_{yx} because of the low number of observations for some DBH classes).

Table 4 – Parameter estimates of Kozak (1988) taper model for comparison of model equality of the genotypes and F value for the identity test.

Tabela 4 – Estimativas dos parâmetros do modelo de Kozak (1988), para comparação da igualdade de tratamentos e correspondente estatística F do teste de identidade.

Treatments	Estimates of Reduced Model Parameters								F(H ₀)
	α_1	α_2	α_3	β_1	β_2	β_3	β_4	β_5	
G1 × G2 × G3	1.126417	0.861247	1.005866	0.11343	0.05241	0.214200	0.180505	0.01327	14.58*
G1 × G2	1.154825	0.843323	1.007321	0.16495	0.07089	0.497001	0.099817	0.06878	43.26*
G1 × G3	0.986572	0.936553	1.00191	0.13347	0.08122	0.520698	0.098094	0.16346	23.48*
G3 × G5	1.186154	0.836148	1.006253	0.16368	0.04264	0.02765	0.279462	0.00504	30.27*

*Significant at 5% probability.

(Weiskittel et al., 2011). The generation of accurate volume estimates was insufficient to achieve satisfactory performance in describing the stem profile of the trees. Nevertheless, Môra et al. (2014) used this compatible model to yield estimates with a low bias for eucalyptus trees aged 8 years.

The segmented model of Max and Burkhart (1976) outperformed the variable exponent model of Kozak

(1988) in some sections of the stem. The performance of the segmented model for diameter estimates was not the most accurate, but showed better results than the sigmoid and compatible models. Except for the variable exponent model of Kozak (1988), the segmented model of Max and Burkhart (1976) showed lower dispersion of errors. Andrade et al. (2014) and Muhairwe (1999) also confirmed in comparison with the exponential and

segmented models that despite the satisfactory performance of the segmented model of Max and Burkhart (1976), it did not present the best performance, which agrees with the results of the present work. Souza et al. (2008) tested some segmented models for eucalyptus trees and obtained the best results using the segmented model of Max and Burkhart (1976). Muhairwe (1999) confirmed that this model showed better results using data (sample trees) containing a low range of DBH and H, or even when the models were fitted by the diameter class. The segmented model of Max and Burkhart (1976) has the disadvantage of additional computational demands on simultaneous fitting of equations and the significant variation of the initial value of the parameters found in literature.

The exponential model of Kozak (1988), which is also called the variable exponent equation, showed great flexibility to describe the stem form of the genotypes, yielding accurate diameter and volume estimates. The successful performances of Kozak (1988) in predicting the diameters are attributed to the focus given by the author on the proposed equation, which assumptions are centered in modeling the tree bole. Kozak (1988) proposed a model whose restrictions determined a fixed inflection point and considers the geometric form variations along the stem, such as neiloid, paraboloid, and conic form. Similar to Andrade (2014), working with eucalyptus aged up to seven years, the performance of the estimates by Kozak (1988) was better than the compatible and sigmoid models. The good performance of this model could be associated with the size of the sample trees. The assumed inflection point (0.25 of the total height) was the assigned value chosen by the author of the equation in the original work for large trees in Canada. Modeling the stem taper of native eucalyptus trees in Australia, Muhairwe (1999) confirmed a better fit of the Kozak (1988) model to large trees in accordance with this study, and encourages the use of these equations for subsequent studies. Although the inflection point is fixed to eucalyptus and *Pinus* trees, this value may vary and should be changed for other tree species with previous estimation of the rate over the dataset.

The models of Max and Burkhart (1976) and Kozak (1988) showed the best performances for modeling the largest diameters, i.e., the diameter at the base region of the stem tree. Souza et al. (2008) elucidated that based on the occurrence of the greatest deformation of the stem in a tree with an abrupt change of geometric form, a consequent variation in the stem diameter values occurs. Bias related to small values of diameter estimates

can be tolerated because of its negligible effect on commercial volume calculus. However, when related to larger diameters, bias has an increasing effect and should be accounted for in cases where these diameters occur in relevant commercial sections (Figueiredo Filho et al., 1996).

Even if the parameters in Kozak (1988) were not restricted to generate a volume equation similar to the compatible models, the variable exponent model showed the most accurate individual tree volume estimates in this comparison. Goodwin (2009) in a study listing advantages and disadvantages of the taper models, points to the low ability of Kozak (1988) for modeling small trees of some species. Therefore, it is suggested that for the recognition of the variable exponent model as a reference to the stem taper of the eucalyptus trees, its accuracy on the estimate age classes can be evaluated, similar to Figueiredo Filho et al. (2015) for *Araucaria angustifolia* in southern Brazil.

5. CONCLUSION

The variable exponent model of Kozak (1988) was the model that fitted stem taper data in the most suitable manner, presenting the most accurate estimates for diameter and individual tree volume.

Based on Kozak (1988), it was possible to conclude that the genotype has a significant effect on the stem taper of eucalyptus trees, which must be considered when estimating the model parameters.

6. REFERENCES

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