Nonlinear Height-DBH Model Analysis For Three Tropical Tree Species In Mt. Makiling, Philippines

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\textbf{ABSTRACT}

Nonlinear growth functions have been commonly used for modeling tree height–diameter at breast height (H-DBH) relationships. The development of a simple yet accurate H-DBH equation to predict the height of individual tree species is a need because using the appropriate model will give precise estimation of the forest inventory resources. In this study, six H-DBH models (CR, EX, KF, ML, SC, and WE) were used to derive and estimate the height of three species in Mt. Makiling, specifically Parashorea malaanonan, Diplodiscus paniculatus, and Celtis luzonica using the DBH as the only predicting variable. The DBH and tree height of the representative trees per species were measured for this study through nondestructive and random sampling. A total of 175 trees represented the P. malaanonan; 178 trees represented D. paniculatus, while 191 trees were measured to represent C. luzonica. Based on the evaluation criteria which include $R^2$, RMSE, $E$, AMD, AIC, and AIC\textsubscript{w}, the performance of the WE model was determined to be the best in predicting the height of P. malaanonan species while the performance of the KL model was the best both for the D. paniculatus, and C. luzonica species.

\textbf{KEYWORDS}

H-DBH models; tropical species; Mt. Makiling; Philippines

\section*{Introduction}

Tree height (H) and diameter at breast height (DBH) are the most important measures of tree growth and are fundamental individual tree variables that underpin the calculation of other important variables as well as the development of forest growth and yield models (Arcangeli et al., 2013). The relationship between H and DBH is very significant in determining site-index, calculating tree volume, evaluating site-quality and predicting future growth of the stand (Jayaraman & Zakrzewski, 2001; Wagle & Sharma, 2012). In addition, a correlation exists between H and growing conditions, forest density, tree age, basal area and dominant H and DBH with that of the relationship of H and DBH (Liu et al., 2017). The DBH are easily and directly measured with the use of measuring instruments, hence accuracy is ensured. The observation of H is usually influenced by many forest factors, including uneven distribution of forest cover, density and rough topography (Temesgen et al., 2014; Xu et al., 2014) and is therefore prone to errors. In addition, it
takes time and effort to measure H since there are limitations caused by observational error and visual disturbance (Colbert et al., 2002), which increase the cost of the forest survey and are often time-consuming (Dorado et al., 2006; C. Peng et al., 2004; Rimondo, 1995; Sharma & Parton, 2007; Zhang et al., 2002).

Due to the existence of an allometric relationship between H and DBH, it is common practice among foresters to measure DBH on all trees in a plot (Arcangeli et al., 2013) without measuring the H. Models for estimating H with DBH as the sole predictor are then required for each species. Simple yet accurate tree H-DBH models to estimate the H of trees (Haikui & Fa, 2011) of specific tree species are vital, since the correct choice of allometric model is the key in accurate prediction of forest inventory resources (Chave et al., 2004). In addition, the use of a local model may provide the best unbiased estimates of H if based on sufficient collected data (Van Laar & Acka, 2007).

Many studies of H-DBH models have already been conducted for different tree species to predict H. The non-linear function fitting is relatively easy and has achieved good results in application (Ahmadi et al., 2013; Fan et al., 2011; Huang et al., 1992; Lumbres et al., 2011, 2013, 2015; C.H. Peng et al., 2001; Sharma & Parton, 2007). However, H-DBH models of many species in the Philippines are still lacking, including those species found within the Mt. Makiling Forest Reserve.

The Mt. Makiling Forest Reserve (MMFR) is famous among the megadiverse tropical rain forests in the Philippines (Lapitan et al., 2013) and is dominated by tree species such as Bagtikan (Parashorea malaanonan), Balobo (Diplodiscus paniculatus), and Magabuyo (Celtis luzonica) and by palm species including Kaong (Arenga pinnata) and Sarawag (Pinanga insignis) (ASEAN-Korea Environmental Cooperation Unit, 2002; Fernando et al., 2008). Naturally, species thriving in volcanic rich-soil environments have an average yearly increase in DBH of 0.81 cm and 0.78 m, respectively. These mean annual increments are exemplified by the growth of native P. malaanonan, D. paniculatus, while C. Luzonica, which also grows favorably in the same ecosystem and soil type, would probably show a similar growth rate, although its distribution is reducing due to the threatened habitat (Garcia et al., 2013).

The dominant tree species in a forest is key during forest resource inventories. P. malaanonan, D. paniculatus, and C. luzonica dominate the MMFR but are some of the species for which H-DBH models are still to be developed. This study aimed to develop H-DBH models for P. malaanonan, D. paniculatus, and C. luzonica of Mt. Makiling, Philippines. Developing H-DBH models for P. malaanonan, D. paniculatus, and C. luzonica is important to forest resource managers who have to acquire precise data regarding their forest resources to formulate better forest administration plans and eventually improve the sustainability of the forest cover under their management.

**Materials and methods**

**Study site**

The data collection for this study of H-DBH models for three species in Mt. Makiling was carried out at the Permanent Field Laboratory Area at MMFR in the southcentral region of Luzon Island, Philippines. The current vegetation is typical secondary tropical rainforest since most of the original vegetation that formed at the base of the mountain was selectively
logged between 1942 and 1944 (Luna et al., 1999). Four types of vegetation are recognized in Mt. Makiling based on altitude; upper montane rain forest (above 1000 masl), lower montane rain forest (750–1000 masl), lowland evergreen rain forest (100–500 masl), and Parang vegetation consisting of a mixture of grassland and second-growth forest (Fernando et al., 2004). The forest reserve is classified into four zones based on vegetation type; the mossy forest zone (900 to 1,109 masl), the dipterocarp mid-montane forest zone (100 to 900 masl), the grassland zone, and the agroforestry zone (Gruezo, 1997). The P. malaanonan, D. paniculatus, and C. luzonica are found below 1000 masl and belong to the dipterocarp mid-montane forest zone. The data were collected in areas with an elevation of less than 140 masl. Mt. Makiling has two pronounced seasons: the dry season lasts from January to April while the wet season lasts from May to December. It has an annual rainfall ranging from 1645 to 2299 mm and yearly temperature of 25.90°C to 29.30°C.

**Data collection**

The DBH and H of the representative trees per species were measured through nondestructive sampling for this study. The DBH of trees without buttress were observed at 1.30 m above the ground while trees with buttress were observed 30 cm from the uppermost part of the buttress. The three species in this study all exhibit buttresses. The DBH was measured using a standard diameter tape while the H was determined using a Haglof Vertex III and Transponder. A total of 175 representative trees were measured for P. malaanonan; 178 trees for D. paniculatus; and 191 trees for C. Luzonica. The selected trees represented different DBH classes (Table 1).

The P. malaanonan had an average DBH of 27.39 cm ranging from 5.20 to 93.80 cm and average H of 20.13 m ranging from 6.20 to 39.40 m; the D. paniculatus had an average DBH of 22.78 cm ranging from 5.20 to 81.70 cm and average H of 14.80 m ranging from 4.60 to 32.40 m; while the C. luzonica had an average DBH of 16.16 cm that ranged from 5.00 to 70.60 cm and average H of 12.48 m that ranged from 5.00 to 30.70 m.

**Data analysis**

Six non-linear H-DBH models were chosen as candidates for these three tropical tree species of Mt. Makiling, namely P. malaanonan, D. paniculatus, and C. luzonica. The six H-DBH models were Chapman-Richards (Chapman, 1961; Richards, 1959), Exponential (Ratkowsky, 1990), Korf/Lundqvist (Stage, 1963; Zeide, 1989), Modified Logistic (S. Huang et al., 1992; Ratkowsky & Reedy, 1986), Schnute (Schnute, 1981), and Weibull (Yang et al., 1978). The equations of the models are shown in Table 2. These models were selected as

**Table 1. Summary of observed statistics for three tropical tree species in Mt. Makiling, Philippines.**

| Statistics | *Parashorea malaanonan* | *Diplodiscus paniculatus* | *Celtis luzonica* |
|------------|------------------------|--------------------------|------------------|
| n          | 175                    | 175                      | 191              |
| Mean (SD)  | 27.39 (19.82)          | 20.13 (9.14)             | 14.80 (14.45)    |
| Range      | 5.20–93.80            | 6.20–39.40               | 4.60–32.40       |

DBH = diameter at breast height; H = total height; n = number of observations; SD = standard deviation.
they had shown satisfactory results in previous studies (Ahmadi et al., 2013; Dorado et al., 2006; Fan et al., 2011; Fang & Bailey, 1998; Huang et al., 2000; Lumbres et al., 2011, 2013, 2015; C.H. Peng et al., 2001; Sharma & Parton, 2007). Nonlinear models have a biological basis, which gives reasonable estimations outside the scope of the collected data, and are generally more adaptable than linear models which are less adjustable and need more predictors to define the data (Corral-Rivas et al., 2004). The six candidate models define sigmoid curves and have three parameters, the upper asymptote, a scale parameter and a shape parameter, that characterize the different growth stages as influenced by biological processes and behaviors (C.H. Peng et al., 2001).

The H-DBH models have fitted different tree species well, including Gmelina arborea in Ibadan, Nigeria (Eby et al., 2017), ten coniferous species collected in the inland northwest of the United States (Zhang, 1997), Jack pine, Black spruce, White spruce, Trembling aspen, White pine, Red pine, Balsam fir, Yellow birch, and Balsam poplar in Ontario Boreal Forests in Canada (C.H. Peng et al., 2001), balsam fir, balsam poplar, Black spruce, jack pine, red pine, trembling aspen, white birch, and white spruce growing in the boreal forests of Ontario, Canada (Sharma & Parton, 2007), oriental beech (Fagus orientalis Lipsky) in the Hyrcanian forests, Iran (Ahmadi et al., 2013), Pinus kesiya Royle ex Gordon of Benguet, Philippines (Lumbres et al., 2013), and Acacia mangium and Eucalyptus pellita in the forest plantation of Pangkalan Bun, Kalimantan, Indonesia (Lumbres et al., 2015).

The parameters of the six H-DBH models were estimated using the Statistical Analysis System (SAS) NLIN procedure (SAS Institute Inc., 2004). Fit statistics, including the coefficient of determination ($R^2$), root mean square error (RMSE), bias (Ē), absolute mean difference (AMD), Akaikie information criterion (AIC) of Akaikie (1974), and AIC weight (AIC_w), were used to analyze the accuracy of the candidate H-DBH models. They are referred to as fit statistics as they were used to evaluate the entire dataset of this study. The use of the fit statistics as evaluation criteria has already been proven to be reliable (Koirala et al., 2017; Liu et al., 2017). Table 3 shows the equation and corresponding ideal result of each of the evaluation criteria that were used to evaluate the performance of the six H-DBH models for the three tropical tree species of Mt. Makiling.

**Table 2.** The candidate H-DBH models for three tropical tree species in Mt. Makiling, Philippines.

| Model (code) | Equations | References |
|--------------|-----------|------------|
| Chapman-Richards (CR) | $H = 1.3 + a(1 - e^{-b\cdot DBH})^c$ | Richards (1959), Chapman (1961) |
| Exponential (EX) | $H = 1.3 + a \cdot e^{\frac{b}{DBH}}$ | Ratkowsky (1990) |
| Korf/Lundqvist (KL) | $H = 1.3 + a \cdot e^{-b\cdot DBH}$ | Stage (1963), Zeide (1989) |
| Modified Logistic (ML) | $H = 1.3 + \frac{a}{(1 + b \cdot DBH)}$ | Ratkowsky and Reedy (1986), Huang et al. (1992) |
| Schnute (SC) | $H = \left\{1.3^b + (e^{b} - 1.3^b) \frac{1-e^{-DBH}}{1-e^{-DBH_{max}}} \right\}^c$ | Schnute (1981) |
| Weibull (WE) | $H = 1.3 + a(1 - e^{-b\cdot DBH})$ | Yang et al. (1978) |

H = tree total height (m); DBH = tree diameter at breast height (cm); 1.3 (m) = distance from the ground to the tree where DBH was measured; $a =$ asymptote; $b =$ scale parameter; $c = $ shape parameter; $e = $ base of natural logarithm; $DBH_{min} = $ minimum DBH and $DBH_{max} = $ maximum DBH.
Table 3. Mathematical equation and the corresponding ideal result of the different evaluation criteria used for the evaluation of the performance of the different candidate H-DBH models.

| Fit statistics                          | Equation                                                                 | Ideal result/preferable/basis |
|----------------------------------------|--------------------------------------------------------------------------|-------------------------------|
| Coefficient of determination (R²)      | \[ R^2 = 1 - \frac{\sum_{i=1}^{n} (Y_i - \hat{Y}_i)^2}{\sum_{i=1}^{n} (Y_i - \overline{Y})^2} \] | Higher R² value               |
| Root mean square error (RMSE)          | \[ \text{RMSE} = \sqrt{\frac{\sum_{i=1}^{n} (Y_i - \hat{Y}_i)^2}{n}} \] | Smaller RMSE value; ideal value is 0 |
| Mean bias (E)                          | \[ \hat{E} = \frac{\sum_{i=1}^{n} (Y_i - \hat{Y}_i)}{n} \] | Lower bias                    |
| Absolute mean deviation (AMD)          | \[ \text{AMD} = \frac{\sum_{i=1}^{n} |Y_i - \hat{Y}_i|}{n} \] | Lower AMD value               |
| Akaike Information Criterion (AIC)     | \[ \text{AIC} = n \ln(RSS/n) + 2k \] | Smaller AIC value             |
| Akaike weight (AICw)                   | \[ \text{AIC}_w = \frac{\text{exp}(-0.5\Delta r)}{\sum_{j=1}^{m} \text{exp}(-0.5\Delta r_j)} \] | Higher AICw value             |

\( Y_i \) = observed value of the \( i \)th observation; \( \hat{Y}_i \) = predicted value of the \( i \)th observation; \( \overline{Y} \) = mean of the \( Y \); \( n \) = number of observations in the dataset; \( k \) = number of estimated parameters; \( \text{RSS} \) = residual sum of squares; \( \ln \) = natural logarithm; \( \Delta i \) = difference between the AIC corrected of the best fitting equation and that of the \( i \) (model); \( R \) = relative likelihood of all the equations; and \( \Delta r \) = normalized relative likelihoods of the candidate equations.

In addition to the fit statistics as evaluation criteria, lack-of-fit statistics were also used to assess further the accuracy of the H-DBH models. Lack-of-fit statistics were used instead of re-sampling to give two independent data sets representing the same area since the re-sampling approach has an accompanying loss of information in model development and the validation estimates are not that stable due to fewer observations.

A cross-validation procedure is favored by most practitioners as it provides independent prediction residuals (Kozak & Kozak, 2003). Additionally, no particular set of criteria or assessment can be easily applied to assess the relevance of a model: nevertheless, a minimum assessment procedure is required to guarantee the reliability and acceptable performance of a new model (Huang et al., 2003). Kozak and Kozak (2003) further stated that, although statistics like R², RMSE, \( \hat{E} \), AMD, and SEE are sufficient measures of the appropriateness of a model, they are not enough to select the “best” model to predict the dependent variable, and therefore recommended the use of lack-of-fit parameters in combination with one or more of the above statistics; for example, plotting the residuals to determine the best appropriate regression model. Calculating \( \hat{E} \) and SEE for various sub groups of the independent variable, indicated as lack-of-fit statistics, is favored. In this study, the combination of \( \hat{E} \), AMD and SEE was used to validate the H-DBH models for every 10 cm DBH class.

The 100% dataset of the three tropical tree species was used for both the fit statistics and lack-of-fit statistics. The best-fitted H-DBH models on both evaluation using fit statistics and lack-of-fit statistics were selected for predicting the H of *P. malaanonan*, *D. paniculatus*, and *C. luzonica* from DBH.

The best nonlinear H-DBH model was selected with the use of the ranking of methods demonstrated by Poudel and Cao (2013). The ranking of methods is different from that of
the traditional standard or ordinal ranking as it shows not just the sequence of the models but also the extent of variation between the models, as was demonstrated in previous studies by N.D. Doyog et al. (2017), Lee et al. (2017) and N. Doyog et al. (2019). The order of the models based on their performance was assessed using the following formula:

$$R_i = 1 + \left[ \frac{(m - 1) \times (S_i - S_{\text{min}})}{S_{\text{max}} - S_{\text{min}}} \right]$$

where $R_i$ is the relative rank of model $i$ ($i = 1, 2, \ldots, m$); $S_i$ is the goodness-of-fit statistic produced by model $i$; $S_{\text{min}}$ is the minimum value of the goodness-of-fit statistic; and $S_{\text{max}}$ is the maximum value of the goodness-of-fit statistic.

Number 1 represents the best rank and m the poorest rank for each statistical measure. For instance, relative ranks of 1.0160, 1.0752, 2.2500, 2.7499, 4.7825, and 6.0000 in the case of six H-DBH models signifies that the standing of the models in predicting height of a certain species does not have a close gap.

Results

**Model performance evaluations (Fit statistics)**

The parameter estimates and evaluation statistics of the six H-DBH models, estimated using the SAS-NLIN procedure using the 100% dataset, are set out in Table 4 for *P. malaanonan*, 5 for *D. paniculatus*, and 6 for *C. luzonica*. Table 4 shows that the parameter estimates of all the H-DBH models for *P. malaanonan* had a significant difference from zero ($p$-value of <.0001). The table shows that, based on the six fit statistics that were used in this study, the WE model achieved the best overall rank of 1.2442. The WE model ($R^2$:0.9732; RMSE:3.4714; $E$:0.0296; AMD:2.5791; AIC:438.5687; and AIC$_w$:0.4733) was followed in

| Statistics | CR     | EX     | KL     | ML     | SC     | WE     |
|------------|--------|--------|--------|--------|--------|--------|
| a          | 33.7509| 44.699 | 57.186 | 39.722 | 0.0257 | 33.0018|
| (1.4835)   | (2.4854)| (10.214)| (3.063) | (0.007) | (1.4487)|
| b          | 0.0414 | -25.863| 7.3816 | 0.012  | 1.4324 | 0.0197 |
| (0.0064)   | (3.572) | (1.187) | (0.0032) | (0.1654) | (0.0039)|
| c          | 1.2654 | 5.8268 | 0.5962 | 1.3593 | 22.8771| 1.1814 |
| (1.1429)   | (1.8641)| (0.102) | (0.1277) | (-0.4132)| (0.0801)|
| F value    | 2070.98| 2029.32| 1986.72| 2042.59| 1981.64| 2078.86|
| P >F       | <.0001 | <.0001 | <.0001 | <.0001 | <.0001 | <.0001 |
| $R^2$      | 0.9731 | 0.9725 | 0.9720 | 0.9727 | 0.9719 | 0.9732 |
| (1.3893)   | (3.4874)| (5.7270) | (2.8099) | (6.0000) | (1.0000)|
| RMSE       | 3.4778 | 3.5124 | 3.5488 | 3.5013 | 3.5352 | 3.4714 |
| (1.3924)   | (3.5037)| (5.7297) | (2.8246) | (6.0000) | (1.0000)|
| E          | 0.0230 | 0.0085 | 0.0299 | 0.0352 | 0.0805 | 0.0296 |
| (2.0069)   | (1.0000)| (2.4861) | (2.8542) | (6.0000) | (2.4653)|
| AMD        | 2.5810 | 2.5892 | 2.6380 | 2.5901 | 2.6861 | 2.5791 |
| (1.0888)   | (1.4720)| (3.7523) | (1.5140) | (6.0000) | (1.0000)|
| AIC        | 439.2177| 442.6742| 446.2902| 441.5636| 446.7259| 438.5687|
| (1.3978)   | (3.5165)| (5.7329) | (2.8369) | (6.0000) | (1.0000)|
| AIC$_w$    | 0.3422 | 0.0068 | 0.0100 | 0.1058 | 0.0080 | 0.4733 |
| (2.4093)   | (5.4331)| (5.9790) | (4.9494) | (6.0000) | (1.0000)|
| Over all Rank | 1.6141 | 3.0688 | 4.9012 | 2.9649 | 6.0000 | 1.2442 |

Parameter estimates (standard error); fit statistics (relative rank).
order by the CR model, ML model, EX model, KL model, and SC model. The CR, ML, EX, KL, and SC models had overall ranks of 1.6141, 2.9649, 3.0688, 4.9012, and 6.0000, respectively.

The $R^2$ by the six H-DBH models in this study for *P. malaanonan* vary very little; all six models had an $R^2$ value close to 1 indicating that the models fitted the species well. C.H. Peng et al. (2001) stated that a model is better the nearer the value is to 1. However, based on all the fit statistics and rank analysis as shown in Table 4, the WE model was the best for estimating the height of *P. malaanonan* with DBH as the only variable. The rank of the models based on the different evaluation criteria is shown through the radar chart at Figure 1(a).

The estimates of the parameters for each of the six H-DBH models for *D. paniculatus* showed a significant difference from zero as indicated by the *p*-value of <.0001, as shown in Table 5. Table 5 also shows the fit statistics derived from the SAS-NLIN. The best H-DBH model for the *D. paniculatus* species is the KL model, with $R^2$ value of 0.9461, the closest to 1, the best RMSE value of 3.4109 and an $\hat{E}$ value of -0.0019. The negative $\hat{E}$ values from all the H-DBH models indicate that the models over predicted the height of the *D. paniculatus* species. The $\hat{E}$ values of all the models had a mean of 0.007 m. The model with the least $\hat{E}$ indicates the best model although the KL model did not attain the least $\hat{E}$. Nevertheless, the KL model was still the best for the *D. paniculatus* species as it was the best for the rest of the evaluation criteria. In addition, the KL model had the best AMD value of 2.4511, the best AIC (439.7787) and AIC$_w$ (0.2309) values.

![Rank analysis of the six candidate H-DBH models](image)

**Figure 1.** Rank analysis of the six candidate H-DBH models for (a) *P. malaanonan*, (b) *D. paniculatus*, and (c) *C. luzonica* species in Mt. Makiling, Philippines using the 100% dataset (The model with the smallest area represents the best model).
Table 5. The estimated parameters and fit statistics of the six H-DBH models for the Diplodiscus paniculatus species in Mt. Makiling, Philippines.

| Statistics | CR     | EX     | KL     | ML     | SC     | WE     |
|------------|--------|--------|--------|--------|--------|--------|
| a          | 18.6041| 21.9194| 22.9057| 20.4362| 0.037  | 18.7153|
|            | (1.1228)| (1.5581)| (3.3182)| (1.9504)| (0.0177)| (1.2952)|
| b          | 0.0663 | -10.5485| 7.5324 | 0.0248 | 2.0424 | 0.0516 |
|            | (0.0182)| (2.6671)| (2.8674)| (0.0126)| (0.383 )| (0.0163)|
| c          | 1.1332 | 0.8632 | 0.8723 | 1.4348 | 16.6952| 1.0492 |
|            | (0.2646)| (1.9371)| (0.2182)| (0.2602)| (0.3594)| (0.1438)|
| F value    | 1011.31| 1022.32| 1022.95| 1018.76| 1022.24| 1010.45|
| P>F        | <.0001 | <.0001 | <.0001 | <.0001 | <.0001 | <.0001 |
| R²         | 0.9455 | 0.9460 | 0.9461 | 0.9458 | 0.9460 | 0.9454 |
|            | (5.6639)| (1.2521)| (1.0000)| (2.6807)| (1.2941)| (6.0000)|
| RMSE       | 3.4294 | 3.4119 | 3.4109 | 3.4176 | 3.4121 | 3.4308 |
|            | (5.6519)| (1.2542)| (1.0000)| (2.6674)| (1.2837)| (6.0000)|
| E          | -0.0120| -0.0008| -0.0019| -0.0090| -0.0017| -0.0180|
|            | (4.2558)| (1.0000)| (1.3198)| (3.3837)| (1.2616)| (6.0000)|
| AMD        | 2.4680 | 2.4522 | 2.4511 | 2.4578 | 2.4550 | 2.4714 |
|            | (5.1626)| (1.2709)| (1.0000)| (2.6502)| (1.9606)| (6.0000)|
| AIC        | 441.7090| 439.8836| 439.7787| 440.4767| 439.9010| 441.8474|
|            | (5.6657)| (1.2535)| (1.0000)| (2.6872)| (1.2957)| (6.0000)|
| AICw       | 0.0879 | 0.2191 | 0.2309 | 0.1629 | 0.2172 | 0.0821 |
|            | (5.8025)| (1.3963)| (1.0000)| (3.2855)| (1.4604)| (6.0000)|
| Over all Rank | 5.3671 | 1.2378 | 1.0533 | 2.8925 | 1.4260 | 6.0000 |

Parameter estimates (standard error); fit statistics (relative rank).

Based on the six evaluation criteria and rank analysis (Figure 1(b)), the H-DBH model that best predicted the H of D. paniculatus was the KL model with an overall rank of 1.0533, followed by EX (1.2378), SC (1.4260), ML (2.8925), CR (5.3671), and WE model (6.0000), respectively. Although the KL model was the best, all six H-DBH models fitted the data of D. paniculatus species well, as indicated by the R² values of the models being close to 1.

The parameter estimates of the six H-DBH models for C. luzonica shown in Table 6 also showed significant difference from zero as supported by the p-value of <.0001, the same as for P. malaanonan and D. paniculatus. The KL model best predicted the H of C. luzonica species based on the different fit statistics criteria and rank analysis (Figure 1(c)) compared with the other models assessed. The KL model had the highest rank (1.0160) and R² value of 0.9638, RMSE of 2.3972, E of 0.0011, AMD of 1.5934, AIC value of 336.9673, and AICw of 0.3096. The KL model ranking was followed by the EX model, ML model, SC model, CR model, and WE model, respectively. The EX, ML, SC, CR, and WE models had overall ranks of 1.0752, 2.2500, 2.7499, 4.7825, and 6.0000, respectively. The ranking indicates that the performance of most of the models is similar, except for models CR and WE which were separated by a large gap.

The following are the H-DBH models developed for the tree tropical tree species of Mt. Makiling based on this study:

\[
P. \text{ malaanonan} \quad \text{HT} = 1.3 + 33.0018 \left( 1 - e^{-0.0197 \times \text{DBH}^{1.1814}} \right) \quad (2)
\]
Table 6. The estimated parameters and fit statistics of the six H-DBH models for the Celtis luzonica species in Mt. Makiling, Philippines.

| Statistics | CR         | EX         | KL         | ML         | SC         | WE         |
|------------|------------|------------|------------|------------|------------|------------|
| a          | 19.0235    | 23.4236    | 24.3033    | 21.0512    | 0.0371     | 19.1136    |
|            | (0.683)    | (1.1221)   | (2.2367)   | (1.156)    | (0.0117)   | (0.7055)   |
| b          | 0.0831     | −10.5877   | 7.8173     | 0.0188     | 1.9978     | 0.0366     |
|            | (0.0126)   | (1.6365)   | (1.5665)   | (0.0052)   | (0.1995)   | (0.0067)   |
| c          | 1.4149     | 0.7991     | 0.8868     | 1.5697     | 17.6745    | 1.2064     |
|            | (0.1878)   | (1.0122)   | (0.1274)   | (0.1531)   | (0.3216)   | (0.0884)   |
| F value    | 163.43     | 1668.78    | 1668.95    | 1660.99    | 1650.98    | 1623.69    |
| P >F       | <.0001     | <.0001     | <.0001     | <.0001     | <.0001     | <.0001     |
| R²         | 0.9631     | 0.9638     | 0.9638     | 0.9636     | 0.9634     | 0.9628     |
|            | (4.7931)   | (1.0172)   | (1.0000)   | (1.8621)   | (2.9483)   | (6.0000)   |
| RMSE       | 2.4215     | 2.3973     | 2.3972     | 2.4027     | 2.4098     | 2.4292     |
|            | (4.8071)   | (1.0196)   | (1.0000)   | (1.8667)   | (2.9619)   | (6.0000)   |
| Ê          | −0.0100    | 0.0007     | 0.0011     | −0.0064    | 0.0053     | −0.0215    |
|            | (3.2356)   | (1.0000)   | (1.0962)   | (2.3702)   | (2.1058)   | (6.0000)   |
| AMD        | 1.6250     | 1.5959     | 1.5934     | 1.6048     | 1.5941     | 1.6292     |
|            | (5.4134)   | (1.3492)   | (1.0000)   | (2.5922)   | (1.0978)   | (6.0000)   |
| AIC        | 340.8176   | 336.9850   | 336.9673   | 337.8492   | 338.9546   | 342.0265   |
|            | (4.8052)   | (1.0175)   | (1.0000)   | (1.8716)   | (2.9641)   | (6.0000)   |
| AICw       | 0.0452     | 0.3068     | 0.3096     | 0.1992     | 0.1146     | 0.0247     |
|            | (5.6405)   | (1.0478)   | (1.0000)   | (2.9372)   | (4.4216)   | (6.0000)   |
| Over all Rank | 4.7825     | 1.0752     | 1.0160     | 2.2500     | 2.7499     | 6.0000     |

Parameter estimates (standard error); fit statistics (relative rank).

\[ D. \text{paniculatus} \]

\[ HT = 1.3 + 22.9057 \times e^{(7.523a)} \]  

\[ C. \text{luzonica} \]

\[ HT = 1.3 + 24.3033 \times e^{(-7.8173 \times \text{DBH}^{0.8868})} \]

The predicted height, using the best model for each species, was plotted with the observed H and DBH as shown in Figure 2.

**Model performance evaluation (Lack-of-fit statistics)**

Lack-of-fit statistics were used in this study to further validate the performance of the six H-DBH models. This method is necessary since no single overall value from the fit statistics indicates which model best predicts the total height at any given DBH (Kozak & Kozak, 2003; Kozak & Smith, 1993). There is no consistent H-DBH model to determine the best model for height prediction of a species at a given DBH class. It is commonly recommended to use various measures of lack-of-fit in combination with one or more of the statistics above for the determination of the most appropriate regression model. Calculation of Ê and AMD for various sub-groups of the independent variables, usually referred to as lack-of-fit statistics, is preferred (Kozak & Kozak, 2003; Kozak & Smith, 1993). The performance of the six models, based on Ê, AMD, and SEE per DBH class, was analyzed. The result of the lack-of-fit analysis for P. malaanonan, D. paniculatus and C. luzonica is presented in Tables 7 and 8, and 9, respectively.
For the *P. malaanonan*, the ML model had the least Ė among the candidate H-DBH models. The least Ė indicates the best model. The least bias among the models was observed at DBH class 21–30 cm, while the model with the highest bias was SC observed at DBH class 11–20 cm. For the AMD value, the EX model had the best, observed at DBH class <11 cm, while the worst AMD was from the SC model observed at DBH class 11–20 cm. The best SEE

**Figure 2.** Comparison of the observed dataset with the predicted total heights of (a) *P. malaanonan*, (b) *D. paniculatus*, and (c) *C. luzonica* species in Mt. Makiling, Philippines.
Table 7. Lack-of-fit statistics of the six H-DBH models for Parashorea malaanonan species in Mt. Makiling, Philippines.

| H-DBH models | Lack-of-fit statistics | Less than 11 cm | 11–20 cm | 21–30 cm | 31–40 cm | 41–50 cm | >50 cm |
|--------------|------------------------|-----------------|----------|----------|----------|----------|--------|
| CR           |                        |                 |          |          |          |          |        |
|              | Ŕ                       | 1.62            | 0.62     | 0.21     | 3.10     | 1.52     | 0.51   |
|              | AMD                    | 1.91            | 2.02     | 2.92     | 3.87     | 4.09     | 3.78   |
|              | SEE                    | 2.39            | 2.96     | 3.75     | 5.20     | 6.25     | 4.67   |
|              | **Rank**               | **1.11**        | **1.24** | **1.02** | **1.04** | **1.04** | **1.09**|
| EX           | Ŕ                       | 1.53            | 0.45     | 0.26     | 3.42     | 1.90     | 0.28   |
|              | AMD                    | 1.85            | 1.98     | 2.91     | 4.05     | 4.24     | 3.67   |
|              | SEE                    | 2.32            | 2.93     | 3.74     | 5.42     | 6.39     | 4.65   |
|              | **Rank**               | **1.00**        | **1.13** | **1.03** | **1.23** | **1.21** | **1.00**|
| KL           | Ŕ                       | 1.75            | 0.23     | 0.22     | 3.57     | 2.10     | 0.29   |
|              | AMD                    | 2.04            | 1.94     | 2.90     | 4.14     | 4.36     | 3.65   |
|              | SEE                    | 2.46            | 2.90     | 3.73     | 5.52     | 6.47     | 4.67   |
|              | **Rank**               | **1.28**        | **1.00** | **1.00** | **1.32** | **1.32** | **1.00**|
| ML           | Ŕ                       | 1.73            | 0.53     | 0.19     | 3.27     | 1.79     | 0.44   |
|              | AMD                    | 1.99            | 2.01     | 2.92     | 3.96     | 4.20     | 3.72   |
|              | SEE                    | 2.46            | 2.95     | 3.74     | 5.32     | 6.35     | 4.66   |
|              | **Rank**               | **1.24**        | **1.19** | **1.01** | **1.14** | **1.16** | **1.06**|
| SC           | Ŕ                       | 5.05            | 4.46     | 5.61     | 9.83     | 9.06     | 8.39   |
|              | AMD                    | 5.05            | 4.61     | 5.61     | 9.83     | 9.30     | 8.39   |
|              | SEE                    | 5.51            | 5.45     | 6.94     | 11.26    | 12.39    | 10.07  |
|              | **Rank**               | **6.00**        | **6.00** | **6.00** | **6.00** | **6.00** | **6.00**|
| WE           | Ŕ                       | 1.63            | 0.69     | 0.22     | 3.02     | 1.42     | 0.56   |
|              | AMD                    | 1.92            | 2.05     | 2.93     | 3.84     | 4.05     | 3.81   |
|              | SEE                    | 2.41            | 2.97     | 3.75     | 5.15     | 6.22     | 4.68   |
|              | **Rank**               | **1.13**        | **1.30** | **1.03** | **1.00** | **1.00** | **1.12**|

value was from the EX model, observed at DBH class <11 cm, while the worst was from the SC model observed at DBH class 11–20 cm. Overall, the lack-of-fit analysis for the P. malaanonan species resulted in the least bias for all six H-DBH models at DBH class 21–30 cm, while the best AMD and SEE were both observed at DBH class <11 cm. Considering each DBH class, the EX model was the best at DBH class >11 cm; the KL model for DBH classes 11–20 cm and 21–30; the WE model for DBH classes 31–40 and 41–50 cm; and EX model for DBH class >50. The worst model for all DBH classes was the SC model.

Considering the lack-of-fit statistics of D. Paniculatus, presented in Table 8, the WE model had the least Ŕ, observed at DBH class 41–50 cm; the WE model provided the best AMD and SEE values, both observed at DBH class <11 cm. The least Ŕ of all the H-DBH models were observed all at DBH class 41–50 cm while the best AMD and SEE of all the models were all observed at DBH class <11 cm. Assessing the best model per DBH class, the WE model was the best for DBH class <11 cm; the EX model for DBH class 11–20 cm; the ML model for DBH class 21–30 cm; the CR model for DBH class 31–40 cm; the WE model for DBH class 41–50 cm and the KL model for DBH class >50 cm. The SC model was the worst for all DBH classes, and for the lack-of-fit analysis of P. malaanonan species.

Table 9 shows the lack-of-fit analysis for the C. luzonica species. The KL model was the best in terms of Ŕ value, observed at DBH class 31–40 cm; the WE model had the best AMD and SEE values, both at DBH class <11 cm. Considering the best model per DBH class, the WE model was the best both at DBH classes <11 cm and 41–50 cm; the ML model at DBH class 11–20 cm; the CR model at DBH class 21–30 cm; and the KL model for both the DBH classes 31–40 cm and >50 cm.
Table 8. Lack-of-fit statistics of the six H-DBH models for Diplodiscus paniculatus species in Mt. Makiling, Philippines.

| H-DBH models | Lack-of-fit statistics | DBH Class (cm) | <11 | 11–20 | 21–30 | 31–40 | 41–50 | >51 |
|--------------|------------------------|----------------|-----|-------|-------|-------|-------|-----|
| Frequency    |                        |                | 36  | 59    | 37    | 24    | 14    | 8   |
| CR           | É                      |                | 0.93| 1.30  | 0.87  | 1.06  | 0.16  | 2.91|
|              | AMD                    |                | 1.30| 2.11  | 2.93  | 4.17  | 2.70  | 4.58|
|              | SEE                    |                | 2.01| 2.89  | 4.04  | 5.62  | 3.96  | 7.46|
|              | **Rank**               |                | 1.09| 1.61  | 1.01  | **1.00**| **1.02**| **1.43**|
| EX           | É                      |                | 1.18| 1.09  | 0.91  | 1.26  | 0.29  | 2.60|
|              | AMD                    |                | 1.41| 2.03  | 2.93  | 4.19  | 2.73  | 4.53|
|              | SEE                    |                | 2.09| 2.51  | 4.04  | 5.67  | 3.97  | 7.37|
|              | **Rank**               |                | 1.40| 1.00  | 1.03  | **1.21**| **1.16**| **1.13**|
| KL           | É                      |                | 1.15| 1.10  | 0.95  | 1.27  | 0.26  | 2.48|
|              | AMD                    |                | 1.39| 2.03  | 2.94  | 4.19  | 2.72  | 4.51|
|              | SEE                    |                | 2.08| 2.50  | 4.05  | 5.67  | 3.97  | 7.33|
|              | **Rank**               |                | 1.36| 1.004 | 1.07  | **1.22**| **1.14**| **1.00**|
| ML           | É                      |                | 1.05| 1.17  | 0.88  | 1.19  | 0.25  | 2.70|
|              | AMD                    |                | 1.35| 2.06  | 2.93  | 4.19  | 2.72  | 4.55|
|              | SEE                    |                | 2.04| 2.52  | 4.03  | 5.65  | 3.97  | 7.40|
|              | **Rank**               |                | 1.24| 1.10  | 1.00  | **1.14**| **1.12**| **1.23**|
| SC           | É                      |                | 3.51| 3.47  | 3.58  | 3.98  | 3.01  | 5.42|
|              | AMD                    |                | 3.51| 3.58  | 4.02  | 5.13  | 3.69  | 5.87|
|              | SEE                    |                | 4.08| 4.20  | 5.41  | 6.96  | 5.22  | 9.49|
|              | **Rank**               |                | **6.00**| **6.00**| **6.00**| **6.00**| **6.00**| **6.00**|
| WE           | É                      |                | 0.85| 1.33  | 0.92  | 1.07  | 0.13  | 2.83|
|              | AMD                    |                | 1.26| 2.13  | 2.94  | 4.18  | 2.69  | 4.56|
|              | SEE                    |                | 1.98| 2.56  | 4.05  | 5.62  | 3.96  | 7.41|
|              | **Rank**               |                | 1.00| 1.32  | 1.07  | 1.01  | **1.00**| **1.32**|

Discussion

The results of this study indicate that different models are best for each species, based on fit statistics. This means that no single H-DBH model is the best for predicting the H of all species given the DBH as predictor. This is because each species exhibits a different growth curve pattern.

The same is true from the analysis of the lack-of-fit statistics. This shows that no single H-DBH model is best for predictions for a single species at any given DBH. A model may be the best for predicting the H of a particular species at a certain DBH class but this does not mean that it is the best for all DBH classes.

This study only used H-DBH models which utilize DBH as the only predictor for the H of a certain species. Other recently published research suggests that the inclusion of other covariates to predict H could improve the predictive capacity of a certain model. According to Saud et al. (2016), the inclusion of the quadratic mean diameter substantially improved the predictive capacity of the existing H-DBH models for naturally occurring shortleaf pine forests (Pinus echinata Mill) of western Arkansas and eastern Oklahoma. Other stand variables aside from DBH could also be included as predictors in different H-DBH models to predict H of a certain species. Coral-Rivas et al. (2014) included other stand variables, including stand density, stand basal area, mean square diameter, dominant H, and dominant diameter as predictors for H estimation. Ige et al. (2013) recommended incorporating more variables including the tree age, crown width and soil richness in H-DBH models in future predictions of the tree H of Gmelina arborea in Ibadan, Nigeria.
Table 9. Lack-of-fit statistics of the six H-DBH models for Celtis luzonica species in Mt. Makiling, Philippines.

| H-DBH models | Lack-of-fit statistics | <11 | 11–20 | 21–30 | 31–40 | 41–50 | >51 |
|--------------|------------------------|-----|-------|-------|-------|-------|-----|
| CR           | È                      | 1.02| 1.48  | 1.12  | −1.07 | 1.59  | 2.46|
| AMD          | 1.39                   | 2.12| 2.33  | 2.11  | 3.57  | 2.96  |
| SEE          | 1.69                   | 3.52| 4.46  | 3.24  | 5.16  | 4.06  |
| Rank         | 1.06                   | 1.08| 1.00  | 2.14  | 1.06  | 2.21  |
| EX           | È                      | 1.03| 1.42  | 1.46  | −0.76 | 1.60  | 1.79|
| AMD          | 1.41                   | 2.12| 2.32  | 1.97  | 3.65  | 2.38  |
| SEE          | 1.70                   | 3.49| 4.59  | 3.12  | 5.23  | 3.36  |
| Rank         | 1.10                   | 1.02| 1.28  | 1.08  | 1.21  | 1.12  |
| KL           | È                      | 1.02| 1.43  | 1.51  | −0.74 | 1.60  | 1.71|
| AMD          | 1.41                   | 2.13| 2.33  | 1.96  | 3.65  | 2.31  |
| SEE          | 1.70                   | 3.50| 4.61  | 3.11  | 5.23  | 3.28  |
| Rank         | 1.09                   | 1.04| 1.32  | 1.00  | 1.21  | 1.00  |
| ML           | È                      | 1.03| 1.42  | 1.30  | −0.87 | 1.63  | 2.09|
| AMD          | 1.41                   | 2.10| 2.31  | 2.02  | 3.63  | 2.63  |
| SEE          | 1.70                   | 3.49| 4.52  | 3.16  | 5.22  | 3.66  |
| Rank         | 1.10                   | 1.00| 1.13  | 1.43  | 1.19  | 1.60  |
| SC           | È                      | 3.56| 4.04  | 4.40  | 2.21  | 4.58  | 4.84|
| AMD          | 3.58                   | 4.05| 4.40  | 2.45  | 5.05  | 4.84  |
| SEE          | 3.89                   | 5.26| 6.55  | 3.95  | 7.32  | 6.61  |
| Rank         | 6.00                   | 6.00| 6.00  | 6.00  | 6.00  | 6.00  |
| WE           | È                      | 0.98| 1.56  | 1.12  | −1.12 | 1.55  | 2.48|
| AMD          | 1.36                   | 2.14| 2.33  | 2.14  | 3.55  | 2.98  |
| SEE          | 1.67                   | 3.56| 4.46  | 3.26  | 5.14  | 4.09  |
| Rank         | 1.00                   | 1.19| 1.01  | 2.33  | 1.00  | 2.25  |

Although the inclusion of different variables in the H-DBH models can improve the predictive capability of a model for H estimation, the models developed in this study for P. malaanonan, D. paniculatus and C. luzonica already provide accurate enough estimates of H using DBH as the single predictor for practical forest resource inventories. The direct measurement of DBH in the field makes it a very reliable variable to use as a predictor for height estimation.

The development of H-DBH models of the three species could provide reliable estimates of the H information of the species from accurate field data. The H and DBH are fundamental for the development and application of growth and yield models that are generally used to predict the temporal development of forest stands (Costa et al., 2018). Forest managers can use this reliable information about the fluctuating growth of their forest resources to develop plans tailored to their forest, thus ensuring the sustainability of the forest resources.

**Conclusion**

Six H-DBH models (CR, EX, KF, ML, SC, and WE) were used to derive estimations of the H of three tree species in Mt. Makiling, P. malaanonan, D. paniculatus, and C. Luzonica, using the DBH as the only predicting variable.

This study showed that the H-DBH models fitted well for the three tropical species. The WE model was determined to perform best in predicting the H of P. malaanonan.
species, while the KL model performed best both for the *D. paniculatus*, and *C. luzonica* species.

Even though this study utilized only one, the DBH, to estimate the H of the three species, the H-DBH models that were developed provide accurate estimates of H. The DBH can be directly measured in the field, providing sufficient accuracy for use as the only predictor for stem volume estimation or biomass estimation when H is unavailable and in the absence of other stand variables.

**Conflict of interest**

None of the authors have any conflict of interest to declare for this study.

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