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A new site-specific height-diameter model for Crimean pine stands in the Black Sea Backward Region, Türkiye†

Ferhat Bolat*, Alkan Günlü and İlker Ercanlı

Çankırı Karatekin University, Faculty of Forestry, Department of Forest Engineering, 18200, Çankırı/Türkiye

*Corresponding author: fbolat@karatekin.edu.tr

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Abstract

Background: Relationship between height (H) and diameter (D) highly depends on site conditions and stand structures. In this regard, this study aimed to build a new site-specific model based on the Chapman-Richards function, for the Crimean pine stands in the Black Sea Backward Region of Türkiye.

Methods: The model was developed using the mixed-effects framework and its accuracy and performance were assessed using a validation data set. The model was then compared to two highly predictive models derived from the Chapman-Richards function through fit statistics, curvature and bias measures of nonlinearity, and biological principles.

Results: The new model resulted in the most favourable fit statistics and nonlinearity measures, and also exhibited a suitable H-D curve that was compatible with the ecological conditions of the study area. While the alternative models in the current literature showed good fit statistics, they resulted in biased parameter estimates and produced inappropriate H-D curves. The proposed model, however, demonstrated a satisfactory accuracy when validated using the validation data set.

Conclusions: (1) It is essential to assess H-D models by considering both fit statistics and curvature and bias measures of nonlinearity; and (2) it is crucial to examine whether H-D models are appropriate for the specific ecological conditions of a particular region.

Keywords: allometry; forest management; mixed-effects model; parametric nonlinearity; *Pinus nigra*

Introduction

Crimean pine (*Pinus nigra* Arnold. subsp. *pallasiana* [Lamb.] Holmboe) is one of the most important tree species in Türkiye, with a distribution of approximately four million ha, representing 18% of total forest area in the country (GDF 2020). The Crimean pine is economically and ecologically valuable species of the Black Sea Backward Region as it has great potential for timber production due to its high wood quality. Tree height is an important variable for estimating site index, developing growth and yield models, and thus determining growing stock.

There are many height-diameter (H-D) models developed for tree species around the world (Peng et al. 2004; Sharma 2016; Song et al. 2024; Salekin et al. 2025). In our country, for the Crimean pine stands grown in the coastal belt and the Western Backward Region of the Black Sea, Seki and Sakıcı (2022) utilised a generalised H-D model developed by Sharma and Parton (2007). In our study, nearly 23% of H-D pairs was collected from the southern part of the Black Sea Backward Region nearest to the Inner Anatolia. There are still no H-D models specific to the stands of Crimean

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† Data considered in this paper were used in IV National Black Sea Forestry Congress, 2021.

pine or other tree species in these areas. This limitation results in foresters facing challenges when trying to accurately determine the volume of growing stock in the Crimean pine-dominated forests within the country. This, in turn, leads to further costs for researchers, professionals, and policymakers involved in forest inventory processes.

Without a valid H-D model tailored to the specific site, relying on models developed for different geographical areas may lead to significant estimation biases. The site-specific H-D models are crucial for accurate height estimation, given that the relationship between height and diameter varies according to the unique characteristics of the site and the stand (Kearsley et al. 2017; Seki & Sakıcı 2022). A study conducted by Özçelik and Çapar (2014) demonstrated that the H-D model developed by Pienaar (1991) was the most suitable for Brutian pine stands in the Antalya region of Türkiye. However, a subsequent study by Sağlam and Sakıcı (2025) found the H-D model proposed by Mirković (1958) as the most appropriate for the same species in a different region (the Adana district). Moreover, the studies by Seki and Sakıcı (2022) and Sağlam and Sakıcı (2024) highlighted that ecological variability within the same region can significantly influence the H-D relationships of Crimean pine and Scots pine, respectively.

In this context, variations in growth and yield can be observed among the subspecies of Black pine. Kalıpsız (1963) reported that Crimean pine stands had a greater average volume increment than Corsican pine (*Pinus nigra* subsp. *laricio*) stands, but less than Austrian pine (*Pinus nigra* subsp. *nigra*) stands. Therefore, the development of models specific to the site and species becomes necessary to improve the reliability of height estimates. To achieve this goal, the base nonlinear models should be parameterised with stand- and site-level variables (Sharma & Parton 2007; Corral-Rivas et al. 2014).

Fit statistics (e.g., the Akaike Information Criterion and the root mean square error) have been widely used to evaluate the effectiveness of nonlinear H-D models incorporating site and stand properties (Sharma & Parton 2007; Corral-Rivas et al. 2014). However, the models should be compared not only by the fit statistics. The parameters in nonlinear regression models sometimes exhibit the asymmetric confidence intervals which indicates a high degree of nonlinearity of the models – that is, the parameter estimates are biased and standard errors, confidence intervals and t-tests are misleading (Fischer & Schönfelder 2017; Diel et al. 2018). Therefore, the patterns of nonlinearity should be inspected using some curvature measures in order to assess the suitability of the asymptotic standard statistics in the output of nonlinear regression models (Ratkowsky 1986). Moreover, it is necessary to examine the profile of confidence interval for each model parameter in order to assess if the fit statistics are valid or not. These intrinsic statistical properties provide a convincing argument for the further use of nonlinear regression models. Nonetheless, this essential statistical exploration has remained largely unexplored in forestry research related to the nonlinear H-D models.

The objectives of this study are to (1) develop a new site-specific nonlinear height-diameter model for the Crimean pine stands, (2) examine its suitability with curvature and bias measures of nonlinearity, (3) evaluate its effectiveness with statistical and biological criteria, and (4) compare its performance with other alternative models.

Methods

Site description and sampling design

In this study, monospecific Crimean pine stands in the inner Anatolian region of Türkiye were sampled (30°53’13”-34°6’59” E, 39°50’6”-41°5’45” N; Figure 1). The stands cover about 45% (approximately 13,698.6 ha) of total forest area in the region (GDF 2020). Various Oak species (i.e., *Quercus cerris* L., *Quercus infectoria* Olivier, *Quercus frainetto* Ten., *Quercus robur* L., and *Quercus petraea* Matt.) and Scots pine (*Pinus sylvestris* L.) stands are also distributed in this region. Elevation of the study area varies from 239 m to 2,541 m above sea level. While mean annual precipitation is about 393.2 mm, mean annual temperature of the study area is 11.9 °C (TSMS 2024).

The sample plots were randomly selected to represent available site qualities, stand densities, and stand ages. A total of 180 circular sample plots were inventoried to investigate H-D relationships of Crimean pine. Sample plot sizes were organised ranging from 400, 600 or 800 m^2 based on the crown closure, following the forest management guidelines of Türkiye (GDF 2008). Overall, 1696 H-D pairs were gathered from the 180 sample plots. Note that care was taken to ensure that the measured sample trees were without broken tops, multiple stems and rotten parts. Then, the data were randomly divided into two groups: one group for model development (1360 trees from 140 sample plots, approximately 80% of the data) and the other group for model validation (336 trees from 40 sample plots, approximately 20% of the data). Descriptive statistics of model development and validation data are summarised in Table 1.

Height-diameter models

The relationships can significantly vary from stand to stand, and even within the same stand (Sağlam & Sakıcı 2024). Therefore, simple H-D models containing only the variable D may be insufficient to explain the H-D relationship. Accordingly, the stand characteristics such as dominant height and basal area have often been included as nonlinear models’ asymptote, rate or shape parameters (Temesgen & von Gadow 2004; Sharma & Parton 2007; Zang et al. 2016). It is crucial to consider the stand characteristics in a study area in order to develop a realistic H-D model (Huang et al. 2000; Castedo Dorado et al. 2006).

The stands sampled in the present study exhibited a great variability regarding the stand characteristics such as dominant height (the average height of the 100 tallest trees per hectare; H_0), dominant diameter (the mean diameter of the 100 thickest trees per hectare; D_0), and

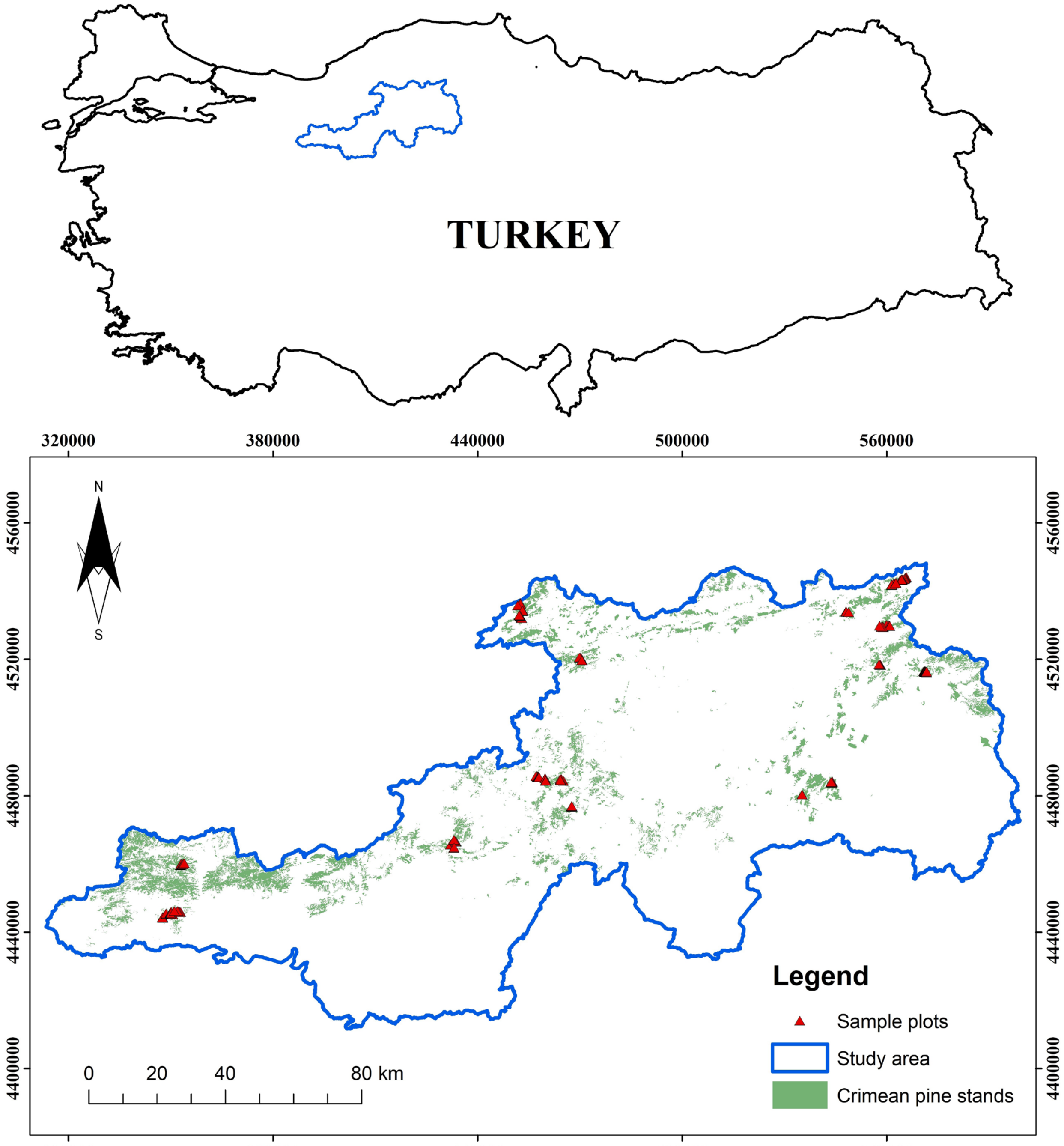

FIGURE 1: Location of study area and sampling units

basal area (BA). These variables were also included in the parameters of Chapman-Richards function (Richards 1959). It may be thought that the use of H_0 as a predictor variable may restrict the applicability of H-D models. However, as outlined above, the plot sizes in the national forest inventory studies in Türkiye are set depending on the crown closure. To utilise the H-D models including H_0 in the country, a little sampling effort is sufficient; that is to say, measuring heights of the four, six and eight tallest trees in plots of 400, 600 and 800 m^2, respectively are adequate. Furthermore, the relevant literature shows that the inclusion of H_0 in the base H-D models improves considerably the accuracy of height estimates (Sharma & Parton 2007; Adame et al. 2008; Crecente-Campo et al. 2010; Raptis et al. 2021; Patrício et al. 2022). In this context, considering H_0 as an explanatory variable seems to be a fairly reasonable decision.

The variable H_0 has a significant effect on both diameter and height growth, though the variables D_0 and BA affect diameter growth rather than height growth. Therefore, the variable H_0 was expressed as both asymptote and rate parameters of the Chapman Richards function, even though the variables D_0 and BA were identified as only asymptote parameter. While the

TABLE 1: Explanatory statistics for the Crimean pine stands measured in this study. H: Height (m), D: Diameter at breast height (cm), D_0: the mean diameter of the 100 thickest trees per hectare (cm), H_0: the average height of the 100 tallest trees per hectare (m), BA: basal area (m^2/ha), and N: the number of trees (ha).

Data set	Variables	Mean	Standard Deviation	Minimum	Maximum
Model	H (m)	15.37	6.83	1.60	39.90
	D (cm)	27.59	12.98	1.10	72.20
	D_0 (cm)	36.55	11.35	7.80	65.53
	H_0 (m)	17.36	6.93	3.20	36.28
	BA (m^2/ha)	33.72	17.07	2.00	114.25
	N (number/ha)	826	917	138	6950
Validation	Height (m)	15.64	7.31	2.70	36.90
	Diameter (cm)	28.97	13.77	1.10	70.00
	D_0 (cm)	37.21	11.96	7.20	61.40
	H_0 (m)	17.49	7.04	3.00	33.40
	BA (m^2/ha)	33.18	15.12	2.00	67.00
	N (number/ha)	822	975	163	5300

variables D_0 and BA distinctly manifest the competitive dynamics among individual trees (Crecente-Campo et al. 2010; Zang et al. 2016), the variable H_0 succinctly indicates the overall stand productivity.

With this functional configuration, the convergence criterion was satisfied with a small number of iterations. Of greater significance, the attainment of symmetric-standard statistics signified the successful achievement of unbiased parameter estimates. The resulting model Eq. (1) was then compared with two highly flexible nonlinear H-D models in the literature, which are different variants of Chapman-Richards function i.e., Eq. (2) (Sharma & Parton 2007) and Eq. (3) (Crecente-Campo et al. 2010). The related equations are given below:

$$H = 1.3 + \left(\beta_1 H_0 + \beta_2\left(\frac{D_0}{BA}\right)\right)\left(1 - exp(-\beta_3(H_0{}^{\beta_4})D)\right)^{\beta_5} \quad (1)$$

$$H = 1.3 + (\beta_1 H_0{}^{\beta_2})\left(1 - exp(-\beta_3\left(\frac{N}{BA}\right)^{\beta_4} D)\right)^{\beta_5} \quad (2)$$

$$H = 1.3 + (\beta_1 H_0{}^{\beta_2})\left(1 - exp - \left(\beta_3 D_0{}^{\beta_4} D\right)\right)^{\beta_5} \quad (3)$$

where H is tree height (m), D is tree diameter at breast height (cm), D_0 is the mean diameter of the 100 thickest trees per hectare (cm), H_0 is the average height of the 100 tallest trees per hectare (m), BA is basal area (m^2/ha), N is the number of trees (ha), and β_1, β_2, β_3, β_4, and β_5 are parameters to be estimated.

An initial estimate of starting values for model parameters is essential to meet the convergence criterion. The wrong starting values can lead to non-significant and biased parameter estimates, and thus the models may not have the desirable statistical and biological behaviors. In the literature, trying different initial values until achieving a global minimum is a common approach. However, this approach is laborious, especially in developing nonlinear models with four and five-parameters (Fang & Bailey 2001). Therefore, we used the Generalized Simulated Annealing package (GenSA) in the R Studio for this purpose (Xiang et al. 2013). This package provided good initial values (significant at the 5% level) at the first attempt. In order to calculate fit statistics, the nonlinear models were then refitted using the starting values generated from GenSA via the nlme package in the R Studio (R Core Team 2022).

Nonlinear mixed-effects modeling

H-D pairs are collected from the sample plots with different characteristics in terms of site index, stand density and age. In addition, H and D of several trees in each sample plot are measured in this kind of studies. This type of forest inventory leads to a hierarchical structure, i.e., a spatially correlated data within each sample plot and variable relationships across the sample plots. Fixed-effects models assume that H-D relationships are similar for all sample plots. In other words, the relationships are normally distributed around the mean function, so the conditional expectation is identical for each sample plot. However, this is unlikely as the sample plots are expected to behave differently. Since the mixed-effects models can account for both fixed and random-effects, they can identify the spatial correlations within a sample plot and explain the variabilities between different sample plots. In this way, they provide an agreement between stands and sample plots, without fitting each sample plot separately (Lindstrom & Bates 1990). Capitalising on this advantageous aspect, the mixed-effects models contribute to increasing the reliability of inferences. In the present study, the mixed-effects models were fitted with the maximum likelihood estimation method using the NLMIXED procedure in SAS program (version 9.4).

The general expression of mixed effects models is:

$$y_{ij} = f(\phi_{ij}, x_{ij}) + \varepsilon_{ij} \qquad i = 1, \dots, M \qquad j = 1, \dots, n_i \quad (4)$$

$$\phi_{ij} = A_{ij}\beta + B_{ij}b_i \qquad b_i \sim N(\sigma^2 D) \quad (5)$$

f specifies model form. M is the number of sample plots, and n_i is the number of observations within each sample plot. β is fixed-effects parameters that are the identical across sample plots, b_i is random-effects parameters specific to the sample plots, and ε_{ij} is residual terms assumed to be independent and normally distributed. A_{ij} and B_{ij} are design matrices for fixed and mixed-effects, respectively, and $\sigma^2 D$ is a variance-covariance matrix.

Model evaluation and comparison

This study used fit statistics, estimation behavior of the models, and biological principles in order to compare the H-D models. The values of the intrinsic and parameter-effect curvatures suggested by Bates and Watts (1980), and the value of the bias measure proposed by Box (1971) were accounted for examining the estimation behavior of the H-D models. While the intrinsic and parametric nonlinearity values of these models were expected to be less than 0.3 and 1.0 respectively, the percentage value of bias measure for each parameter was expected to be less than 1% (Ratkowsky 1986; Diel et al. 2018). The SAS software (version 9.4) was used to obtain the non-linearity measures and the Box's bias. In addition, fifty thousand bootstrap samples were used to visually assess the curvature of each model parameter. This is the most influential method for analysing the distributional properties of the parameters. This analysis was conducted using the function bootci in MATLAB program (version 2020b). After the appropriate models were determined based on the evaluation criteria mentioned above, their predictive ability was also justified based on the root mean square error using the validation data. In addition, the biological characteristics of the model predictions were analysed considering following the recommendations by Yuancai and Parresol (2001), i.e., sigmoid pattern, inflection point, horizontal asymptote, and H should be zero when D is zero.

The fit criteria used in this study were the Akaike information criterion (AIC), the Bayesian information criterion (BIC), the root-mean square error (RMSE), and the mean bias ($\bar{E}$). While the conditional predictions were utilised to compare the mixed-effects models in the model data set, the marginal predictions (the fixed parts of the mixed-effects models) were used in validation data set. Additionally, only RMSE was considered to compare the mixed-effects models in the validation data set. The model residuals were visually checked for their normality and homogeneity. While a loess curve was used to check the homogeneity of the residual variance, a frequency histogram was used to check the normality of the residuals.

$$\text{AIC} = -2ln(L) + 2p \tag{6}$$

$$\text{BIC} = -2ln(L) + p \times ln(n) \tag{7}$$

$$\text{RMSE} = \sqrt{\frac{\sum_{i=1}^{n}(y_i - \hat{y}_i)^2}{n}},\ i = 1, \ldots, n_i. \tag{8}$$

$$\bar{E} = \frac{\sum_{i=1}^{n} y_i - \hat{y}_i}{n_i} \tag{9}$$

where y_i and $\hat{y}_i$ are the ith observed and predicted height values, respectively. The indexes n_i and p are the number of observations and parameters, respectively. L is log-likelihood value of fitted model.

Results

Nonlinear fixed-effects models

The estimated parameters and fit statistics for Eq. (1), Eq. (2) and Eq. (3) are shown in Table 2. As indicated in the table, all parameters held significance at the 0.05 level. Equation (1), with the lowest ranking value, outperformed alternative models. Eq. (2) was less accurate compared to Eq. (3). On the other hand, the values of parameter-effect curvature and of bias measure indicated that Eq. (1) and Eq. (2) yielded accurate and reliable estimates in

TABLE 2: Parameter estimates with standard errors in brackets and fit statistics for the nonlinear fixed-effects models

Parameters/Fit statistics	Eq. (1)	Eq. (2)	Eq. (3)
β_1	0.9123 (0.0125)	1.1223 (0.0636)	0.9213 (0.0488)
β_2	-0.8902 (0.1151)	0.0504 (0.0044)	0.9747 (0.0160)
β_3	2.4460 (0.3373)	0.0504 (0.0044)	2.9537 (0.6531)
β_4	-1.0245 (0.0426)	0.2780 (0.0219)	-0.8877 (0.0595)
β_5	2.0210 (0.1798)	2.3657 (0.2427)	2.3950 (0.2427)
AIC	6090.1	6248.0	6176.9
BIC	6116.1	6274.1	6274.1
RMSE (m)	2.2702	2.4060	2.3439
$\bar{E}$ (m)	0.0058	0.0124	0.0021
Ranking score†	4.00	12.00	7.28

† Poudel and Cao (2013)

contrast to Eq. (3) (Table 3). The statistical validity of Eq. (3) was questionable, even though it had reasonable and acceptable model performance. The Eq. (1) and Eq. (2) provided good fit statistics and unbiased parameter estimates. However, the parameters of Eq. (2) were not as stable as that of Eq. (1). It was appeared that Eq. (1) was the most suitable for describing H-D relationships.

The parameter-effect curvature of the equations was also visually investigated for each parameter using the QQ plot based on fifty thousand bootstrap samples (Figure 2). The most accurate parameter estimates were achieved when Eq. (1) was fitted to the observed data. Four of the five parameters of Eq. (1) followed the reference line exactly, suggesting that these parameters had approximately normal distributions. The remaining parameter of Eq. (1) deviated slightly from the straight

TABLE 3: Curvature measures of nonlinearity and Box's bias for the nonlinear fixed-effects models

Parameters	**Box's bias (%)**		
	Eq. (1)	Eq. (2)	Eq. (3)
β_1	0.044	0.220	0.200
β_2	0.064	0.000	-0.010
β_3	0.870	0.310	2.360
β_4	0.007	0.018	0.063
β_5	0.530	0.750	0.690
Parameter-effects curvature	0.892	0.672	2.6395
Intrinsic curvature	0.0496	0.0582	0.0543

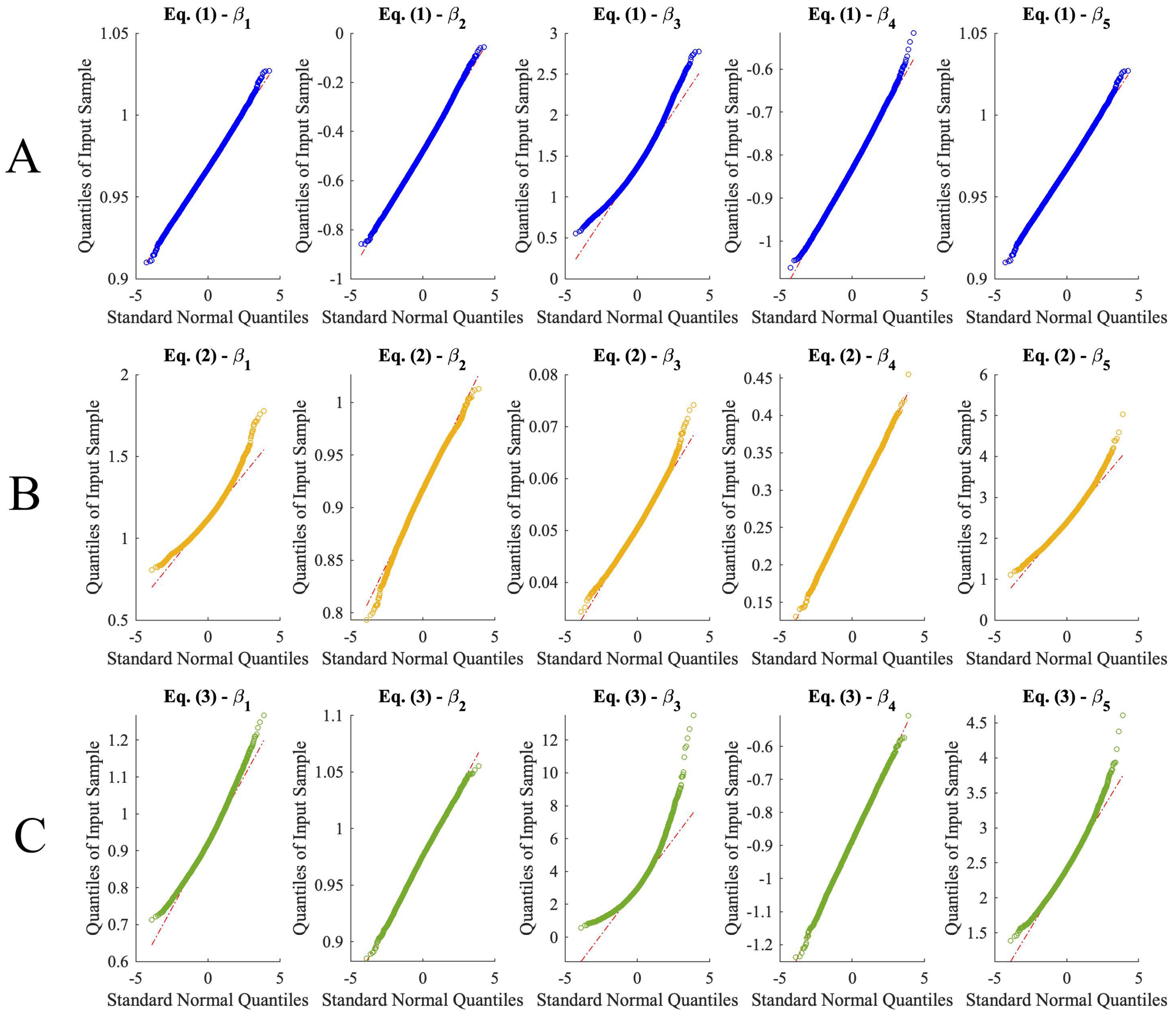

FIGURE 2: Normal QQ plots of parameter estimates based on fifty thousand bootstrap samples (A: Eq. (1), B: Eq. (2), and C: Eq. (3)).

line (Figure 2A). Contrary to the Eq (1), the divergence from normal distribution became more apparent for more parameters when the Eq. (2) was fitted to the observed data (Figure 2B). It was clear that there was a significant bias in the estimation of the parameter β_3 of Eq. (3) (Figure 2C). This evidence also proved that Eq. (3) was an inappropriate model to predict tree heights. With this evidence in mind, Eq. (3) was excluded from the following statistical analysis step.

Nonlinear mixed-effects models

In the mixed-effects models, each parameter was initially assumed to have a random effect. However, all models failed to meet the convergence criterion in this case. When the parameters β_1, β_2, and β_4 of Eq. (1) and Eq. (2) were specified as random-effects, the convergence criterion was satisfied. Then, the variance of the estimated random parameters was used to determine the significant random-effects parameters. The parameter with negligible variance ($\sigma^2 < 1\times10^{-4}$) was assessed as only the fixed-effects to simplify model complexity and improve prediction accuracy. Accordingly, the variance of the parameters β_1 ($\sigma^2_{\beta1}$=0.0012) and β_4 ($\sigma^2_{\beta4}$=0.0053) in Eq. (1) was considerable. Similarly, the variance of the same parameters ($\sigma^2_{\beta1}$=0.0007 and $\sigma^2_{\beta4}$=0.0088) in Eq. (2) was significant. The fit statistics for both full and simplified models, and the estimated parameters for only the simplified model with standard error in brackets are displayed in Table 4.

As seen in Table 4, dropping the parameter with a negligible variance improved prediction accuracy. There was an exception for the mean error of Eq. (2), which was the same for both full and simplified mixed-effects models.

The residuals against predicted heights and the frequency histogram of residuals are illustrated for the simplified models in Figure 3. The loess curves in the residual plots were almost horizontal throughout the predictions, indicating that the predictions were unbiased for both models (Figures 3A and 3C). The frequency histogram of residuals also implied that the model residuals were normally distributed (Figures 3B and 3D).

The RMSE for the validation data set was calculated using the fixed-effects part of the simplified mixed-effects models. While the RMSE for Eq. (1) was 2.5011 m, it was 2. 5601 m for Eq. (2). Furthermore, the biological characteristics of these models were investigated based on the H-D curves for different dominant heights (Figures 4A and 4C). As demonstrated in Figure 4, there was a significant difference in the height-diameter curves at H_0=34 m (FIGURE 4C), although the curves were similar at H_0=14 m and H_0=24 m (Figures 4A and 4B). Moreover, Eq. (2) exhibited faster height growth from the juvenile development stage to the immature stage and demonstrated a more rapid convergence toward the asymptote in contrast to Eq. (1).

TABLE 4: Parameter estimates with standard errors in brackets and fit statistics for the nonlinear mixed-effects models (a: full model and b: simplified models).

Parameters/Fit statistics	Eq. (1)	Eq. (2)
β_1	0.9633 (0.0120)	0.8266 (0.0471)
β_2	-0.3367 (0.1142)	1.0434 (0.0184)
β_3	0.8078 (0.1423)	0.0401 (0.0043)
β_4	-0.6518 (0.0590)	0.3899 (0.0364)
β_5	2.2762 (0.2004)	2.2463 (0.1964)
$\sigma^2_{\beta1}$	0.0012 (0.0006)	0.0007 (0.0002)
$\sigma^2_{\beta4}$	0.0053 (0.0010)	0.0088 (0.0013)
σ^2_{ε}	3.9749 (0.1610)	3.9673 (0.1599)
^{a}AIC	5960.9	6022.4
^{b}AIC	5955.7	6020.4
^{a}BIC	5984.3	6049.1
^{b}BIC	5979.4	6044.1
^{a}RMSE (m)	2.0147	1.9314
^{b}RMSE (m)	1.9838	1.9307
$^a\bar{E}$ (m)	-0.0038	0.0303
^{b}E (m)	-0.0005	0.0303

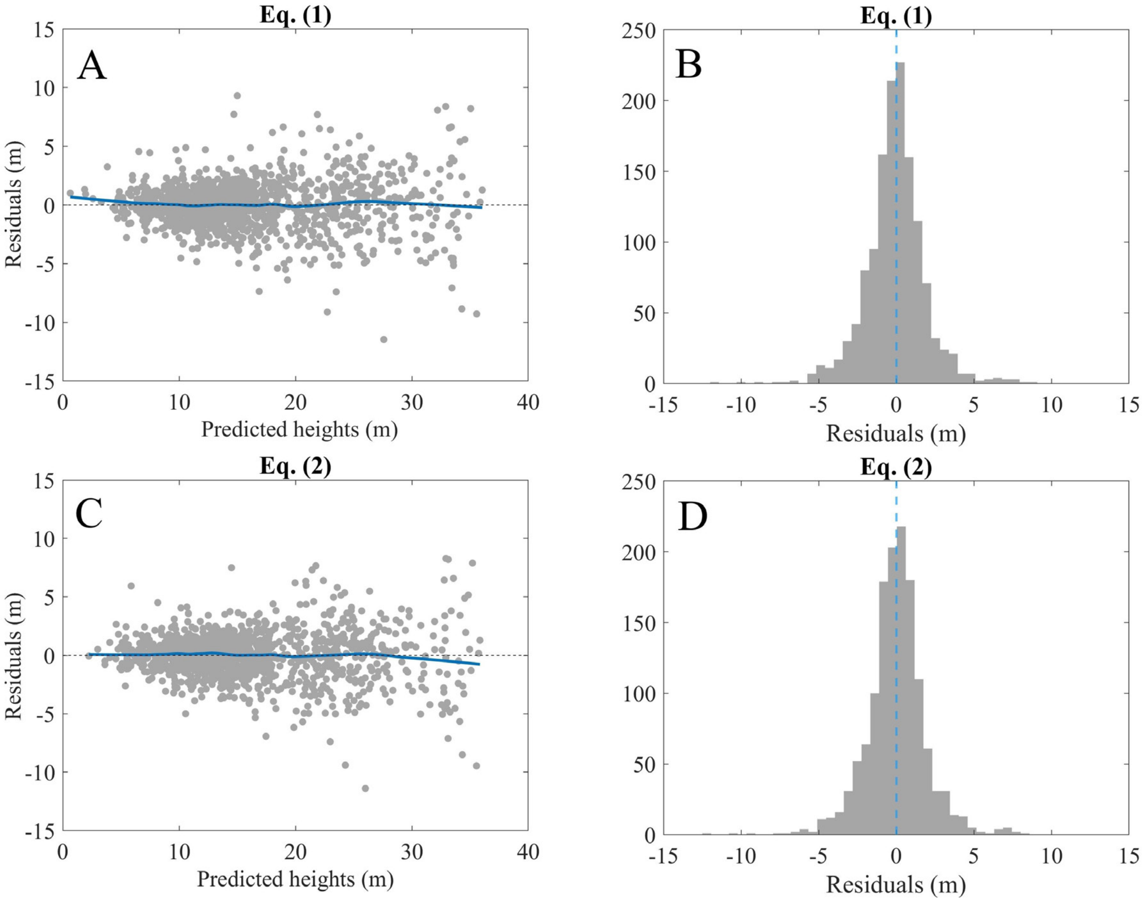

FIGURE 3: Scatter plots of residuals against predictions with a loess curve (A: Eq. (1) and C: Eq. (2)), and frequency histograms for residuals (B: Eq. (1) and D: Eq. (2)). Blue solid line shows the variance of residuals over predictions and blue dashed line indicates the average of residuals.

Discussion

This study developed a new H-D model, Eq. (1), for the Crimean pine stands in the Black Sea Backward region nearest to the inner Anatolian region of Turkiye. The proposed model outperformed its counterparts in terms of the fit statistics such as AIC and BIC. Diel et al. (2018) stated that the curvature measures of nonlinearity were more important than the fit statistics to determine the best model. Therefore, the predictive ability of the parameterised models should be tested using the appropriate methods such as the curvature measures of intrinsic and parameter-effects nonlinearities (Bates & Watts, 1980) and the bias measure (Box, 1971). In addition, Ratkowsky (1986) pointed out the importance of the bootstrap samples to assess the reliability of model estimates. Overall, Eq. (1) was superior to the alternative

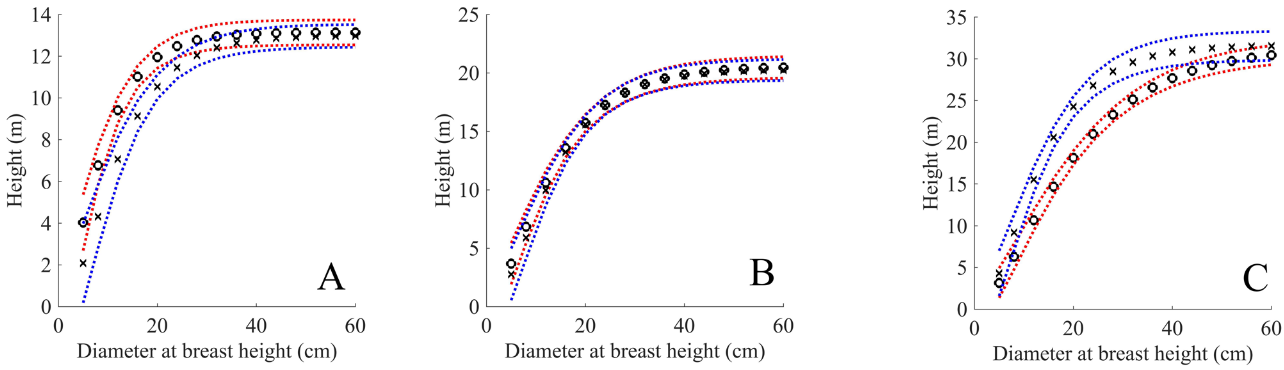

FIGURE 4: H-D curves of fitted models for different dominant heights (A: H_0=14 m, B: H_0=24 m and C: H_0=34 m. Blue and red dotted lines show 95% confidence intervals of the fitted values).

models with regard to the statistical criteria indicated in this study.

Furthermore, Ratkowsky (1986) claimed that a parameterised model with good statistical properties may be unacceptable in terms of biological soundness due to the unsuitable parameterisation. Eq. (1) met the biological expectations that Yuancai and Parresol (2001) reported, i.e., S-shaped curve, inflection point, and horizontal asymptote. Moreover, as noted by Fang and Bailey (1998), the S-shaped curve initiated from the origin and maintained a positive slope across the entire range of data, gradually approaching zero as the variable D increased. Crecente-Campo et al. (2010) did not obtain the S-shaped curve, noting that while this feature was not unavoidable for height-diameter relationships, it was essential for capturing dominant height growth patterns. We hold a somewhat differing viewpoint on this matter, as we believe that realistic H-D models are essential for promoting sustainable forest management. In our perspective, the adaptability of H-D models and the inherent characteristics of the data, such as minimum and maximum values, can greatly influence the fulfillment of biological expectations. Since our data covered juvenile, adolescent, and mature stands, the S-shaped curve could be achieved in this study. Equally crucial was the flexibility inherent in the proposed model, guaranteeing adherence to biological principles.

The unique characteristics of the site and stand play a crucial role in the success of height–diameter (H-D) modeling studies (Long et al. 2020). Although the alternative model (Eq. 2) complies with biological principles, it exhibited biologically unrealistic behavior, particularly at H_0=34m—by predicting a rapid height increase approaching the upper asymptote. This contradicts the slower growth rates typically observed under the ecological conditions of the study area. As clearly demonstrated by Bolat (2025), Crimean pine forests are significantly affected by unfavourable climatic conditions, such as low precipitation and high temperatures. Therefore, the behavior of Eq. (2) might only be valid for Crimean pine stands growing in more favourable environments, such as those with annual precipitation exceeding 500 mm and soils rich in water and organic matter. The findings of Seki and Sakıcı (2022) support this perspective. Similar to Sharma and Parton (2007), they collected a significant portion of their H-D data (approximately 80%) from humid-mild and subhumid forests. As a result, they might have found the Sharma and Parton (2007) model as the most effective in capturing the H-D relationship in their study. This evidence underscores the necessity of considering site condition for reliable height estimates.

The asymptote, rate, and shape parameters of the Chapman-Richards function are expected to vary randomly across the sample plots, as these parameters specifiy the properties of H-D curves. The random-effects parameters are commonly included sequentially with the fixed-effects parameters at a given level (e.g., sample plot). Then, the different alternatives of fixed and random-effects parameters are compared based on fit statistics to determine the best model form (Raptis et al. 2021; Şahin 2025). In contrast to this standard implementation, we looked at the variance of the random-effects parameters. We assessed the parameters with a variance less than 1×10^{-4} to be negligible at the sample plot level in order to simplify model complexity and improve model accuracy. Fang and Bailey (2001) suggested that the variability of parameters across sample plots should be considered if there is sufficient data for each sample plot. In the absence of such information, they suggested taking into account the estimated variance of parameters. In this study, we followed the model specification of Fang and Bailey (2001). Accordingly, the first and fourth parameters of the proposed model were assigned as random-effects. This result was in accordance with the biological expectations since these random parameters controlled the maximum value and rate of change in height depending on diameter.

Conclusions

This study drew attention to the role of site-specific H-D models in order to improve the reliability of height estimates. It also pointed out the importance of curvature and bias measures such as parameter-effect curvature in the step of model selection. Although fit statistics indicated that all the models were well-fitted to the observed height pattern (RMSE≅2m), the nonlinearity measures brought out that Eq. (3) had an unstable H-D model form, despite ranking second among the H-D models in terms of fit statistics. This finding invalidated the success of Eq. (3) in terms of fit statistics. From a biological viewpoint, the ecological suitability of the stable H-D models, Eq. (1) and Eq. (2), were further investigated. It was inferred that Eq. (1), which was tailored to site conditions, exhibited more realistic behavior, particularly at high productive sites. However, Eq. (2) predicted unexpectedly rapid height growth, which was inconsistent with the ecological characteristics of the study area. On the basis of this study's results, we can suggest the inspection of inherent statistical properties to approve the validity of outputs such as parameter estimates and fit statistics in nonlinear regression models and the careful observation of stand structures throughout data collection in order to build a proper nonlinear model.

List of abbreviations

H: Tree height
D: Diameter at breast height
H_0: The average height of the 100 tallest trees per hectare
D_0: The mean diameter of the 100 thickest trees per hectare
BA: Basal area per hectare
N: The number of trees per hectare

Authors' contributions

FB was the primary author, carried out the sampling, completed the statistical analyses and writing the manuscript draft. AG and İE contributed to idea, reviewed and edited the manuscript. All authors read and approved the final manuscript.

Competing interests

The authors declare that they have no competing interests.

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