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Individual Plant Allometric Equations for Estimating Aboveground Biomass and Its Components for a Common Bamboo Species (*Bambusa procera* A. Chev. and A. Camus) in Tropical Forests

Bao Huy [1], Giang Thi Thanh [2], Krishna P. Poudel [3] and Hailemariam Temesgen [4,*]

[1] Department of Forest Resources and Environment Management, Tay Nguyen University, 567 Le Duan, Buon Ma Thuot, Dak Lak 630000, Vietnam; BaoHuy.frem@gmail.com
[2] Forest Science Institute of Central Highlands and South of Central Viet Nam, 09 Hung Vuong, Da Lat, Lam Dong 670000, Vietnam; GiangThanh136@gmail.com
[3] Department of Forestry, Mississippi State University, P.O. Box 9681, Starkville, MS 39762, USA; Krishna.Poudel@msstate.edu
[4] Department of Forest Engineering, Resources and Management, Oregon State University (OSU), Corvallis, OR 97333, USA
* Correspondence: Hailemariam.Temesgen@oregonstate.edu; Tel.: +1-5417378549; Fax: +1-5417379126

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Abstract: Bamboo forests play an important role in achieving the objectives of the United Nations program on Reducing Emission from Deforestation and Forest Degradation. We developed and validated a modeling system that simultaneously estimate aboveground biomass and its components for a common bamboo species (*Bambusa procera* A. Chev. and A. Camus) in tropical forests. Eighty-three bamboo culms were destructively sampled from seventeen 100 m^2 sample plots located in different parts of the Central Highlands in Viet Nam to obtain total plant aboveground biomass (*AGB*) and its components. We examined the performance of weighted nonlinear models fit by maximum likelihood and weighted nonlinear seemingly unrelated regression fit by generalized least squares for predicting bamboo biomass. The simultaneous estimation of *AGB* and its components produced higher reliability than the models of components and total developed separately. With a large number of bamboo species, it may not be feasible to develop species- specific biomass models, hence genus-specific allometric models may be considered.

Keywords: bamboo biomass; genus-specific model; seemingly unrelated regression; simultaneous biomass estimation

1. Introduction

Natural bamboo forests help fight against poverty and to mitigate climate change [1,2] and offer a variety of products for livelihoods and forest ecosystem services in the tropical regions. Bamboos are multipurpose plants [3], and sustainable management of natural bamboo forests helps to stabilize the livelihoods of millions of poor people in rural and mountainous areas [4]. Active management of fast-growing bamboo species will contribute to the United Nations Collaborative Programme on Reducing Emissions from Deforestation and Forest Degradation in Developing Countries (UN-REDD).

Bamboo is widely distributed in the subtropics and tropics of Asia, Africa, and Latin America, has a fast growth rate, and is very well capable of regenerating naturally [5–7]. There are 1250–1500 bamboo species globally consisting of 75–107 genera [4]. Bamboo forests cover approximately 31.5 million hectares, mostly in China and India [4]. In Viet Nam, bamboo forests are widely and naturally distributed. There are approximately 200 bamboo species belonging to about 20–25 genera in the country [8,9], and *Bambusa procera* A. Chev. and A. Camus plays an important role in the local economy [10]. The Central Highlands of Viet Nam has 186,309 hectares of natural forest of pure bamboo forests and mixed forest of woody and bamboo species representing 8.3% of total natural forest area in this eco-region [11]. Throughout the country, the natural bamboo forests cover about 12% of total forested area [11]. *Bambusa procera* can be used to produce paper, textile, its leaves are used to feed animals, and culms for making many kinds of handcrafts and housing materials. This species is mainly distributed in the uplands where it helps in preventing land slide, regulating water, reducing flooding, and it has potential in climate change mitigation due to its ability to sequester carbon.

Regardless of the botanical classification, bamboo is a woody grass, but it is capable of accumulating carbon similar to other woody forest types [1,5]. With the high growth rate, organic carbon accumulation due to photosynthesis is high in culms, branches, leaves, and in the network of bamboo roots and persistent rhizomes [4]. Carbon accumulation in bamboo forests is similar to, or higher than that of fast-growing timber plantations [2]. Yuen et al. (2017) [4] in a review indicated that the aboveground carbon of bamboo forests ranged from 16–128 Mg C ha^{-1}, which is substantial compared to tropical rain forest in Asia which contains 56–320 Mg C ha^{-1} [12,13]. Therefore, bamboo needs to be recognized better in forest policy and management and needs to be included in Measurement, Reporting and Verification (MRV) of the UN-REDD program. To do this, an important task is to develop a system of allometric equations for estimating and monitoring biomass and carbon of the bamboo forest in this region.

Allometric equations for estimating forest biomass have been developed for many geographical regions [4], but they mostly focus on large tree species [14–17]. In Viet Nam, previously developed models for biomass estimation have mainly focused on trees of major tropical forests types [18–21]. Despite bamboo forests being a unique forest ecosystem with substantial carbon storage capacity, there are very few models available for bamboo biomass and carbon estimation [22]. Current the Intergovernmental Panel on Climate Change (IPCC) guidelines [12,13] ignore bamboo forests and there are no guidelines for biomass and carbon inventories in the greenhouse gas emission reports [2].

Major genera of bamboo include *Bambusa*, *Dendrocalamus*, *Gigantochloa*, and *Guadua*, with *Bambusa* being the most common. Most biomass models for bamboo have been developed in China, India, Japan, and Taiwan. Yuen et al. (2017) [4] reviewed 184 studies related to 70 bamboo species belonging to 22 genera around the world. They found that the biomass models were mostly developed for species *Phyllostachys edulis* (Carriere) J.Houz and *Dendrocalamus latiflorus* Munro. GlobAllomeTree database, an online data repository for global biomass data, contains 65 biomass equations for six bamboo species (*Bambusa balcooa* Roxb., *Bambusa bambos* (L.) Voss, *Bambusa cacharensis* R.B.Majumdar, *Bambusa procera* A.Chev. & A.Camus, *Bambusa vulgaris* Schrad., and *Indosasa angustata* McClure) developed in India and Viet Nam [23]. However, in Vietnam, there is a need to validate their reliability to assess the contribution of the widely distributed bamboo forests as the country prepares to implement the UN-REDD programme.

The objectives of this study were to develop a modeling system that simultaneously estimates aboveground biomass (*AGB*) and its components for a common bamboo species (*Bambusa procera* A. Chev. and A. Camus) in tropical forests of Viet Nam. With a large number of bamboo species, it is not feasible to develop species-specific biomass models. Therefore, the study also focused on evaluating the performance of genus-specific bamboo biomass models.

2. Materials and Methods

2.1. Study Sites

The study area was located in two provinces (Dak Lak and Dak Nong) of the Central Highlands in Viet Nam (Figure 1). Some of the ecological, environmental, and forest characteristics of the study area are summarized in Table 1.

Figure 1. Map of natural bamboo distribution and location of sample plots in the Central Highlands of Viet Nam.

Table 1. Summary of selected variables at the sample plot locations and summary statistics for variables of destructively sampled bamboo culm.

Factor/Variable	Minimum	Average	Maximum	SD
Mean annual rainfall (mm)	1800	2119	2300	
Mean annual temperature (°C)	22.3	22.6	23.0	
Source: Hydrometeorology Center in the Central Highlands Viet Nam, 2017				
Bedrock	Acid Magma, Basalt, Shale			
Soil unit	Geri-Acric Ferralsols, Haplic Acrisols, Epileptic Acrisols, Endoleptic Acrisols			
Source: The Map of Soil Units in Dak Lak and Dak Nong provinces, 2008				
Altitude (m)	575	700	898	91.1
Soil layer depth (cm)	30	60	100	29.4
Slope (degree)	3.0	20.5	48.0	11.7
Bamboo culm density ha^{-1}	4000	6965	13,500	2583
Source: Sample plots				
D (cm)	3.6	6.20	9.5	1.3
H (m)	6.1	14.52	25.4	4.0
A (year)	1	3	5	1.4
Bcu (kg plant^{-1})	1.97	7.83	26.13	4.85
Bbr (kg plant^{-1})	0.13	2.11	5.48	1.17
Ble (kg plant^{-1})	0.04	0.75	1.92	0.37
AGB (kg plant^{-1})	2.65	10.69	33.53	6.11
Source: Destructively sampled trees				

Note: D, H, and A are the diameter at breast height of bamboo culms, height of bamboo culms, and bamboo culm age, respectively; Bcu, Bbr, Ble, and AGB are the biomass of bamboo culms, branches, leaves, and total plant aboveground biomass, respectively.

Sample plots were distributed in areas that were different in elevation, rainfall, bedrock, soil unit, slope, and density of bamboo culms. There are two ecological sub-zones in Dak Lak and Dak Nong provinces with rainfall ranging from 1800–2300 mm year^{-1} (averaged over five years) and dry season lasting 3–5 months (Table 1, Figure 1).

2.2. Bamboo Species

In this study, the bamboo species we considered is *Bambusa procera* A. Chev. and A. Camus in the genus *Bambusa* that belongs to the Poaceae family. Briefly, the *Bambusa procera* species reaches heights over 25 m, diameters larger than 9 cm, has no thorns, straight culm, is hollow, and the age spans a range of 1–5 years (Table 1). Note that the culm developed in the study year is regarded as one-year old culm even though some researchers use the term "current-year-old", e.g., [24]. Bamboos of this study were of natural origin, distributed in larger areas or intermingling with evergreen broadleaf forests.

2.3. Sample Plot, Destructive Sample, and Measurement of Variables

Seventeen sample plots of 100 m^2 (10 × 10 m) were selected in different ecological conditions with varying rainfall, temperature, bedrock, soil unit, altitude, soil layer depth, and slope; and in different bamboo forest stand structure (Table 1). The size and shape of the sample plots were consistent with Zhuang et al. (2015) [25] for the Moso bamboo survey. Within a plot, the diameter at breast height (D, cm) and height (H, m) were recorded, and bamboo age (A, year) was identified directly from its morphological features [7,26]. A total of 83 bamboo culms covering the full range of sizes were destructively sampled with D ranging from 3.6–9.5 cm, with H of 6.1–25.4 m, and bamboo culms of 1, 2, 3, 4, and 5 years old (Table 1). The diameter and height distributions of the sampled bamboo are shown in Figure 2. The diameter distribution of destructively sampled bamboo culms was the same with the diameter distribution of the bamboo forests (Figure 2).

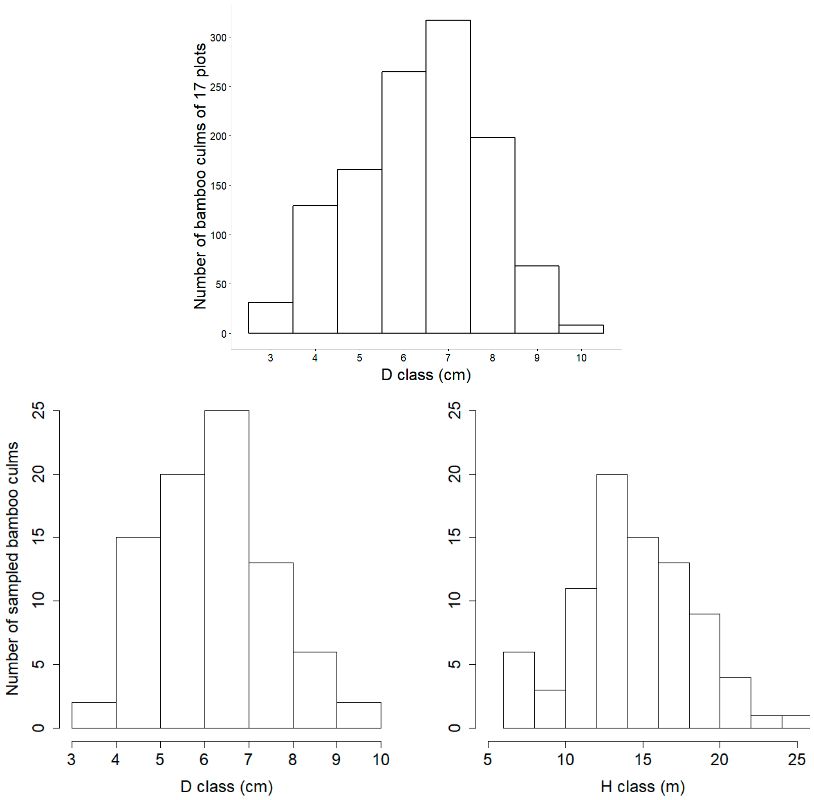

Figure 2. Top: Distribution of bamboo culm diameter (D, cm) of 17 sample plots of 100 m^2. Bottom: Distribution of bamboo culm diameter (D, cm) and bamboo culm height (H, m) of destructively-sampled bamboo culms.

Sampled bamboo culms after cutting were re-measured for height that were used in the modeling. Fresh biomass of three components of the bamboo culm, branches, and leaves were separated and weighed at the site. Approximately 100–300 g sub-samples for each component—culm (at three positions on the culm: root collar, middle, and top), branches, and leaves included young and old ones.

In the laboratory, the samples were dried at 105 °C until constant weight to obtain the fresh-to-dry mass ratio of each bamboo component to calculate dry biomass of the culm (*Bcu*, kg plant^{-1}), branches (*Bbr*, kg plant^{-1}), leaves (*Ble*, kg plant^{-1}), and total bamboo aboveground biomass (*AGB*, kg plant^{-1}) = *Bcu* + *Bbr* + *Ble*. Table 1 presents the summary statistics for each of the predictors and the response variables of the destructive sampled bamboo culms; and Figure 3 shows scatterplots of *Bcu*, *Bbr*, *Ble*, and *AGB* versus diameter (*D*) and the combined variable $D^2H = D^2$ (cm) × H (m).

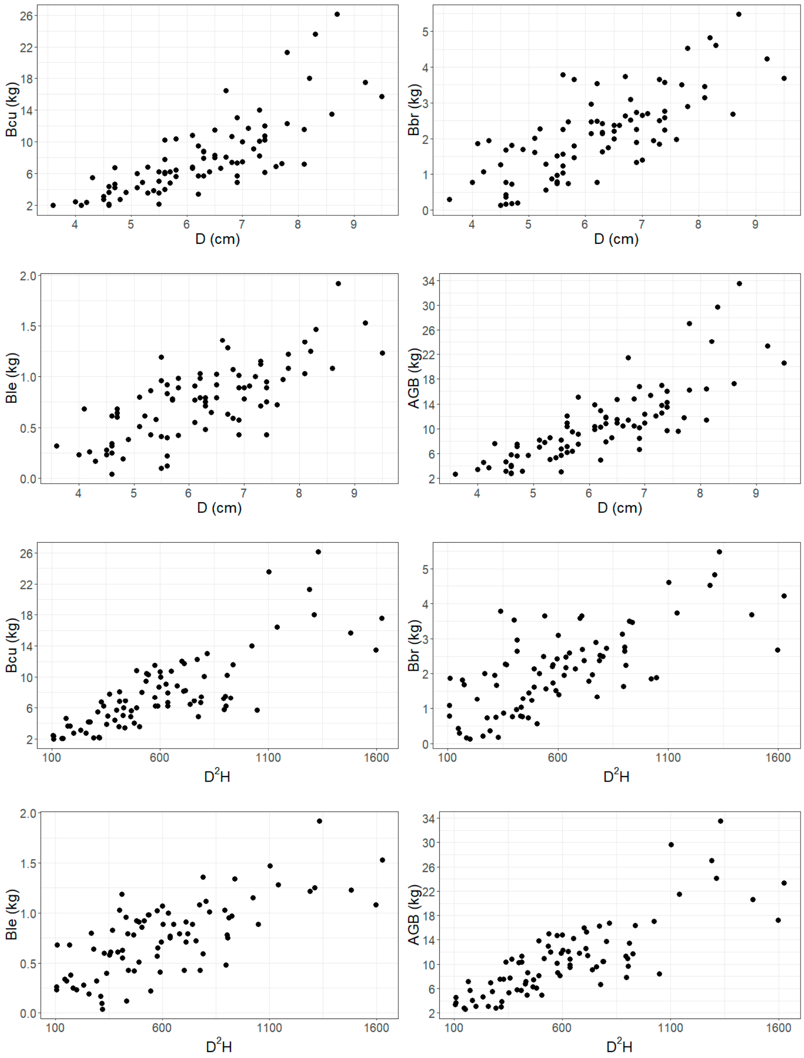

Figure 3. Scatterplots of biomass of culm (*Bcu*, kg), branches (*Bbr*, kg), leaves (*Ble*, kg), and bamboo aboveground biomass (*AGB*, kg) versus diameter (*D*) and $D^2H = D^2$ (cm) × H (m).

2.4. Methods to Fit and Validate the Bamboo Biomass Model Systems

The process of developing, comparing, selecting and cross-validating the biomass model system is summarized below:

- Develop and cross-validate to select independent models with appropriate predictors for each component and *AGB*, using weighted nonlinear model fit by maximum likelihood.
- Develop and cross-validate a system of component models and *AGB* fitted simultaneously, using weighted nonlinear SUR fit by generalized least squares; and compare with independent selected models and previously published bamboo biomass equations.
- Finally, obtain the parameters of all selected model systems by fitting models with the entire dataset.

2.4.1. Covariates and Model Form

This study used predictors of D, H, or combination of D^2H and power model to fit the model systems for estimating bamboo AGB and its components Bcu, Bbr, and Ble. Selection of the predictors and the model form for bamboo biomass is consistent with existing literature [4,22,27–29], that used the power form with one predictor of D for estimating total biomass, AGB, and its components biomass for *Phyllostachys pubescens* J.Houz., *Phyllostachys edulis*, *Bambusa bambos*, and the genus of *Bambusa*. Li et al. (2016) [7] used covariate D or D and H for estimating biomass of some bamboo species. Covariate D^2H is the best for thorny bamboo biomass of components [7], and for *Bambusa vulgaris* [2]. However, most bamboo biomass models used D as a sole predictor because it is both cheap and easy to measure. Therefore, we evaluated models with combination of different predictors and also developed models with D as the only predictor for application when other predictors are unavailable.

The power function has been widely used for biomass prediction [16,17,20,21] even though it is outperformed by other allometric models [30]. Yuen et al. [4] and Ricardo et al. [1] also demonstrated the power-law relation as one of the most common forms for estimating AGB and its components of different bamboo species worldwide.

2.4.2. Log-Transformation vs. Nonlinear Fit

The power equation can be fit in two ways, as a linear model of the log-transformed data or as a nonlinear model. Most power equations for estimating tree biomass in pantropical region were performed by log-transformation [12,14,16,17]. Kumar et al. (2005) [27] and Yuen et al. (2017) [4] also used log-log transformation to fit power model for *Bambusa nutans* Wall. ex Munro. Huy et al. (2016a, b, c, 2019) [18–21] used nonlinear modeling approach to develop the models for AGB estimates in tropical forests. Xiao et al. (2011) [31] suggested that the method chosen to fit power law should be based on analyses on both error distribution and biological structure. Huy et al. (2016c) [20] compared log-linear and non-linear models using the Furnival index [32] and showed that the power equation nonlinear fit produced higher reliability. Therefore, we assumed nonlinear relationship to fit biomass model for bamboo.

2.4.3. Weighted Nonlinear Models Fit by Maximum Likelihood

Weighted non-linear fit was used to account for heteroscedasticity in residuals [21,33] and to compare and select the best predictor(s) for each biomass component of bamboo and AGB independently [18,34,35]. Models were fitted using 'nlme' packages in statistical software R [36]. The form of the allometric equation, after Huy et al. (2016a, b, 2019) [18,19,21], was:

$$\mathrm{Y}_i = \alpha \times \mathrm{X}_i{}^{\beta} + \varepsilon_i \tag{1}$$

$$\varepsilon_i \sim iid\, \mathcal{N}\left(0, \sigma_i^2\right) \tag{2}$$

where Y_i is the Bcu, Bbr, Ble, or AGB in kg for the i^{th} bamboo culm; α and β are the parameters of the model; and X_i is the covariate D (cm), H (m), or D^2H for the i^{th} sampled culm; and ε_i is the random error associated with the i^{th} sampled culm.

The variance function was determined as follow [18,19,21]:

$$\mathrm{Var}(\varepsilon_i) = \hat{\sigma^2}(\nu_i)^{2\delta} \tag{3}$$

where $\hat{\sigma^2}$ is the estimated error sum of squares; ν_i is the weighting variable (D, D^2H in this study) associated with the i^{th} sampled culm; and δ is the variance function coefficient to be estimated.

2.4.4. Weighted Nonlinear Seemingly Unrelated Regression (SUR) Fit by Generalized Least Squares

When the models of each component and the *AGB* are fit independently the total biomass calculated from the component models is different from the estimate obtained from the independently developed *AGB* model [37–39]. Seemingly unrelated regression (SUR) can solve that limitation by allowing simultaneous estimation of the component biomass as well as *AGB*. Additionally, the SUR takes into account the cross-equation correlation (i.e., correlation among error terms of the biomass equations) among the equations and ensures the additivity among components and *AGB* predictions [38–41]. The weighted nonlinear SUR was implemented by using SAS procedure Proc Model with the generalized least squares (GLS) method [21,42].

The model system in this study had following general form [21,38,40,41]:

$$Bcu \ = a_1 \times {X_1}^{b1} + \varepsilon_1 \tag{4}$$

$$Bbr \ = a_2 \times {X_2}^{b_2} + \varepsilon_2 \tag{5}$$

$$Ble \ = a_3 \times {X_3}^{b3} + \varepsilon_3 \tag{6}$$

$$AGB \ = Bcu + Bbr + Ble = \ a_1 \times {X_1}^{b1} + \ a_2 \times {X_2}^{b_2} + a_3 \times {X_3}^{b_3} + \varepsilon_4 \tag{7}$$

where *Bcu*, *Bbr*, *Ble*, and *AGB* are biomass of culm, branches, leaves, and total aboveground in kg respectively; a_i and b_i are parameters of the power model i (i = 1, 2, 3 for culm, branches, and leaves, respectively); X_i is the predictor variable or combination of predictor variables (D, H, or D^2H) for the i^{th} equation; and ε_i is the residuals for the i^{th} equation (i = 1, 2, 3, 4). The weighting function is $1/{X_i}^{2\delta}$ with δ is the variance function coefficient to be estimated [21].

2.4.5. Model Comparison, Selection, and Cross-Validation

The dataset was randomly split into two parts with 70% for model development and 30% for validation. The cross-validation process was repeated 200 times, and statistics for comparison and validation of the models were averaged over 200 realizations [43].

Models were selected based on the Akaike information criterion (AIC) [44], the model that had lower AIC value was preferred; along with AIC, adj. R^2 (the larger the better), statistical significance of parameters (p-value < 0.05), and diagnostic plots of the trend of weighted residuals were also used to assess model performance.

Cross-validation of the model was done using percent bias, root mean squared error (RMSE, kg), and mean absolute percent error (MAPE, %). Equations that produced smaller values of cross-validation errors were preferred:

$$Bias\ (\%) = \frac{1}{R}\sum_{r=1}^{R}\frac{100}{n}\sum_{i=1}^{n}\frac{\boldsymbol{y_i} - \boldsymbol{\hat{y}_i}}{\boldsymbol{y_i}} \tag{8}$$

$$RMSE\ (kg) = \frac{1}{R}\sum_{r=1}^{R}\sqrt{\frac{1}{n}\sum_{i=1}^{n}(\boldsymbol{y_i} - \boldsymbol{\hat{y}_i})^2} \tag{9}$$

$$MAPE\ (\%) = \frac{1}{R}\sum_{r=1}^{R}\frac{100}{n}\sum_{i=1}^{n}\frac{|y_i - \ \hat{y}_i|}{y_i} \tag{10}$$

To assess the applicability of genus-specific models, we assessed the goodness of fit of the previously published models that were either developed for same [4,7] or different [1,45] genera of bamboo studied in this study using the Fit Index (FI) [21,46,47]. Models that have larger FI values are preferred:

$$FI = \ 1 - \frac{\sum_{i=1}^{N}(y_i - \hat{y}_i)^2}{\sum_{i=1}^{N}\,(y_i - \overline{y})^2} \tag{11}$$

where, R is the number of realizations (200); n, N are the number of bamboo plant samples per realization R and number of the entire plant samples, respectively; and y_i, $\hat{y}_i$ and $\overline{y}$ are the observed, predicted and averaged *Bcu*, *Bbr*, *Ble*, and *AGB* for the i^{th} bamboo culm in realization R, respectively.

3. Results

3.1. Components and AGB Models Fit Independently

Separate models for bamboo biomass components and *AGB* were developed and cross-evaluated for different covariates including D, D and H, and D^2H (Table 2). The results showed that cross-validation statistics had little differences among the different predictors in each component and *AGB* models. Most bamboo biomass components and *AGB* were closely related to the predictors but the *Bbr* and *Ble* models had a weaker relation with adj. $R^2 \geq 0.5$, whereas *Bcu* and *AGB* models were more closely related with adj. $R^2 > 0.6$ (Table 2). Therefore, the model chosen was based primarily on smaller AIC, combined with narrow variation and even distribution of weighted residuals at predicted biomass (Figure 4). For example, the *AGB* model with the D^2H predictor had AIC slightly larger than the models of predictor D, (not comparing with the *AGB* model with D and H predictors because of H variable's parameter had p-value > 0.05), but its weighted residuals graph produced the narrowest variation and spread evenly (Figure 4), so the model with the D^2H input variable was selected. Figure 4 also showed the homoscedastic weighted residuals were improved, as shown by even spread of the variation of weighted residuals.

Table 2. Cross-validation and comparison of selected biomass models for each component and bamboo aboveground biomass.

Model Form	Weight Variable	AIC	Adj. R^2	Averaged Bias (%)	Averaged RMSE (kg)	Averaged MAPE (%)
For *Bcu*:						
$Bcu = a \times D^b$	$1/D^{\delta}$	275.4	0.606	−11.4	3.0	29.7
$Bcu = a \times D^b \times H^c$	$1/D^{\delta}$	275.6	0.634	−10.1	2.9	29.8
$\mathbf{Bcu = a \times (D^2H)^b}$	$\mathbf{1/(D^2H)^{\delta}}$	269.6	0.610	−11.2	3.0	31.9
For *Bbr*:						
$\mathbf{Bbr = a \times D^b}$	$\mathbf{1/D^{\delta}}$	142.9	0.548	−44.3	0.8	66.2
$Bbr = a \times D^b \times H^c$	$1/D^{\delta}$	143.4	0.533	−44.1	0.8	66.2
$Bbr = a \times (D^2H)^b$	$1/(D^2H)^{\delta}$	151.7	0.466	−47.4	0.9	72.6
For *Ble*:						
$\mathbf{Ble = a \times D^b}$	$\mathbf{1/D^{\delta}}$	11.2	0.512	−34.6	0.3	55.8
$Ble = a \times D^b \times H^c$ *	$1/D^{\delta}$	11.4	0.521	−35.5	0.3	57.0
$Ble = a \times (D^2H)^b$	$1/(D^2H)^{\delta}$	13.5	0.487	−35.7	0.3	56.9
For *AGB*:						
$AGB = a \times D^b$	$1/D^{\delta}$	298.5	0.651	−9.1	3.6	26.9
$AGB = a \times D^b \times H^c$ *	$1/D^{\delta}$	302.7	0.668	−10.7	3.5	28.0
$\mathbf{AGB = a \times (D^2H)^b}$	$\mathbf{1/(D^2H)^{\delta}}$	304.9	**0.633**	**−11.9**	3.8	**31.3**

Note: All statistics were calculated using the cross-validation procedure with 200 realizations, 70% randomly split dataset for developing models, and 30% randomly split dataset for validation. *: Parameter with $p_{\text{value}} > 0.05$. δ: the variance function coefficient; Bold: Selected model based on cross-validation statistics and diagnostic plots. *Bcu*, *Bbr*, *Ble*, and *AGB* are biomass of bamboo culm, branches, leaves, and total aboveground biomass, respectively.

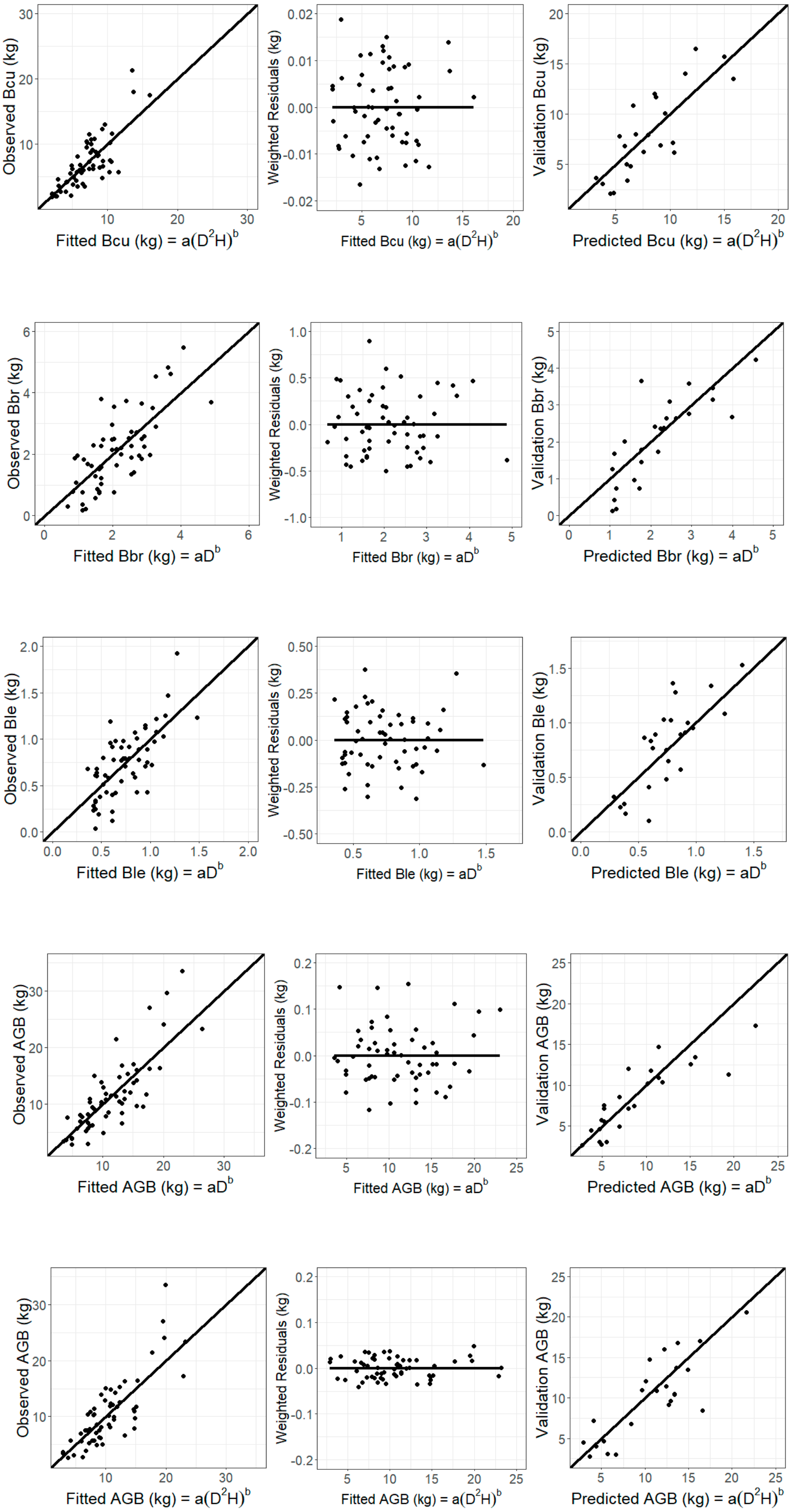

Figure 4. Plots of separate selected models for bamboo aboveground biomass (*AGB*) and its components with different predictor(s): Left: Observed was randomly split from 70% dataset vs. weighted fitted biomass; Middle: Maximum likelihood weighted residuals vs. fitted biomass; and Right: Validation data was randomly split from 30% dataset vs. predicted biomass. *Bcu*, *Bbr*, *Ble*, and *AGB* are biomass of bamboo culm, branches, leaves, and total aboveground biomass, respectively.

The selected models for each bamboo biomass component and *AGB* were in the following form:

$$Bcu = a \times (D^2H)^b \tag{12}$$

$$Bbr = a \times D^b \tag{13}$$

$$Ble = a \times D^b \tag{14}$$

$$AGB = a \times (D^2H)^b \tag{15}$$

3.2. Simultaneous Model System Fit by the SUR Method

We used weighted nonlinear SUR to develop and validate simultaneously fitted models for component and AGB of the bamboo and compared them with the models developed by fitting them independently. The simultaneous modeling systems included combinations of three components of bamboo (*Bcu*, *Bbr* and *Ble*) with different predictors such as *D*, *D* and *H*, or D^2H. Results of the establishment and evaluation of covariates in the separate component models revealed that the *Ble* and *AGB* models had variable *H* with a *p*-value > 0.05 (Table 2). Thus, the variable *H* was ignored in combinations of model systems. Three component models (*Bcu*, *Bbr*, and *Ble*) and two predictors (*D* and D^2H) form eight combinations of model systems.

Table 3 shows the results of developing simultaneously and cross-validating the eight combinations of the model systems applying weighted nonlinear SUR. Combination 6 produced the smallest bias, RMSE, and MAPE for most biomass components.

Table 3. Using SUR method to develop and validate simultaneously model combinations with 200 realizations; 70% randomly split dataset for developing simultaneous models; and 30% randomly split dataset for validation, calculation of averaged bias, RMSE, and MAPE.

Combination of Component Equation Systems	Weight Variable	Averaged Bias (%)	Averaged RMSE (kg)	Averaged MAPE (%)
Combination 1:				
$Bcu = a_1 \times D^{b1}$	$1/D$	−10.7	3.3	32.2
$Bbr = a_2 \times D^{b2}$	$1/D$	−57.0	0.8	78.9
$Ble = a_3 \times D^{b3}$	$1/D$	−32.0	0.3	53.5
$AGB = Bcu + Bbr + Ble$	$1/D$	−10.7	3.9	29.3
Combination 2:				
$Bcu = a_1 \times (D^2H)^{b1}$	$1/D^2H$	−4.1	3.4	33.3
$Bbr = a_2 \times (D^2H)^{b2}$	$1/D^2H$	−63.5	1.0	87.5
$Ble = a_3 \times (D^2H)^{b3}$	$1/D^2H$	−42.7	0.3	63.5
$AGB = Bcu + Bbr + Ble$	$1/D^2H$	−7.8	4.1	30.5
Combination 3:				
$Bcu = a_1 \times D^{b1}$	$1/D$	−16.5	3.4	35.1
$Bbr = a_2 \times (D^2H)^{b2}$	$1/D^2H$	−52.4	0.9	79.0
$Ble = a_3 \times D^{b3}$	$1/D$	41.4	0.7	90.3
$AGB = Bcu + Bbr + Ble$	$1/D^2H$	−9.2	3.9	28.4
Combination 4:				
$Bcu = a_1 \times D^{b1}$	$1/D$	−21.9	3.5	38.5
$Bbr = a_2 \times D^{b2}$	$1/D$	15.2	1.5	86.4
$Ble = a_3 \times (D2H)^{b3}$	$1/D^2H$	29.5	0.5	75.6
$AGB = Bcu + Bbr + Ble$	$1/D^2H$	−4.3	4.0	27.8
Combination 5:				
$Bcu = a_1 \times (D^2H)^{b1}$	$1/D^2H$	−1.0	3.3	30.2
$Bbr = a_2 \times D^{b2}$	$1/D$	−103.1	1.1	115.0
$Ble = a_3 \times D^{b3}$	$1/D$	61.1	0.6	79.8
$AGB = Bcu + Bbr + Ble$	$1/D^2H$	−4.2	3.9	27.8

Table 3. *Cont.*

Combination of Component Equation Systems	Weight Variable	Averaged Bias (%)	Averaged RMSE (kg)	Averaged MAPE (%)
Combination 6:				
$Bcu = a_1 \times (D^2H)^{b1}$	$1/D$	−1.8	3.2	30.5
$Bbr = a_2 \times (D^2H)^{b2}$	$1/D^2H$	−44.7	0.9	74.1
$Ble = a_3 \times D^{b3}$	$1/D^2$	−28.9	0.3	50.8
$AGB = Bcu + Bbr + Ble$	$1/D^2$	−2.2	3.8	28.3
Combination 7:				
$Bcu = a_1 \times D^{b1}$	$1/D$	−10.5	3.2	31.6
$Bbr = a_2 \times (D^2H)^{b2}$	$1/D^2H$	−56.4	0.9	81.5
$Ble = a_3 \times (D^2H)^{b3}$	$1/D^2H$	19.6	0.5	74.0
$AGB = Bcu + Bbr + Ble$	$1/D^2H$	−6.4	3.8	27.1
Combination 8:				
$Bcu = a_1 \times (D^2H)^{b1}$	$1/D^2H$	−11.1	3.2	32.3
$Bbr = a_2 \times D^{b2}$	$1/D$	−55.7	0.9	76.8
$Ble = a_3 \times (D^2H)^{b3}$	$1/D^2H$	−31.7	0.3	52.5
$AGB = Bcu + Bbr + Ble$	$1/D^2H$	−11.2	3.8	30.0

Note: Bold: Selected simultaneous model combination based on cross validation statistics. *Bcu*, *Bbr*, *Ble*, and *AGB* are biomass of bamboo culm, branches, leaves, and total aboveground biomass, respectively.

The forms of simultaneous model system were selected as follows:

$$Bcu = a_1 \times (D^2H)^{b1} \tag{16}$$

$$Bbr = a_2 \times (D^2H)^{b2} \tag{17}$$

$$Ble = a_3 \times D^{b3} \tag{18}$$

$$AGB = Bcu + Bbr + Ble = a_1 \times (D^2H)^{b1} + a_2 \times (D^2H)^{b2} + a_3 \times D^{b3} \tag{19}$$

Table 4 shows the model system parameters obtained from final models fit simultaneously with the entire dataset. However, in practice, the measurement of bamboo height (H) is difficult and costly, so we estimated the parameters for the model system simultaneously with sole D predictor and have presented this system in Table 5.

Table 4. SUR method estimating parameters of selected model combination of bamboo biomass components using the entire dataset.

Model Form	Weight Variable	Parameter	Estimate ± Approx. Std Error	Entire RMSE (kg)	Adj. R^2
$Bcu = a_1 \times (D^2H)^{b1}$	$1/D$	a_1 b_1	0.02269 ± 0.00746 0.90703 ± 0.04890	2.95	0.631
$Bbr = a_2 \times (D^2H)^{b2}$	$1/D^2H$	a_2 b_2	0.02015 ± 0.01010 0.72251 ± 0.07280	0.84	0.488
$Ble = a_3 \times D^{b3}$	$1/D^2$	a_3 b_3	0.03420 ± 0.01760 1.67330 ± 0.25700	0.25	0.535
$AGB = Bcu + Bbr + Ble = a_1 \times (D^2H)^{b1} + a_2 \times (D^2H)^{b2} + a_3 \times D^{b3}$	$1/D^2$	$a_1, b_1, a_2, b_2, a_3, b_3$	idem	3.62	0.649

Note: *Bcu*, *Bbr*, *Ble*, and *AGB* are biomass of bamboo culm, branches, leaves, and total aboveground biomass, respectively. All parameter have a p-value < 0.05.

Table 5. SUR method estimating parameters of simple model combination with single variable D of bamboo biomass components using the entire dataset.

Model Form	Weight Variable	Parameter	Estimate ± Approx. Std Error	Entire RMSE (kg)	Adj. R^2
$Bcu = a_1 \times D^{b1}$	$1/D$	a_1 b_1	0.098137 ± 0.00976 2.365691 ± 0.04930	2.96	0.627
$Bbr = a_2 \times D^{b2}$	$1/D$	a_2 b_2	0.052164 ± 0.01570 2.004830 ± 0.15030	0.77	0.567
$Ble = a_3 \times D^{b3}$	$1/D$	a_3 b_3	0.030439 ± 0.00948 1.741870 ± 0.15720	0.25	0.536
$AGB = Bcu + Bbr + Ble = a_1 \times D^{b1} + a_2 \times D^{b2} + a_3 \times D^{b3}$	$1/D$	$a_1, b_1, a_2, b_2, a_3, b_3$	idem	3.58	0.657

Note: *Bcu*, *Bbr*, *Ble*, and *AGB* are biomass of bamboo culm, branches, leaves, and total aboveground biomass, respectively. All parameter have a p-value < 0.05.

3.3. Comparison with Previously Published Models

The validation dataset of 30% random splitting data was also used and repeated 200 times to validate the performance of other allometric equations developed in the tropics and compared with the selected *AGB* equation fit by SUR in this study.

As a result, the errors of predicted *AGB* using models with the same genus *Bambusa* such as model of Yuen et al. (2017) [4] for *Bambusa nutans* species and model of Li et al. (2016) [7] for *Bambusa stenostachya* Hack. species were not substantially different from the errors of the selected model of this study for *Bambusa procera* species. The FI statistic of the model selected in this study and two of the previously published models for the *Bambusa* genus suggested that these models well (Table 6 and Figure 5, left)

Table 6. Cross validation of *AGB* model fitted by SUR of this study and other *AGB* models worldwide with the different/same genus.

Source	Genus/Species-Specific	Selected Model	Fit Index (FI)	Averaged Bias (%)	Averaged RMSE (kg)	Averaged MAPE (%)
This study, 2018, Viet Nam	*Bambusa procera*	$AGB = Bcu + Bbr + Ble = 0.02269 \times (D^2H)^{0.90703} + 0.02015 \times (D^2H)^{0.72251} + 0.03420 \times D^{1.67330}$	0.66	−2.2	3.8	28.3
Yuen et al., 2017 [4] in Thailand	*Bambusa nutans*	$AGB = 0.269 \times D^{2.107}$	0.48	−17.4	3.7	31.4
Li et al., 2016 [7] in Taiwan	*Bambusa stenostachya*	$AGB = 0.0262 \times (D^2H)^{0.9215}$	0.62	5.5	3.9	27.6
Ricardo et al., 2013 [1] in Bolivia	*Guadua angustifolia*	$AGB = 2.6685 \times D^{0.9879}$	−0.23	−87.5	6.8	90.8
Yen et al., 2010 [45] in Taiwan	*Phyllostachys makinoi*	$AGB = 1.112 \times D^{2.695} \times H^{-1.175}$	0.04	19.2	6.1	39.4

Note: Using SUR method to develop and validate simultaneously model combinations with 200 realizations; 70% randomly split dataset for developing simultaneous models; and 30% randomly split dataset for validation, calculation of averaged Bias, RMSE and MAPE for this study model system and other compared models. *Bcu*, *Bbr*, *Ble*, and *AGB* are biomass of bamboo culm, branches, leaves, and total aboveground biomass, respectively.

While *AGB* models of other bamboo species from different genera such as Ricardo et al. (2013) [1] for the species *Guadua angustifolia* Kunth overestimated *AGB* and gave very high errors and significant differences with the errors of the *Bambusa procera* model in this study (Table 6 and Figure 5, right). Yen et al. (2010) [45] models for *Phyllostachys makinoi* Hayata had high errors compared with the errors of the *Bambusa* genus models (Table 6), and the plot of prediction vs. observation (Figure 5, right) shows that the model of Yen et al. (2010) [45] underestimated *AGB*. Models developed for different genera from *Bambusa* genus of this study showed very low or negative FI statistics (Table 6).

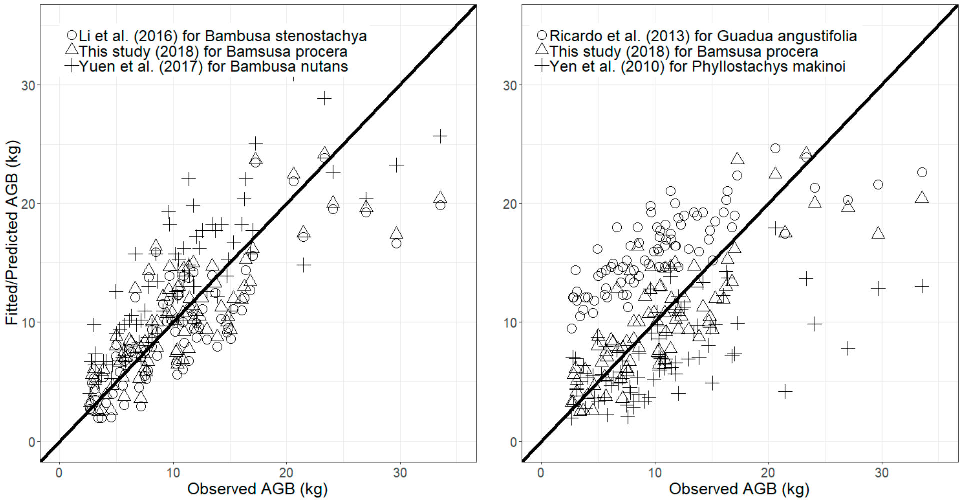

Figure 5. Plots of Fitted/Predicted *AGB* vs. Observed *AGB*: (**left**) Comparison of selected model of this study with other models in the same genus *Bambusa*; (**right**) comparison of selected *Bambusa* genus model of this study with other models in different genera.

4. Discussion

4.1. Predictors for Bamboo AGB and its Components

Biomass of bamboo branches (*Bbr*) and leaves (*Ble*) are highly variable and difficult to predict through empirical models (Figure 3, Figure 4). The relationship between *Bbr*, *Ble* with covariates *D*, D^2H usually only reached R^2 of approximately 0.5. This is consistent with the results of Melo et al. (2015) [28] and Li et al. (2016) [7]. Yen et al., (2010) [45] showed that the relationship between carbon biomass of foliage, branches for Makino bamboo species (*Phyllostachys makinoi*) with variable *D* of power function had R^2 = 0.5–0.6.

The biomass of the culm (*Bcu*) and *AGB* were closely related to the *D* variable or combination of variables D^2H, this result is consistent with Melo et al. (2015) [28] and Li et al. (2016) [7]. However, the *H*-variable model is difficult to apply to bamboo, as *H* is difficult to measure due to culm density [4,48]. Thus, many models for bamboo components and *AGB* used sole variable *D* (e.g., Kaushal et al., 2016) [49] for *Dendrocalamus strictus* (Roxb.) Nees. However, components and *AGB* models with the addition of the variable *H* to the variable combination (D^2H) reduced the uncertainty, this is consistent with results of Yiping et al. (2010) [5], Ricardo et al. (2013) [1], Li et al. (2016) [7], and Yuen et al. (2017) [4]. Nevertheless, sole *H* variable is site index if the *H* involved in the D^2H variable combination reduced the site model specificity [50].

There are very few models for estimating belowground biomass (*BGB*) for bamboo plant that includes rhizome, coarse and fine roots. The reason is mainly the difficulty of collecting datasets of bamboo root system to develop the allometric equations. Yuen et al. (2017) [4] indicated that there are no bamboo plant *BGB* models found in Southeast Asia. Some *BGB* equations exist for *Bambusa bambos* in India, *Phyllostachys edulis* in China [4]. *BGB* is sometimes estimated via root-shoot ratio (RSR), it is ratio of *BGB* to *AGB* [4].

4.2. Independent vs. Simultaneous Model Fit

Using the biomass models of *AGB* and its components developed simultaneously reduced the errors in biomass prediction compared to the models fitted independently (Table 2 vs. Table 3). This result is consistent with the findings of Poudel and Temesgen (2016) [38]. The simultaneously fitted model system decreased percent bias and MAPE by −10%, and 3%, respectively, compared to the models fitted independently (Table 2 vs. Table 3). A Bland–Altman plot [51] also indicated the significant difference between predicted *AGB* from SUR model system and non- SUR model (Figure 6).

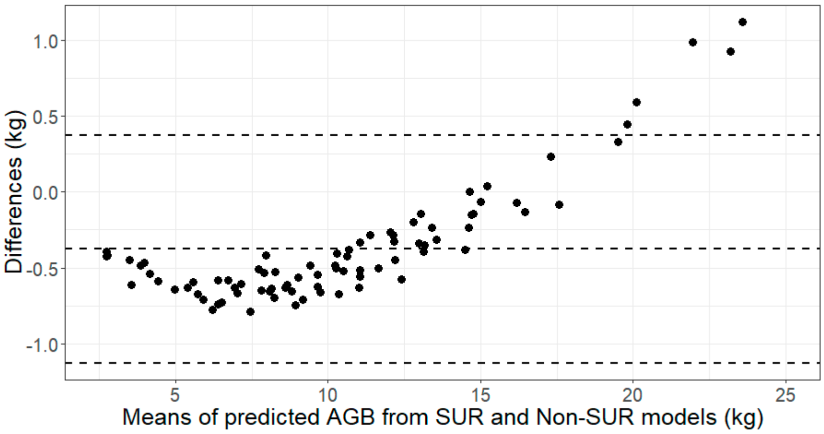

Figure 6. Bland- Altman plot: differences vs. means of predicted *AGB* from SUR and non-SUR models.

In addition, SUR provided the additivity that ensures the aboveground biomass was equal to the sum of the biomass of the bamboo components [39]. Therefore, this approach should be promoted to develop and estimate simultaneously biomass of components and total [37].

It should be noted that, the RMSE and R^2 of the two modeling systems were not substantially different (Table 4 vs. Table 5). However, the errors of the modeling system that uses two predictors *D* and *H* (Combination 6) were smaller than the errors produced by the modeling system that used *D* as the only predictor (Combination 1). The best modeling system using two predictors of *D* and *H* is shown in Table 4. The modeling system using *D* as the only predictor (Table 5) should only be applied when measuring *H* is difficult and/or costly.

4.3. Species-Specific vs. Genus-Specific Models

Yuen et al. (2017) [4] showed that most bamboo biomass models were species-specific. Our results showed that the biomass models developed for same *Bambusa* genus were similar in terms of the goodness of fit whereas models developed for the *Guadua* and *Phyllostachy* genera showed a large bias (Figure 5). Therefore, while bamboo biomass models have not been totally established, developing genus-specific bamboo models should be considered to reduce the volume of model establishment. However, the uncertainty around model parameters should be tested using statistics such as percent relative standard error [52].

5. Conclusions

The modeling system for estimating *AGB* and its components simultaneously produced higher reliability compared to independently developed models. The forms of simultaneous model system for estimating *AGB* and its component of *Bambusa procera* species were developed and selected as follows: $Bcu = a_1 \times (D^2H)^{b1}$, $Bbr = a_2 \times (D^2H)^{b2}$, $Ble = a_3 \times D^{b3}$ and $AGB = Bcu + Bbr + Ble = a_1 \times (D^2H)^{b1} + a_2 \times (D^2H)^{b2} + a_3 \times D^{b3}$.

Development of genus-specific bamboo models should be considered to reduce the volume of developing species-specific models for estimating the bamboo biomass.

Author Contributions: B.H. and G.T.T. collected the datasets and analyzed the raw data; B.H., H.T., and K.P.P. developed the hypotheses and methodology; B.H., G.T.T., K.P.P., and H.T. wrote the paper.

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