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Taxon-specific modeling systems for improving reliability of tree aboveground biomass and its components estimates in tropical dry dipterocarp forests

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ABSTRACT

The dry dipterocarp forest (DDF) is a major and unique forest type in Asia providing both protection and production functions. DDF's role as a carbon sink is important in Asia, but there is a deficiency in existing biomass models for these forests. This study aimed to develop simultaneous modeling systems to estimate tree aboveground biomass (*AGB*) and its components for mixed species, dominant family, genera, and species. Twenty-eight 0.25 ha plots in the Central highlands and one 1 ha plot in the Southeast ecoregion in Viet Nam were measured. A total of 329 trees were destructively sampled to obtain a dataset of the dry biomass of the stem (*Bst*), branches (*Bbr*), leaves (*Ble*), bark (*Bba*), and *AGB*. Using K-fold cross validation, we compared *AGB* predictions from independently developed *AGB* equation and from a system of biomass equations that estimated component biomass and *AGB* simultaneously. The estimation methods for independent equation was weighted nonlinear regression fit by maximum likelihood and for simultaneous system it was weighted nonlinear seemingly unrelated regression (SUR) fit by generalized least squares. We also examined different modeling systems for different plant classification at taxonomic levels. The selected form of taxon-specific modeling systems were $AGB = a_1 \times D^{b11} \times H^{b12} \times WD^{b13} + a_2 \times D^{b21} + a_3 \times D^{b31} + a_4 \times D^{b41}$ for mixed species and dominant Dipterocarpaceae family and $AGB = a_1 \times D^{b11} + a_2 \times D^{b21} + a_3 \times D^{b31} + a_4 \times D^{b41}$ for dominant genera of *Dipterocarpus* and *Shorea*. The predictors of *D, H,* and *WD* are diameter at breast height, tree height and wood density, respectively. Compared to the mixed species modeling system, genus-specific modeling systems improved the reliability of *AGB* estimation substantially and will reduce the cost of application because the only predictor required for measurement is *D*. The pantropical genus-specific modeling systems are more reliable than pantropical mixed species models.

1. Introduction

The dry dipterocarp forest (DDF) is a major and unique forest type in Asia, distributed in tropical and subtropical regions (Wohlfart et al., 2014). Its distribution extends from northwestern India and Myanmar across Thailand to the Mekong River, Laos, Cambodia and Vietnam (Maury-Lechon and Curtet, 1998; Rundel et al., 2017; Khamyong et al., 2018; Huy et al., 2018).

Omar et al. (2015) indicated that the DDF supports both protection and production functions by providing good timber and a diverse non-timber forest products such as medicinal goods, food plants and large amounts of resin from species of dipterocarpaceae family. However, in recent years, this forest type has been degraded by overlogging and conversion into industrial crops such as rubber, which has had an unexpected impact on the environment (Huy et al., 2018). The areas in which DDF exists exhibit extreme environmental conditions such as drought, forest fires in the dry season, and flooding in the rainy season which can cause soil depths and soil types to fluctuate. Only dipterocarpaceae species that can adapt to these harsh living conditions can exist. Thus, the DDF is of high significance in environmental protection

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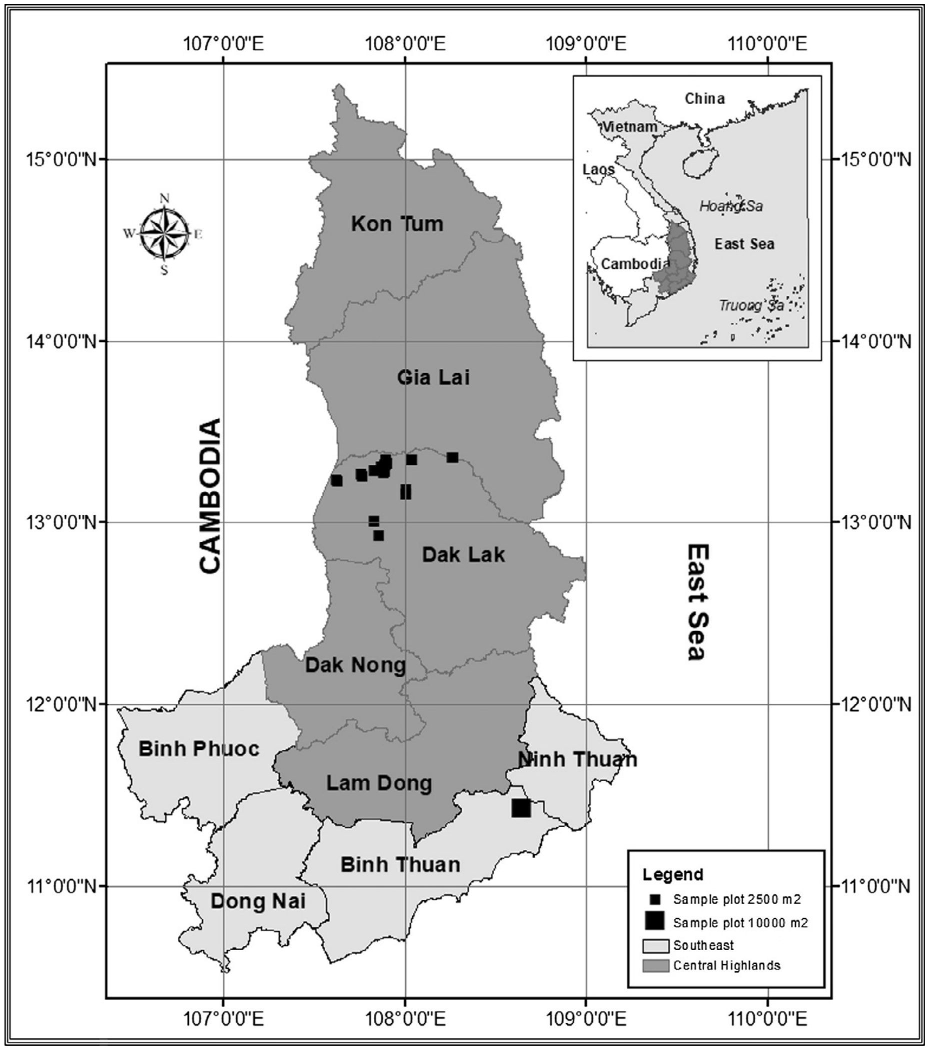


Fig. 1. Map of the distribution of sample plots in tropical dry dipterocarp forests in the Central Highlands and Southeast ecoregions of Viet Nam.

(Huy et al., 2018), especially carbon sequestration to mitigate climate change.

There is currently a lack of information on the carbon storage capacity of the DDF. Matthew et al. (2018) showed that carbon stocks of the DDF including above-ground carbon (AGC) content was about 222 Mg ton ha^{-1} and below-ground carbon (*BGC*) was 53 Mg ton ha^{-1}. Laumonier et al. (2010) indicated in the dipterocarp forest of Sumatra, average above-ground biomass was 361 ± 7 Mg ton ha^{-1}, which is also the higher than the default value in IPCC (2006) guidelines.

After years of unsustainable logging, the DDFs in Vietnam are mostly degraded and distributed in two major ecological regions: the Central Highlands and the South East (Huy et al., 2016b, 2018). It is therefore important to rehabilitate the degraded DDF by enrichment planting which will also improve the carbon absorption capacity of this forest type. This sort of rehabiliation effort stands in contrast to the production of industrial crops such as rubber, cashew and acacia species, which are unsuitable to these extreme ecological conditions (Huy et al., 2018).

So far there are some pantropical models developed to estimate tree above-ground biomass (*AGB*) e.g. Brown (1997), IPCC (2003), and Chave et al. (2005, 2014). However, Nelson et al. (1999), Cairns et al. (2003), Basuki et al. (2009), and Huy et al. (2016b,c) determined that site-specific allometric equations shoud be developed to improve the accuracy of biomass estimates.

Even though the DDFs are ancarbon sink in the Asian region and to enforce the UN-REDD program, there have been very few models developed for this forest type (Basuki et al., 2009; Rutishauser et al., 2013; Huy et al., 2016b). Up to now, there are only a few biomass models for the DDF. Cairns et al. (2003) developed species-specific biomass models for the six most common species in dry forest in Mexico. Chave et al. (2005) set up a dry forest specific *AGB* estimation model for the tropics. Basuki et al. (2009) built *AGB* model for mixed species, and some dominant genera such as *Dipterocarpus, Hopea, Palaquium, Shorea* in Indonesia. Niiyama et al. (2010) developed a below-ground biomass (*BGB*) model with predictor of diameter at breast height (*D*) on peninsular Malaysia; and Kralicek et al. (2017) established models that concern dipterocarp forests in Viet Nam. These are rare works that mentioned the *BGB* – a difficult and costly variable to measure. The biomass models for the tree components are also found in an article by Hanpattanakit et al. (2016). The authors created three models for estimating biomass of stem together with branches, leaves, and roots with predictor combination of $D^2 \times H$, for the 5 dominant species of the DDF in Thailand. Huy et al. (2016b) established *AGB* model for mixed species and two domiant genera of *Dipterocarpus* and *Shorea* in Vietnam. The results indicated that site-specific models and genus-specific models improved the estimate of *AGB* in the DDF. However, due to the small sample size used for developing genus-specific models (e.g. *Shorea* genus had only 36 destructively sampled trees), authors also argued that this conclusion should be further assessed with the additional data.

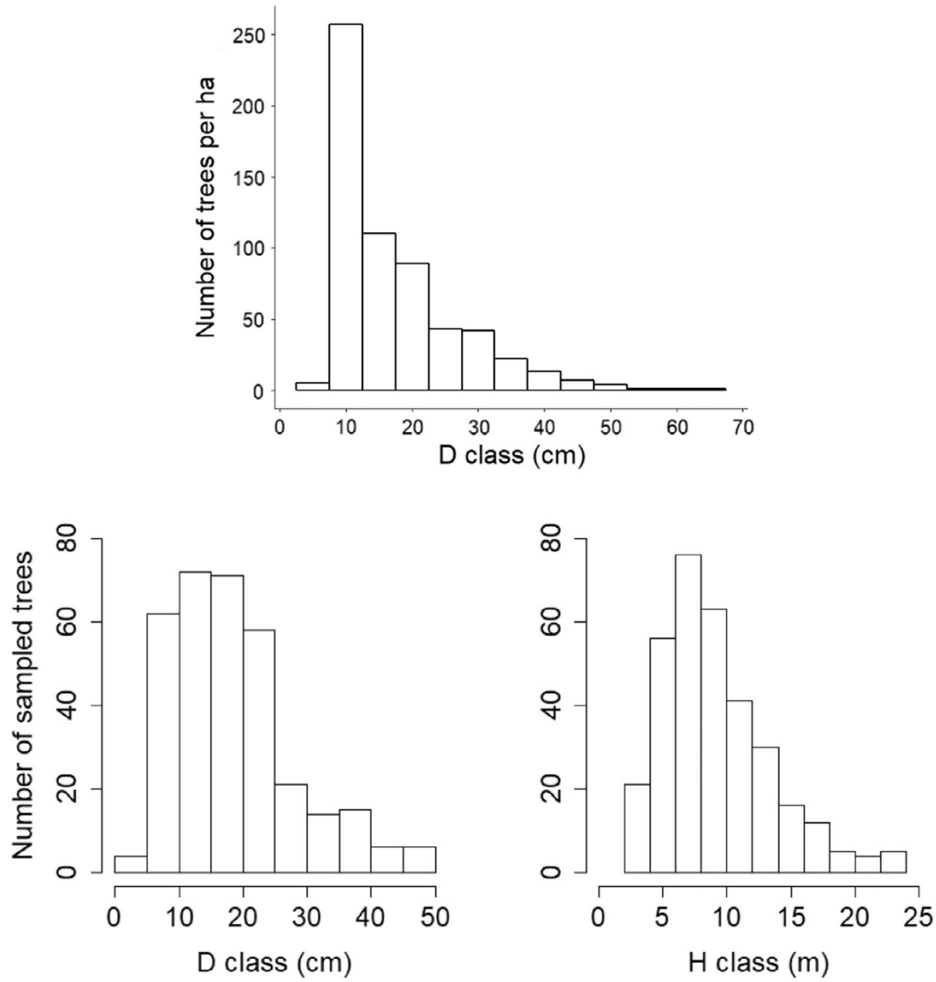


Fig. 2. Distribution of diameter (*D*, cm) in all sample plots per ha (top). Distribution of diameter (*D*, cm) (bottom left) and height (*H*, m) of destructively sampled trees (bottom right) (below).

To improve the impact of the deficiency of the existing biomass model for the DDF, this study increases the sample size of 329 destructively sampled trees, including 222 sampled trees from Huy et al. (2016b) and 107 newly sampled trees which focused on collection of dominant species, genera, and family of the DDF. We use this data to examine the hypotheses: (1) Taxon-specific models fitted using seemingly unrelated regression (SUR) increase reliability and decrease uncertainty in comparison with the mixed species models developed independently; and (2) The genus-specific models are better than mixed species models for the tropical region. The objective of this research is to develop modeling systems that simultaneously estimate *AGB* and its components in the DDF for mixed species, dominant family, genera, and species to improve reliability in forest biomass and carbon estimates. We also provide cross-assessment of pantropic biomass models and DDF-specific models in different ecological regions to propose appropriate applications.

2. Materials and methods

2.1. Study sites

The data were collected in two ecological regions of the eight agro-ecological regions of Viet Nam, which are the Central Highlands (CH) and South East (SE) regions. The study sites are located in the north latitude: 11°20′N–13°30′N and east longitude: 107°35′E–108°45′E (Fig. 1). The average annual rainfall in CH is 1600 mm year^{-1} and in SE is 1003 mm year^{-1}, with an average annual temperature of 25.5 °C, the dry season lasts 3–4 months. The altitude of the DDF in this study ranges from 171 to 417 m, and has an igneous rock parent material. The terrain of the study area is relatively flat with density from 228 to 1291 tree ha^{-1} (with D ≥ 5 cm), total basal area ranges from 3.8 to 23.4 m^2 ha^{-1} (This study; Hydrometeorology Center in the Central Highlands, Viet Nam, 2017; Hijmans et al., 2005; Fischer et al., 2008)

2.2. Measurements

Twenty eight 0.25 ha square plots in the CH, home of the dipterocarp forests in Viet Nam, and one square 1 ha plot in the SE ecoregion were inventoried. Within each sample plot several variables were measured for each tree ≥5 cm diameter at breast height including species name, diameter at breast height (*D*, cm), and tree height (*H*, m). The selection of sampled trees was proportional to the diameter distribution of the DDF (Fig. 2) and density, biomass of dominant species (Basuki et al., 2009). A total of 329 trees were destructively sampled, this includes the 222 trees from the dataset used by Huy et al. (2016b) and 107 newly sampled trees from the current study that emphasized collection of samples in domiant family, genera and species in the stands.

Prior to felling the sample trees, species name was recorded, *D* and *H* were measured. Height was remeasured after the sample trees were cut. Aboveground biomass components including stem and bark, branches, and leaves were separated to obtain the green weights in the field.

To obtain the fresh bark biomass, stems of the sampled trees were

Table 1
Summary statistics for predictor and response variables of destructively sampled tree using plant classification hierarchy.

Plant classification hierarchy	Variable	Min	Mean	Max	Sd
Mixed species N = 329	*D* (cm)	3.4	18.1	48.8	9.751
	H (m)	2.5	9.2	23.5	4.238
	WD (g/cm^3)	0.379	0.662	0.953	0.096
	Bst (kg)	0.5	95.1	885.3	148.704
	Bbr (kg)	0.2	49.8	607.5	86.939
	Ble (kg)	0.1	5.3	42.4	6.238
	Bba (kg)	0.1	27.7	311.0	45.638
	AGB (kg)	1.3	177.9	1719.8	277.770
Dominant family					
N = 228	Dipterocarpaceae family:				
	D (cm)	4.9	19.1	48.8	10.058
	H (m)	2.7	9.1	23.5	4.308
	WD (g/cm^3)	0.379	0.664	0.917	0.091
	Bst (kg)	0.6	106.0	885.3	165.106
	Bbr (kg)	0.2	57.9	607.5	98.704
	Ble (kg)	0.2	5.9	42.4	6.751
	Bba (kg)	0.3	31.9	311.0	51.222
	AGB (kg)	1.5	201.7	1710.8	311.298
Dominant genera					
N = 150	*Dipterocarpus* genus:				
	D (cm)	4.9	20.0	48.8	11.058
	H (m)	2.7	9.7	23.5	4.825
	WD (g/cm^3)	0.379	0.633	0.858	0.079
	Bst (kg)	0.6	128.0	885.3	188.052
	Bbr (kg)	0.2	69.1	607.5	114.190
	Ble (kg)	0.2	6.6	42.4	7.825
	Bba (kg)	0.3	36.7	311.0	61.527
	AGB (kg)	1.5	240.4	1710.8	359.983
N = 78	*Shorea* genus:				
	D (cm)	5.6	17.3	48.2	7.512
	H (m)	3.1	7.9	14.1	2.709
	WD (g/cm^3)	0.507	0.724	0.917	0.083
	Bst (kg)	1.2	63.8	752.1	95.834
	Bbr (kg)	0.2	36.4	377.7	52.694
	Ble (kg)	0.3	4.4	19.3	3.540
	Bba (kg)	1.2	22.7	101.7	16.697
	AGB (kg)	2.9	127.3	1250.8	162.445
Dominant species					
N = 75	*Dipterocarpus tuberculatus* Roxb.:				
	D (cm)	4.9	16.1	40.5	9.357
	H (m)	2.7	8.5	19.0	3.922
	WD (g/cm^3)	0.379	0.624	0.858	0.090
	Bst (kg)	0.6	69.1	548.5	104.9
	Bbr (kg)	0.2	42.9	377.7	76.666
	Ble (kg)	0.2	5.0	42.4	6.977
	Bba (kg)	0.3	13.1	67.5	14.434
	AGB (kg)	1.5	130.1	993.5	196.348
N = 54	*Dipterocarpus obtusifolius* Teijsm. Ex Miq.:				
	D (cm)	5.6	20.3	41.2	8.019
	H (m)	3.4	8.3	16.4	2.774
	WD (g/cm^3)	0.495	0.663	0.826	0.060
	Bst (kg)	1.6	97.6	446.2	98.317
	Bbr (kg)	0.7	47.6	236.7	52.673
	Ble (kg)	0.5	5.4	16.6	3.942
	Bba (kg)	1.2	26.9	87.4	17.724
	AGB (kg)	4.0	177.5	736.9	166.810
N = 42	*Shorea obtusa* Wall. Ex Blume:				
	D (cm)	7.5	16.1	28.5	4.718
	H (m)	3.3	8.4	13.8	2.939
	WD (g/cm^3)	0.555	0.744	0.917	0.085
	Bst (kg)	5.1	54.3	262.1	45.702
	Bbr (kg)	0.5	27.7	151.6	28.469
	Ble (kg)	0.4	4.2	11.8	2.856
	Bba (kg)	2.7	18.6	55.1	11.110
	AGB (kg)	9.1	104.8	470.5	82.634
N = 36	*Shorea siamensis* Miq.:				
	D (cm)	5.6	18.6	48.2	9.726
	H (m)	3.1	7.3	14.1	2.317
	WD (g/cm^3)	0.507	0.700	0.818	0.074
	Bst (kg)	1.2	74.9	752.1	132.4
	Bbr (kg)	0.2	46.6	377.7	70.452
	Ble (kg)	0.3	4.6	19.3	4.234
	Bba (kg)	1.2	27.5	101.7	20.625
	AGB (kg)	2.9	153.5	1250.8	220.776

Note: Response variables including Bst, Bbr, Ble, Bba and AGB are biomass of tree stem, branches, leaves, bark and total above-ground biomass, respectively. Predictor variables consisting of D, H and WD are diameter at breast height, tree height and wood density, respectively. N: Number of destructively sampled trees.

split into five logs of equal length and then the diameters with and without bark at the base of each log were measured, volume of five equal logs with and without bark was calculated using Huber's formula (Chapman, 1921; Huy et al., 2016c) and then fresh bark volume of sampled trees V_{ba} (m^3) was calculated as the difference between volume of stem with bark and without bark whereas the fresh bark density (df_{ba} g cm^{-3}) was recorded as the average density of five bark samples at five equal logs. The fresh bark biomass per sampled tree (Bf_{ba} kg tree^{-1}) was computed using the following formula (Huy et al., 2016c):

$$Bf_{ba} = df_{ba} \times V_{ba} \times 10^3 \tag{1}$$

where Bf_{ba} is fresh bark biomass (kg tree^{-1}), df_{ba} is fresh bark density (g cm^{-3}) and V_{ba} is fresh bark volume (m^3 tree^{-1}).

Fresh biomass of the stem was then computed by subtracting fresh bark biomass from the fresh weight of stem with bark (Huy et al., 2016c). To obtain the fresh-to-dry ratio of each sampled tree component, five samples for stem (500 g) and bark (300 g) at the base of each equal log were collected, along with three for branches (500 g) (at big, medium and small branches), and two for old and new leaves (300 g) and sent to the laboratory to determine their dry mass. Samples were dried at 105 °C until a constant weight was attained. This provided the average fresh-to-dry mass ratio of the four tree components to calculate the total dry biomass of the tree. We define the four components as stem (*Bst*), branches (*Bbr*), leaves (*Ble*) and bark (*Bba)* and total tree above-ground biomass: $AGB = Bst + Bbr + Ble + Bba$ (Huy et al., 2016b,c; Kralicek et al., 2017). The wood density variable (*WD*) was then computed and averaged as the ratio of dry biomass to the volume of wood disk samples taken from every one-fifth of stem length (Huy et al., 2016a). Table 1 shows the summary statistics for each of the predictors and the response variables of the destructive sampled trees for mixed species, a dominant family (Dipterocarpaceae), two dominant genera (*Dipterocarpus* and *Shorea)*; and four dominant species (*Dipterocarpus tuberculatus* Roxb., *Dipterocarpus obtusifolius* Teijsm. Ex Miq., *Shorea obtusa* Wall. Ex Blume, and *Shorea siamensis* Miq.).

2.3. Approaches to developing allometric equations

Most tropical forest types have a diversity of tree species, with the dominance of plant species, genus and family being often unclear. In contrast, the DDF dominated by the Dipterocarpaceae family with several dominant genera and dozen dominant species within. Therefore, the approach of developing biomass models by dominant plant family and dominant plant genera using hierarchical modeling should be considered in this forest type to improve the reliability and reduce uncertainty (Huy et al., 2016b).

Basuki et al. (2009) used a dataset from the tropical lowland Dipterocarp forests in Indonesia for developing *AGB* models for four common genera – *Dipterocarpus*, *Hopea*, *Palaquium* and *Shorea.* The genera of *Dipterocarpus, Hopea,* and *Shorea* belong to the Dipterocarpaceae family while the *Palaquium* genus belongs to the Sapotaceae

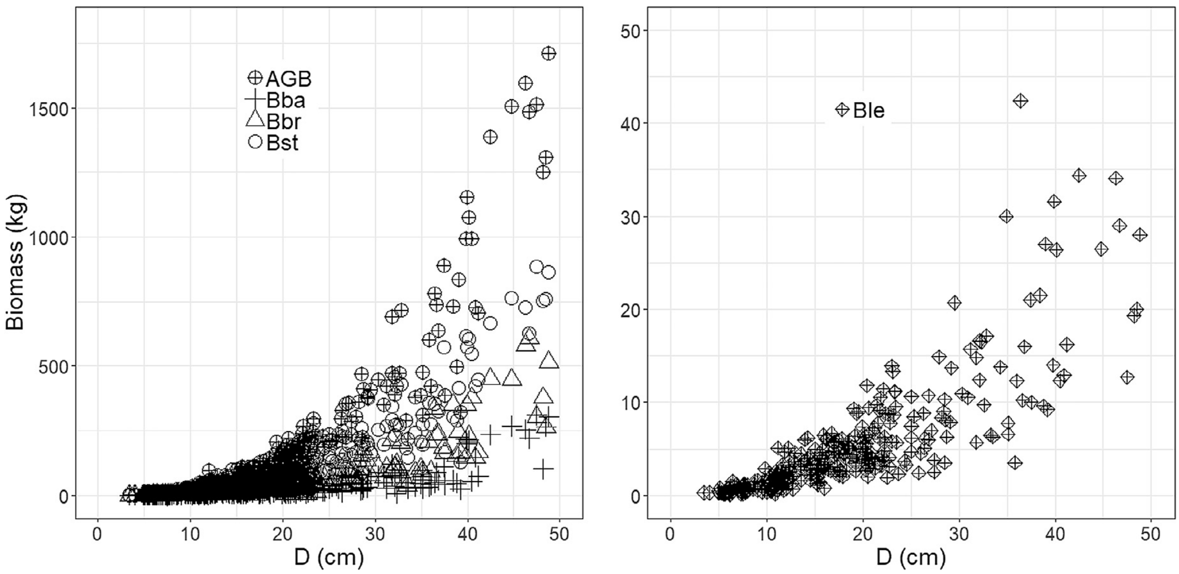


Fig. 3. Scatter plot of biomass for four components, tree stem (Bst, kg), branches (Bbr, kg), leaves (Ble, kg), bark (Bba, kg), and total aboveground biomass (AGB, kg) for mixed species by diameter at breast height (D, cm).

family. Rundel et al. (2017) and Khamyong et al. (2018) asserted that the DDF in Southeast Asia (Thailand, Laos and Viet Nam) has two dominant families, Dipterocarpaceae and Fabaceae with two dominant genera *Dipterocarpus* and *Shorea* with four dominant species namely *Dipterocarpus obtusifolius, Dipterocarpus tuberculatus, Shorea obtusa*, and *Shorea siamenesis*.

The data used in this study belonged to four main families – Dipterocarpaceae, Combretaceae, Leguminosaceae and Rubiaceae with Dipterocarpaceae being the most dominant. There are three distinct dominant genera: *Dipterocarpus, Shorea* and *Terminalia*; with 6 distinctly dominant species – *Dipterocarpus tuberculatus* Roxb., *Dipterocarpus obtusifolius* Teijsm. Ex Miq., *Shorea obtusa* Wall. ex Blume, *Shorea siamensis* Miq., *Terminalia alata* Wall., and *Dipterocarpus intricatus* Dyer.

Given the destructively sampled trees and the predominance of the timber plants of the DDF, this study examined and cross-valiadated biomass modeling systems along with the order of the mixed species, dominant Dipterocarpaceae family, dominant genus including two genera of *Dipterocarpus* and *Shorea*, and dominant species consist of 4 species of *Dipterocarpus obtusifolius* Teijsm. Ex Miq., *Dipterocarpus tuberculatus* Roxb., *Shorea obtusa* Wall. ex Blume and *Shorea siamensis* Miq.

2.4. Model fitting

We compared two methods to fit systems of equations for *AGB* and its components: weighted nonlinear models fit by maximum likelihood and weighted nonlinear models fit with seemingly unrelated regression (SUR).

Predictor(s): Three predictors have commonly been suggested for pantropic *AGB* models. These are *D (cm), H (m), WD* ($g\ cm^{-3}$) or combinations of these predictors: $D^2H\ (m^3) = (D\ (cm)/100)^2 \times H\ (m)$, $D^2HWD\ (kg) = D^2H\ (m^3) \times WD\ (g\ cm^{-3}) \times 10^3$ (Brown, 1997; IPCC, 2003; Cairns et al., 2003; Basuki et al., 2009; Chave et al., 2005, 2014; Huy et al., 2016a,b,c; Kralicek et al., 2017). These previous studies indicate *AGB* and its components are highly correlated with *D* and *H*, where *H* also reflects difference of the sites. With the mixed species models, *WD* is correlated with the species (Huy et al., 2016a). We investigated all three predictors *D, H, WD* and combinations D^2H and D^2HWD in order to choose the right variables for biomass models according to the order of plant classification such as mixed species, family, genera, species and for models for each of the four *AGB* components.

Power form: Power function has been proposed for most of the pantropical biomass models (Chave et al., 2005, 2014; Picard et al., 2015; Huy et al., 2016a, b, c; Kralicek et al., 2017). Figs. 3 and 4 show that the *AGB* and its components versus *D* exhibit compliance with the power law. Therefore, this study applies the power form to appraise the biomass modeling system with various predictors.

Weighted nonlinear models fit by Maximum Likelihood: To correct for heteroscedasticity in residuals (Davidian and Giltinan, 1995; Picard et al., 2012), weighted nonlinear regression was used in this study. Using the Furnival index (Furnival, 1961; Jayaraman, 1999), we compared the performance of log-linear and non-linear models to predict. Based on the results of that comparison, nonlinear models were selected. This is consistent with Huy et al. (2016c). Weighted nonlinear models fit by maximum likelihood were examined to select the best predictor(s) for *AGB* and its biomass component (Bates, 2010; Pinheiro et al., 2014). The nlme packages in statistical software R (R Core Team, 2018) was used with the form after Huy et al. (2016a,b,c), Kralicek et al. (2017) was:

$$Y_i = \alpha \times X_i^{\beta} + \varepsilon_i \tag{2}$$

$$\varepsilon_i\ iid\mathcal{N}(0,\ \sigma_i^2) \tag{3}$$

where Y_i is the *Bst, Bbr, Ble, Bba* or *AGB* in kg for the *i*th sampled tree; α and β are the parameters of the model; and X_i is the predictor(s) such as *D, H, WD* or some combinations thereof D^2H (m^3) or $D^2H(WD)$ (kg) for the *i*th sampled tree; and ε_i is the random error associated with the *i*th sampled tree.

The variance function was as follows (Huy et al., 2016a,b,c):

$$\mathrm{Var}(\varepsilon_i) = \widehat{\sigma^2}(\nu_i)^{2\delta} \tag{4}$$

where $\widehat{\sigma^2}$ is the estimated error sum of squares; ν_i is the weighting variable (*D*, D^2H *or* D^2HWD) associated with the *i*th sampled tree; and δ is the variance function coefficient to be estimated.

Weighted nonlinear models fit by seemingly unrelated regression (SUR): It has been shown that the sum of power functions of component biomass models is not a power function of the *AGB* equation (Picard et al., 2012; Sanquetta et al., 2015; Poudel and Temesgen, 2016), so establishing independent biomass component models to estimate total tree AGB will give a significant deviation compared to the independent model AGB. Additionally, to account for the cross-equation correlation among the equations of the different biomass components, the modeling system is simultaneously fit rather than separately (Parresol,

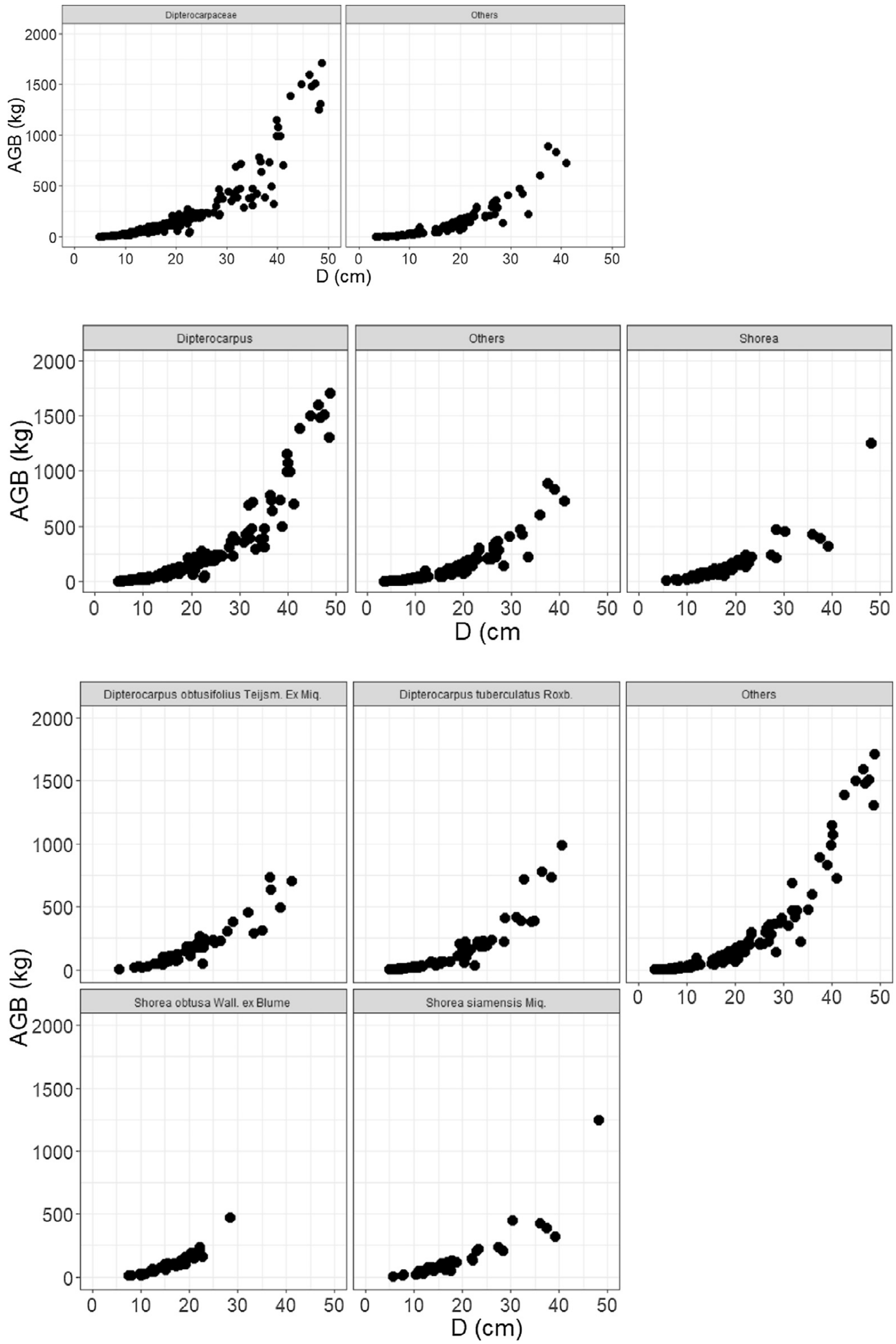


Fig. 4. Scatter graph of total tree above-ground biomass (*AGB*, kg) versus diameter at breast height (*D*, cm) by dominant plant families (top), dominant plant genera (middle) and dominant plant species (bottom).

2001; Picard et al., 2012; Poudel and Temesgen, 2016).

The weighted nonlinear SUR (Parresol, 2001; Poudel and Temesgen, 2016; Kralicek et al., 2017) was performed using the SAS procedure Proc Model with the generalized least squares (GLS) method (SAS Institute Inc., 2014; Affleck and Dieguez-Aranda, 2016). The modeling system had the following general form (Sanquetta et al., 2015):

$$Stem: Bst = a_1 \times X_{1j}{}^{b1j} + \varepsilon_1 \tag{5}$$

$$Branches: Bbr = a_2 \times X_{2j}{}^{b2j} + \varepsilon_2 \tag{6}$$

$$Leaves: Ble = a_3 \times X_{3j}{}^{b3j} + \varepsilon_3 \tag{7}$$

$$Bark: Bba = a_4 \times X_{4j}{}^{b4j} + \varepsilon_4 \tag{8}$$

Table 2
Nonlinear model development and K-fold cross validation to select plant classification hierarchy-specific equations for above-ground biomass (*AGB*) estimates.

Model form	Weight variable	AIC	Adj. R^2	Bias (%)	RMSE (%)	MAPE (%)
Mixed species models						
$AGB = a \times D^b$	$1/D^\delta$	2675	0.914	−12.5	50.4	29.2
$AGB = a \times D^b \times H^c$	$1/D^\Delta$	2678	0.927	−12.4	46.8	28.9
$AGB = a \times (D^2H)^b$	$1/(D^2H)^\delta$	2957	0.935	−24.0	63.5	43.3
$AGB = a \times D^b \times WD^c$	$1/D^\delta$	2662	0.890	−11.4	46.9	27.6
$\mathbf{AGB = a \times D^b \times H^c \times WD^d}$	$\mathbf{1/D^\delta}$	**2664**	**0.910**	**−11.1**	**44.6**	**27.1**
$AGB = a \times (D^2H \times WD)^b$	$1/(D^2H \times WD)^\delta$	2938	0.922	−19.2	54.8	37.2
Dominant family-specific models						
Dipterocarpaceae family						
$AGB = a \times D^b$	$1/D^\delta$	1902	0.915	−11.6	48.4	28.5
$AGB = a \times D^b \times H^c$	$1/D^\delta$	1906	0.930	−11.3	46.3	28.0
$AGB = a \times (D^2H)^b$	$1/(D^2H)^\delta$	2089	0.945	−24.3	66.4	43.9
$AGB = a \times D^b \times WD^c$	$1/D^\delta$	1891	0.884	−10.4	43.3	27.0
$\mathbf{AGB = a \times D^b \times H^c \times WD^d}$	$\mathbf{1/D^\delta}$	**1893**	**0.910**	**−9.9**	**41.7**	**26.4**
$AGB = a \times (D^2H \times WD)^b$	$1/(D^2H \times WD)^\delta$	2070	0.945	−18.5	53.7	37.4
Dominant genera-specific models						
Dipterocarpus genus						
$\mathbf{AGB = a \times D^b}$	$\mathbf{1/D^\delta}$	**1262**	**0.936**	**−12.2**	**46.3**	**29.2**
$AGB = a \times D^b \times H^{c*}$	$1/D^\delta$	1268	0.944	−12.2	46.6	29.3
$AGB = a \times (D^2H)^b$	$1/(D^2H)^\delta$	1404	0.952	−26.7	69.0	46.5
$AGB = a \times D^b \times WD^c$	$1/D^\delta$	1265	0.923	−11.7	45.2	28.6
$AGB = a \times D^b \times H^c \times WD^d$	$1/D^\delta$	1271	0.937	−11.3	45.6	28.2
$AGB = a \times (D^2H \times WD)^b$	$1/(D^2H \times WD)^\delta$	1392	0.952	−21.8	56.9	40.4
Shorea genus						
$\mathbf{AGB = a \times D^b}$	$\mathbf{1/D^\delta}$	**639**	**0.816**	**−8.8**	**33.2**	**24.6**
$AGB = a \times D^b \times H^c$	$1/D^\delta$	643	0.840	−8.7	34.4	24.5
$AGB = a \times (D^2H)^b$	$1/(D^2H)^\delta$	691	0.869	−14.9	45.3	33.8
$AGB = a \times D^b \times WD^c$	$1/D^\delta$	634	0.824	−7.9	31.4	23.6
$AGB = a \times D^b \times H^{c*} \times WD^d$	$1/D^\delta$	641	0.841	−7.4	31.5	23.7
$AGB = a \times (D^2H \times WD)^b$	$1/(D^2H \times WD)^\delta$	686	0.863	−11.8	38.8	31.1
Dominant species-specific models						
Dipterocarpus tuberculatus Roxb.						
$\mathbf{AGB = a \times D^b}$	$\mathbf{1/D^\delta}$	**554**	**0.916**	**−13.4**	**47.2**	**31.5**
$AGB = a \times D^b \times H^{c*}$	$1/D^\delta$	561	0.916	−13.2	46.7	31.4
$AGB = a \times (D^2H)^b$	$1/(D^2H)^\delta$	630	0.880	−24.3	60.3	44.1
Dipterocarpus obtusifolius Teijsm. Ex Miq.						
$\mathbf{AGB = a \times D^b}$	$\mathbf{1/D^\delta}$	**480**	**0.854**	**−10.5**	**36.8**	**25.8**
$AGB = a \times D^b \times H^c$	$1/D^\delta$	480	0.854	−10.5	36.8	25.9
$AGB = a \times (D^2H)^b$	$1/(D^2H)^\delta$	528	0.827	−20.0	56.3	39.9
Shorea obtusa Wall.						
$\mathbf{AGB = a \times D^b}$	$\mathbf{1/D^\delta}$	**323**	**0.931**	**−4.4**	**22.3**	**18.0**
$AGB = a \times D^b \times H^c$	$1/D^\delta$	326	0.924	−3.8	21.3	17.3
$AGB = a \times (D^2H)^b$	$1/(D^2H)^\delta$	366	0.681	−10.8	33.4	26.5
Shorea siamensis Miq.						
$\mathbf{AGB = a \times D^b}$	$\mathbf{1/D^\delta}$	**314**	**0.862**	**−13.3**	**41.5**	**33.8**
$AGB = a \times D^b \times H^{c*}$	$1/D^\delta$	322	0.850	−12.6	41.6	33.9
$AGB = a \times (D^2H)^b$	$1/(D^2H)^\delta$	329	0.895	−21.3	55.8	43.6

Note: In K-fold cross validation, the dataset is randomly split into K (K = 10 folds) equal sized subsamples, K − 1 subsamples used for developing models, calculation of AIC, Adj. R^2; and K remaining subsample used for validation, calculation of Bias, RMSE, MAPE; finally, all those statistics averaged over 10 realizations. *: Parameter with $p_{value} > 0.05$. δ: the variance function coefficient; Predictor: D^2H (m^3) = (D (cm)/100)^2 × H (m); $D^2H \times WD$ (kg) = D^2H (m^3) × WD (g/cm^3) × 1000. For species-specific models, predictor of *WD* was not examined. Bold: Selected model based on K-fold cross validation statistics and diagnostic plots.

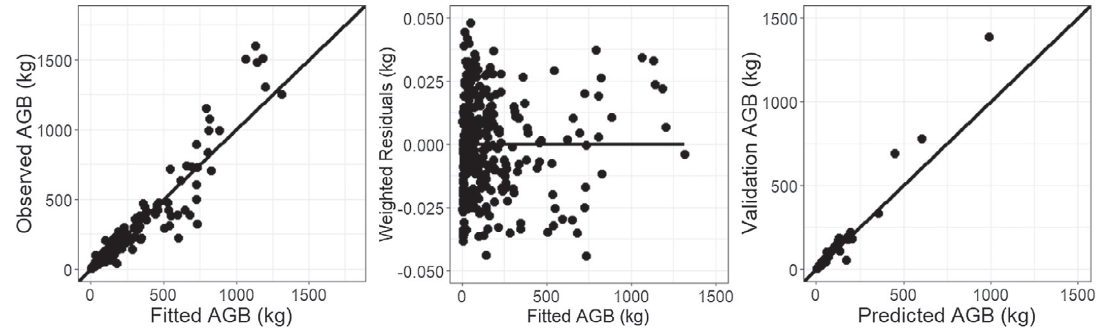
$$\textit{Above ground biomass}: \; AGB = Bst + Bbr + Ble + Bba = a_1 \times X_{1j}{}^{b1j} + a_2 \times X_{2j}{}^{b_{2j}} + a_3 \times X_{3j}{}^{3j} + a_4 \times X_{4j}{}^{4j} + \varepsilon_5 \quad (9)$$

where *Bst*, *Bbr*, *Ble*, *Bba* and *AGB* are biomass of stem, branches, leaves, bark and total in kg respectively; a_i and b_i are parameters of the power model i (i = 1, 2, 3, 4 for stem, branches, leaves and bark respectively); X_{ij} is the predictor variables (*D, H, D^2H or D^2HWD*) for the ith equation and the jth predictor; and ε_i is the residuals for the ith equation (i = 1, 2, 3, 4, 5). The weighting function is $1/X_{ij}{}^{2\delta}$ (Picard et al., 2012) with δ is the variance function coefficient to be estimated.

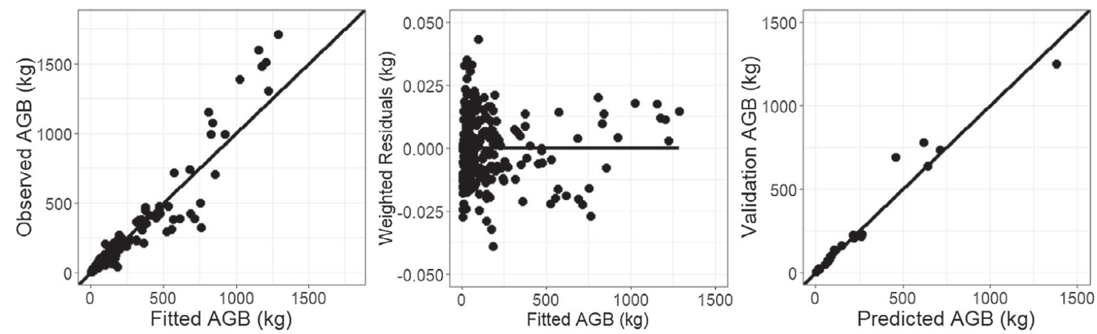
2.5. Model comparison, selection and cross validation

K-fold with K = 10 cross validation (Kohavi, 1995; Picard et al., 2012) was performed to cross-validate the selected models and other pantropics models included in the analysis. The dataset was randomly split into K equal sized subsamples, in which K − 1 subsamples were used to develop models and the K remaining subsamples were used to assess model performance. The cross-validation process was repeated 10 times, and statistics for comparison and validation of the models were averaged over 10 realizations.

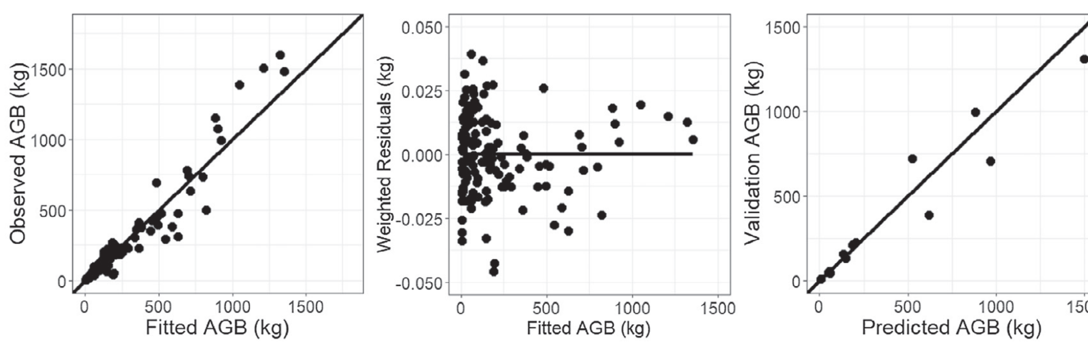
The Akaike information criterion (AIC) (Akaike, 1973) was used as a key statistic to compare and select the optimal models. The model that had the lowest AIC value was selected as the best model. Along with AIC, adj. R^2, statistical significance of parameters (p-value < 0.05), diagnostic plots of the trend of residuals were also used to assess model



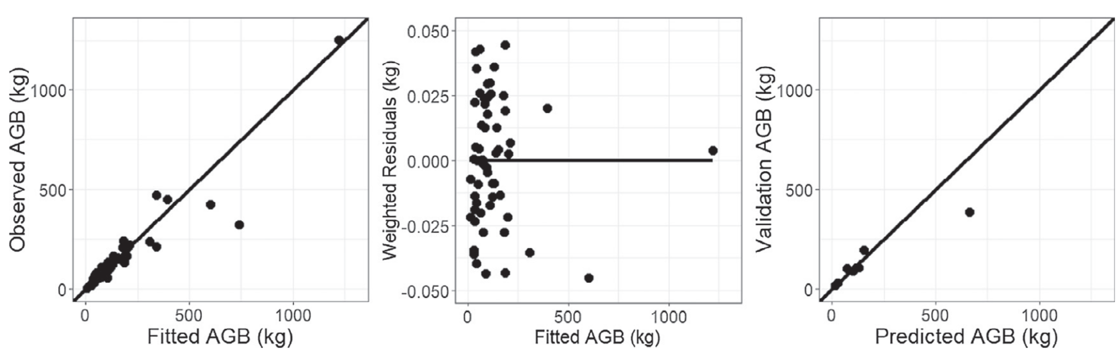
For Mixed- species: $AGB = a \times D^b \times H^c \times WD^d$



For Dipterocarpaceae Family: $AGB = a \times D^b \times H^c \times WD^d$



For *Dipterocarpus* Genus: $AGB = a \times D^b$



For *Shorea* Genus: $AGB = a \times D^b$

Fig. 5. Plots of selected aboveground biomass (*AGB*) models for mixed-species, dominant family, dominant genus left column: Observed was randomly split from 9/10 dataset vs fitted *AGB*; middle column: Maximum likelihood weighted residuals vs fitted *AGB*; and right column: Validation data of *AGB* was randomly split from 1/10 dataset vs predicted *AGB*. k-fold cross validation with k = 10.

performance. All statistics used in this fashion were calculated using the cross-validation procedure.

For cross-validation of the selected model and the pantropics models included in the analysis, bias (%), root mean square error (RMSE, %), and mean absolute percent error (MAPE, %) (Basuki et al., 2009; Swanson et al., 2011; Huy et al., 2016a,b,c) were calculated. Bias, RMSE and MAPE were also calculated using the cross-validation procedure. Smaller values for indicators are preferred.

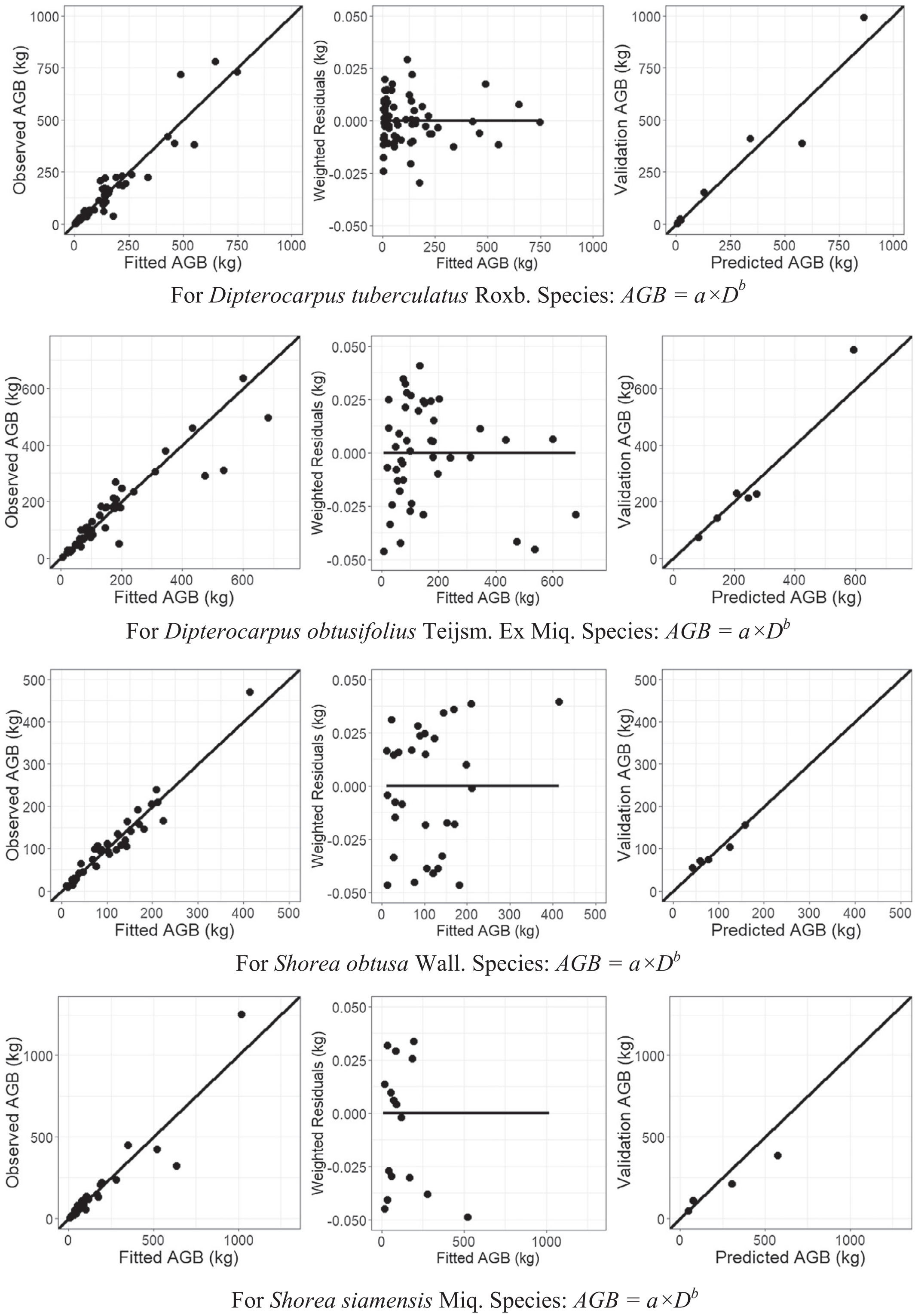


Fig. 6. Plots of selected aboveground biomass (*AGB*) models for dominant species specific. Left: Observed was randomly split from 9/10 dataset vs fitted *AGB*; Middle: Maximum likelihood weighted residuals vs fitted *AGB*; and Right: Validation data of *AGB* was randomly split from 1/10 dataset vs predicted *AGB*. K-fold cross validation with k = 10.

$$Bias\,(\%) = \frac{1}{K}\sum\nolimits_{k=1}^{K}\frac{100}{n}\sum_{i=1}^{n}\frac{\boldsymbol{y_i}-\boldsymbol{\hat{y}_i}}{\boldsymbol{y_i}} \tag{10}$$

$$\boldsymbol{RMSE}\,(\%) = \frac{1}{\boldsymbol{K}}\sum\nolimits_{\boldsymbol{k}=1}^{\boldsymbol{K}}100\sqrt{\frac{1}{n}\sum_{i=1}^{n}\left(\frac{y_i-\hat{y}_i}{y_i}\right)^2} \tag{11}$$

$$MAPE\,(\%) = \frac{1}{K}\sum\nolimits_{k=1}^{K}\frac{100}{n}\sum_{i=1}^{n}\frac{|y_i-\hat{y}_i|}{y_i} \tag{12}$$

Additionally, Fit Index (FI) (Parresol, 1999; Subedi et al., 2010) was also used to validate the goodness of fit among the selected models in this study and the pantropics models and larger values for FI are

Table 3
K-fold cross validations to select separate equations for biomass components including *Bst, Bbr, Ble* and *Bba* (biomass of stem, branches, leaves and bark, respectively) for mixed species.

Model form	Weight variable	AIC	Adj. R^2	Bias (%)	RMSE (%)	MAPE (%)
$Bst = a \times D^b$	$1/D^\delta$	2355	0.916	−15.8	56.4	34.2
$Bst = a \times D^b \times H^c$	$1/D^\delta$	2311	0.945	−13.8	51.0	30.8
$Bst = a \times (D^2H)^b$	$1/(D^2H)^\delta$	2499	0.938	−20.9	60.8	38.6
$Bst = a \times D^b \times WD^c$	$1/D^\delta$	2347	0.901	−14.6	53.5	32.8
$\mathbf{Bst = a \times D^b \times H^c \times WD^d}$	$\mathbf{1/D^\delta}$	**2282**	**0.945**	**−11.3**	**43.8**	**28.1**
$Bst = a \times (D^2H \times WD)^b$	$1/(D^2H \times WD)^\delta$	2471	0.941	−16.3	48.6	32.4
$\mathbf{Bbr = a \times D^b}$	$\mathbf{1/D^\delta}$	**2222**	**0.822**	**−51.2**	**133.9**	**75.6**
$Bbr = a \times D^b \times H^c$	$1/D^\delta$	2213	0.781	−50.3	142.6	74.9
$Bbr = a \times (D^2H)^b$	$1/(D^2H)^\delta$	2512	0.792	−93.2	206.6	117.4
$Bbr = a \times D^b \times WD^c$	$1/D^\delta$	2224	0.814	−50.2	142.0	73.9
$Bbr = a \times D^b \times H^c \times WD^{d*}$	$1/D^\delta$	2219	0.771	−50.2	137.7	75.2
$Bbr = a \times (D^2H \times WD)^b$	$1/(D^2H \times WD)^\delta$	2498	0.794	−83.4	190.9	106.4
$\mathbf{Ble = a \times D^b}$	$\mathbf{1/D^\delta}$	**1127**	**0.690**	**−31.0**	**86.2**	**54.4**
$Ble = a \times D^b \times H^c$	$1/D^\delta$	1132	0.702	−30.6	86.1	54.0
$Ble = a \times (D^2H)^b$	$1/(D^2H)^\delta$	1184	0.708	−34.9	92.2	57.9
$Ble = a \times D^b \times WD^c$	$1/D^\delta$	1129	0.682	−30.8	88.3	54.1
$Ble = a \times D^b \times H^c \times WD^d$	$1/D^\delta$	1134	0.699	−30.2	83.8	53.1
$Ble = a \times (D^2H \times WD)^b$	$1/(D^2H \times WD)^\delta$	1167	0.711	−33.2	92.1	55.8
$\mathbf{Bba = a \times D^b}$	$\mathbf{1/D^\delta}$	**1991**	**0.724**	**−40.7**	**128.6**	**64.2**
$Bba = a \times D^b \times H^{c*}$	$1/D^\delta$	1999	0.720	−40.8	129.6	64.6
$Bba = a \times (D^2H)^b$	$1/(D^2H)^\delta$	2104	0.790	−51.6	137.1	76.0
$Bba = a \times D^b \times WD^c$	$1/D^\delta$	1994	0.676	−39.9	126.8	63.9
$Bba = a \times D^b \times H^{c*} \times WD^d$	$1/D^\delta$	2004	0.674	−41.0	128.8	65.4
$Bba = a \times (D^2H \times WD)^b$	$1/(D^2H \times WD)^\delta$	2083	0.735	−48.4	141.6	72.6

Note: In K-fold cross validation, the dataset is randomly split into K (K = 10 folds) equal sized subsamples, K − 1 subsamples used for developing models, calculation of AIC, Adj. R^2; and K remaining subsample used for validation, calculation of Bias, RMSE, MAPE; finally, all those statistics averaged over 10 realizations. *: Parameter with $p_{value} > 0.05$. δ: the variance function coefficient; Predictor: D^2H (m^3) = (D (cm)/100)$^2 \times H$ (m); $D^2H \times WD$ (kg) = D^2H (m^3) $\times WD$ (g/cm^3) × 1000. Bold: Selected model based on K-fold cross validation statistics and diagnostic plots.

Table 4
K-fold cross validations to select separate equations for biomass components including *Bst, Bbr, Ble* and *Bba* (biomass of stem, branches, leaves and bark, respectively) for dominant Dipterocarpaceae family.

Model form	Weight variable	AIC	Adj. R^2	Bias (%)	RMSE (%)	MAPE (%)
$Bst = a \times D^b$	$1/D^\delta$	1663	0.919	−14.3	52.8	33.1
$Bst = a \times D^b \times H^c$	$1/D^\delta$	1638	0.947	−13.1	46.4	30.4
$Bst = a \times (D^2H)^b$	$1/(D^2H)^\delta$	1769	0.935	−21.3	64.4	40.1
$Bst = a \times D^b \times WD^c$	$1/D^\delta$	1657	0.901	−13.3	48.6	31.7
$\mathbf{Bst = a \times D^b \times H^c \times WD^d}$	$\mathbf{1/D^\delta}$	**1615**	**0.952**	**−10.2**	**41.3**	**27.0**
$Bst = a \times (D^2H \times WD)^b$	$1/(D^2H \times WD)^\delta$	1742	0.956	−16.3	49.1	33.4
$\mathbf{Bbr = a \times D^b}$	$\mathbf{1/D^\delta}$	**1618**	**0.825**	**−50.1**	**125.8**	**74.1**
$Bbr = a \times D^b \times H^c$	$1/D^\delta$	1615	0.780	−48.2	135.2	72.9
$Bbr = a \times (D^2H)^b$	$1/(D^2H)^\delta$	1802	0.805	−93.1	202.4	118.2
$Bbr = a \times D^b \times WD^{c*}$	$1/D^\delta$	1612	0.817	−47.9	132.0	71.4
$Bbr = a \times D^b \times H^c \times WD^{d*}$	$1/D^\delta$	1623	0.764	−48.0	138.0	72.4
$Bbr = a \times (D^2H \times WD)^b$	$1/(D^2H \times WD)^\delta$	1792	0.820	−81.5	180.4	105.5
$\mathbf{Ble = a \times D^b}$	$\mathbf{1/D^\delta}$	**808**	**0.691**	**−25.0**	**66.8**	**48.2**
$Ble = a \times D^b \times H^c$	$1/D^\delta$	811	0.707	−24.5	67.8	47.5
$Ble = a \times (D^2H)^b$	$1/(D^2H)^\delta$	842	0.715	−27.3	72.6	50.3
$Ble = a \times D^b \times WD^c$	$1/D^\delta$	811	0.683	−24.4	68.6	47.2
$Ble = a \times D^b \times H^c \times WD^d$	$1/D^\delta$	812	0.716	−23.6	67.5	46.2
$Ble = a \times (D^2H \times WD)^b$	$1/(D^2H \times WD)^\delta$	829	0.733	−24.9	68.9	46.8
$\mathbf{Bba = a \times D^b}$	$\mathbf{1/D^\delta}$	**1433**	**0.710**	**−27.1**	**76.4**	**49.7**
$Bba = a \times D^b \times H^{c*}$	$1/D^\delta$	1439	0.737	−27.3	73.1	49.5
$Bba = a \times (D^2H)^b$	$1/(D^2H)^\delta$	1477	0.808	−34.3	90.9	58.2
$Bba = a \times D^b \times WD^c$	$1/D^\delta$	1430	0.613	−24.9	68.8	48.0
$Bba = a \times D^b \times H^{c*} \times WD^d$	$1/D^\delta$	1438	0.643	−25.2	72.8	48.4
$Bba = a \times (D^2H \times WD)^b$	$1/(D^2H \times WD)^\delta$	1460	0.763	−31.1	79.4	55.3

Note: In K-fold cross validation, the dataset is randomly split into K (K = 10 folds) equal sized subsamples, K − 1 subsamples used for developing models, calculation of AIC, Adj. R^2; and K remaining subsample used for validation, calculation of Bias, RMSE, MAPE; finally, all those statistics averaged over 10 realizations. *: Parameter with $p_{value} > 0.05$. δ: the variance function coefficient; Predictor: D^2H (m^3) = (D (cm)/100)$^2 \times H$ (m); $D^2H \times WD$ (kg) = D^2H (m^3) $\times WD$ (g/cm^3) × 1000. Bold: Selected model based on K-fold cross validation statistics and diagnostic plots.

Table 5
Development of simultaneously fit models using SUR and cross-validation using K-fold for mixed-species, dominant family, dominant genera and dominant species.

Plant classification hierarchy level	Modeling system	Bias (%)	RMSE (%)	MAPE (%)
Mixed-species	$Bst = a_1 \times D^{b11} \times H^{b12} \times WD^{b13}$	1.0	45.6	26.2
	$Bbr = a_2 \times D^{b21}$	−33.0	127.3	59.9
	$Ble = a_3 \times D^{b31}$	−44.6	96.7	62.9
	$Bba = a_4 \times D^{b41}$	−14.3	66.6	46.6
	$AGB = Bst + Bbr + Ble + Bba$	−1.8	51.4	25.4
Dominant family	Dipterocarpaceae:			
	$Bst = a_1 \times D^{b11} \times H^{b12} \times WD^{b13}$	−0.5	38.0	31.0
	$Bbr = a_2 \times D^{b21}$	−75.1	151.5	91.6
	$Ble = a_3 \times D^{b31}$	−74.0	129.4	86.0
	$Bba = a_4 \times D^{b41}$	4.1	58.2	48.6
	$AGB = Bst + Bbr + Ble + Bba$	−5.9	36.2	27.7
Dominant genera	*Dipterocarpus:*			
	$Bst = a_1 \times D^{b11}$	−20.3	45.3	29.3
	$Bbr = a_2 \times D^{b21}$	−2.2	31.4	26.1
	$Ble = a_3 \times D^{b31}$	−55.0	121.1	65.1
	$Bba = a_4 \times D^{b41}$	−30.9	90.3	74.0
	$AGB = Bst + Bbr + Ble + Bba$	−8.5	27.2	20.4
	Shorea:			
	$Bst = a_1 \times D^{b11}$	−6.4	36.5	30.5
	$Bbr = a_2 \times D^{b21}$	−12.9	44.5	36.8
	$Ble = a_3 \times D^{b31}$	−43.8	83.2	63.8
	$Bba = a_4 \times D^{b41}$	−11.7	39.1	31.9
	$AGB = Bst + Bbr + Ble + Bba$	−3.4	23.8	20.9
Dominant species	*Dipterocarpus tuberculatus* Roxb.:			
	$Bst = a_1 \times D^{b11}$	−26.6	42,4	34.6
	$Bbr = a_2 \times D^{b21}$	−28.9	51.1	43.0
	$Ble = a_3 \times D^{b31}$	5.7	25.7	18.9
	$Bba = a_4 \times D^{b41}$	−25.4	62.0	43.1
	$AGB = Bst + Bbr + Ble + Bba$	−15.1	26.6	20.9
	Dipterocarpus obtusifolius Teijsm. Ex Miq.:			
	$Bst = a_1 \times D^{b11}$	−22.4	64.9	40.0
	$Bbr = a_2 \times D^{b21}$	−112.8	217.1	134.6
	$Ble = a_3 \times D^{b31}$	−17.5	39.0	32.9
	$Bba = a_4 \times D^{b41}$	−14.4	41.6	33.5
	$AGB = Bst + Bbr + Ble + Bba$	−25.8	65.6	36.1
	Shorea obtusa Wall. Ex Blume:			
	$Bst = a_1 \times D^{b11}$	−8.5	50.4	37.6
	$Bbr = a_2 \times D^{b21}$	−22.1	67.4	58.9
	$Ble = a_3 \times D^{b31}$	−92.9	177.5	94.5
	$Bba = a_4 \times D^{b41}$	−16.6	32.7	31.6
	$AGB = Bst + Bbr + Ble + Bba$	−7.7	37.0	26.7
	Shorea siamensis Miq.:			
	$Bst = a_1 \times D^{b11}$	−6.2	28.5	24.4
	$Bbr = a_2 \times D^{b21}$	1.9	44.5	35.9
	$Ble = a_3 \times D^{b31}$	−47.5	78.0	63.3
	$Bba = a_4 \times D^{b41}$	17.9	24.1	20.3
	$AGB = Bst + Bbr + Ble + Bba$	7.0	20.9	18.5

Note: In K-fold cross validation, the dataset is randomly split into K (K = 10 folds) equal sized subsamples, K − 1 subsamples used for developing models, calculation of AIC, Adj. R^2; and K remaining subsample used for validation, calculation of Bias, RMSE, MAPE; finally, all those statistics averaged over 10 realizations. *Bst, Bbr, Ble, Bba* and *AGB* are biomass of stem, branches, leaves, bark and total above-ground biomass, respectively.

preferred.

$$FI = 1 - \frac{\sum_{i=1}^{N} (y_i - \hat{y}_i)^2}{\sum_{i=1}^{N} (y_i - \bar{y})^2} \quad (13)$$

where K is the number of folds (10); n, N are the number of sampled trees in fold K and number of the entire dataset, respectively; and y_i, $\hat{y}_i$ and$\bar{y}$ are the observed, predicted and averaged *Bst*, *Bbr*, *Ble*, *Bba* and *AGB* for the *i*th sampled tree in realization K, respectively.

Final parameter estimates for all of the selected modeling systems were obtained by fitting models with the entire dataset.

3. Results

3.1. Selection of taxon-specific models – independent fit

Weighted nonlinear models were fit via Maximum Likelihood to develop and select the appropriate predictor(s) of *AGB* models for mixed species, dominant Dipterocarpaceae family-specific, two dominant genera-specific of *Dipterocarpus* and *Shorea,* and four dominant species-specific of *Dipterocarpus tuberculatus* Roxb., *Dipterocarpus obtusifolius* Teijsm. Ex Miq., *Shorea obtusa* Wall., *Shorea siamensis* Miq and K-fold cross validation was employed to select the best models (Table 2).

The three predictors including *D, H,* and *WD* were evaluated, except in the case of the species-specific model where the *WD* is considered the same value for a given species.

The best *AGB* models for mixed species and dominant Dipterocarpaceae family-specific involved all three of *D, H* and *WD*. Meanwhile, among the *AGB* models that were specific to each dominant genus and species, very similar values of AIC, R^2 and cross-validation statistics were observed (Table 2), therefore the simplest models with only D as a predictor were for parsimony.

The forms of the *AGB* models obtained by independent fitting were:

For mixed species and dominant dipterocarpaceae family:

$$AGB = a \times D^b \times H^c \times WD^d \quad (14)$$

Table 6
Comparison of K-fold cross validation statistics between two methods (independent and SUR fits) to fit selected *AGB* models for plant classification hierarchy-specific levels.

Plant classification hierarchy-specific level	Method to fit the model	Selected model form	Bias (%)	RMSE (%)	MAPE (%)
Mixed-species	Independent	$AGB = a \times D^b \times H^c \times WD^d$	−11.1	44.6	27.1
	SUR	$AGB = Bst + Bbr + Ble + Bba = a_1 \times D^{b11} \times H^{b12} \times WD^{b13} + a_2 \times D^{b21} + a_3 \times D^{b31} + a_4 \times D^{b41}$	−1.8	51.4	25.4
Dipterocarpaceae family	Independent	$AGB = a \times D^b \times H^c \times WD^d$	−9.9	41.7	26.4
	SUR	$AGB = Bst + Bbr + Ble + Bba = a_1 \times D^{b11} \times H^{b12} \times WD^{b13} + a_2 \times D^{b21} + a_3 \times D^{b31} + a_4 \times D^{b41}$	−5.9	36.2	27.7
Dipterocarpus genus	Independent	$AGB = a \times D^b$	−12.2	46.3	29.2
	SUR	$AGB = Bst + Bbr + Ble + Bba = a_1 \times D^{b11} + a_2 \times D^{b21} + a_3 \times D^{b31} + a_4 \times D^{b41}$	−8.5	27.2	20.4
Shorea genus	Independent	$AGB = a \times D^b$	−8.8	33.2	24.6
	SUR	$AGB = Bst + Bbr + Ble + Bba = a_1 \times D^{b11} + a_2 \times D^{b21} + a_3 \times D^{b31} + a_4 \times D^{b41}$	−3.4	23.8	20.9
Dipterocarpus tuberculatus Roxb species	Independent	$AGB = a \times D^b$	−13.4	47.2	31.5
	SUR	$AGB = Bst + Bbr + Ble + Bba = a_1 \times D^{b11} + a_2 \times D^{b21} + a_3 \times D^{b31} + a_4 \times D^{b41}$	−15.1	26.6	20.9
Dipterocarpus obtusifolius Teijsm. Ex Miq. species	Independent	$AGB = a \times D^b$	−10.5	36.8	25.8
	SUR	$AGB = Bst + Bbr + Ble + Bba = a_1 \times D^{b11} + a_2 \times D^{b21} + a_3 \times D^{b31} + a_4 \times D^{b41}$	−25.8	65.6	36.1
Shorea obtusa Wall. species	Independent	$AGB = a \times D^b$	−4.4	22.3	18.0
	SUR	$AGB = Bst + Bbr + Ble + Bba = a_1 \times D^{b11} + a_2 \times D^{b21} + a_3 \times D^{b31} + a_4 \times D^{b41}$	−7.7	37.0	26.7
Shorea siamensis Miq. species	Independent	$AGB = a \times D^b$	−13.3	41.5	33.8
	SUR	$AGB = Bst + Bbr + Ble + Bba = a_1 \times D^{b11} + a_2 \times D^{b21} + a_3 \times D^{b31} + a_4 \times D^{b41}$	7.0	20.9	18.5

Note: In K-fold with K = 10 folds. *Bst, Bbr, Ble, Bba* and *AGB* are biomass of stem, branches, leaves, bark and total above-ground biomass, respectively.

For two dominant genera of *Dipterocarpus* and *Shorea,* and four dominant species of *Dipterocarpus tuberculatus, Dipterocarpus obtusifolius, Shorea obtuse and Shorea siamensis*:

$$AGB = a \times D^b \tag{15}$$

Figs. 5 and 6 demonstrate plots of selected *AGB* models at different levels of mixed species, family, genera and species for observed vs fitted, weighted residuals vs fitted, and validation data vs predicted *AGB*.

Because the selected genus-specific and species-specific *AGB* models had only one variable D (Table 2), its components models for *Bst*, *Bbr*, *Ble* and *Bba* also only included *D* in the SUR modeling system. Meanwhile, the selected *AGB* models for mixed species and for the Dipterocarpaceae family consisted of all three variables, *D, H* and *WD* (Table 2); Therefore development and cross-validation were done independently to select optimal predictor(s) for each model component *Bst*, *Bbr*, *Ble* and *Bba* (Tables 3 and 4); As a result, given the case of mixed species and the Dipterocarpaceae family, the selected *Bst* model included three variables of *D, H* and *WD*. Whereas the selected models of *Bbr*, *Ble* and *Bba* only included *D* (Tables 3 and 4).

3.2. Models fit as a system with SUR

To simultaneously estimate tree *AGB* and its components, the weighted nonlinear SUR method was performed. We then compared the reliability and uncertainty of the SUR method against the *AGB* and components models fitted independently.

Based on the optimal predictor(s) determined from the previous step, the SUR modeling system was constructed and predictions for *AGB* and its components were produced using the cross-validation procedure for each level of plant classification (Table 5). Comparative results showed that the modeling systems fit simultaneously by SUR produced substantially lower errors (Bias, RMSE, and MAPE) than models that developed separately at levels of mixed species, family and genera (Table 6). Figs. 7–9 show predictions of simultaneously fit (using SUR) models against observed *AGB* and its components for mixed species and two dominant genera.

In addition, the results indicated that the modeling system improved reliability of predictions for groups further down the hierarchy (for example from mixed species to family, and then to genus). The uncertainty of species-specific models did not show improvement relative to the genus-specific models (Tables 5 and 6). Therefore, we used the entire dataset to estimate the parameters for simultaneous systems for estimating *AGB* and its components for the levels of mixed species, dominant family and dominant genus (Table 7). Sometimes only the predictor *D* is measured in the field, hence the modeling system with only the *D* variable also developed and the results presented in Table 8.

The forms of selected modeling systems developed simultaneously by SUR at different plant classification levels as follows:

For mixed species and dominant Dipterocarpaceae family:

$$AGB = Bst + Bbr + Ble + Bba = a_1 \times D^{b11} \times H^{b12} \times WD^{b13} + a_2 \times D^{b21} + a_3 \times D^{b31} + a_4 \times D^{b41}.$$

For dominant genera of *Dipterocarpus* and *Shorea*:

$$AGB = Bst + Bbr + Ble + Bba = a_1 \times D^{b11} + a_2 \times D^{b21} + a_3 \times D^{b31} + a_4 \times D^{b41}$$

4. Discussion

4.1. Variability of tree biomass components in the DDF

The *Ble* and *Bba* are highly variable (Figs. 3, 7–9), which resulted in models that had slightly lower adj. $R^2 = 0.6–0.7$ and its Bias, RMSE and MAPE were larger than those errors of the *Bst* and *AGB* models (Table 5). This reflects the variation of the foliage and the thickness of the bark among different species in the DDF. For example, *Dipterocarpus tuberculatus* and *Shorea siamenesis* have large foliage and very wide and thick leaves, while *Dipterocarpus obtusifolious* has medium-size foliage and leaves; *Shorea obtusa* shows the smallest foliage and leaves. Additionally, the plants in the DDF are also adapted to wild-fire. This adaptation is reflected in the Dipterocarpaceae family, with its thicker and harder bark relative to other species. This drives the higher variation of bark biomass among the plant species, genera, and family in the DDF.

4.2. Independent vs. simultaneous model fit

The structure of the equation system ensures additivity, while fitting

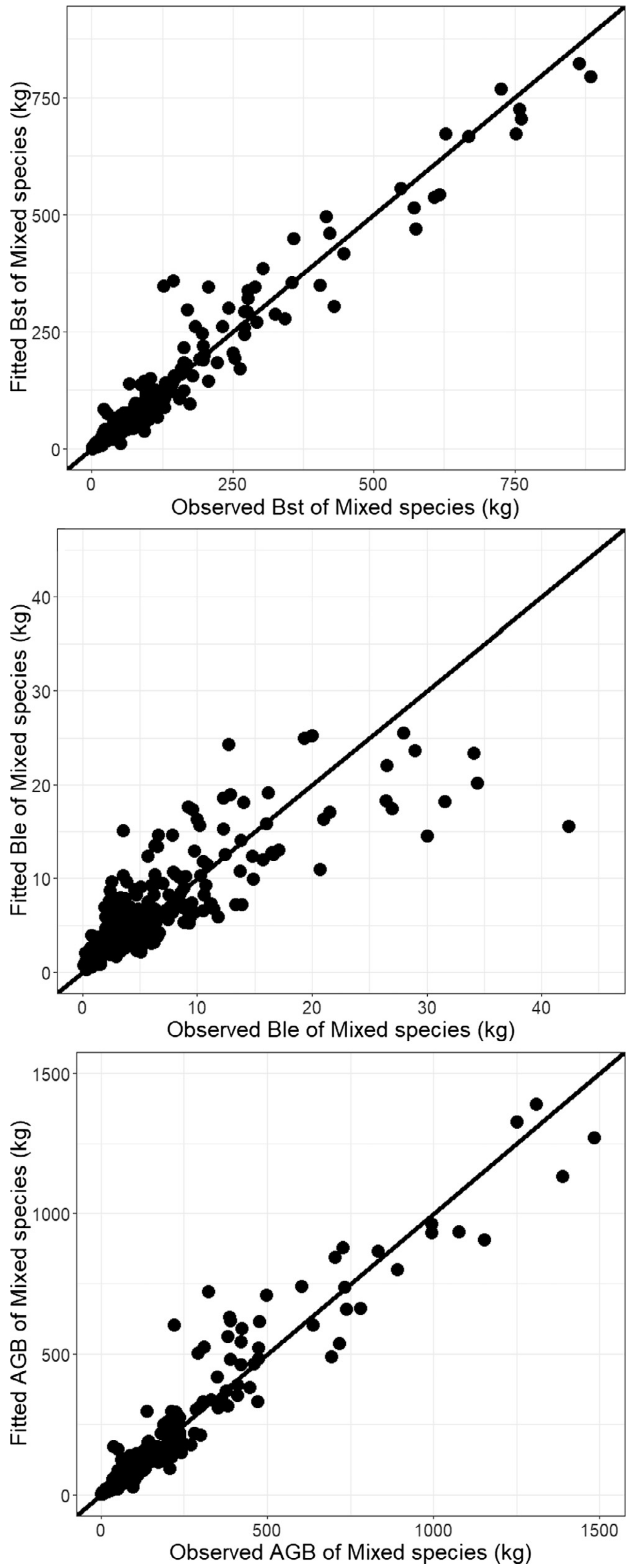


Fig. 7. Simultaneously fit of biomass of tree stem (*Bst*), branches (*Bbr*), leaves (*Ble*), bark (*Bba*), and total aboveground biomass (*AGB*), using SUR for mixed species vs observed entire datasets.

the system with SUR to deal with the correlation among equations may achieve more efficient estimates. Compared to fitting models separately (Tables 3 and 4 vs. Tables 5 and 6), the errors in *AGB* estimation improved by fitting models as a system of equations with SUR. This finding is consistent with Poudel and Temesgen (2016) that used SUR systems to predict biomass components. These improvements are biggest at the genus-level (Table 6).

Additionally, with the variation of component biomass in the DDF,

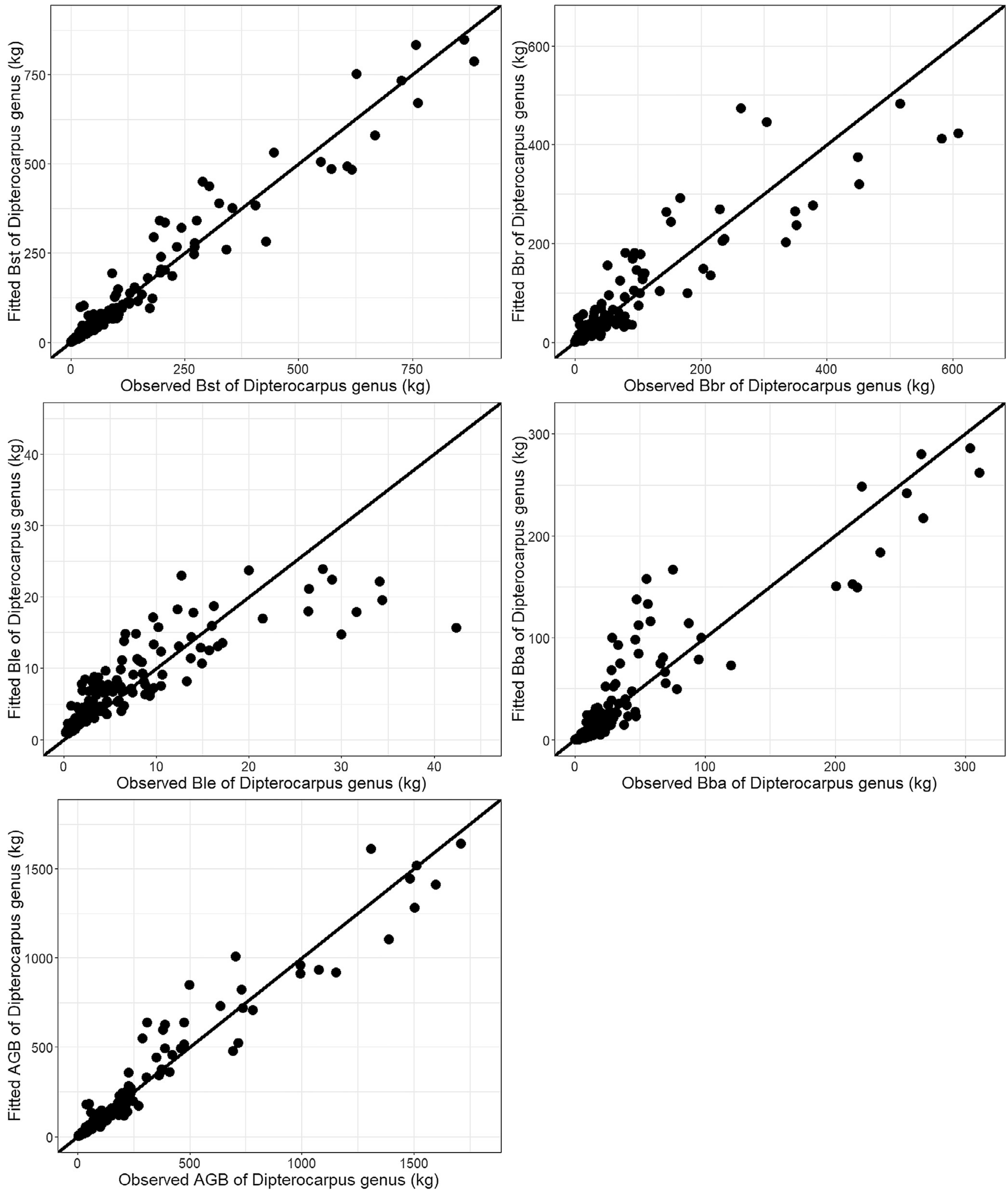


Fig. 8. Simultaneously fit of biomass of tree stem (*Bst*), branches (*Bbr*), leaves (*Ble)*, bark (*Bba*), and total aboveground biomass (*AGB*), using SUR for *Dipterocarpus* genus vs observed entire datasets.

the use of SUR better accommodates the interactions between the parameters of the component models (Parresol, 2001; Poudel and Temesgen, 2016), and reduced the uncertainty of parameter estimates of the component models fitted. Therefore, we encourage the weighted nonlinear SUR to develop simultaneous models for *AGB* and its components in the tropical forests.

4.3. Mixed species vs genus-specific models

The simultaneous modeling systems for mixed species or Dipterocarp family need all three predictors (*D, H,* and *WD*), meanwhile in the modeling of genus-and species-specific systems, only *D* variable was selected. This shows that the *WD* predictor is only necessary for the

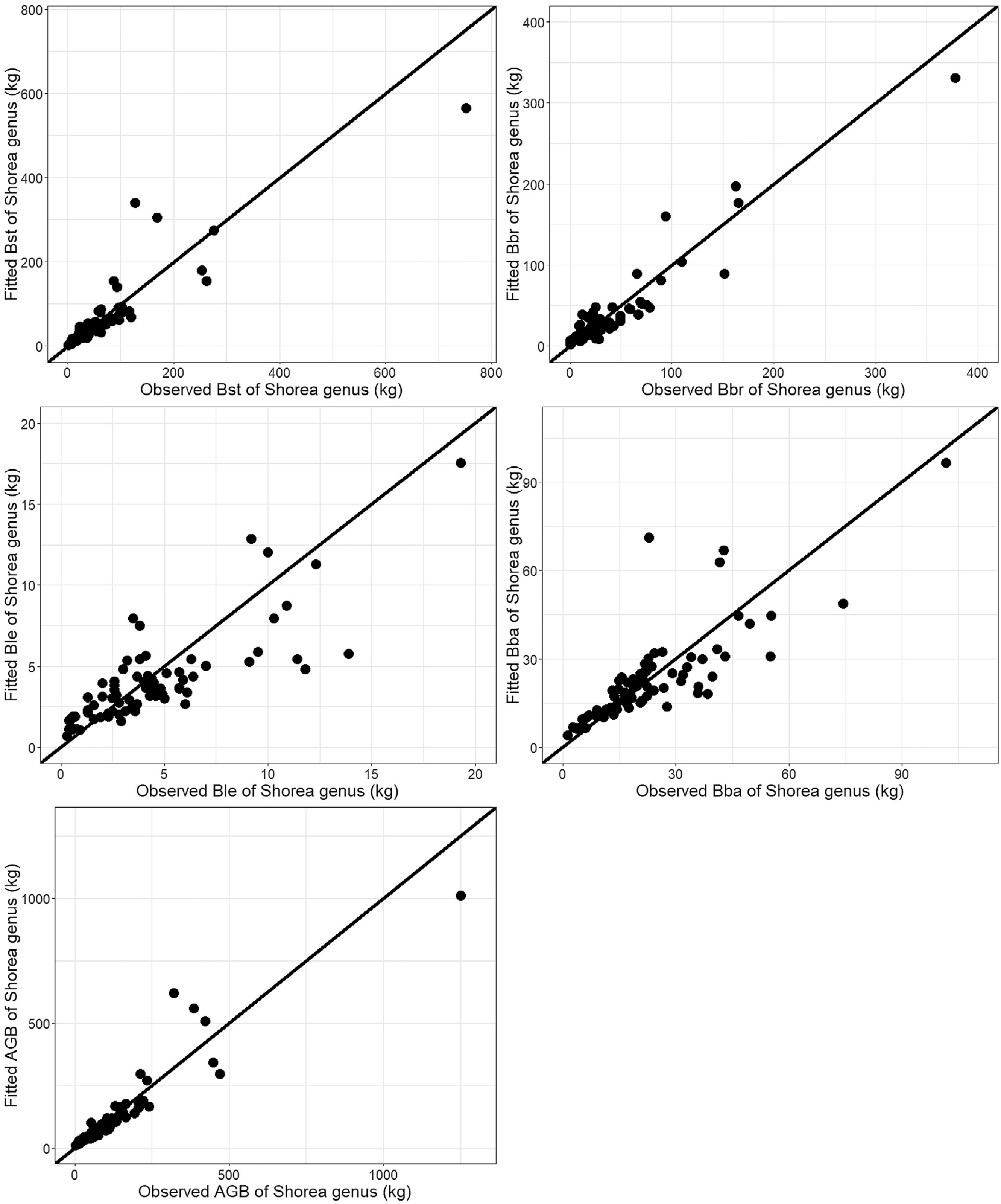


Fig. 9. Simultaneously fit of biomass of tree stem (*Bst*), branches (*Bbr*), leaves (*Ble*), bark (*Bba*), and total aboveground biomass (*AGB*), using SUR for *Shorea* genus vs observed entire datasets.

mixed-species model rather than for genus and species (Basuki et al., 2009; Huy et al., 2016b).

The genus-specific models fit by SUR significantly reduced uncertainty compared with the mixed-species or family-specific models (Table 6), meanwhile models at genus level only required a simple variable *D*. It is also worth noting that the number of genera in DDF is low; consequently, we recommend the use of genus-species modeling systems for tropical DDF to improve reliability and reduce costs of field measurement associated with species-specific models. This reinforces the finding of Huy et al. (2016b).

Table 7
Estimated parameters to simultaneously predict *AGB* and its components for plant classification hierarchy-specific levels using SUR method (based on the entire dataset).

Plant classification hierarchy-specific level	Model form	Parameter	Estimate ± Approx. Std Error	RMSE (kg)	Adj. R^2
Mixed-species	$Bst = a_1 \times D^{b11} \times H^{b12} \times WD^{b13}$	a_1	0.02055 ± 0.00215	32.7	0.952
		b_{11}	2.35241 ± 0.03490		
		b_{12}	0.59142 ± 0.03210		
		b_{13}	0.69609 ± 0.07980		
	$Bbr = a_2 \times D^{b21}$	a_2	0.00669 ± 0.00190	36.4	0.824
		b_{21}	2.85742 ± 0.07880		
	$Ble = a_3 \times D^{b31}$	a_3	0.03701 ± 0.01310	3.5	0.694
		b_{31}	1.68095 ± 0.09680		
	$Bba = a_4 \times D^{b41}$	a_4	0.01541 ± 0.00445	23.1	0.744
		b41	2.43959 ± 0.08360		
	$AGB = Bst + Bbr + Ble + Bba$	idem	idem	68.5	0.939
Dipterocarpaceae family	$Bst = a_1 \times D^{b11} \times H^{b12} \times WD^{b13}$	a_1	0.02548 ± 0.00390	32.7	0.961
		b_{11}	2.25377 ± 0.04780		
		b_{12}	0.69531 ± 0.03900		
		b_{13}	0.95381 ± 0.12130		
	$Bbr = a_2 \times D^{b21}$	a_2	0.01097 ± 0.00356	41.1	0.827
		b_{21}	2.73663 ± 0.08850		
	$Ble = a_3 \times D^{b31}$	a_3	0.04559 ± 0.01490	3.7	0.696
		b_{31}	1.63322 ± 0.09000		
	$Bba = a_4 \times D^{b41}$	a_4	0.00399 ± 0.00174	25.2	0.758
		b41	2.83670 ± 0.11690		
	$AGB = Bst + Bbr + Ble + Bba$	idem	idem	72.1	0.946
Dipterocarpus genus	$Bst = a_1 \times D^{b11}$	a_1	0.01831 ± 0.00348	43.9	0.945
		b_{11}	2.76361 ± 0.05260		
	$Bbr = a_2 \times D^{b21}$	a_2	0.00481 ± 0.00220	47.6	0.827
		b_{21}	2.96217 ± 0.12500		
	$Ble = a_3 \times D^{b31}$	a_3	0.08921 ± 0.02840	4.3	0.691
		b_{31}	1.43840 ± 0.09600		
	$Bba = a_4 \times D^{b41}$	a_4	0.00116 ± 0.00040	24.4	0.843
		b41	3.19340 ± 0.09160		
	$AGB = Bst + Bbr + Ble + Bba$	idem	idem	88.1	0.940
Shorea genus	$Bst = a_1 \times D^{b11}$	a_1	0.03925 ± 0.01190	42.1	0.807
		b_{11}	2.47118 ± 0.09070		
	$Bbr = a_2 \times D^{b21}$	a_2	0.02130 ± 0.00631	16.7	0.900
		b_{21}	2.49004 ± 0.08800		
	$Ble = a_3 \times D^{b31}$	a_3	0.05119 ± 0.01070	2.1	0.634
		b_{31}	1.50629 ± 0.05890		
	$Bba = a_4 \times D^{b41}$	a_4	0.31967 ± 0.09090	9.9	0.649
		b41	1.47380 ± 0.09610		
	$AGB = Bst + Bbr + Ble + Bba$	idem	idem	60.2	0.863

Note: *Bst, Bbr, Ble, Bba* and *AGB* are biomass of stem, branches, leaves, bark and total above-ground biomass, respectively. All parameters with $p_{value} < 0.05$.

Table 8
Estimated parameters for sole predictor of diameter at breast height (D) to estimate simultaneously *AGB* and its components for mixed species using SUR method (based on the entire dataset).

Model form	Parameter	Estimate ± Approx. Std Error	RMSE (kg)	Adj. R^2
$Bst = a_1 \times D^{b11}$	a_1	0.02384 ± 0.00262	42.8	0.917
	b_{11}	2.67666 ± 0.03020		
$Bbr = a_2 \times D^{b21}$	a_2	0.00748 ± 0.00207	36.5	0.824
	b_{21}	2.82670 ± 0.07660		
$Ble = a_3 \times D^{b31}$	a_3	0.03874 ± 0.01290	3.5	0.693
	b_{31}	1.66726 ± 0.09140		
$Bba = a_4 \times D^{b41}$	a_4	0.01827 ± 0.00521	23.4	0.738
	b41	2.38654 ± 0.08340		
$AGB = Bst + Bbr + Ble + Bba$	idem	idem	80.6	0.916

4.4. *Pantropic models vs. site-specific models and pantropic mixed-species vs. pantropic genus-specific models*

The K-Fold cross-validation with K = 10 was undertaken to validate the performance of other allometric equations developed for the pantropics (Chave et al., 2005, 2014), and Southeast Asia for the DDF (Basuki et al., 2009) relative to the selected *AGB* equations fit by SUR in this study. We did this for mixed species and genus-specific models (Table 9).

The K-Fold cross-validation results showed the pantropical mixed-species model developed by Chave et al. (2005) with *D* and *WD* producing high errors and overestimated *AGB* versus *AGB* data evaluation, whereas the models with all three variables *D, H* and *WD* (Chave et al., 2005, 2014) gave the same errors as our *AGB* model fit by SUR in this study. The Fit Index (FI) is high at approximately 0.93 (Table 9, Fig. 10, above). The finding is also consistent with Rutishauser et al. (2013) in

Table 9

K-fold cross validation of *AGB* models fitted by SUR of this study compared to other AGB models for Dipterocarp forest in worldwide at Mixed species and Genus-specific levels.

Plant classification hierarchy-specific level	Source	Selected model	Fit Index (FI)	Bias (%)	RMSE (%)	MAPE (%)
Mixed species	This study, (2018), for Dipterocarp forest in Viet Nam	$AGB = Bst + Bbr + Ble + Bba = 0.02055 \times D^{2.35241} \times H^{0.59142} \times WD^{0.69609} + 0.00669 \times D^{2.85742} + 0.03701 \times D^{1.68095} + 0.01541 \times D^{2.43959}$	0.940	−1.8	51.4	25.4
	Chave et al. (2005), for dry forests in pantropic	*Model I:* $AGB = WD \times \exp(-0.667 + 1.784 \times \log(D) + 0.207 \times (\log(D))^2 - 0.0281 \times (\log(D))^3)$	0.764	−84.0	123.9	84.1
		Model II: $AGB = 0.112 \times (D^2 \times H \times WD)^{0.916}$	0.926	−23.1	65.4	40.9
	Chave et al. (2014), for all forest types in pantropic	Model III: $AGB = 0.0673 \times (D^2 \times H \times WD)^{0.976}$	0.923	−12.1	58.5	37.1
	Basuki et al. (2009), for Dipterocarp forest in Indonesia	Model I: $AGB = \exp(-1.201 + 2.196 \times \log(D))$	0.833	−100.3	139.6	100.3
		Model II: $AGB = \exp(-0.744 + 2.188 \times \log(D) + 0.832 \times \log(WD))$	0.704	−112.5	152.5	112.5
Genus-specific						
Dipterocarpus genus	This study, (2018), Viet Nam	$AGB = Bst + Bbr + Ble + Bba = 0.01831 \times D^{2.76361} + 0.00481 \times D^{2.96217} + 0.08921 \times D^{1.43840} + 0.00116 \times D^{3.19340}$	0.941	−8.5	27.2	20.4
	Basuki et al. (2009), Indonesia	$AGB = \exp(-1.232 + 2.178 \times \log(D))$	0.901	−70.9	95.2	70.9
Shorea genus	This study, (2018), Viet Nam	$AGB = Bst + Bbr + Ble + Bba = 0.03925 \times D^{2.47118} + 0.02130 \times D^{2.49004} + 0.05119 \times D^{1.50629} + 0.31967 \times D^{1.47380}$	0.868	−3.4	23.8	20.9
	Basuki et al. (2009), Indonesia	$AGB = \exp(-2.193 + 2.371 \times \log(D))$	0.861	−1.2	23.7	20.7

Note: In K-fold cross validation, the dataset is randomly split into K (K = 10 folds) equal sized subsamples, K − 1 subsamples used for developing models; and K remaining subsample used for validation, calculation of averaged Bias, RMSE and MAPE for this study model system and other compared models, and all those statistics averaged over 10 realizations; *Bst, Bbr, Ble, Bba* and *AGB* are biomass of stem, branches, leaves, bark and total above-ground biomass, respectively.

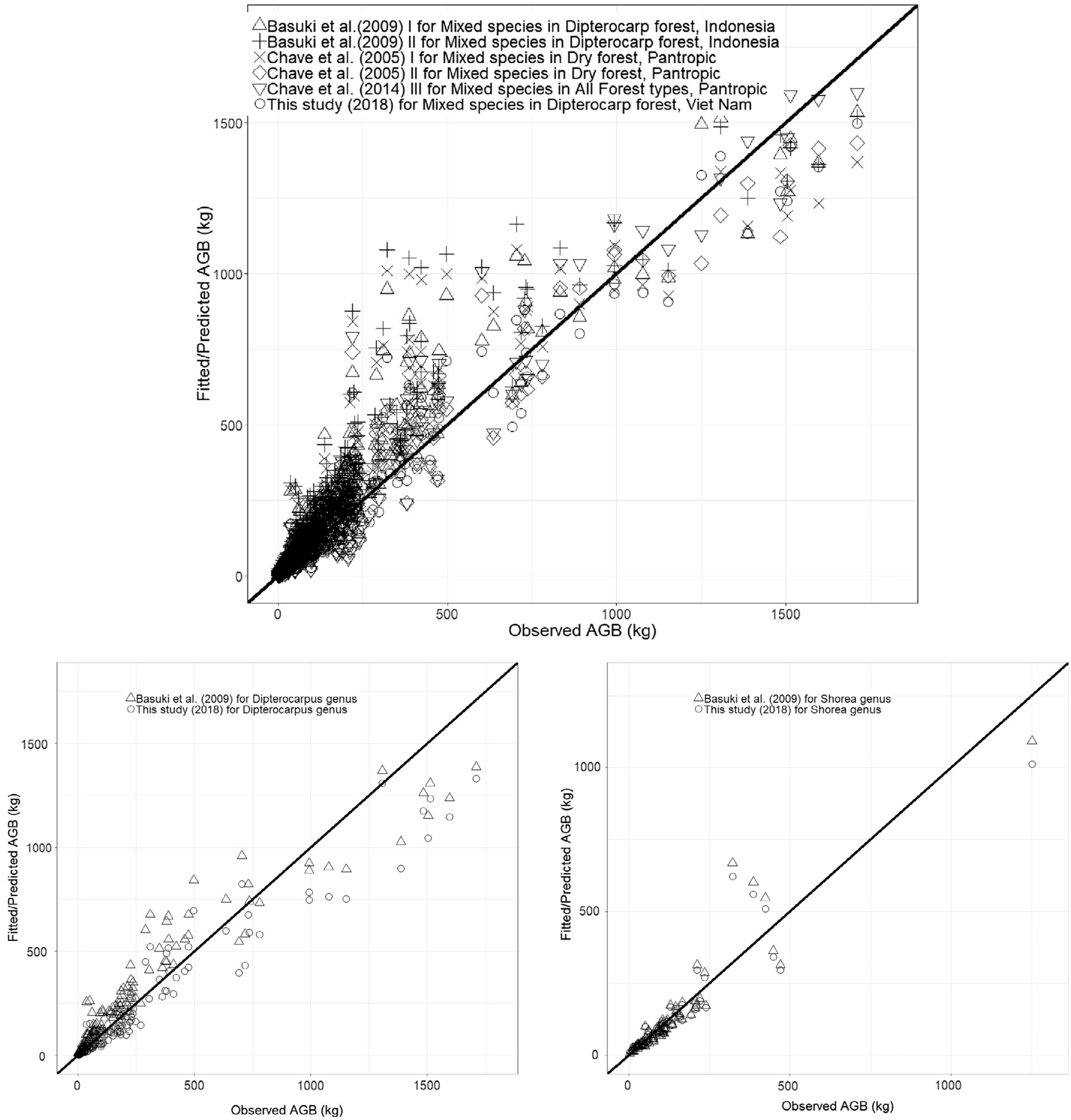


Fig. 10. Plots of Fitted/Predicted *AGB* vs Observed *AGB*: top: Comparison of selected model fit by SUR of this study for the same mixed species with other models in different regions, pantropic in dry dipterocarp forest, all forest types; bottom panel from left to right: Comparisons of selected models of this study with other models developed in Indonesia with the same *Dipterocarpus* and *Shorea* genus, respectively.

Indonesia who used the pantropical model developed by Chave et al. (2005) and found that including tree height provided the best biomass estimates for locally measured samples of *AGB*. However, it is different from the recommendations of Huy et al. (2016b,c) and Basuki et al. (2009) who suggested the site-specific is better than pantropics models.

Meanwhile, site-specific models for mixed species in the DDF developed by Basuki et al. (2009) in Indonesia gave high errors and substantially overestimated *AGB* using our dataset (Table 9; Fig. 10, above). This suggests that site-specific models do not transfer well across ecological regions.

Validations for genus-specific models of both *Dipterocarpus* and *Shorea* published by Basuki et al. (2009) in Indonesia using our dataset showed that those genus-specific models produced FI values and predicted *AGB* values very similar to the genus-specific models developed in this study (Table 9 and Fig. 10, below). This result confirms the finding of Huy et al. (2016b) that genus-specific models can perform well at different site conditions.

Pantropical genus-specific models will improve the reliability compared to pantropical mixed species models (Table 9). Bias, RMSE and MAPE were remarkably reduced using our newly developed genus-specific models, these models achieved −1.6%, 27.6% and 4.5% respectively (Table 9).

5. Conclusion

Developing simultaneous modeling systems using SUR for *AGB* and its components in the DDF produced substantially lower uncertainty than models developed separately. The forms of simultaneous modeling systems for estimating *AGB* and its components were developed and selected at different taxonomic hierarchies and as follows:

For mixed species and dominant Dipterocarpaceae family:

$$AGB = a_1 \times D^{b11} \times H^{b12} \times WD^{b13} + a_2 \times D^{b21} + a_3 \times D^{b31} + a_4 \times D^{b41}.$$

For dominant genera of *Dipterocarpus* and *Shorea*:

$$AGB = a_1 \times D^{b11} + a_2 \times D^{b21} + a_3 \times D^{b31} + a_4 \times D^{b41}$$

In comparison to the mixed species modeling system, genus-specific modeling systems substantially improved the reliability of *AGB* and component predictions. It will also reduce the cost of application because only one variable *D*, is required for measurement; the pantropical genus-specific modeling systems are more reliable than pantropical mixed species models.

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Appendix A. Supplementary material

Supplementary data to this article can be found online at https://doi.org/10.1016/j.foreco.2019.01.038.

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