

Allometric equations for estimating biomass of community forest tree species in Madiun, Indonesia

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Abstract. Wirabuana PYAP, Setiahadi R, Sadono R, Lukito M, Martono DS, Matatula J. 2020. Allometric equations for estimating biomass of community forest tree species in Madiun, Indonesia. *Biodiversitas* 21: 4291-4300. The capability of community forests for offsetting carbon emissions highly depends on their biomass production. Unfortunately, the measurement of tree biomass in community forests using a destructive method is expensive and time-consuming. It is also almost impossible to conduct this method for all trees in the observation area. Therefore, the development of allometric equations is essential to support tree biomass estimation in community forests. This study was designed to construct specific models for predicting individual tree biomass in community forests, located in Madiun, Indonesia. We destructively sampled approximately 120 trees from four different species (30 trees for each species), i.e., *Falcattaria moluccana*, *Melia azedarach*, *Swietenia macrophylla*, and *Tectona grandis*. For every tree sample, the measurement of biomass was conducted in each tree's component, namely roots, stem, branches, and leaves. The allometric equations were developed with regression analysis using predictor variables, like diameter at breast height (D), squared diameter at breast height combined with tree height (D²H), as well as D and H separately. Results found that for four species, the mean biomass in the stem was 50.3%, followed by branches 25.4%, roots 15.9%, and leaves 8.3%. The best equation for estimating biomass in every component and total of four species was different. However, our study showed that the equation $\ln \hat{Y} = -3.037 + 1.430 \ln D + 1.684$ was reliable to estimate total individual tree biomass of four species in the surveyed area since this model had accuracy of 90.8%. Referring to these findings, we recommended the utilization of an allometric equation as an alternative method for facilitating more efficient biomass measurement in the community forests.

Keywords: Best model, biomass distribution, carbon emissions, destructive sampling, reliable

INTRODUCTION

The community forests make a meaningful contribution to the reduction of carbon emissions in the atmosphere at global and regional scales. However, the capacity of community forests as carbon sequestrators principally depends on their biomass production (Setiahadi 2017). As one of the important attributes in community forests, biomass accumulation plays a fundamental role in biogeochemical cycles, especially carbon cycle (Chen et al. 2017). Higher biomass production indicates greater carbon storage, since approximately 50% of biomass is composed of carbon (Latifah et al. 2018; Viera and Rodríguez-Soalleiro 2019; Wirabuana et al. 2020). Therefore, the scenario of sustainable management in community forests becomes one of the primary focuses related to climate change mitigation.

In the context of global climate change, the quantification of biomass production in community forests is necessary as an indicator to assess carbon storage and forest productivity (Zhang et al. 2017). Unfortunately, the direct measurement of tree biomass in community forests using a destructive method is expensive and time-consuming. It is also almost impossible to conduct this

approach for all trees in the study area. Thus, the development of allometric equations for predicting tree biomass is required to facilitate a more efficient biomass estimation in community forests (Altanzagas et al. 2019). Several studies also confirm that the use of allometric equations is helpful to conduct the estimation of tree biomass rapidly (Nogueira Junior et al. 2014; Nam et al. 2016; Daba et al. 2019). This method also has a potential contribution to predict the biomass change from different observation periods (Kebede and Soromessa 2018).

The construction of allometric models for computing tree biomass in community forests is substantially more difficult than plantation forests. Besides having various species, the community forests also have a high variation in tree growth rates and age distribution (Baral et al. 2018). Therefore, the prediction model in community forests should be reliable to estimate the individual tree biomass from various species. This reliability is important because the accurate biomass estimation in forest levels is principally affected by the high precision of biomass measurement in tree levels. Thus, the allometric models which have good accuracy are highly required for facilitating biomass assessment. Several studies have evidenced the reliability of allometric models for

estimating biomass from different types of forest. A study conducted in Northeastern China reported that the accuracy level of allometric equations for estimating aboveground biomass of various tree components in various species forests ranged from 83.7 to 97.2% (He et al. 2018). Another research undertaken in Papua, recorded that the use of allometric models for predicting total aboveground biomass from 8 genera resulted in the accuracy level of approximately 91% (Maulana et al. 2016). Both literature obviously confirms the capability of allometric equation as a proxy approach to predict biomass accumulation from various species.

This study was designed to develop allometric models for estimating the individual tree biomass in community forests, located in Madiun. It was required to facilitate the rapid assessment of biomass accumulation to encourage the effort of climate change mitigation. Before this study was conducted, no specific equations had been constructed to calculate the individual tree biomass from various species in this area. The specific objectives of our study were: (i) To quantify individual tree biomass in each component and total from various species in community forest; (ii) To assess the relative contribution of each tree component to total individual tree biomass from various species in community forests; (iii) To construct specific allometric models for estimating individual tree biomass in each component and total from various species; (iv) To discover the best allometric equation which is generally reliable to

estimate total individual tree biomass for all species in community forests.

MATERIALS AND METHODS

Study area

The study area is situated in community forests around Madiun District, East Java Province, Indonesia covering four villages, namely Kuwiran, Morang, Randualas, and Kare. The study site has a geographic position of $7^{\circ}41'1.42''$ to $7^{\circ}45'31.14''$ S and $111^{\circ}39'19.27''$ to $111^{\circ}42'17.30''$ E. Topography is relatively flat, having slope level approximately 0-8%. Altitude varies from 100 to 500 m. The mean daily temperature is 29°C with average minimum of 25°C and maximum of 35°C . Annual rainfall ranges from 1,554 mm to 1,754 mm.year⁻¹. The majority of rainfall occurs in December and January. Dry period lasts around 5 months from June to October. The air humidity of study area varies from 70.5% to 85.6%. Soil types are dominated by alfisols which have high clay content, around 39-42%. The level of cation exchange capacity is relatively moderate, ranging from 14 to 28%. Soil acidity is classified as slightly acid, with a pH of 5.5-6.0 due to the high content of soil organic matter which ranges from 17% to 23% (Setiahadi 2017).

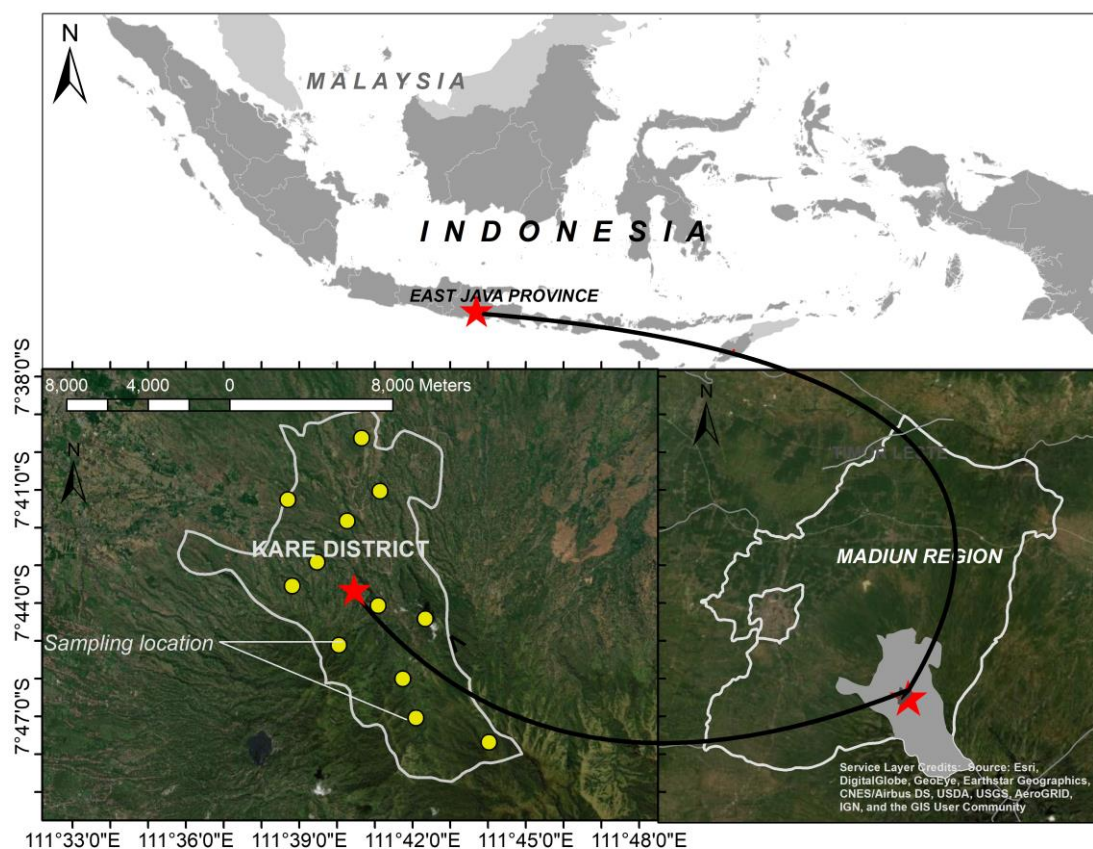


Figure 1. Distribution of sampling locations for measuring tree biomass in each component and total from various species in community forests, Madiun, East Java, Indonesia

Data collection

We destructively sampled 120 trees consisting of four different species, i.e. *Falcataria moluccana*, *Melia azedarach*, *Swietenia macrophylla*, and *Tectona grandis*. Those were the species of trees mostly planted by societies in community forests around Madiun District because of their prospective economic values (Setiahadi 2017). Total sample trees for each species were 30 (Table 1). The sample trees were selected by considering the diameter distribution to obtain the balance growth dimension from small trees to the big ones (Guendehou et al. 2012). We classified trees' diameter into four different classes (Table 2), i.e. smaller than 10 cm, 10-20 cm, 21-30 cm, and bigger than 30 cm (Altanzagas et al. 2019).

The process of destructive sampling was implemented step by step in a chronological manner. After the selected

trees were felled, the tree components were separated into stem, branches, and leaves. Moreover, the root excavation was also done to record biomass distribution in roots. However, this study was only able to measure the smallest size of root diameter until 5 cm. The fresh weight of every component was measured using a hanging balance in the field. Then, 500 g sub-sample from each part was taken to the laboratory to be dried (Wirabuana et al. 2019). The drying process was done using an oven at 70°C for 48 hours before weighting for biomass determination (Hakamada et al. 2017). Total biomass in each component of sample trees was computed by multiplying the ratio of dry-fresh weight from sub-sample with the total fresh weight of each component which was recorded from the field survey (Hakamada et al. 2017; Altanzagas et al. 2019; Wirabuana et al. 2019).



Figure 2. Documentation of data collection process: A. Stand condition in the observation area; B. Designing measurement plot in the field; C. Labeling name tag in each sampling plot; D. Destructive sampling for selected tree; E. Excavating root component

Table 1. Total sample trees of each species taken from different locations of community forests in Madiun District

Site	Number of samples in each species			
	<i>Falcataria moluccana</i>	<i>Melia azedarach</i>	<i>Swietenia macrophylla</i>	<i>Tectona grandis</i>
Kuwiran	7	6	6	9
Morang	8	8	7	7
Randualas	7	6	8	7
Kare	8	10	9	7
Total	30	30	30	30

Table 2. Number of sample trees in each diameter class from four different species in the study area

Species	Number of sample trees in each diameter class			
	<10 cm	10-20 cm	21-30 cm	>30 cm
<i>F. moluccana</i>	5	13	9	3
<i>M. azedarach</i>	3	6	10	11
<i>S. macrophylla</i>	3	11	10	6
<i>T. grandis</i>	5	13	8	4
Total	16	43	37	24

Data analysis

The process of data analysis was conducted with R software version 3.6.1. with a significant level of 5% using *easyreg* package (Arnhold 2018). Descriptive test was conducted to identify some data attributes, i.e., minimum, maximum, mean, and standard deviation. Normality of data was assessed using Shapiro-Wilk test. Homogeneity of variance among the relative contribution of every tree component to total biomass was examined with Bartlett's test. Comparison average of biomass in each component was evaluated with ANOVA and followed with HSD Tukey. Then, three general allometric equations were examined for estimating biomass allocation in each component and total of trees by using some different predictor variables, i.e., diameter at breast height (D), squared diameter at breast height (D²) combined by tree height (H), as well as D and H separately (Battulga et al. 2013; Dong et al. 2015; Xue et al. 2016). The measurement unit of D and H for each variable was in cm and m. Those allometric equations are expressed below:

$$\hat{Y} = aD^b \quad (1)$$

$$\hat{Y} = a(D^2H)^b \quad (2)$$

$$\hat{Y} = aD^bH^c \quad (3)$$

Where: \hat{Y} is the estimated biomass value in kg unit and a, b, and c are the fitted parameters.

In general, nonlinear models for biomass studies based on arithmetical units do not have constant value of the error variances overall observations in most cases (Zeng and Tang 2012). It is commonly called heteroscedasticity. Thereby, to eliminate the effect of heteroscedasticity, the use of data transformation in natural log-form is frequently conducted to change the nonlinear model into a linear regression when calculating the parameters for equations

(He et al. 2018). Therefore, those above equations are converted into the following models:

$$\ln \hat{Y} = \ln a + b \times \ln D \quad (4)$$

$$\ln \hat{Y} = \ln a + b \times \ln (D^2H) \quad (5)$$

$$\ln \hat{Y} = \ln a + b \times \ln D + c \times \ln H \quad (6)$$

Where: $\ln \hat{Y}$ is the predicted biomass value in the logarithmic unit and $\ln a$, b, and c are the fitted parameters

Many studies have adopted a similar method (log-transformed linear regression) for modeling tree biomass (Xue et al. 2016; He et al. 2018; Altanzagas et al. 2019). The allometric models were calculated separately for roots, stem, branches, leaves, and total. The best model was determined by assessing statistical indicators, i.e., coefficient of determination (R²), root means square error (RMSE), mean absolute bias (MAB), and Akaike information criteria (AIC). Highest R² value, smallest RMSE, MAB, and AIC values indicate the best prediction model. The details formula for calculating those statistical indicators are presented below:

$$R^2 = 1 - (\sum (\ln Y - \ln \bar{y})^2 / \sum (\ln Y - \ln \hat{Y})^2) \quad (7)$$

$$RMSE = (\sum (\ln Y - \ln \hat{Y})^2 / (n-p-1))^{0.5} \quad (8)$$

$$MAB = \sum (|\ln Y - \ln \hat{Y}|) / n \quad (9)$$

$$AIC = n \log (RSS/n) + 2k + ((2k(k+1)) / (n-k-1)) \quad (10)$$

where $\ln Y$ is the actual log-transformed biomass, $\ln \hat{Y}$ is the estimated log-transformed biomass from the fitted model, n is the sample size, $\ln \bar{y}$ is the mean of the actual log-transformed biomass, p is the number of terms in the model, RSS is the residual sum of squares from the fitted model, and k is the number of parameters.

Because of our small sample size, the validation process was conducted by comparing the best allometric model with other equations from the previous studies. In addition, our study also proposed an additional criterion to select the best model, namely simplicity. This criterion is really important since it would facilitate more efficient forest inventory in community forests particularly related to biomass monitoring. According to a study reported by Setiahadhi (2017), the species composition of community forests in Madiun consisted of many tree species which had irregular age distribution pattern. Therefore, it would be better to discover a single equation which is applicable over various species.

RESULTS AND DISCUSSION

Biomass accumulation in four species of community forests

Summarized results of the observation documented that the highest average total biomass was recorded in *M. azedarach* (371.72 ± 236.05 kg), followed by *T. grandis* (283.41 ± 261.06 kg), *S. macrophylla* (214.16 ± 235.93 kg), and *F. moluccana* (71.52 ± 65.30 kg) (Table 3). Furthermore, the greatest mean biomass was discovered in

the stem (50.31%), followed by branches (25.40%), roots (15.96%), and leaves (8.33%) when the four species were combined (Table 4). These results indicated that more than 80% of tree biomass in the study area were accumulated aboveground. Our study also noted the mean ratio between aboveground and belowground tree biomass in the study site reached 5:1 wherein the quantity of aboveground biomass was considerably higher than that belowground. It was also consistently similar to other studies conducted in different forest regions (Mendoza-Ponce and Galicia 2010; Ekoungoulou et al. 2015; Nam et al. 2016).

The allocation of total tree biomass into the tree components from four species along diameter classes is demonstrated in Figure 3. The biggest biomass proportion was found in the stem for every species, i.e., approximately 43–57%, but the pattern was not similar for each tree species. In *M. azedarach*, the contribution of stem biomass to the total tree biomass slightly decreased from 54% for the smallest-diameter class (<10 cm) to 48% for the largest one (>30 cm) due to extensively greater contribution of branch biomass to the total tree biomass with the increasing diameter classes. The same trend was also noted in *T. grandis*; however, the decline of stem biomass percentage was higher than in *M. azedarach* by approximately 11%. In contrast, the relative contribution of stem biomass to the total individual tree biomass increased by approximately 13% in *F. moluccana* and *S. macrophylla* from the lowest-diameter class to the highest one. Overall, the relative contribution of branches' biomass to total tree biomass increased for the four species with increasing diameter

classes. Consequently, the relative contribution of root and leaf biomass from various species declined with the increasing diameter classes. These results indicate that the biomass in each tree component is different for each species (Mate et al. 2014; Zhang et al. 2015; Yue et al. 2018). This process is also affected by specific factors such as site quality and silviculture treatment (Rodríguez-Soalleiro et al. 2018). For example, the application of pruning can reduce the relative contribution of branches biomass to the total biomass (Velázquez-Martí et al. 2011).

Our study obviously observed that the dimension size of tree diameter had a relationship to the biomass allocation. Moreover, the percentage of leaf biomass also declined rapidly with the increasing tree diameter, which indicated that relatively more biomass was distributed to the trunk for improving growth and accelerating translocation process. It was consistent with the result of previous studies (Zeng and Tang 2012; Dong et al. 2018; He et al. 2018). Additionally, this study found the proportion of root biomass decreased gradually with the increasing tree diameter in various species. It was caused by natural pruning in root component. Principally, the primary function of root system is to absorb water and nutrient. When the root becomes older, it regenerates naturally to guarantee the continuity of water and nutrient absorption (Jing et al. 2018). This outcome was similar to the previous studies which were implemented in different forest locations (Mendoza-Ponce and Galicia 2010; Maulana et al. 2016; Purwanto et al. 2015; Nam et al. 2016; Altanzagas et al. 2019).

Table 3. Minimum (min), maximum (max), average (mean), and standard deviation (sd) of biomass in each component and total from four tree species at the sampling location

Species	Value	D (cm)	H (cm)	Roots (kg)	Stem (kg)	Branches (kg)	Leaves (kg)	Total (kg)
<i>F. moluccana</i>	min	5.4	4.6	0.69	1.67	0.56	0.39	3.31
	max	40.1	11.1	45.07	149.27	47.74	22.84	264.92
	mean	19.7	7.3	13.47	37.45	13.74	6.85	71.52
	sd	8.9	1.6	11.19	36.95	11.66	5.76	65.30
<i>M. azedarach</i>	min	6.4	6.3	2.02	11.13	5.29	2.27	20.71
	max	42.3	16.8	103.26	405.22	288.64	52.19	849.31
	mean	26.3	10.7	43.86	180.39	121.73	25.75	371.72
	sd	10.1	2.8	29.23	111.60	80.40	16.11	236.05
<i>S. macrophylla</i>	min	8.9	4.8	2.67	12.33	5.40	0.92	22.48
	max	40.4	13.0	171.58	392.08	272.46	23.23	859.34
	mean	19.8	8.2	39.35	101.81	65.81	7.18	214.16
	sd	9.6	2.2	46.55	108.38	75.17	6.39	235.93
<i>T. grandis</i>	min	8.9	4.8	5.05	9.52	5.18	3.00	23.28
	max	41.4	15.6	101.39	487.04	191.78	87.17	867.38
	mean	23.4	9.0	37.44	153.24	62.40	30.34	283.41
	sd	10.0	3.4	30.13	145.75	59.04	26.71	261.06
Total species	min	5.41	4.60	0.69	1.67	0.56	0.39	3.31
	max	42.32	16.80	171.58	487.04	288.64	87.17	867.38
	mean	22.30	8.81	33.53	118.22	65.92	17.53	235.20
	sd	9.93	2.83	33.60	120.01	72.87	19.22	238.62

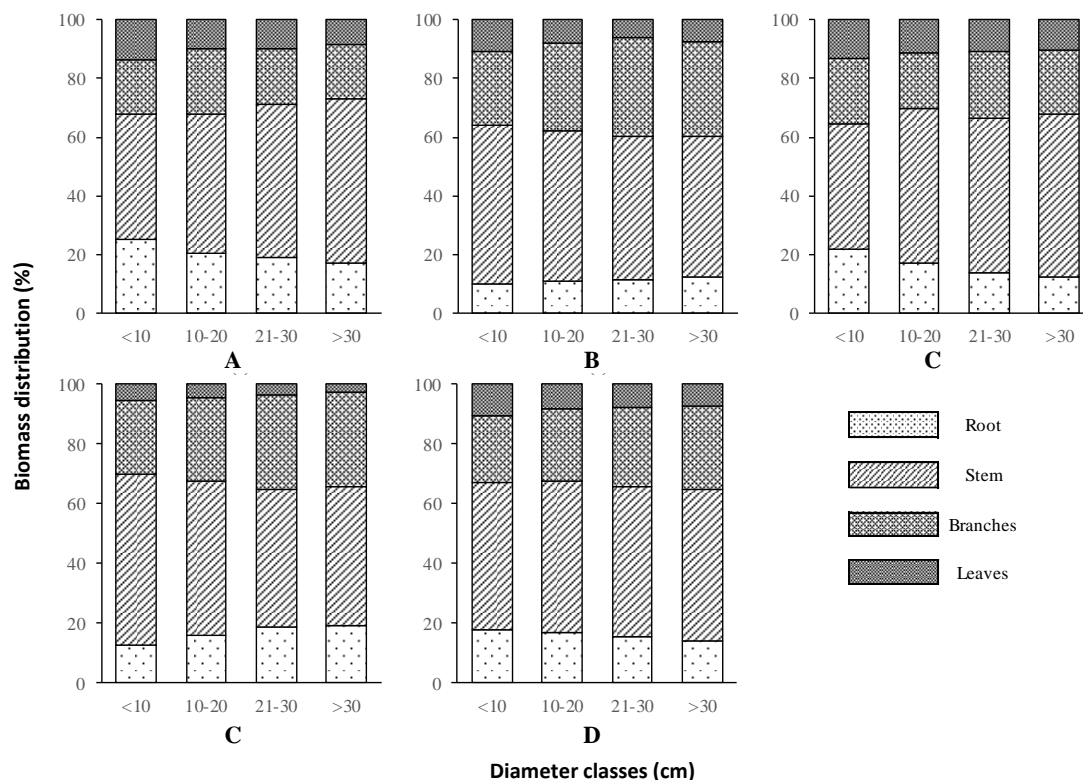


Figure 3. Biomass allocation in tree components across the diameter classes. A. *F. moluccana*, B. *M. azedarach*, C. *S. macrophylla*, D. *T. grandis*, E. Various species. Data are presented in the percentage unit

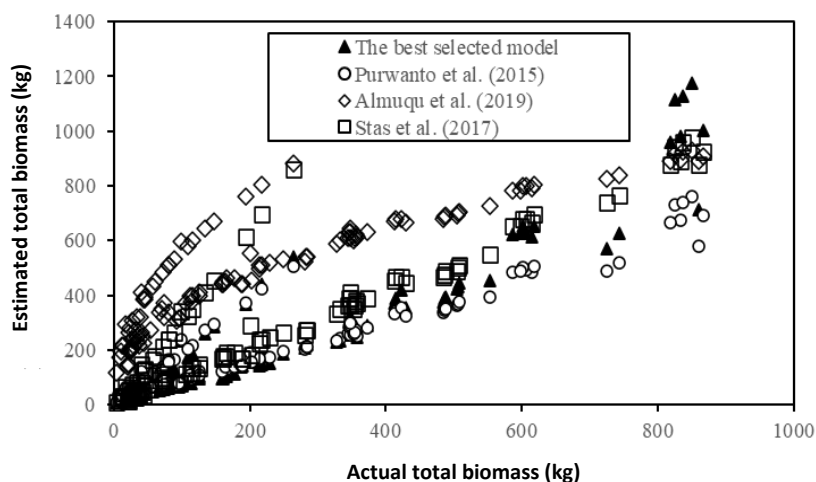


Figure 4. Comparison among the predicted total biomass from the best-selected models for various species and the estimated total biomass using other equations from previous studies

Table 4. Ratio of the biomass of roots, stem, branches, and leaves to the total biomass from sample trees. Data are presented in average (mean) and standard deviation (sd)

Species	RB/TB		SB/TB		BB/TB		LB/TB	
	mean	sd	Mean	Sd	mean	sd	mean	sd
<i>F. moluccana</i>	20.40a	3.17	49.07b	5.12	20.16a	5.16	10.38c	2.23
<i>M. azedarach</i>	11.42a	0.81	49.56b	1.92	31.56c	2.94	7.47d	1.80
<i>S. macrophylla</i>	15.56a	3.24	52.15b	4.58	21.12c	2.73	11.18d	0.95
<i>T. grandis</i>	16.46a	3.14	50.45b	6.69	28.79c	4.47	4.30d	1.67
Total Species	15.96a	4.22	50.31b	4.97	25.40c	6.27	8.33d	3.20

Note: root biomass (RB); stem biomass (SB); branch biomass (BB); leaf biomass (LB); total biomass (TB). The similar letter in row indicated the mean value was not significantly different

Table 5. Summary evaluation statistics of each allometric model for estimating the biomass of roots, stem, branches, and leaves for the four species in the community forests around Madiun District, East Java, Indonesia

Component	Equations*	Lna	b	c	R ²	RMSE	MAB	AIC
<i>F. moluccana</i>								
Root	$\ln \hat{Y} = \ln a + b \ln D$	-3.325	1.933	-	0.982	0.129	0.064	-4.101
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	3.422	0.798	-	0.974	0.156	0.110	-3.651
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-3.182	2.005	-0.177	0.982	0.130	0.069	-4.051
Stem	$\ln \hat{Y} = \ln a + b \ln D$	-3.451	2.284	-	0.991	0.107	0.063	-4.472
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	4.521	0.944	-	0.985	0.139	0.104	-3.875
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-3.426	2.296	-0.031	0.991	0.109	0.063	-4.406
Branches	$\ln \hat{Y} = \ln a + b \ln D$	-3.664	2.041	-	0.907	0.324	0.169	-2.258
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	3.464	0.845	-	0.903	0.330	0.201	-2.152
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-3.764	1.991	0.124	0.907	0.329	0.168	-2.192
Leaves	$\ln \hat{Y} = \ln a + b \ln D$	-4.015	1.934	-	0.974	0.155	0.090	-3.728
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	2.734	0.798	-	0.965	0.182	0.136	-3.339
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-3.787	2.048	-0.282	0.975	0.156	0.086	-3.689
Total	$\ln \hat{Y} = \ln a + b \ln D$	-2.245	2.114	-	0.985	0.127	0.070	-4.133
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	5.135	0.874	-	0.980	0.149	0.108	-3.746
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-2.266	2.103	0.025	0.985	0.129	0.070	-4.066
<i>M. azedarach</i>								
Root	$\ln \hat{Y} = \ln a + b \ln D$	-3.211	2.091	-	0.993	0.096	0.058	-4.690
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	3.863	0.847	-	0.990	0.111	0.091	-4.332
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-3.402	1.992	0.216	0.993	0.096	0.060	-4.669
Stem	$\ln \hat{Y} = \ln a + b \ln D$	-1.178	1.912	-	0.998	0.050	0.035	-5.980
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	5.294	0.775	-	0.994	0.077	0.065	-5.061
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-1.301	1.849	0.139	0.998	0.050	0.035	-5.982
Branches	$\ln \hat{Y} = \ln a + b \ln D$	-2.367	2.145	-	0.999	0.025	0.018	-7.399
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	4.890	0.868	-	0.995	0.085	0.067	-4.877
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-2.375	2.141	0.009	0.999	0.025	0.018	-7.333
Leaves	$\ln \hat{Y} = \ln a + b \ln D$	-2.371	1.682	-	0.920	0.264	0.141	-2.667
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	3.321	0.683	-	0.923	0.260	0.164	-2.628
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-2.813	1.454	0.497	0.923	0.264	0.154	-2.632
Total	$\ln \hat{Y} = \ln a + b \ln D$	-0.698	1.983	-	0.997	0.054	0.037	-5.838
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	6.012	0.803	-	0.994	0.081	0.069	-4.962
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-0.827	1.916	0.145	0.998	0.053	0.037	-5.837
<i>S. macrophylla</i>								
Root	$\ln \hat{Y} = \ln a + b \ln D$	-2.947	2.028	-	0.987	0.109	0.084	-4.435
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	3.958	0.732	-	0.984	0.122	0.097	-4.146
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-2.926	1.942	0.113	0.988	0.111	0.082	-4.377
Stem	$\ln \hat{Y} = \ln a + b \ln D$	-3.395	2.576	-	0.998	0.049	0.035	-6.014
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	5.375	0.928	-	0.992	0.111	0.086	-4.341
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-3.432	2.724	-0.195	0.999	0.047	0.032	-6.080
Branches	$\ln \hat{Y} = \ln a + b \ln D$	-4.160	2.529	-	0.974	0.198	0.113	-3.237
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	4.454	0.915	-	0.975	0.195	0.128	-3.208
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-4.054	2.106	0.557	0.975	0.196	0.119	-3.235
Leaves	$\ln \hat{Y} = \ln a + b \ln D$	-4.185	2.330	-	0.985	0.138	0.090	-3.962
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	3.751	0.842	-	0.983	0.146	0.110	-3.781
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-4.137	2.141	0.249	0.985	0.139	0.092	-3.922
Total	$\ln \hat{Y} = \ln a + b \ln D$	-2.344	2.446	-	0.995	0.081	0.051	-5.019
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	5.986	0.883	-	0.992	0.107	0.088	-4.402
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-2.326	2.373	0.096	0.995	0.082	0.053	-4.964
<i>T. grandis</i>								
Root	$\ln \hat{Y} = \ln a + b \ln D$	-4.728	2.671	-	0.990	0.132	0.062	-4.054
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	4.435	1.071	-	0.978	0.197	0.137	-3.189
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-4.612	2.745	-0.159	0.990	0.133	0.068	-4.008
Stem	$\ln \hat{Y} = \ln a + b \ln D$	-2.320	2.226	-	0.965	0.211	0.119	-3.116
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	5.328	0.901	-	0.973	0.185	0.115	-3.307
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-2.938	1.830	0.847	0.973	0.189	0.068	-4.008
Branches	$\ln \hat{Y} = \ln a + b \ln D$	-3.833	2.556	-	0.987	0.145	0.076	-3.865
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	4.933	1.023	-	0.971	0.216	0.143	-3.000
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-3.566	2.727	-0.365	0.988	0.141	0.079	-3.892
Leaves	$\ln \hat{Y} = \ln a + b \ln D$	-3.893	1.900	-	0.916	0.285	0.145	-2.513
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	2.621	0.759	-	0.900	0.311	0.179	-2.270
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-3.642	2.060	-0.343	0.918	0.287	0.152	-2.467
Total	$\ln \hat{Y} = \ln a + b \ln D$	-2.039	2.369	-	0.989	0.124	0.068	-4.170
	$\ln \hat{Y} = \ln a + b \ln(D^2 H)$	6.094	0.954	-	0.985	0.144	0.098	-3.807
	$\ln \hat{Y} = \ln a + b \ln D + c \ln H$	-2.244	2.238	0.282	0.990	0.122	0.067	-4.179

Total								
Root	$\ln\hat{Y} = \ln a + b \ln D$	-3.704	2.226	-	0.919	0.333	0.263	-2.199
	$\ln\hat{Y} = \ln a + b \ln(D^2 H)$	-4.108	0.871	-	0.922	0.326	0.266	-2.223
Stem	$\ln\hat{Y} = \ln a + b \ln D + c \ln H$	-3.983	1.920	0.562	0.923	0.325	0.260	-2.241
	$\ln\hat{Y} = \ln a + b \ln D$	-2.946	2.367	-	0.864	0.472	0.384	-1.502
	$\ln\hat{Y} = \ln a + b \ln(D^2 H)$	-3.493	0.940	-	0.895	0.416	0.348	-1.738
Branches	$\ln\hat{Y} = \ln a + b \ln D + c \ln H$	-3.842	1.384	1.803	0.904	0.399	0.333	-1.829
	$\ln\hat{Y} = \ln a + b \ln D$	-3.984	2.476	-	0.796	0.631	0.503	-0.922
	$\ln\hat{Y} = \ln a + b \ln(D^2 H)$	-4.599	0.989	-	0.833	0.571	0.460	-1.105
Leaves	$\ln\hat{Y} = \ln a + b \ln D + c \ln H$	-5.142	1.205	2.331	0.852	0.540	0.451	-1.223
	$\ln\hat{Y} = \ln a + b \ln D$	-4.191	2.152	-	0.812	0.522	0.479	-1.302
	$\ln\hat{Y} = \ln a + b \ln(D^2 H)$	3.181	0.849	-	0.828	0.498	0.448	-1.376
Total	$\ln\hat{Y} = \ln a + b \ln D + c \ln H$	-4.751	1.539	1.126	0.829	0.499	0.442	-1.383
	$\ln\hat{Y} = \ln a + b \ln D$	-2.200	2.348	-	0.873	0.451	0.367	-1.593
	$\ln\hat{Y} = \ln a + b \ln(D^2 H)$	5.850	0.932	-	0.901	0.398	0.326	-1.827
$\ln\hat{Y} = \ln a + b \ln D + c \ln H$		-3.037	1.430	1.684	0.908	0.385	0.322	-1.902

Note: *indicated that the p -value for all models was <0.001 ; $\ln a$, b , and c were the fitted parameters; R^2 was the coefficient of determination; $RMSE$ was root mean square error; MAB was mean absolute bias; AIC was Akaike information criterion; the best models for biomass prediction were printed in bold

Allometric models for estimating biomass

The results obviously showed that every allometric model had good fits ($p < 0.001$) (Table 5). However, the most accurate allometric equations for estimating biomass were different in each tree species. These findings were similar to the previous studies conducted in other forest sites (Maulana et al. 2016; Purwanto et al. 2015; Stas et al. 2017; Almuqu et al. 2019; Altanzagas et al. 2019). For example, the equation $\ln\hat{Y} = \ln a + b \times \ln D$ was the best model for predicting biomass in each component and the total tree from *F. moluccana*. But, the model showed lower precision for estimating stem biomass in *M. azedarach*, *T. grandis*, and *S. macrophylla*. On the other hand, the equation $\ln\hat{Y} = \ln a + b \times \ln D + c \times \ln H$ was the most suitable to predict the biomass in branches, stem, and the total tree of *T. grandis*, but it generated smaller accuracy when it was used to estimate the root and leaf biomass (Table 5). Interestingly, the mean R^2 values for all of the best models were more than 80%. These findings documented that the best-selected models could explain more than 80% of the variation in the majority of the component and the total tree biomass. Those values were high enough since the stand attributes of community forests in the study area had great variation, particularly in the species composition and growth distribution.

The results of validation process showed there were similar patterns of estimated biomass values using our best models with other equations from the previous studies (Purwanto et al. 2015; Stas et al. 2017; Almuqu et al. 2019) (Figure 4). It indicated that our best-selected equations were reliable and could be utilized in the monitoring of forest biomass at community forests, mainly in the study area. Nevertheless, the value of estimated total biomass from our model was relatively lower than allometric equation recommended by Almuqu et al. (2019). In contrast, it provided higher estimation than model from Purwanto et al. (2015). It occurs because the accuracy of allometric equations for estimating tree biomass are also determined by certain factors, such as type of forest ecosystems, stand condition, management practice, and number of samples for direct measurement (destructive

method) (Maulana et al. 2016; Nam et al. 2016; Altanzagas et al. 2019). This study discovered the utilization of equation $\ln\hat{Y} = -3.037 + 1.430 \ln D + 1.684 \ln H$ was principally good enough to facilitate the rapid assessment of the total tree biomass from various species in the study area since it provided an accuracy around 90.8% (Table 5).

Similar to the previous studies, our allometric equation with one predictor variable, $\ln\hat{Y} = \ln a + b \times \ln D$, showed reasonably accurate biomass estimation for various species (Guendehou et al. 2012; He et al. 2018; Altanzagas et al. 2019), but the addition of tree height as independent variable in the equation resulted in more accurate biomass prediction (Li and Zhao 2013; Dong et al. 2015; Chen et al. 2017). The equation $\ln\hat{Y} = \ln a + b \times \ln D + c \times \ln H$ was the most suitable to estimate biomass for various species. Besides providing high accuracy, this model was reliable to predict biomass from different tree species. It was also consistent with the previous studies which focused on the development of allometric models for mixed forest (Hosoda and Iehara 2010; Battulga et al. 2013; Altanzagas et al. 2019). Nevertheless, the biomass models resulted in this study had certain regional limitations since the equations were constructed based on the growth performance of stand in the study area. Therefore, the model requires further verification to be used in other areas.

In conclusion, this study clearly demonstrated that the biomass in each of four tree species of community forests in Madiun greatly varied in which the majority of biomass was accumulated in the stem. The best allometric equations for estimating individual tree biomass was different for each tree species. However, to facilitate the rapid assessment of tree biomass in the context of climate change mitigation, we recommended the use a general model, namely $\ln\hat{Y} = -3.037 + 1.430 \ln D + 1.684 \ln H$. This model was reliable to estimate total individual tree biomass from various species in the study area with high accuracy. By adopting this equation, the forest managers of study site could conduct more efficient forest inventory and derive accurate data related to biomass.

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