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Tree allometric equation development for estimation of forest above-ground biomass in Viet Nam -
Evergreen broadleaf and Bamboo forests in the North Central region

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EXECUTIVE SUMMARY

The main objective of this study is to develop allometric equation for biomass estimation of two forest types in North Central Coastal Vietnam of evergreen broadleaf (EB) forests and bamboo forests (*Dendrocalamus barbatus*). Four representative rectangular sample plots (1.0 ha each) were established for EB forests and one sample plot was established for bamboo forests. The sample trees and bamboo were selected based on the dominant species and number of trees in each diameter class. Destructive method was used to collect the samples and measure the fresh biomass. The number of sample trees in EB forests was 221, with DBH ranging from 5.0 cm to 90.0 cm, of which 201 sample trees were used to develop equations and 20 trees for validation of the developed equations. In bamboo forests, 100 sample bamboo trees was selected for fresh biomass measurement and 51 sample trees for dry biomass analysis and equations development. The control data from 20 independent sample trees were also collected in bamboo forest for validation. Diameter at breast height (DBH), total height (H) and wood density (WD) were used as predictors (independent variables) for dry mass of total above ground biomass (tAGB). For comparison and selection of optimal equations, significance of coefficients, adjusted R-square, Sum of Square Error (SSE), average deviation and Akaike Information Criterion (AIC) were employed.

The results indicate that the most suitable equations are

EB forests (general) $tAGB = b_1*DBH^{b2}WD^{b3}$in case of

EB forests (for plant family and species) $tAGB = b_1*DBH^{b2}*H^{b3}$ by

Bamboo forests $tAGB = b_1*DBH^{b2}$

The average deviation of these equations ranges from 5.75% to 18.05% for EB forests and from 7.41% to 10.55% for bamboo forests. Comparing the developed equations with published equations indicates that, the selected equations from this study are more reliable for biomass estimation.

Keywords: Allometric equation, destructive sampling, above ground biomass, evergreen broadleaf-forest, bamboo forest.

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ABBREVIATION AND ACRONYMS

AGB	Above Ground Biomass
AE(s)	Allometric Equation(s)
AIC	Akaike Information Criterion
BA	Basal Area
BA%	Percentage of basal area
BCEF	Biomass Conversion and Expansion Factor
BEF	Biomass Expansion Factor
BGB	Below Ground Biomass
Bio_{Stem}	Stem biomass
Bio_{Branch}	Branch biomass
Bio_{Leaf}	Foliage biomass
C	Carbon
CO_2	Carbon dioxide
D	Diameter at 1.3m
DBH	Diameter at breast height (at 1.3m in this study)
EB	Evergreen Boardleaf
$\Delta_i(\%)$	Relative error or deviation between observed and predicted values
FAO	Food and Agriculture Organization
H	Total height
IV%	Important Value (%)
n	Sample size
N%	Percentage of number of tree
R^2	Coefficient of determination (*R*-square)
$\bar{R}^2$	Adjusted *R*-square
REDD	Reducing Emission from Deforestation and Forest Degradation
SSE	Sum of Squared Error
tAGB	Total Above Ground Biomass
WD	Wood density

1. INTRODUCTION

This study was implemented from November 2011 to November 2012, by Vietnam Forestry University under the UN-REDD Program in Vietnam, with technical support from FAO.

The study aims to collect field and laboratory measurements and synthesize data through statistical analysis in order to develop allometric equations for estimation of forest biomass for natural forests of EB and bamboo forests in the North Central Coastal region of Vietnam.

The main outputs included in this report include: Forest structure, individual tree biomass and wood density (WD), allometric equation for biomass prediction.

2. MATERIAL AND METHODS

2.1 Study Area

2.1.1 Location and topography

The study area is situated in two provinces (Ha Tinh and Nghe An) of the North Central region in Vietnam; on the eastern trailing edge of the Truong Son, with a large elevation gradient towards the east.

Ha Tinh and Nghe An provinces have the complicated topography fragmented by mountain ranges and river systems and streams. Overall, the terrain tilt in the direction northwest-southeast with more than 80% of the territory area is mountainous areas.

2.1.2 Climate

The North Central region is located in the tropical monsoon area with cold winters and divided into two distinct seasons: summer with hot, humid and rainy and cool winter with less rain. The rainy season is from the May to October with the rainfall accounts for approximately 80% of annual rainfall. The average rainfall is about 1200 – 2000 mm/year. The average temperature is about 23-25^{o}C. The average humidity fluctuates from 80-90%.

2.1.3 Soils

Soils in the study area are mainly formed from shale, sandstone or conglomerate. The physical texture is light to medium. The soil thickness is ranging from 30-100 cm.

2.1.4 Vegetation

The main types of forest in the study area are evergreen boardfeaf (EB) forest, nutural bamboo forest, mixed woody and bamboo forest and plantations. Vegetation in the study area is very diverse and rich with more than 90 families and 500 species of different trees. The main species are *Erythrophleum fordii, Castanopsis chinensis, Vatica odorata, Endospermum sinensis, Gironniera subaequalis, Alangium ridleyi... etc.*

2.2 Sampling strategy

2.2.1 Location and design of the plots

Location of the plots

The study sites were in Ha Tinh and Nghe An provinces of the North Central Coastal region of Vietnam. Four sample plots in total (three in Ha Tinh and one in Nghe An province) were established for EB forests, and the one plot for bamboo (*Dendrocalamus barbatus*) was located in Yen Khe commune, Con Cuong district of Nghe An province. The area is managed by Con Cuong Forestry Company.

The geographical characteristics of these sample plots are shown in the Table 2-1 Characteristics of geographical location of sample plots:

Table 2-1 Characteristics of geographical location of sample plots

#	Plot	Location	Forest Type	Area (ha)	Latitude	Longitude	Elevation (m)
1	HT00	Ha Tinh	EB	1.0	18°05’32.0” N	105°39’59.0” E	200
2	HT01	Ha Tinh	EB	1.0	18°05’29.0” N	105°36’28.7” E	197
3	HT02	Ha Tinh	EB	1.0	18°05’14.3” N	105°36’42.0” E	198
4	NA01	Nghe An	EB	1.0	19°29’22.4” N	105°07’36.1” E	416
5	NA02	Nghe An	Bamboo	1.0	19°00’50.7” N	104°49’41.2” E	215

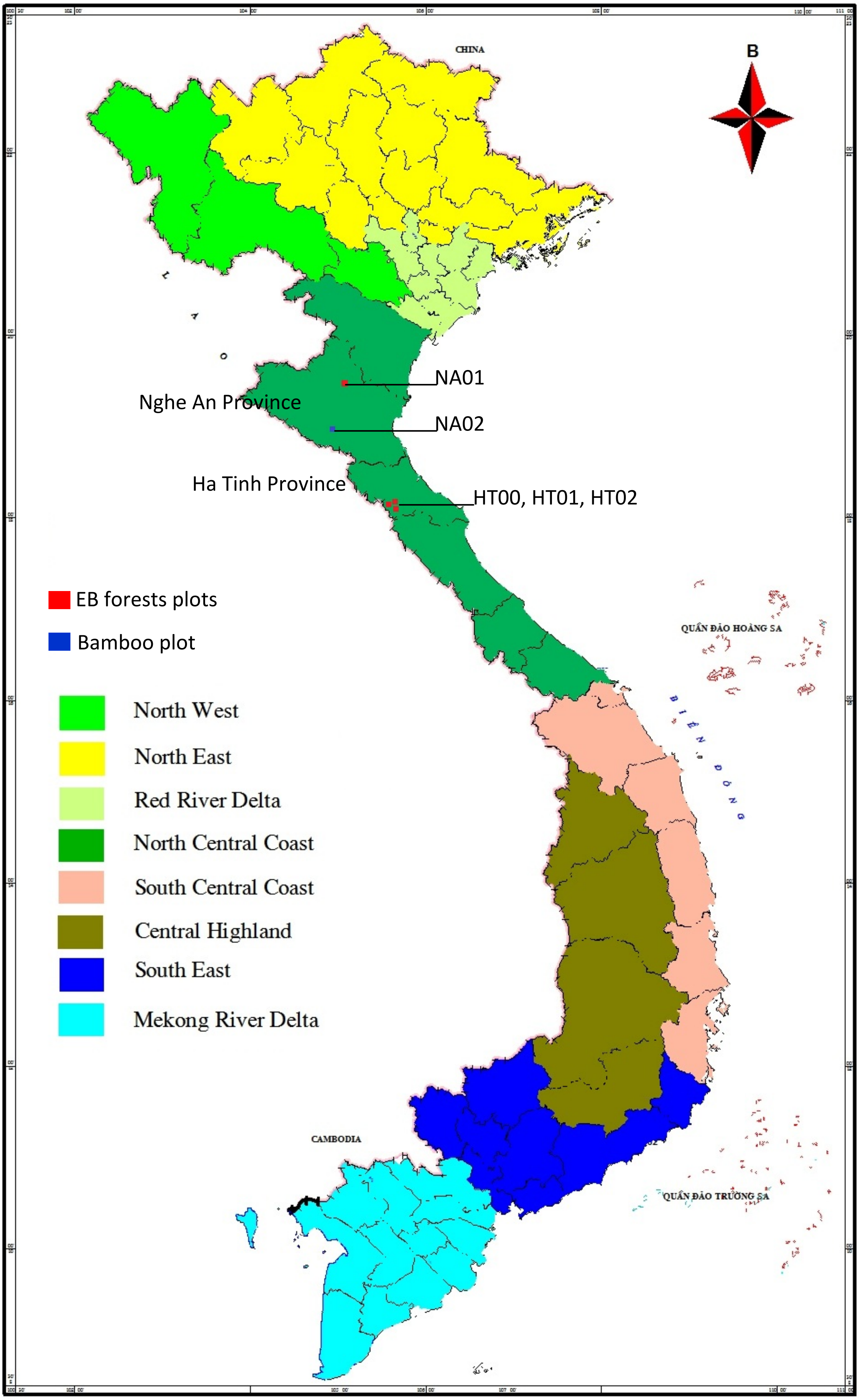

Figure 2.1 Location of sample plots in North Central Coast region

Plot design

For each forest type (EB forests and bamboo forests), sample plots locations were selected and plots established. The location of sample plots was chosen based on the following criteria:

representativeness of the forest type being studied;
representativeness for topographic conditions of the general site location;
representativeness of the number and trees sizes occurring in the general site location; and
even distribution of trees in the plot area, avoiding large gaps.

Each sample plot has area of one ha (100m x 100m). The boundaries of each sample plot were identified in the field and marked the corners by stakes (Figure 2.2). The location of sample plots is recorded using a GPS receiver, at the center point of the plot.

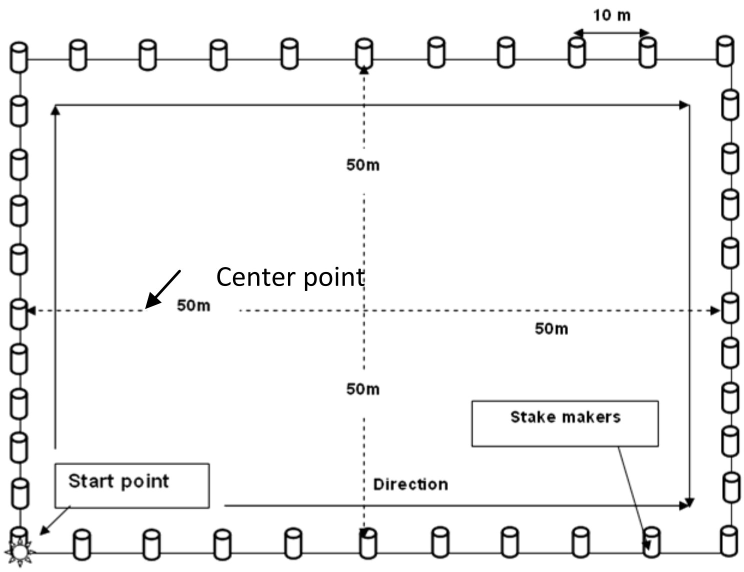

Figure 2.2 One hectare sample plot establishment diagram

2.2.2 Selection of the sampling trees

The selection of the tree is the result of diameter measurement of all the trees within each plot. All the trees in the sample plots are grouped into DBH classes. The interval of DBH classes is 10 cm, and the DBH classes are: 5 – 14.9 cm; 15 – 24.9 cm; 25 – 34.9 cm; 35 – 44.9 cm; 45 – 54.9 cm; 55 – 64.9 cm; 65 – 74.9 cm. Select randomly the sample trees in each DBH class in the sample plots. The total number of sample trees for harvesting is 55 trees for each forest type (50 trees for development of allometric equations and 5 trees for validation). The number of felled sample trees for each DBH class and each family and each species are given in the following tables:

Table 2-2 Number of standing and felled trees divided by DBH classes in EB forest

DBH class (cm)	#of standing trees in the sample plot				# of felled trees for modeling				# of felled trees for validation				Total # of trees cut for modeling	Total #of trees cut for validation
	HT 00	HT 01	HT 02	NA 01	HT 00	HT 01	HT 02	NA 01	HT 00	HT 01	HT 02	NA 01		
5 –15	533	179	173	194	20	10	8	2	1	2	2	2	40	7
15 –25	113	142	136	127	15	13	11	9	1	1	1	1	48	4
25 –35	28	73	102	118	8	7	12	13	1	1	1		40	3

DBH class (cm)	#of standing trees in the sample plot				# of felled trees for modeling				# of felled trees for validation				Total # of trees cut for modeling	Total #of trees cut for validation
	HT 00	HT 01	HT 02	NA 01	HT 00	HT 01	HT 02	NA 01	HT 00	HT 01	HT 02	NA 01		
35 - 45	4	34	53	59	5	6	9	12			1	1	32	2
45 - 55	3	23	23	25	2	6	3	8		1	1		19	2
55 - 65		14	7	12		5	4	5			1		14	1
65 - 75		8	5	2		3	4	1			1		8	1
75 - 85		3	1	2										
85 - 95			1											
Total	**681**	**681**	**501**	**539**	**50**	**50**	**51**	**50**	**3**	**5**	**8**	**4**	**201**	**20**

Table 2-3 Number of felled trees divided by tree family

No	Family	# of felled trees for modeling				# of felled trees for validation				Total # of trees cut for modeling	Total #of trees cut for validation
		HT 00	HT 01	HT 02	NA01	HT 00	HT 01	HT 02	NA01		
1	Alangiaceae		2	6				1		8	1
2	Anacardiaceae	1								1	
3	Annonaceae	2								2	
4	Apocynaceae				1					1	
5	Bignoniaceae			1						1	
6	Burseraceae	2	3							5	
7	Cactaceae				1					1	
8	Caesalpiniaceae	2	1	1	3					7	
9	Clusiaceae		2	4						6	
10	Dipterocarpaceae	4	12	6	2	1	1	1	1	24	4
11	Elaeocarpaceae	1	3	3				1		7	1
12	Euphorbiaceae	3		3	20	1		1	2	26	4
13	Fabaceae	3	1	6	2	1	1			12	2
14	Fagaceae	6	4	4	8					22	
15	Juglandaceae	1	7		1					9	
16	Lauraceae	4	2	4	2		1	1		12	2
17	Magnoliaceae	1		1	1		1	1		3	2
18	Meliaceae	1			2					3	
19	Mimosaceae	7							1	7	1
20	Moraceae	2		1						3	
21	Myristicaceae	1	1	1						3	

No	Family	# of felled trees for modeling				# of felled trees for validation				Total # of trees cut for modeling	Total #of trees cut for validation
		HT 00	HT 01	HT 02	NA01	HT 00	HT 01	HT 02	NA01		
22	Myrtaceae	1			1					2	
23	Proteaceae	1								1	
24	Rosaceae	1	1	1	2					5	
25	Sapindaceae		1	2	1					4	
26	Sapotaceae		2	1						3	
27	Symplocaceae	1	1							2	
28	Theaceae	1	1	1	1			1		4	1
29	Ulmaceae	4	3	2	1					10	
30	unidentified		3	3	1		1	1		7	2
	Total	**50**	**50**	**51**	**50**	**3**	**5**	**8**	**4**	**201**	**20**

Table 2-4 Number of felled trees divided by tree species

No	Species	# of felled trees for modeling				# of felled trees for validation				Total # of trees cut for modeling	Total #of trees cut for validation
		HT 00	HT 01	HT 02	NA 01	HT 00	HT 01	HT 02	NA 01		
1	*Actinodaphne ellipticibacca*		1							1	
2	*Actinodaphne pilosa*			1						1	
3	*Aglaia macrocarpa*				2					2	
4	*Aidia pycnantha*	1								1	
5	*Alangium barbatum*			1						1	
6	*Alangium ridleyi King*		2	5						7	
7	*Aleurites montana*			1						1	
8	*Alstonia scholaris*				1					1	
9	*Andinandra intalgerrima*				1					1	
10	*Antheroporum pierre*			4						4	
11	*Archidendron balansae*	2								2	
12	*Archidendron eberhardtia*		1	2						3	
13	*Artocarpus rigidus*			1						1	
14	*Camellia sp*	1								1	
15	*Canarium tramdenum*	2	3							5	
16	*Castanopsis acuminatissima*				1					1	
17	*Castanopsis cerebrina*				1					1	
18	*Castanopsis chinensis*	2	1	2	2					7	
19	*Castanopsis hystrix*		3	2						5	

No	Species	# of felled trees for modeling				# of felled trees for validation				Total # of trees cut for modeling	Total #of trees cut for validation
		HT 00	HT 01	HT 02	NA 01	HT 00	HT 01	HT 02	NA 01		
20	*Castanopsis pierrei Hance*				4					4	
21	*Castanopsis tesselata*	3								3	
22	*Cinnadenia paniculata*	2								2	
23	*Cinnamomum parthenoxylon*				1					1	
24	*Cryptocarya lenticellata*		1	1						2	
25	*Cryptocarya sp*				1					1	
26	*Dracontomelon duperreanum*	1								1	
27	*Dysoxylum binectariferum*	1								1	
28	*Eberhardtia tonkinensis*		2	1						3	
29	*Elaeocarpus griffithii*	1	3	3						7	
30	*Endiandra hainanensis*			2						2	
31	*Endospermum sinensis*	1		2	18					21	
32	*Engelhardtia roxburghiana*	1	7		1					9	
33	*Erythrophleum fordii*	2		1	2					5	
34	*Ficus sp.*	2								2	
35	*Garcinia oblongifolia*		2	4						6	
36	*Gironniera subaequalis*	4	3	2	1					10	
37	*Goniothalamus macrocalyx*	1								1	
38	*Helicia cochinchinensis*	1								1	
39	*Knema conferta*	1	1	1						3	
40	*Lithocarpus pseudosundaicus*	1								1	
41	*Litsea sp*	2								2	
42	*Mallotus macrostachyus*	1								1	
43	*Manglietia conifera*				1					1	
44	*Manglietia dandyi*	1		1						2	
45	*Nephelium cuspidatum*		1	2						3	
46	*Ormosia balansae*	2			2					4	
47	*Oroxylum indicum (L.)*			1						1	
48	*Peltophorum pterocarpum*		1		1					2	
49	*Pithecolobium acumiratum*	5								5	
50	*Polyalthia sp*	1								1	
51	*Pometia pinnata*				1					1	

No	Species	# of felled trees for modeling				# of felled trees for validation				Total # of trees cut for modeling	Total #of trees cut for validation
		HT 00	HT 01	HT 02	NA 01	HT 00	HT 01	HT 02	NA 01		
52	*Prunus arborea*	1			2					3	
53	*Rubus parvifolius*		1	1						2	
54	*Sapium discolor*				2					2	
55	*Sapium sebiferum*	1								1	
56	*Schima superba*		1	1						2	
57	*Symolocos laurina var.acumilanata*		1							1	
58	*Symolocos sp*	1								1	
59	*Syzygium jambos*	1								1	
60	*Syzygium wightianum*				1					1	
61	*Vatica chevalieri*				1					1	
62	*Vatica odorata*	4	12	6	1					23	
63	*Zygocaeus truncatus*				1					1	
64	*Spp.*		3	3	1					7	
Total		**50**	**50**	**51**	**50**	**3**	**5**	**8**	**4**	**201**	**20**

EB forests

In each sample plot, 55 sample trees were randomly selected for felling (50 trees to develop equations and five trees for validation). These sample trees are selected based on the following criteria:

- An equal number of sample trees for each DBH class (classes established for each 10 cm interval);
- Representative of the species as occurring in the general plot location;
- Avoiding hollow trees, trees with broken crowns or truncated trees.

After felling, measurements were taken including tree height and diameters of logs segmented into two meter lengths from the base of tree. The sample trees were also separated into three components of bole, branches and foliage and then weighed to measure fresh biomass.

Bamboo forests

120 sample bamboo trees were randomly selected for felling (100 trees to develop equations and 20 for validation). These sample trees are selected based on the following criteria:

- An equal number of sample trees for each DBH class (classes established for each 2 cm interval) and for each of the three age classes;
- Avoiding diseased, broken or truncated trees.

After felling, measurements were taken including DBH and total height, and then separated into components of stem, branches and foliage and weighed immediately for measuring fresh biomass of each component.

2.3 Variables measurement and calculation for volume and biomass

2.3.1 Field measurements

The methodology for field data gathering followed the "Guidelines on Destructive Measurement for Forest Biomass Estimation" prepared by UN-REDD Program (UN-REDD 2012).

The following present the main steps involved in biomass measurement and allometric equation development.

EB forests

After sample plots were established, general information on slope, average elevation, soil and coordinate of plot center was recorded. Then, each tree with diameter at breast height (DBH) of 5 cm and above was tallied, and the species name of these trees identified. DBH and tree height were measured (diameter tape was used for DBH and Vertex III was used for tree height measurement).

Sampling for analysis of dry biomass and wood density

Samples were taken from sample trees to analyze dry biomass and wood density (WD). Three samples were taken for each of the three components; different parts of bole and branches were taken to weigh about 0.5-1.0 kg per sample and 0.2-0.5 kg for foliage. WD analysis was done only for boles at four positions: namely, 0 m, ¼, ½, and ¾ of total tree length. At every position, a disc of 5-10 cm in thickness was cut out. In case of the large-sized wood disc (diameter >50 cm), a radial wood disc was taken instead.

All samples were immediately stored in plastic bags. The following information was marked on the samples: sample plot code, sample tree code, component name, and sample position.

Bamboo forests

For bamboo forests, measurements were applied to diameter of bamboo clusters and bamboo trees. The bamboo height was not recorded due to the difficulty of the task, considering the curved shape of bamboo stems. All bamboo trees were classified into three age classes of young, medium and old.

Sampling for analysis of dry biomass and wood density

For bamboo, only dry biomass analysis was undertaken. From 100 sample bamboo trees for fresh biomass measurement, 50 sample trees were randomly selected to analyze dry biomass. In each sample tree for dry biomass analysis, six samples were taken, of which four samples were of stem, one for branches and one for foliage. The four samples of stem were produced by segmenting at one fourth, half, and three fourths of total tree height. The weighing, storing and marking of samples follow the same procedures as in EB forests.

2.3.2 Laboratory measurements

The samples for dry biomass analysis were first weighed for fresh biomass using a chemical scale with accuracy of 0.01 g immediately after arrival at the laboratory. The samples were dried at 105^{o}C until constant weight was reached, then weighed by use of chemical scales.

Analysis of WD was carried out for every wood disc sample following method stated in TCVN 8048-2:2009 (Ministry of Science and Technology, 2009).

The wood discs for WD analysis were firstly measured and calculated the volume (V_{WD}) by using cylinder formula:

$$V_{WD} = \frac{\pi}{4} * \bar{d}_{WD}^2 * \bar{l}_{WD}$$

where, d_{WD} and l_{WD} are the diameter and length of wood disc that measured in eight directions. Then, the samples were dried at 105°C to get the dried mass (M_{WD}). WD, therefore, is calculated as follows:

$$WD = \frac{M_{WD}}{V_{WD}}$$

2.3.3 Other variables

The stem volume of the tree was calculated by applying Smalian formula(West, 2004 #15):

$$v_c = \frac{\pi}{4}\left(\frac{d_0^2 + d_n^2}{2} + d_2^2 + d_4^2 + ... + d_{n-2}^2\right) * 2 + \frac{1}{3} * \frac{\pi}{4} * d_n^2 * l_n$$

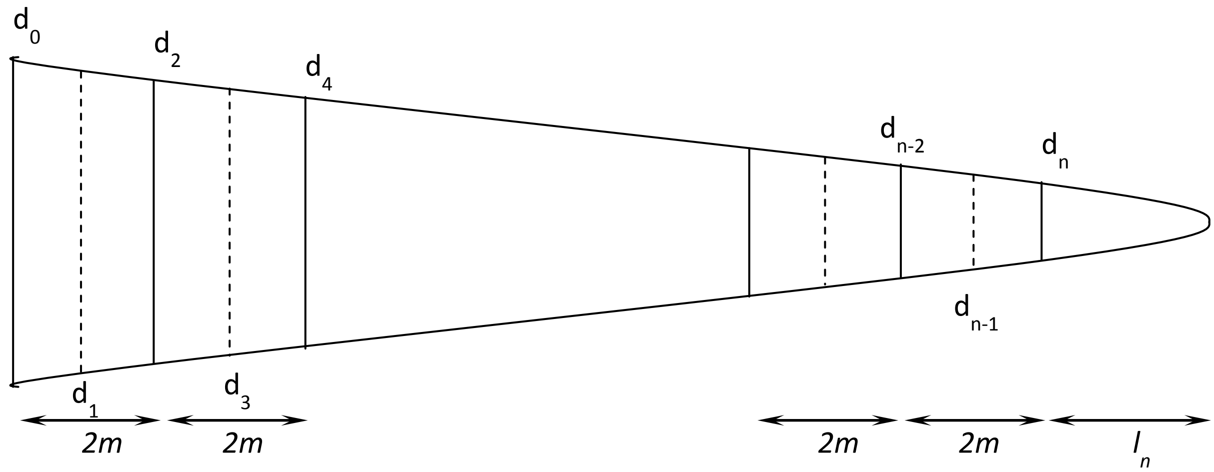

Figure 2.3 Diagram of sample tree measurement of diameter

BCEF is a fairly straightforward way to convert stem volume directly to dry mass of each tree compartment (Schroeder, P.*, et al.* 1997). In its simplest form, the conversion formula can be described as follows:

$$BCEF = \frac{tAGB}{V_{stem}}$$

where, V_{stem} is stem volume. The value of BCEF indicates the mass of tree per unit stem volume and its commonly expressed in Mg m^{-3}.

According to IPCC 2003, BEF is – when used to calculate aboveground biomass of forests – the ratio of aboveground oven-dry biomass of trees to oven-dry biomass of the commercial volume, dimensionless. The biomass of commercial volume can be calculated as commercial volume times wood density or directly measured as the biomass of tree bole. In this study the formula used is (IPCC 2003):

$$BEF = \frac{tAGB}{Bio_{stem}}$$

2.4 Model fitting and selection

All data from field or laboratory measurements were entered into a spreadsheet (using Microsoft Excel)and were analyzed with Statistica 10 (StatSoft, Inc.).

Firstly, descriptive statistics of DBH, height, basal area, tree volume and WD were generated for each sample plot. (For bamboo forests, descriptive statistics of basal area, tree volume and wood density were omitted.) Then, diameter distributions were generated using 10 cm intervals for EB forests and 2 cm intervals for bamboo forests. Following this, correlation of tree height (H) and DBH for each sample plot was developed to estimate H particularly for bamboo and calculations including of volume. In EB forests, tree volume equations were also developed to estimate the growing stock.

The allometric equations for estimation of biomass were developed for both linear and non-linear forms. The dependent variables are tree biomass (*tAGB*), and biomass of bole, branches and foliage. The independent variables are DBH, tree height (H) and/or WD for EB forests; and DBH and/or H for bamboo forests. The equations were developed for the individual sample plots and for the whole North Central Coastal region. Equations were also developed for some main tree species and plant families.

Optimal equation selection was based on the following criteria:

The significance of the regression coefficients;
The highest value of adjusted coefficient of determination ($\bar{R}^2$);
The lowest value of sum of square error (SSE) in nested equations;
The lowest value of Akaike Information Criterion (AIC) in non-nested equations; and
The accuracy of the equation.

$\bar{R}^2$ was calculated as follows (Cohen, J., *et al.* 2003):

$$\bar{R}^2 = 1 - \left(\frac{n-1}{n-p-1}\right)(1 - R^2)$$ Formula (1.1)

*AIC*criteria (Kuiper, R.M., *et al.* 2011):

$$AIC = n \ln\left(\frac{SSE}{n}\right) + 2p$$ Formula (1.2)

where, *p* is the total number of parameters in the equation and *n* is the sample size.

To assess the accuracy of each equation, deviation of the predicted and observed dry weight was calculated as follows (Basuki, T.M., *et al.* 2009):

$$\Delta_i(\%) = \frac{\hat{Y}_i - Y_i}{Y_i} 100$$ Formula (1.3)

where, $\Delta_i(\%)$ is the deviation or relative error of predicted versus observed[1] dry weight, Y_i is the observed dry weight, $\hat{Y}_i$ is the predicted dry weight.

To check the hypothesis of the residuals, the normal probability plots of residuals (a normal quantile-quantile plot), predicted versus residual values plots and predicted versus observed values plots were generated.

Finally, published equations (Brown, S. 1997; Chave, J., *et al.* 2005) were used to compare with the result of this study.

[1] The observed dry weight is derived from the control data (i.e. five sample trees from each of the four sample plots for EB forests and 20 sample trees for bamboo forest).

3. RESULTS FOR EVEGREEN BROADLEAF FORESTS

3.1 Result 1: forest and trees characteristics

3.1.1 Forest characteristics: species composition and forest structure

Species composition

Based on analyzed field data, the number of species and species composition formula were calculated (Table 3-1, and details in Annex A.1).

Table 3-1 Number of species in sample plots and species occurrence formula

Plot ID	Density (tree/ha)	Identified species	Formula of species percentage (%)
HT00	681	91	8.6DeG+8.2PhM+7.0LiX+6.9Tau+5.2Com+5.2CoT+4.4SoP+ 4.0LaN+3.3ChT+3.3TrT+3.0ReN+2.9NgA+2.9RRM+35.1KH
HT01	476	91	12.8Tau+6.1CoS+5.0Nan+5.0TrT+4.8ChT+4.4VaR+4.2DeG+ 3.6Com+3.6Bua+3.2ĐaB+47.3KH
HT02	501	95	9.0Nan+8.2CoS+5.2Tau+4.8TrT+4.4DeG+4.0Nga+3.4TrĐ+ 3.0Com+3.0Bua+3.0BuP+3.0VaR+49.0KH
NA01	539	88	20.0VaT+13.7Tau+5.0Nga+3.5DeG+3.5TrĐ+3.2SoT+ 51.1KH
General		116	9.56Tau+5.51DeG+5.23VaT+3.91CoS+3.73TrT+3.55Nga+ 3.46Com+3.28Nan+2.82LiX+58.94KH

The occurrence of each species is formulated based on IV% (important value), with IV% = (N% + BA%)/2; formulae for all species with IV% ≥ 5% are presented (Table 3-2).

Table 3-2 Species formulae based on IV%

Plot ID	Identified species	Formula of species based on IV%	Total IV% in formula
HT00	91	7.50DeG+6.42PhM+6.34LiX+6.23CoT+5.30Tau	31.97
HT01	91	17.81Tau+6.91Nan+6.66ChT+5.57CoS	36.96
HT02	95	9.11Nan+7.48CoS+5.68Tau+5.41Nga+5.19DeG	32.87
NA01	88	21.48VaT+13.61Tau+6.68Nga	41.77

Note:

Code	Latin Name	Code	Latin Name
Bua	*Garcinia oblongifolia*	Nga	*Gironniera subaequalis*
BuP	*Mallotus macrostachyus*	PhM	*Archidendron chevalierii balansae*
ChT	*Engelhardtia roxburghiana*	ReN	*Machilus leptophylla*
Com	*Elaeocarpus griffithii*	RRM	*Ormosia balansae*
CoS	*Eberhardtia tonkinensis*	SoP	*Castanopsis cerebrina*
CoT	*Calophyllum calaba var.bracteatum*	SoT	*Sapium discolor*

ĐaB	*Archidendron eberhardtia*	Tau	*Vatica odorata*
DeG	*Castanopsis chinensis*	TrĐ	*Canarium tramdenum*
LaN	*Macaranga denticulata*	TrT	*Syzygium wightianum*
LiX	*Erythrophleum fordii*	VaR	*Nephelium cuspidatum*
Nan	*Alangium ridleyi*	VaT	*Endospermum sinensis*
KH	*Others*		

The number of individual trees per hectare of main species and families in study sites were also analyzed (Table 3-3, details in Annex A.2 and A.3).

Table 3-3 Number of individuals per ha of some main families of EB forests

Family	Sum		HT00		HT01		HT02		NA01	
	n	%	n	%	n	%	n	%	n	%
Total identified families	45		33		33		37		35	
Total individual trees (per ha)	-		681		476		501		539	
Dipterocarpaceae	211	9.60	48	7.05	61	12.82	28	5.59	74	13.73
Euphorbiaceae	189	8.60	31	4.55	5	1.05	19	3.79	134	24.86
Fagaceae	188	8.56	91	13.36	27	5.67	25	4.99	45	8.35
Lauraceae	139	6.33	40	5.87	40	8.40	19	3.79	40	7.42
Fabaceae	132	6.01	33	4.85	43	9.03	41	8.18	15	2.78
Sapotaceae	87	3.96	16	2.35	29	6.09	41	8.18	1	0.19
Myrtaceae	86	3.91	26	3.82	25	5.25	24	4.79	11	2.04
Ulmaceae	78	3.55	20	2.94	11	2.31	20	3.99	27	5.01
Unknown	114	5.19	30	4.41	21	4.41	50	9.88	13	2.41

Table 3-4 Number of individuals per ha of some main species in EB forests

Species	Sum		HT00		HT01		HT02		NA01	
	n	%	n	%	n	%	n	%	n	%
Total identified species	116		91		91		95		75	
Total individual trees (per ha)	-		681		476		501		539	
Vaticaspp.	210	9.56	48	7.05	61	12.82	27	5.39	74	13.73
Castanopsis chinensis	121	5.51	60	8.81	20	4.20	22	4.39	19	3.53

Endospermum sinensis	115	5.23	1	0.15	4	0.84	2	0.40	108	20.04
Eberhardtia tonkinensis	86	3.91	16	2.35	29	6.09	41	8.18	-	-
Syzygium wightianum	82	3.73	23	3.38	24	5.04	24	4.79	11	2.04
Gironniera subaequalis	78	3.55	20	2.94	11	2.31	20	3.99	27	5.01
Elaeocarpus griffithii	76	3.46	36	5.29	17	3.57	15	2.99	8	1.48
Alangium ridleyi	72	3.28	-	-	24	5.04	45	8.98	3	0.56
…										
Unknown	84	3.82	17	2.50	15	3.15	39	7.78	13	2.41

Forest structure

The diameter distribution of trees for each sample plot is shown in the following Table 3-5:

Table 3-5 Diameter distribution of trees in sample plots of EB forests

DBH range[2](cm)	The number of trees per hectare				
	DBH_i (cm)	HT00	HT01	HT02	NA01
5.0<=x<15.0	10	533	179	173	194
15.0<=x<25.0	20	113	142	136	127
25.0<=x<35.0	30	28	73	102	118
35.0<=x<45.0	40	4	34	53	59
45.0<=x<55.0	50	3	23	23	25
55.0<=x<65.0	60		14	7	12
65.0<=x<75.0	70		8	5	2
75.0<=x<85.0	80		3	1	2
85.0<=x<95.0	90			1	
Sum	-	681	476	501	539

[2] The maximum DBH is 51.0 cm; 77.0 cm; 90.0 cm and 76.7 cm in HT00, HT01, HT02 and NA01 respectively

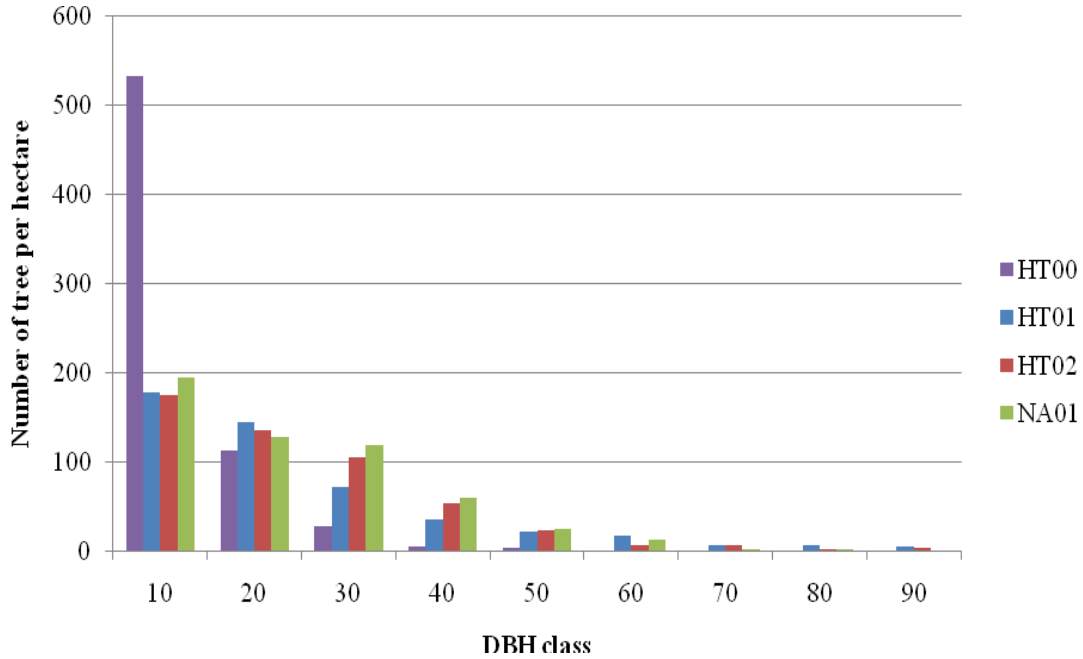

Figure 3.1 The diameter distribution of sample plots

The basal area distribution of trees for each sample plot is shown in the following table:

Table 3-6 Diameter distribution of trees in sample plots of EB forests

DBH range[3] (cm)	The basal area (m^2/ha)				
	DBH_i (cm)	HT00	HT01	HT02	NA01
5.0<=x<15.0	10	4.19	1.41	1.36	1.52
15.0<=x<25.0	20	3.55	4.46	4.27	3.99
25.0<=x<35.0	30	1.98	5.16	7.21	8.34
35.0<=x<45.0	40	0.50	4.27	6.66	7.41
45.0<=x<55.0	50	0.59	4.52	4.52	4.91
55.0<=x<65.0	60	-	3.96	1.98	3.39
65.0<=x<75.0	70	-	3.08	1.92	0.77
75.0<=x<85.0	80	-	1.51	0.50	1.01
85.0<=x<95.0	90	-	-	0.64	-
Sum	**-**	**10.81**	**28.36**	**29.06**	**31.35**

[3] The maximum DBH is 51.0 cm; 77.0 cm; 90.0 cm and 76.7 cm in HT00, HT01, HT02 and NA01 respectively

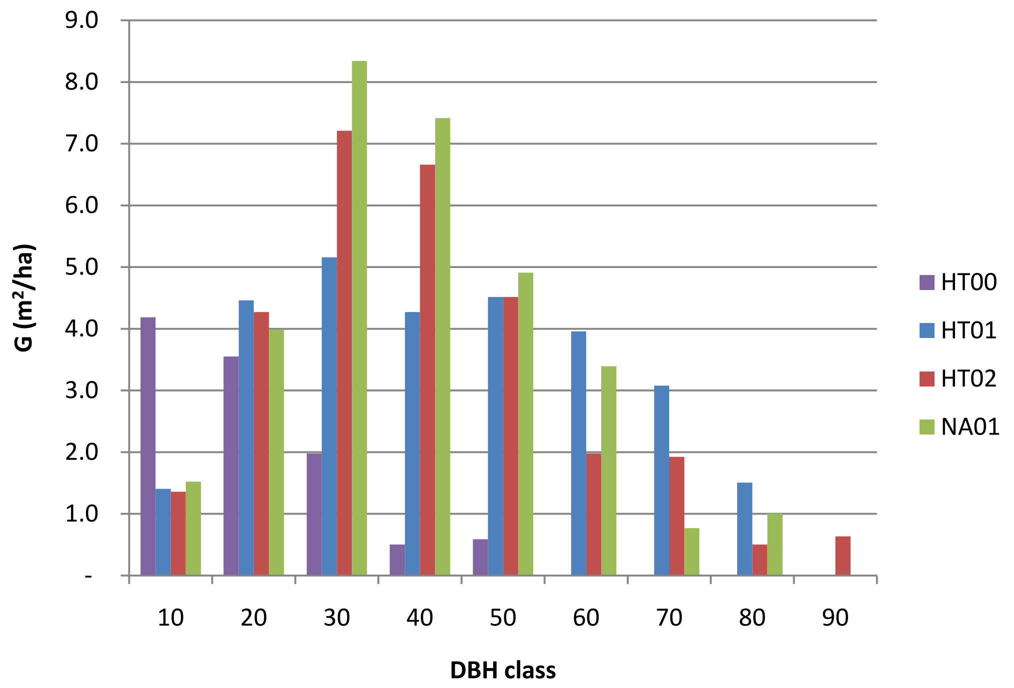

Figure 3.2 The basal area distribution of sample plots

3.1.2 Relation between H and diameter

The relationship between H and DBH was established based on the data of felled sample trees in each sample plot (details in Annex A.4). The three models below were tested for this correlation.

$H = b_1 + b_2*DBH + b_3*DBH^2$ Model (3.1)

$H = b_1 + b_2*log(DBH)$ Model (3.2)

$H = b_1*(DBH)^{b2}$ Model (3.3)

The Table 3-7presents the correlation analysis of above models for data of each sample plot (details in Annex A.5):

Table 3-7 Correlation analysis of H-DBH models per sample plot

Plot ID	H-DBH model	N	b_1	b_2	b_3	$\bar{R}^2$	SSE	AIC
HT00	(3.1)	50	5.5463^{***}	0.5186^{***}	-0.0042^{**}	0.8461^{***}	114.98	47.64
	(3.2)	50	-2.7971^{**}	13.4720^{***}		0.8436^{***}	119.34	47.50
	(3.3)	50	3.7628^{***}	0.4453^{***}		0.8796^{***}	112.63	44.60
HT01	(3.1)	50	6.4390^{***}	0.5360^{***}	-0.0029^{ns}	0.7805^{***}	484.47	119.55
	(3.2)	50	-11.8294^{***}	22.1143^{***}		0.7883^{***}	477.43	116.82
	(3.3)	50	3.5831^{***}	0.5045^{***}		0.7879^{***}	469.25	115.96
HT02	(3.1)	51	6.3502^{***}	0.6027^{***}	-0.0038^{**}	0.7773^{***}	426.70	114.34
	(3.2)	51	-10.4145^{***}	21.6012^{***}		0.7770^{***}	436.11	113.45
	(3.3)	51	4.0862^{***}	0.4780^{***}		0.8073^{***}	429.06	112.62
NA01	(3.1)	50	3.0483^{ns}	0.7462^{***}	-0.0062^{**}	0.6062^{***}	433.20	113.96

	(3.2)	50	-12.6342**	21.9010***		0.6243***	422.15	110.67
	(3.3)	50	4.1808***	0.4521***		0.6495***	459.18	114.87

Note: The statistical analyses are significant at 95% confidence interval. ***p < 0.001; **p < 0.01; *p < 0.05; and non-significant, ^{ns}p> 0.05.

The results indicate that the adjusted coefficient of determination ($\bar{R}^2$) of the models are high, ranging from 0.5997 (model (3.3) for plot NA01) to 0.8555 (model (3.3) for plot HT00). Thus, the relationships between H and DBH in these models are strong and can be considered functional relations.

From comparison of the $\bar{R}^2$,SSE and AIC values from the three equations of four sample plots, Model (3.3) was found to have the smallest SSE and AIC values, therefore Model (3.3) is selected as the optimal equation for the H-DBH relation, with the exception for plot NA01 for which the best fitted Model is (3.2). Optimal equations selected for respective sample plots are:

HT00:	$H = 3.7628 * DBH^{0.4439}$	$\bar{R}^2 = 0.8796$	Equation (H-00)
HT01:	$H = 3.5831 * DBH^{0.5045}$	$\bar{R}^2 = 0.7879$	Equation (H-01)
HT02:	$H = 4.0862 * DBH^{0.4780}$	$\bar{R}^2 = 0.8073$	Equation (H-02)
NA01:	$H = -12.6342 + 21.9010 * \log(DBH)$	$\bar{R}^2 = 0.6243$	Equation (H-03)

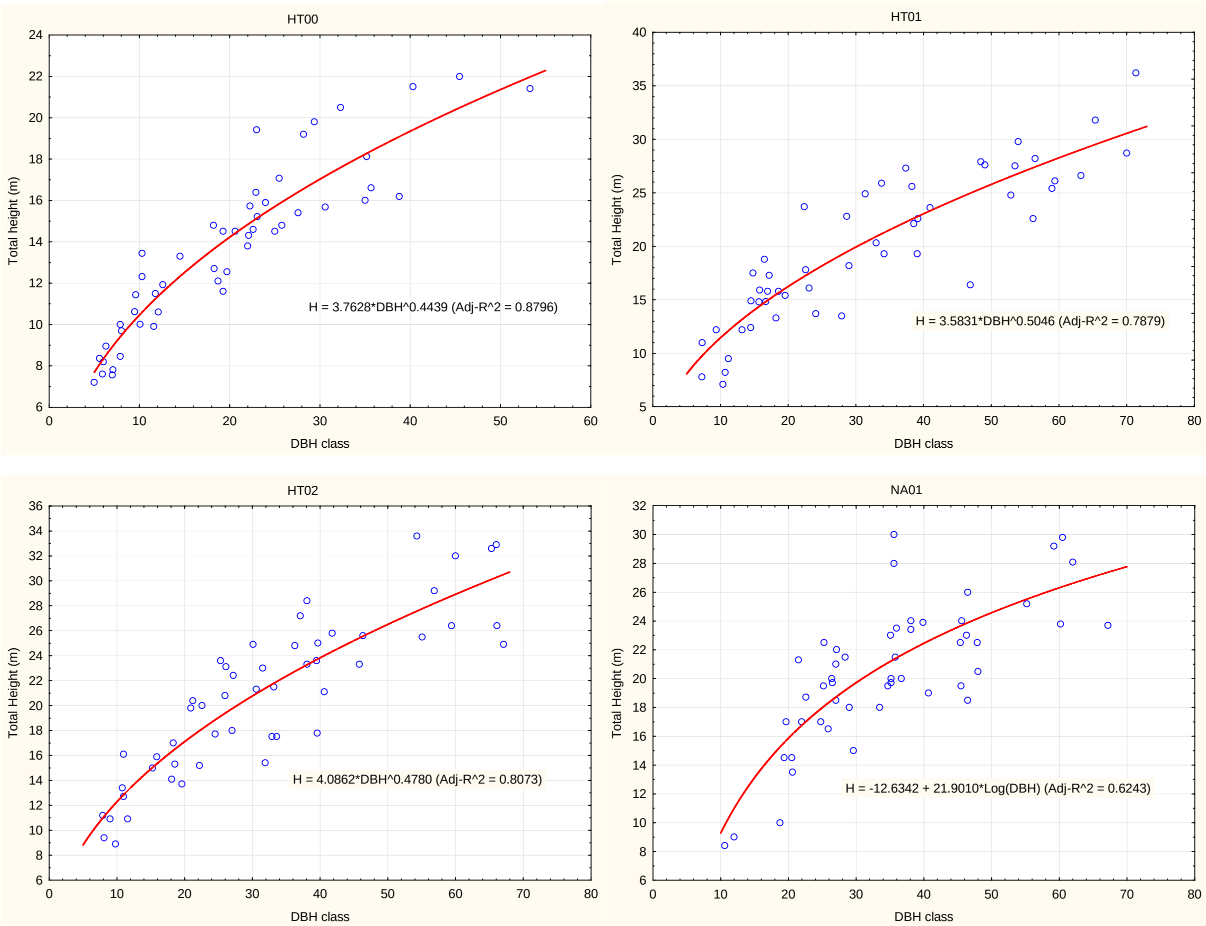

Figure 3.3 The best fitted equations of H-DBH regression

3.1.3 Wood density analysis

To estimate the WD of bole in EB forests, four samples were taken from each sample tree at different locations of the bole: namely at0h, ¼ h, ½ h and ¾ h. The Table 3-9and Table 3-8provides the results of WD analysis for each sample plot and each family (details in Annex A.9).

Table 3-9 WD analysis per sample plot

Plot ID	n_i	Mean	Min	Max	Std.Err.	Coef.Var.
HT00	50	0.4835	0.3419	0.7026	0.0139	20.34
HT01	50	0.6264	0.4373	0.8477	0.0167	18.84
HT02	51	0.5923	0.3888	0.8197	0.0170	20.54
NA01	50	0.5044	0.3813	0.8728	0.0156	21.89
Average	201	0.5519	0.3419	0.8728	0.0089	22.93

Note: *Std.Err.*= Standard Error; *Coef.Var.*= Coefficient of variation (%)

Table 3-10 WD analysis per family

Family	n_i	Mean	Min	Max	Std.Err.	Coef.Var.
Alangiaceae	8	0.6768	0.4290	0.7293	0.1014	14.98
Anacardiaceae	1	0.4621	0.4621	0.4621		
Annonaceae	2	0.4968	0.3917	0.6019	0.1486	29.91
Apocynaceae	1	0.4740	0.4740	0.4740		
Bignoniaceae	1	0.4404	0.4404	0.4404		
Burseraceae	5	0.5910	0.4884	0.7269	0.0979	16.56
Cactaceae	1	0.5659	0.5659	0.5659		
Caesalpiniaceae	7	0.6811	0.5942	0.7943	0.0706	10.36
Clusiaceae	6	0.5454	0.4520	0.5940	0.0522	9.57
Dipterocarpaceae	24	0.7633	0.6402	0.8728	0.0615	8.06
Elaeocarpaceae	7	0.5321	0.4003	0.6207	0.0764	14.36
Euphorbiaceae	26	0.4225	0.3419	0.4909	0.0356	8.43
Fabaceae	12	0.5296	0.4392	0.6355	0.0600	11.33
Fagaceae	22	0.5330	0.3796	0.6809	0.0948	17.78
Juglandaceae	9	0.5743	0.5072	0.6199	0.0421	7.33
Lauraceae	12	0.5137	0.3890	0.6649	0.0872	16.98
Magnoliaceae	3	0.4365	0.4291	0.4407	0.0064	1.47
Meliaceae	3	0.4502	0.3960	0.5490	0.0857	19.03
Mimosaceae	7	0.4440	0.3665	0.4925	0.0410	9.24
Moraceae	3	0.4611	0.4165	0.5135	0.0489	10.61

Myristicaceae	3	0.5301	0.4195	0.7338	0.1767	33.32
Myrtaceae	2	0.5312	0.4851	0.5773	0.0651	12.26
Proteaceae	1	0.5287	0.5287	0.5287		
Rosaceae	5	0.6017	0.4274	0.6776	0.1026	17.05
Sapindaceae	4	0.6834	0.4403	0.8477	0.1726	25.26
Sapotaceae	3	0.4219	0.3888	0.4396	0.0287	6.81
Symplocaceae	2	0.4498	0.3656	0.5340	0.1191	26.47
Theaceae	4	0.5408	0.4343	0.6130	0.0850	15.72
Ulmaceae	10	0.4721	0.3837	0.5323	0.0483	10.22
Unknown	7	0.5725	0.4740	0.6524	0.0716	12.51

Note: *Std.Err.*= Standard Error; *Coef.Var.*= Coefficient of variation (%)

3.1.4 Biomass of sample trees

To measure the fresh biomass of EB forests, 50 sample trees were randomly selected (based on the aforementioned criteria for selection of felling sample trees mentioned)in each sample plot (Table 3-11, details in Annex A.4).

Table 3-11 Sample tree count for fresh biomass measurement of EB forests

DBH range (cm)	DBH_i (cm)	Count of sample trees for fresh biomass measurement				
		Sum	HT00	HT01	HT02	NA01
5.0<=x<15.0	10	40	20	10	8	2
15.0<=x<25.0	20	48	15	13	11	9
25.0<=x<35.0	30	40	8	7	12	13
35.0<=x<45.0	40	32	5	6	9	12
45.0<=x<55.0	50	19	2	6	3	8
55.0<=x<65.0	60	14	-	5	4	5
65.0<=x<75.0	70	8	-	3	4	1
75.0<=x<85.0	80	-	-	-	-	-
85.0<=x<95.0	90	-	-	-	-	-
Sum	-	201	50	50	51	50

The sample trees were separated into components of bole, branch, foliage and buttress (if any) and then weighed for fresh biomass (Table 3-12, details in Annex A.7).

Table 3-12 Average fresh biomass per tree component per sample plot

Plot ID	n_i	Average fresh biomass of a sample tree (kg)									
		Buttress	%	Bole	%	Branch	%	Foliage	%	Sum	%
HT00	50	-	-	272.8	80.5	48.3	14.3	17.7	5.2	338.8	100

HT01	50	-	-	1,386.4	78.3	347.0	19.6	37.6	2.1	1,771.1	100
HT02	51	16.12	1.0	1,231.1	78.6	263.0	16.8	56.1	3.6	1,566.3	100
NA01	50	-	-	1,013.8	81.4	147.9	11.9	83.5	6.7	1,245.3	100

To estimate dry biomass of sample trees, samples were taken for each sample tree component, then analyzed in the laboratory for dry mass (Annex A.8), and finally the ratio of dry-fresh biomass for each tree component was calculated (Table 3-13).

Table 3-13 Dry-fresh mass ratio per tree components per sample plot

Plot ID	**n_i**	**Dry-fresh mass ratio of each tree components**			
		Buttress	Bole	Branch	Foliage
HT00	50	-	0.5086	0.4902	0.3727
HT01	50	-	0.5552	0.5406	0.3746
HT02	51	0.6369	0.5348	0.4951	0.3046
NA01	50		0.5454	0.4019	0.2781

The average dry biomass per component of sample tree per sample plot was estimated (Table 3-14).

Table 3-14 Average dry biomass per tree component per sample plot

Plot ID	**n_i**	**Average dry biomass of a sample tree (kg)**									
		Buttress	%	Bole	%	Branch	%	Foliage	%	Sum	%
HT00	50	-	-	140.8	81.3	25.7	14.8	6.7	3.9	173.2	100
HT01	50	-	-	819.3	79.3	198.2	19.2	15.6	1.5	1,033.0	100
HT02	51	10.2	1.2	672.4	80.6	132.8	15.9	18.6	2.2	834.0	100
NA01	50	-	-	563.5	87.4	59.0	9.1	22.3	3.5	644.7	100
Average					82.15		14.75		2.78		

3.2 Result 2: Modeling of the stem volume

To estimate the standing wood volume (including bark) of EB forests, three volume models were tested for respective sample plots. The data used to develop the volume equations is the data of felled sample trees in each sample plot (Annex A.4). The following models were tested:

$$v = b_1*DBH^{b2}*H^{b3} \qquad \text{Model (3.4)}$$

$$v = b_1*(DBH^2H)^{b2} \qquad \text{Model (3.5)}$$

$$v = b_1+b_2*(DBH^2H) \qquad \text{Model (3.6)}$$

The results of correlation analysis of the alternative models are presented in Table 3-15(details in Annex A.6):

Table 3-15 Correlation analysis of volume models

Plot ID	Volume Model	N	b_1	b_2	b_3	$\bar{R}^2$	SSE	AIC
HT00	(3.4)	50	0.000052^{**}	1.8144^{***}	1.0912^{***}	0.9926^{***}	0.1317	-290.97
	(3.5)	50	0.000009^{***}	1.5931^{***}		0.9927^{***}	0.1597	-283.32
	(3.6)	50	-0.162058^{***}	0.0008^{***}		0.9820^{***}	0.5834	-218.54
HT01	(3.4)	50	0.000122^{***}	1.8439^{***}	0.8031^{***}	0.9951^{***}	0.7829	-201.84
	(3.5)	50	0.000033^{**}	1.4152^{***}		0.9949^{***}	1.6422	-166.80
	(3.6)	50	-0.412309^{***}	0.0011^{***}		0.9886^{***}	3.2573	-132.56
HT02	(3.4)	51	0.000169^{**}	1.9282^{***}	0.6162^{***}	0.9950^{***}	1.3352	-179.78
	(3.5)	51	0.000027^{*}	1.4457^{***}		0.9942^{***}	3.1301	-138.33
	(3.6)	51	-0.476670^{***}	0.0011^{***}		0.9793^{***}	4.5966	-118.73
NA01	(3.4)	50	0.000180^{**}	1.4773^{***}	1.1302^{***}	0.9750^{***}	1.3939	-172.99
	(3.5)	50	0.000051^{**}	1.3651^{***}		0.9748^{***}	1.4987	-171.37
	(3.6)	50	-0.417597^{***}	0.0011^{***}		0.9505^{***}	1.8874	-159.84

Note: The statistical analyses are significant at 95% confidence interval. ***p < 0.001; **p < 0.01; *p < 0.05; and non-significant, ^{ns}p> 0.05.

The adjusted coefficients of determination ($\bar{R}^2$) of the equations are very high, ranging from 0.9505 (Model (3.6) for plot NA01) to 0.9951 (Model (3.4) for plot HT01). Thus, the relationship between the bole volume (with bark) with diameter and height in these model forms are strong and can be considered functional relations.

From comparison of $\bar{R}^2$, *SSE* and *AIC* values from the three models of four sample plots, Model (3.4) was found to have the smallest *SSE* and *AIC* values. Model (3.4) is selected as the optimal volume model. Optimal equations for respective sample plots are:

HT00: $v = 0.000052 * DBH^{1.8144} * H^{1.0912}$ $\bar{R}^2 = 0.9926$ Equation (V-00)

HT01: $v = 0.000122 * DBH^{1.8439} * H^{0.8031}$ $\bar{R}^2 = 0.9951$ Equation (V-01)

HT02: $v = 0.000169 * DBH^{1.9282} * H^{0.6162}$ $\bar{R}^2 = 0.9950$ Equation (V-02)

NA01: $v = 0.000180 * DBH^{1.4773} * H^{1.1302}$ $\bar{R}^2 = 0.9750$ Equation (V-03)

Using the above results standing volume was calculated for each of the sample plots (Table 3-16).

Table 3-16 Standing volume per sample plot

Plot ID	N (tree/ha)	DBH (cm)	H (m)	BA (m^2/ha)	Volume (m^3/ha)
HT00	681	14.2	12.2	10.81	72.8
HT01	481	29.0	19.3	31.86	353.5
HT02	503	27.4	19.5	29.72	341.5
NA01	539	27.2	17.3	31.35	343.3

3.3 RESULT 3: Modeling of Aboveground biomass

3.3.1 Modeling per tree compartment

Bole

Allometric equations were established using data of felled sample trees for each sample plot.

The five following models were chosen to test the correlation of oven-dried biomass with diameter (D), D^2H and WD:

$\ln(y) = b_1 + b_2*ln(D)$ Model (3.7)

$\ln(y) = b_1 + b_2*\ln(D) + b_3*\ln(H)$ Model (3.8)

$\ln(y) = b_1 + b_2*\ln(D^2H)$ Model (3.9)

$\ln(y) = b_1 + b_2*\ln(D) + b_3*\ln(D^2H)$ Model (3.10)

$\ln(y) = b_1 + b_2*\ln(D) + b_3*\ln(WD)$ Model (3.11)

where: y is dependent variable (total tree dry weight or dry weight of bole, branch or foliage; in *kg*); D is DBH(*cm*); D^2H is inm^3; WD is WD (g/cm^3); b_1, b_2,b_3 are regression coefficients

The bulk of tree biomass is located in the main bole(Basuki, T.M.*, et al.* 2009), accounting for about 80% of the total tree biomass (Table III.12). After graphic exploration on scatter plots for bole biomass with variables D and D^2H (Figure 3.4), all five of the above alternative models were tested (Table 3-17, details in Annex A.10):

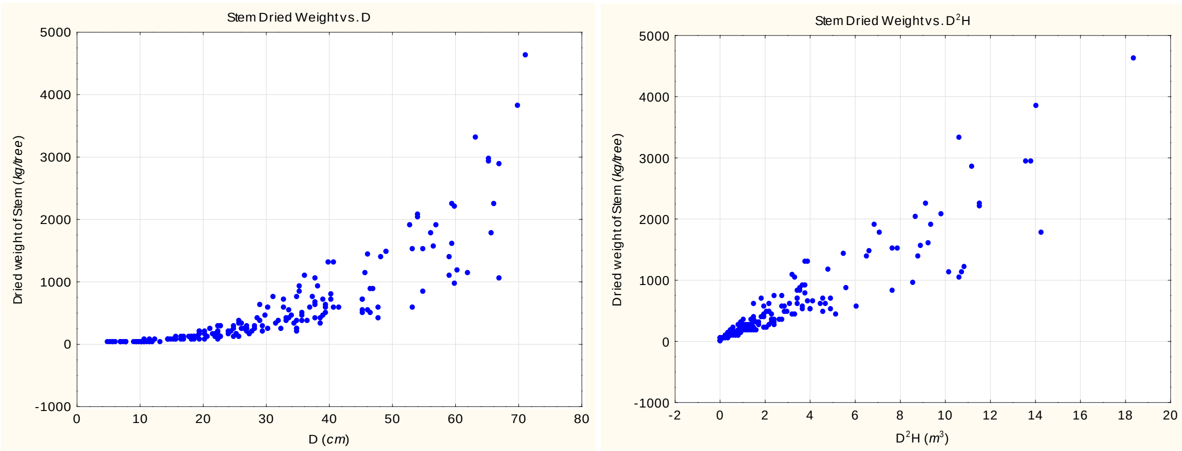

Figure 3.4 Scatter plots between dry weight of bole and variables D and D^2H

Table 3-17 Correlation analysis of bole biomass

Plot ID	Models	N	b_1	b_2	b_3	$\bar{R}^2$	SSE	AIC
HT00	(3.7)	50	-1.8294^{***}	2.1309^{***}		0.9538	4.15	-120
	(3.8)	50	-3.5221^{***}	1.5392^{***}	1.3059^{***}	0.9631	3.24	-133
	(3.9)	50	5.0472^{***}	0.8706^{***}		0.9627	3.35	-131
	(3.10)	50	8.5056^{**}	-1.0726^{ns}	1.3059^{***}	0.9631	3.24	-131
	(3.11)	50	-1.3054^{***}	2.2313^{***}	1.0824^{***}	0.9751	2.19	-150
HT01	(3.7)	50	-2.6683^{***}	2.5423^{***}		0.9745	3.27	-132

	(3.8)	50	-3.3226^{**8}	2.2397^{**8}	0.5655**	0.9778	2.80	-140
	(3.9)	50	5.4093***	0.9978***		0.9760	3.08	-135
	(3.10)	50	1.8863^{ns}	1.1086*	0.5655**	0.9778	2.80	-138
	(3.11)	50	-1.8095***	2.4253***	0.9749***	0.9851	1.87	-158
HT02	(3.7)	51	-2.4515***	2.4572***		0.9639	3.93	-127
	(3.8)		-3.0088***	2.2467***	0.4214^{ns}	0.9648	3.75	-129
	(3.9)	51	5.3043***	0.9778***		0.9626	4.07	-125
	(3.10)	51	0.8720^{ns}	1.4040*	0.4214^{ns}	0.9648	3.75	-127
	(3.11)	51	-1.7846***	2.4118***	0.9477***	0.9809	2.04	-158
NA01	(3.7)	50	-1.0640*	1.9783***		0.8343	6.08	-101
	(3.8)	50	-2.3470***	1.3412***	1.1721***	0.8781	4.38	-118
	(3.9)	50	5.2414***	0.7870***		0.8755	4.56	-116
	(3.10)	50	8.4483***	-1.0029^{ns}	1.1721***	0.8781	4.38	-116
	(3.11)	50	-1.1148**	2.2109***	1.0766***	0.8823	4.23	-118
General[4]	(3.7)	201	-2.3404***	2.3831***		0.9429	26.33	-405
	(3.8)	201	-3.5590***	1.8262***	1.0526***	0.9546	20.84	-452
	(3.9)	201	5.2474***	0.9434***		0.9547	20.90	-451
	(3.10)	201	6.1361***	-0.2791^{ns}	1.0526***	0.9546	20.84	-450
	(3.11)	201	-1.4829***	2.3519***	1.2211***	0.9751	11.40	-571

Note: The statistical analyses are significant at 95% confidence interval. $^{***}p < 0.001$; $^{**}p < 0.01$; $^{*}p < 0.05$; and non-significant, $^{ns}p > 0.05$

The results indicate that the adjusted coefficients of determination ($\bar{R}^2$) of the equations are very high, ranging from 0.8343 (Model (3.7) for plot NA01) to 0.9851 (Model (3.11) for plot HT01). Thus, the relationship between the oven-dried bole biomass with variables *D* or D^2H or *WD* in these equation forms is very strong and can be considered functional relations.

The results in Table 3-17also show that Model (3.10) has a non-significant value of $b_2$or$b_3$at $p<0.05$ except for in plot HT01. The coefficients of Model (3.7), Model (3.9) and Model (3.11) are significant at $p<0.05$ in all sample plots and in general.

On comparing $\bar{R}^2$, *SSE* and *AIC* values, Model (3.11) is selected as the optimal model for estimation of bole biomass of all sample plots and in general. Optimal equations for respective sample plots and in general are:

HT00: $\ln(y) = -1.3054 + 2.2313*\ln(D) + 1.0824*\ln(WD)$ $\bar{R}^2 = 0.9751$

or $y = 0.2711*(D)^{2.2313}*(WD)^{1.0824}$ Equation (S-00)

[4] The "General" category here, and in all other occurrences throughout this report connotes analysis for the regional level (i.e. North Central Coastal region).

HT01: $\ln(y) = -1.8095 + 2.4253*\ln(D) + 0.9749*\ln(WD)$ $\bar{R}^2 = 0.9851$

or $y = 0.1637*(D)^{2.4253}*(WD)^{0.9749}$ Equation (S-01)

HT02: $\ln(y) = -1.7846 + 2.4118*\ln(D) + 0.9477*\ln(WD)$ $\bar{R}^2 = 0.9809$

or $y = 0.1679*(D)^{2.4118}*(WD)^{0.9477}$ Equation (S-02)

NA01: $\ln(y) = -1.1148 + 2.2109*\ln(D) + 1.0766*\ln(WD)$ $\bar{R}^2 = 0.8823$

or $y = 0.3280*(D)^{2.2109}*(WD)^{1.0766}$ Equation (S-03)

General: $\ln(y) = -1.4829 + 2.3519*\ln(D) + 1.2211*\ln(WD)$ $\bar{R}^2 = 0.9751$

or $y = 0.2270*(D)^{2.3519}*(WD)^{1.2211}$ Equation (S-04)

Using the results generated, total bole biomass per hectare was calculated (Table 3-18).

Table 3-18 Total bole biomass estimates

Plot ID	N (tree/ha)	DBH (cm)	H (m)	WD (g/cm^3)	Total bolebiomass (ton/ha)
HT00	681	14.2	12.2	0.4835	31.3
HT01	481	29.0	19.3	0.6264	175.8
HT02	503	27.4	19.5	0.5923	150.8
NA01	539	27.2	17.3	0.5044	125.6
General	551	24.5	17.1	0.5519	111.4

Branches

Similarly to the process of allometric equation development of bole biomass, graphic exploration through scatter plots of branches and variables D and D^2H (Figure 3.5) were undertaken, and based on these results only equations (3.7), (3.9) and (3.11) were tested (Table 3-19, details in Annex A.11):

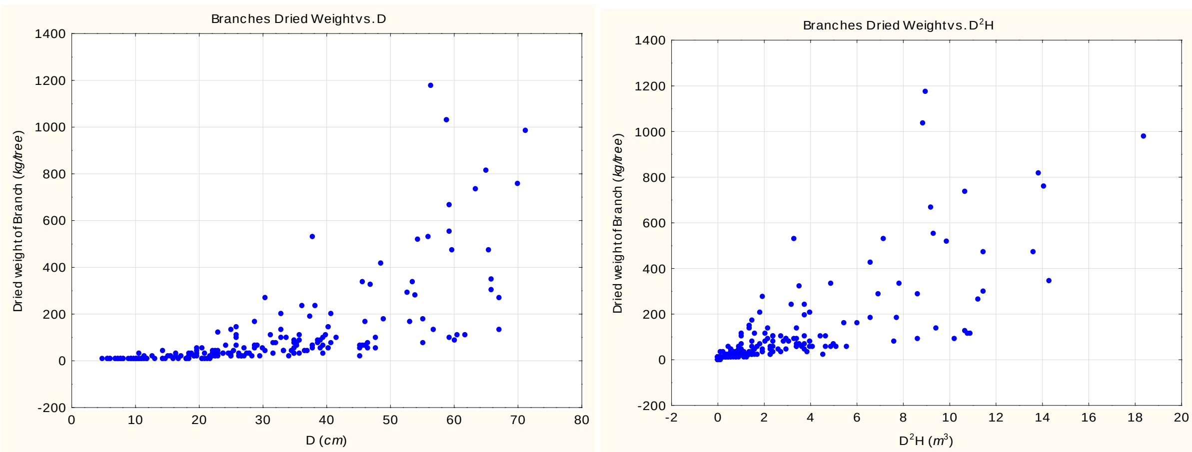

Figure 3.5 Scatter plots between dry weight of branches and D and D^2H

Table 3-19 Correlation analysis of branch biomass

Plot ID	Dry weight model	N	b_1	b_2	b_3	$\bar{R}^2$	SSE	AIC
HT00	(3.7)	50	-3.2129***	1.9846***		0.7710	21.95	-37

	(3.9)	50	3.1854***	0.8046***		0.7660	22.44	-36
	(3.11)	50	-2.6936***	2.0841***	1.0728*	0.7867	20.03	-40
HT01	(3.7)	50	-5.6582***	2.9034***		0.8865	20.86	-40
	(3.9)	50	3.5678***	1.1358***		0.8820	21.68	-38
	(3.11)	50	-4.9728***	2.8100***	0.7780^{ns}	0.8890	19.97	-40
HT02	(3.7)	51	-3.7174***	2.3061***		0.7677	27.78	-27
	(3.9)	51	3.5645***	0.9098***		0.7533	29.51	-24
	(3.11)	51	-2.2635***	2.2070***	2.0661***	0.8397	18.78	-45
NA01	(3.7)	50	-2.4068***	1.7409***		0.6311	13.74	-61
	(3.9)	50	3.1490***	0.6832***		0.6442	13.25	-62
	(3.11)	50	-2.4738***	2.0475***	1.4191***	0.7114	10.52	-72
General	(3.7)	201	-4.0186***	2.3198***		0.7853	112.45	-113
	(3.9)	201	3.3680***	0.9144***		0.7884	110.83	-116
	(3.11)	201	-2.7540***	2.2738***	1.8007***	0.8465	79.97	-179

Note: The statistical analyses are significant at 95% confidence interval. ***$p < 0.001$; **$p < 0.01$; *$p < 0.05$; and non-significant, $^{ns}p > 0.05$.

The results in Table 3-19show that the adjusted coefficient of determination ($\bar{R}^2$) of the models are high, ranging from 0.6311 (Model (3.7) for plot NA01) to 0.8890 (Model (3.11) for plot HT01). Thus, the relationship between the oven-dried branch biomass with variables *D* or D^2H or *WD* in these model forms is very strong and can be considered functional relations.

The results in Table 3-19also show that all models have significant coefficients at $p<0.001$ except Model (3.11) for plots HT00 and HT01.

On comparing $\bar{R}^2$, *SSE* and *AIC* values, Model (3.11) is selected as the optimal model for estimating branch biomass for all sample plots and in general. Optimal equations for respective sample plots and in general are:

HT00: $\ln(y) = -2.6936+2.0841*\ln(D) + 1.0728*\ln(WD)$ $\bar{R}^2 = 0.7867$

or $y = 0.0676*D^{1.9846}*WD^{1.0728}$ Equation (B-00)

HT01: $\ln(y) = -5.6582 + 2.9034*\ln(D)$ $\bar{R}^2 = 0.8865$

or $y = 0.0035*D^{2.9034}$ Equation (B-01)

HT02: $\ln(y) = -2.2635+2.2070*\ln(D) + 2.0661*\ln(WD)$ $\bar{R}^2 = 0.8397$

or $y = 0.1040*D^{2.3061}*WD^{2.0661}$ Equation (B-02)

NA01: $\ln(y) = -2.4738 + 2.0475*\ln(D) + 1.4191*\ln(WD)$ $\bar{R}^2 = 0.7114$

or $y = 0.0843*D^{1.7409}*WD^{1.4191}$ Equation (B-03)

General: $\ln(y) = -2.7540 + 2.2738*\ln(D) + 1.8007*\ln(WD)$ $\bar{R}^2 = 0.8465$

or $y = 0.0636*D^{2.3198}*WD^{1.8007}$ Equation (B-04)

Using the above results, total branch biomass per hectare was calculated (Table 3-20).

Table 3-20 Total branch biomass estimates

Sample plot	N (tree/ha)	DBH (cm)	H (m)	WD (g/cm^3)	Total Branch biomass (ton/ha)
HT00	681	14.2	12.2	0.4835	5.3
HT01	481	29.0	19.3	0.6264	29.6
HT02	503	27.4	19.5	0.5923	26.4
NA01	539	27.2	17.3	0.5044	14.9
General	551	24.5	17.1	0.5519	17.3

Foliage

Taking similar steps as for bole and branches, based on the results of graphic exploration through scatter plots of foliage biomass and variables D and D^2H (Figure 3.6)only Model (3.7), Model (3.9) and Model (3.11) were tested (Table 3-21, details in Annex A.12).

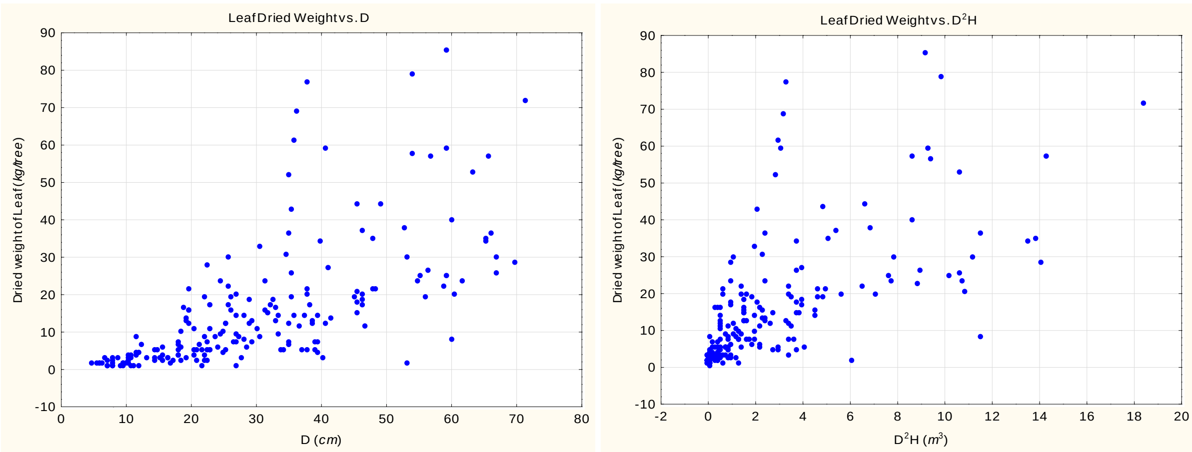

Figure 3.6 Scatter plots between dry weight of foliage and variables D and D^2H

Table 3-21 Correlation analysis of foliage biomass

Plot ID	Model	N	b_1	b_2	b_3	$\bar{R}^2$	SSE	AIC
HT00	(3.7)	50	-1.4212**	1.0164***		0.4276	25.42	-30
	(3.9)	50	1.8571***	0.4137***		0.4284	25.38	-30
	(3.11)	50	-1.4014*	1.0202***	0.0409^{ns}	0.4155	25.41	-28
HT01	(3.7)	50	-4.0811***	1.8527***		0.8172	14.81	-57
	(3.9)	50	1.8050***	0.7279***		0.8203	14.55	-58
	(3.11)	50	-2.7066***	1.6654***	1.5604***	0.8586	11.22	-69
HT02	(3.7)	51	-3.2272***	1.6559***		0.5852	33.28	-18
	(3.9)	51	2.0005***	0.6562***		0.5794	33.75	-17
	(3.11)	51	-2.0906**	1.5784***	1.6152**	0.6465	27.79	-25
NA01	(3.7)	50	-1.7711*	1.2996***		0.4254	17.43	-49

	(3.9)	50	2.3777^{***}	0.5081^{***}		0.4309	17.26	-49
	(3.11)	50	-1.8659^{**}	1.7338^{***}	2.0102^{***}	0.6304	10.98	-70
General	(3.7)	201	-2.8357^{***}	1.5355^{***}		0.6339	103.91	-129
	(3.9)	201	2.0537^{***}	0.6049^{***}		0.6357	103.41	-130
	(3.11)	201	-2.1949^{***}	1.5122^{***}	0.9124^{***}	0.6616	95.57	-143

Note: The statistical analyses are significant at 95% confidence interval. ***$p < 0.001$; **$p < 0.01$; *$p < 0.05$; and non-significant, $^{ns}p > 0.05$.

The results show that the adjusted coefficient of determination ($\bar{R}^2$) of the model are low to high, ranging from 0.4155 (Model (3.11) for plot HT00) to 0.8586 (Model (3.11) for plot HT01).

The results in Table 3-21also show that all models have significant coefficients$b_2$and $b_3$at$p<0.001$ except Model (3.11) for plots HT00 and HT02.

On comparing $\bar{R}^2$, *SSE* and *AIC* values, Model (3.11) is selected as the optimal model for estimating foliage biomass of sample plots HT01, HT02, NA01 and in general; Model (3.9) is selected as the optimal model for sample plot HT00. Optimal equations for respective sample plots and in general are:

HT00: $\ln(y) = 1.8571 + 0.4137*\ln(D^2H)$ $\quad \bar{R}^2 = 0.4284$

or $y = 6.4050*(D^2H)^{0.4137}$ Equation (L-00)

HT01: $\ln(y) = -2.7066 + 1.6654*\ln(D) + 1.5604*\ln(WD)$ $\quad \bar{R}^2 = 0.8586$

or $y = 0.0668*D^{1.6654}*WD^{1.5604}$ Equation (L-01)

HT02: $\ln(y) = -2.0906 + 1.5784*\ln(D) + 1.6152*\ln(WD)$ $\quad \bar{R}^2 = 0.6465$

or $y = 0.1236*D^{1.5784}*WD^{1.6152}$ Equation (L-02)

NA01: $\ln(y) = -1.8659 + 1.7338*\ln(D) + 2.0102*\ln(WD)$ $\quad \bar{R}^2 = 0.6304$

or $y = 0.1548*D^{1.7338}*WD^{2.0102}$ Equation (L-03)

General: $\ln(y) = -2.1949 + 1.5122*\ln(D) + 0.9124*\ln(WD)$ $\quad \bar{R}^2 = 0.6616$

or $y = 0.1114*D^{1.5122}*WD^{0.9124}$ Equation (L-04)

Using the above results, total foliage biomass per hectare was calculated (Table 3-22).

Table 3-22 Total foliage biomass estimates

Plot ID	N (tree/ha)	DBH (cm)	H (m)	WD (g/cm^3)	Total Foliage biomass (ton/ha)
HT00	681	14.2	12.2	0.4835	2.4
HT01	481	29.0	19.3	0.6264	4.2
HT02	503	27.4	19.5	0.5923	5.0
NA01	539	27.2	17.3	0.5044	6.5
General	551	24.5	17.1	0.5519	4.5

3.3.2 Modeling of total aboveground biomass

Development of allometric equations for total above ground biomass (*tAGB*)for some of the main tree species and plant families of EB forests was attempted. Based on the data from Tables III.4, III.5 and III.9, the number of sample trees of some main species and families is presented in following table (Table 3-23):

Table 3-23 Sample tree count of main tree species and plant families

Plant family	Number of samples	%	Tree species	Number of samples	%
Total	201		Total	201	
Euphorbiaceae	26	12.94	*Vaticaodorata*	23	11.44
Dipterocarpaceae	24	11.94	*Endospermumsinensis*	21	10.45
Fagaceae	22	10.95	*Gironnierasubaequalis*	10	4.98
Fabaceae	12	5.97	*Engelhardtiaroxburghiana*	9	4.48
Lauraceae	12	5.97	*Alangiumridleyi*	7	3.48
Ulmaceae	10	4.98	*Castanopsischinensis*	7	3.48
Juglandaceae	9	4.48	*Elaeocarpusgriffithii*	7	3.48
Alangiaceae	8	3.98	*Garciniaoblongifolia*	6	2.99

Based on graphicexploration using scatter plots (Figure 3.7), all alternative models were tested to develop equationsfor *tAGB*with variables D and D^2H (Table 3-24, details in Annex A.13).

Table 3-24 Correlation analysis oftABG biomass

Plot ID	Model	N	b_1	b_2	b_3	$\bar{R}^2$	SSE	AIC
HT00	(3.7)	50	-1.3454***	2.0496***		0.9535	3.87	-124
	(3.8)	50	-2.6531***	1.5925***	1.0088**	0.9591	3.33	-129
	(3.9)	50	5.2677***	0.8363***		0.9598	3.34	-131
	(3.10)	50	6.6387*	-0.4252^{ns}	1.0088**	0.9591	3.33	-129
	(3.11)	50	-0.8290***	2.1485***	1.0669***	0.9759	1.96	-156
HT01	(3.7)	50	-2.5924***	2.5806***		0.9737	3.48	-129
	(3.8)	50	-3.1630***	2.3167***	0.4931**	0.9759	3.12	-133
	(3.9)	50	5.6070***	1.0118***		0.9734	3.52	-129
	(3.10)	50	1.3790^{ns}	1.3304*	0.4931*	0.9759	3.12	-133
	(3.11)	50	-1.8000***	2.4726***	0.8996***	0.9824	2.29	-148
HT02	(3.7)	51	-2.0698***	2.4090***		0.9502	5.27	-112
	(3.8)	51	-2.4438***	2.2678***	0.2827^{ns}	0.9500	5.19	-111

	(3.9)	51	5.5344***	0.9575***		0.9466	5.66	-108
	(3.10)	51	0.1603^{ns}	1.7023*	0.2827^{ns}	0.9500	5.19	-111
	(3.11)	51	-1.2616***	2.3540***	1.1486***	0.9760	2.49	-148
NA01	(3.7)	50	-0.6619^{ns}	1.9106***		0.8224	6.16	-101
	(3.8)	50	-1.9081***	1.2918***	1.1384***	0.8658	4.56	-114
	(3.9)	50	5.4276***	0.7602***		0.8634	4.74	-114
	(3.10)	50	8.5774***	-0.9851^{ns}	1.1384***	0.8658	4.56	-114
	(3.11)	50	-0.7157^{ns}	2.1570***	1.1404***	0.8797	4.08	-119
General	(3.7)	201	-1.9763***	2.3358***		0.9351	28.99	-385
	(3.8)	201	-3.0977***	1.8233***	0.9686***	0.9452	24.34	-418
	(3.9)	201	5.4608***	0.9240***		0.9455	24.35	-420
	(3.10)	201	5.8238***	-0.1140^{ns}	0.9686***	0.9452	24.34	-418
	(3.11)	201	-1.0703***	2.3028***	1.2901***	0.9723	12.32	-555

Note: The statistical analyses are significant at 95% confidence interval. $^{***}p < 0.001$; $^{**}p < 0.01$; $^{*}p < 0.05$; and non-significant, $^{ns}p > 0.05$.

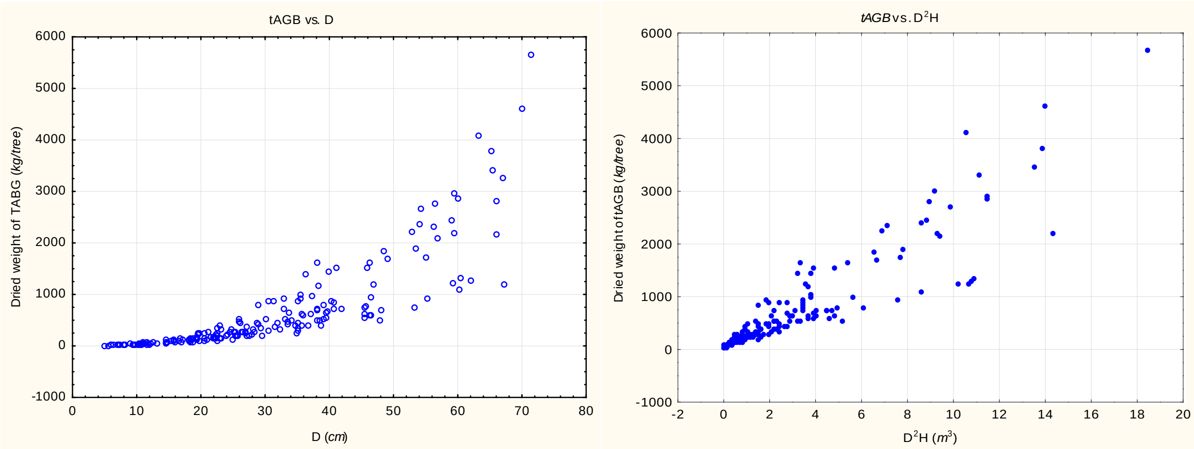

Figure 3.7 Scatter plots between dry weight of tABGand variables D and D^2H

The results indicate that the adjusted coefficient of determinations ($\bar{R}^2$) of the equations are very high, ranging from 0.8224 (Model (3.7) for plot NA01) to 0.9824 (Model (3.11) for plot HT01). Thus, the relationship between the *tAGB* with variables *D* or D^2H or *WD* in these model forms are very strong and can be considered functional relations.

The results also indicate that Model (3.10) has a non-significant value of $b_2$or $b_3$at$p<0.05$except for plot HT01. The coefficients of Model (3.9) are significant at $p < 0.001$ in all sample plots and in the general category.

On comparing $\bar{R}^2$, *SSE* and *AIC* values, Model (3.11) is selected as the optimal model for estimating the *tAGB* of all sample plots and for the general category, with the exception for plot NA01 for which Model (3.9) is the optimal. However, Model (3.11) requires both diameter (*D*) and WD, thus where WD is unknown, Model(3.9) can be used instead of Model (3.11). Specific equations for respective sample plots and in general are:

HT00: $\ln(y) = -0.8290 + 2.1485*\ln(D) + 1.0669*\ln(WD)$ $\bar{R}^2 = 0.9759$

or $y = 0.4365*(D)^{2.1485}*(WD)^{1.0669}$ Equation (T-00)

HT01: $\ln(y) = -1.800 + 2.4726*\ln(D) + 0.8996*\ln(WD)$ $\bar{R}^2 = 0.9824$

or $y = 0.1653*(D)^{2.4726}*(WD)^{0.8996}$ Equation (T-01)

HT02: $\ln(y) = -1.2616 + 2.3540*\ln(D) + 1.1486*\ln(WD)$ $\bar{R}^2 = 0.9760$

or $y = 0.2832*(D)^{2.3540}*(WD)^{1.1486}$ Equation (T-02)

NA01: $\ln(y) = 5.4276 + 0.7602*\ln(D^2H)$ $\bar{R}^2 = 0.8634$

or $y = 227.61*(D^2H)^{0.7602}$ Equation (T-03)

General: $\ln(y) = -1.0703 + 2.3028*\ln(D) + 1.2901*\ln(WD)$ $\bar{R}^2 = 0.9723$

or $y = 0.3429*(D)^{2.3028}*(WD)^{1.2901}$ Equation (T-04)

Using the above results, the *tAGB* per hectare was calculated (Table 3-25).

Table 3-25 Total above ground biomass estimation

Plot ID	N (tree/ha)	DBH (cm)	H (m)	WD (g/cm^3)	tAGB (ton/ha)
HT00	681	14.2	12.2	0.4835	40.9
HT01	481	29.0	19.3	0.6264	215.6
HT02	503	27.4	19.5	0.5923	189.2
NA01	539	27.2	17.3	0.5044	148.0
General	551	24.5	17.1	0.5519	138.1

3.3.3 Modeling of ABG for the main tree families and species

Tree families

Based on the results in Table 3-23, three main plant families of the study sites (i.e. Dipterocarpaceae, Euphorbiaceae and Fagaceae) were selected to develop the biomass equations. All candidate models were tested (Table 3-26, details in Annex A.14):

Table 3-26 Correlation analysis of tABG biomass equations for the Dipterocarpaceae, Euphorbiaceae and Fagaceae plant families

Family	Model	N	b_1	b_2	b_3	$\bar{R}^2$	SSE	AIC
Dipterocarpaceae	(3.7)	24	-1.6473^{***}	2.3849^{***}		0.9926	0.70	-210
	(3.8)	24	-2.4528^{***}	1.9869^{***}	0.7157^{*}	0.9941	0.53	-221
	(3.9)	24	5.8962^{***}	0.9324^{***}		0.9942	0.55	-222
	(3.10)	24	4.1389^{ns}	0.5555^{ns}	0.7157^{*}	0.9941	0.53	-221
	(3.11)	24	-1.3747^{***}	2.3644^{***}	0.7522^{ns}	0.9932	0.62	-214
Euphorbiaceae	(3.7)	26	-1.7462^{***}	2.1691^{***}		0.9593	1.12	-186
	(3.8)	26	-3.1965^{***}	1.5860^{***}	1.1584^{***}	0.9822	0.47	-227
	(3.9)	26	5.1460^{***}	0.8703^{***}		0.9815	0.51	-225

	(3.10)	26	7.4731***	-0.7308ns	1.1584***	0.9822	0.47	-227
	(3.11)	26	-0.5559ns	2.1759***	1.4043**	0.9711	0.77	-203
Fagaceae	(3.7)	22	-1.7608**	2.2948***		0.9230	2.92	-142
	(3.8)	22	-3.1849***	1.6357***	1.2475**	0.9368	2.28	-153
	(3.9)	22	5.5616***	0.9107***		0.9387	2.33	-153
	(3.10)	22	8.3053ns	-0.8594ns	1.2475*	0.9368	2.28	-153
	(3.11)	22	-0.3166ns	2.1243***	1.3576**	0.9503	1.79	-165

Note: The statistical analyses are significant at 95% confidence interval. ****p < 0.001*; ***p < 0.01*; **p < 0.05*; and non-significant, $^{ns}p > 0.05$.

The results show that the adjusted coefficients of determination ($\bar{R}^2$) of the models are very high, ranging from 0.9230 (Model (3.7) for the Fagaceae family) to 0.9942 (Model (3.9) for the Dipterocarpaceae family). Thus, the relationship between the *tAGB* of these families with variables *D* or D^2H or *WD* in these model forms is very strong and can be considered to be functional relations.

The results also indicate that Model (3.10) has a non-significant value of $b_2$at $p<0.05$. The coefficients of Model (3.8) and Model (3.9) are significant at $p < 0.001$for all families.

On comparing $\bar{R}^2$, *SSE* and *AIC* values, Model (3.8) is selected as the optimal model for estimating *tAGB* of the three families. Optimal equations for respective families are:

Dipterocarpaceae:

$\ln(y) = -2.4528 + 1.9869*\ln(D) + 0.7157*\ln(H)$ $\bar{R}^2 = 0.9941$

or $y = 0.0860*D^{1.9869}*H^{0.7157}$ Equation (F-01)

Euphorbiaceae:

$\ln(y) = -3.1965 + 1.5860*\ln(D) + 1.1584*\ln(H)$ $\bar{R}^2 = 0.9822$

or $y = 0.0409*D^{1.5860}*H^{1.1584}$ Equation (F-02)

Fagaceae:

$\ln(y) = -3.1849 + 1.6357*\ln(D) + 1.2475*\ln(H)$ $\bar{R}^2 = 0.9368$

or $y = 0.0414*D^{1.6357}*H^{1.2475}$ Equation (F-03)

Tree species

Based on the results in Table 3-23, two main species of the study sites (i.e. *Vatica odorata* and *Endospermum sinensis*) were selected to develop biomass equations. All candidate models were tested (Table 3-27, details in Annex A.15):

Table 3-27 Correlation analysis of tABG biomass equations for Vatica odorata and Endospermum sinensis species

Species	Model	N	b_1	b_2	b_3	$\bar{R}^2$	SSE	AIC
Vatica odorata	(3.7)	23	-1.6468***	2.3843***		0.9926	0.6965	-210
	(3.8)	23	-2.7128***	1.8646***	0.9434**	0.9945	0.4903	-225
	(3.9)	23	5.9059***	0.9347***		0.9948	0.4904	-227
	(3.10)	23	5.9765*	-0.0223ns	0.9434**	0.9945	0.4903	-225
	(3.11)	23	-1.3688***	2.3630***	0.7663ns	0.9931	0.6145	-214

Endospermum sinensis	(3.7)	21	-1.7692***	2.1666***		0.9496	0.8543	-199
	(3.8)	21	-3.0385***	1.5705***	1.1214***	0.9777	0.3576	-241
	(3.9)	21	5.1394***	0.8603***		0.9773	0.3850	-239
	(3.10)	21	7.2901***	-0.6723^{ns}	1.1214***	0.9777	0.3576	-241
	(3.11)	21	-0.0817^{ns}	2.1435***	1.8411**	0.9692	0.4947	-225

Note: The statistical analyses are significant at 95% confidence interval. ***$p < 0.001$; **$p < 0.01$; *$p < 0.05$; and non-significant, $^{ns}p > 0.05$.

The results indicate that the adjusted coefficient of determinations ($\bar{R}^2$) of the models are very high, ranging from 0.9496 (Model (3.7) for the *Endospermum sinensis* species) to 0.9948 (Model (3.9) for the *Vatica odorata* species). Thus, the relationship between the *tAGB* of these species with variables *D* or D^2H or *WD* in these model forms is very strong and can be considered functional relations.

The results also show that Model (3.10) has non-significant value of $b_2$at $p<0.05$. The coefficients of Model (3.8) and Model (3.9) are significant at $p < 0.001$for all species.

On comparing $\bar{R}^2$, *SSE* and *AIC* values, Model (3.8) is selected as the optimal model for estimating*tAGB* of these two species. Optimal equations for respective species are:

Vatica odorata:

$\ln(y) = -2.7128 + 1.8646*\ln(D) + 0.9434*\ln(H)$ $\bar{R}^2 = 0.9945$

or $y = 0.0860*D^{1.8646}*H^{0.9434}$ Equation (Sp-01)

Endospermum sinensis:

$\ln(y) = -3.0385 + 1.5705*\ln(D) + 1.1214*\ln(H)$ $\bar{R}^2 = 0.9777$

or $y = 0.0409*D^{1.5705}*H^{1.1214}$ Equation (Sp-02)

3.3.4 Validation of equations

To assess the accuracy of the selected equations, 20 felled sample trees were used as the control data (Annex A. 16). These sample trees were not used in the development of equations. Only selected optimal equations were validated. Formula (1.3) was used to estimate the relative error or deviation (Δ%)using given biomass data and predicted data generated from the selected equations and previously published equations for validation (Table 3-28, details in Annex A.17).

The equations subject to the validation exercise are the optimal equations developed for; biomass of components bole, branch, and foliage(equations (S-04), (B-04), and (L-04)); and total tree above ground biomass (equation (T-04)). For the published equation, the equation of Brown (1997) and Chave et al., (2005) were employed.

$tAGB_{Brown} = \exp(-2.134 + 2.53*\ln(D))$ (Brown, S. 1997)

$tAGB_{Chave} = 0.0509*WD*D^2*H$ (Chave, J., *et al.* 2005)

Table 3-28 Percentage error of biomass equations

Equation	No. of control samples	Min Δ%	Max Δ%	$\overline{\Delta}$%	No. of +Δ%	No. of -Δ%
S-04	20	-2.97	-17.80	8.15	7	13
B-04	20	-5.87	-28.72	17.79	8	12

L-04	20	7.95	-27.25	18.05	9	11
T-04	20	0.09	-15.23	5.74	9	11
$tAGB_{Brown}$	20	4.10	-67.60	35.65	4	16
$tAGB_{Chave}$	20	0.19	47.09	20.35	9	11

The maximum error for bole biomass estimation is -17.80%, for branch biomass this is -28.72% and for foliage biomass this is -27.25%. The average error is 8.15% for equation for bolebiomass,17.79% for branch and 18.05% for foliage, respectively. For total tree biomass, Model (3.11) was applied as optimal model and then compared with the previously published models from Brown (1997) and Chave et al., (2005). The result shows that, the average relative error of previously published models is higher than that of model (3.11) for total tree biomass. When the models of Brown (1997) and Chave et al., (2005) were applied to the control data, the predicted values were overestimated (Table 3-29).

Table 3-29 Observed values and predicted values of tAGB from various models

Parameters	Observed	Selected optimal model	Brown (1997)	Chave et al., (2005)
Mean tAGB (kg/tree)	556.3	541.8	959.5	703.8
Standard deviation	723.9	706.5	1384.5	1035.0
Confidence SD -95%	550.1	537.3	1052.9	787.1
Confidence SD +95%	1056.4	1031.9	2022.1	1511.7
Number of observation	20	20	20	20

For equations of plant families, all equations were validated, namely:

Dipterocarpaceae family:

$tAGB = \exp(-1.6473+2.3829*\ln(D))$ Equation (Di-1)

$tAGB = \exp(-2.4528+1.9869*\ln(D)+0.7157*\ln(H))$ Equation (Di-2) = Optimal equation (F-01)

$tAGB = \exp(5.8962+0.9324*\ln(D^2H))$ Equation (Di-3)

Euphorbiaceae family:

$tAGB = \exp(-1.7462+2.1691*\ln(D))$ Equation (Eu-1)

$tAGB = \exp(-3.1965+1.5860*\ln(D)+1.1584*\ln(H))$ Equation (Eu-2) = Optimal equation (F-02)

$tAGB = \exp(5.1460+0.8703*\ln(D^2H))$ Equation (Eu-3)

Fagaceae family:

$tAGB = \exp(-1.7608+2.2948*\ln(D))$ Equation (Fa-1)

$tAGB = \exp(-3.1849+1.6357*\ln(D)+1.2475*\ln(H))$ Equation (Fa-2) = Optimal equation (F-03)

$tAGB = \exp(5.5616+0.9107*\ln(D^2H))$ Equation (Fa-3)

3.3.5 Comparison with generic models

The predicted values of tAGB estimated from previously published models ofBrown (1997) and Chave et al., (2005) were compared with validated equations. For the Dipterocarpaceae family, the following models ofBasuki et al., (2009) were compared:

$$tAGB = \exp(-1.201 + 2.196*\ln(D)) \qquad \textit{Basuki 1}$$

$$tAGB = \exp(-0.744 + 2.188*\ln(D) + 0.832*\ln(WD)) \qquad \textit{Basuki 2}$$

The Table 3-30is the result of relative error for each equation (details in Annex A.18).

Table 3-30Relative error of biomass allometric equations for plant families

Equations	No. of control samples	Min Δ%	Max Δ%	$\overline{\Delta}$%	No. of +Δ%	No. of -Δ%
Dipterocarpaceae family						
(Di-1)	4	1.72	9.08	5.76	2	2
(Di-2)	4	1.02	4.51	2.94	2	2
(Di-3)	4	0.09	-8.22	4.14	3	1
Brown	4	4.10	-9.25	7.34	3	1
Chave	4	0.19	-18.40	8.90	2	2
Basuki 1	4	3.99	38.61	19.07	4	0
Basuki 2	4	-3.14	-15.80	8.85	1	3
Euphorbiaceae family						
(Eu-1)	4	2.09	29.37	11.33	4	0
(Eu-2)	4	6.74	-23.93	13.52	2	2
(Eu-3)	4	-5.74	-19.14	9.75	2	2
Brown	4	-36.89	-56.17	48.98	0	4
Chave	4	-11.71	33.45	20.17	2	2
Fagaceae family						
(Fa-1)	1	-	-	5.97	1	-
(Fa-2)	1	-	-	4.23	1	-
(Fa-3)	1	-	-	5.33	1	-
Brown	1	-	-	-47.85	1	-
Chave	1	-	-	-25.94	1	-

The results indicate that the average deviations for the three main plant families of all models are consistently smaller than that of the previously published models. In the Dipterocarpaceae family, prediction of *tAGB* using validated equations resulted in average deviation ranging from 2.94% to 5.76%. This means all validated equations can be used to estimate the total tree biomass of the

Dipterocarpaceae family. Other previously published models have average deviations lower than 10% with the exception for the equation Basuki 1 of Basuki et al., (2009).

For the Euphorbiaceae family, the previously published models have poor estimation of tAGB with average deviation of 20.17% and 48.98% from the equations of Chave et al., (2005) and Brown (1997), respectively. Meanwhile, the validated equations give average deviation ranging between 9.75-13.52%.

Figure 3.8shows the observed values and the predicted lines using Power model and models of the previously publications.

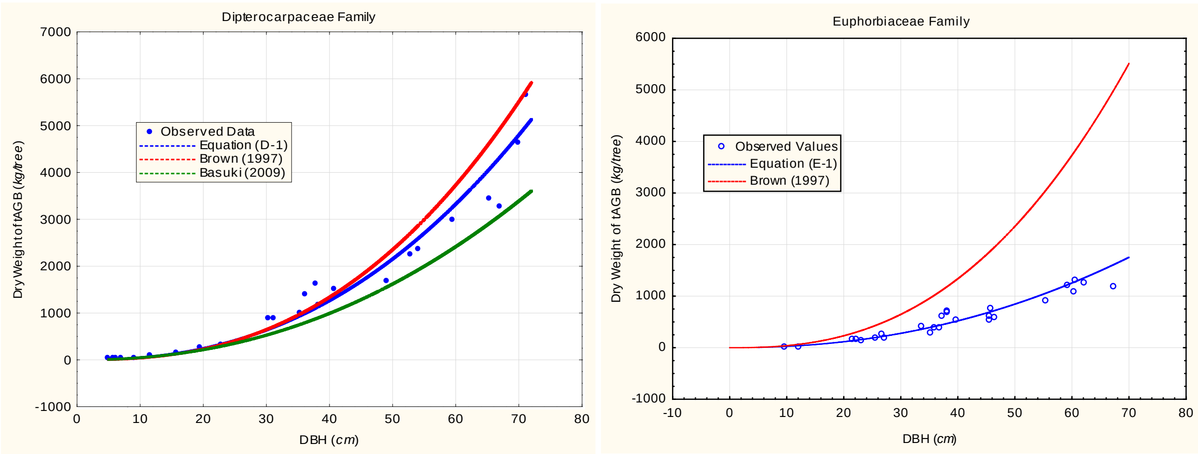

Figure 3.8 DBH and dry weight of the tAGB for Dipterocarpaceae and Euphorbiaceae families from the observed data and the predicted lines using Power model and previously published models

For equations of species, all optimal models were validated. They are:

Vatica odorata species:

$tAGB$ = exp(-1.6468+2.3843*ln(D)) Equation (Vo-1)

$tAGB$ = exp(-2.7128+1.8646*ln(D)+0.9434*ln(H)) Equation (Vo-2) = Optimal equation (Sp-01)

$tAGB$ = exp(5.9059+0.9347*ln(D^2H)) Equation (Vo-3)

Endospermum sinensis species:

$tAGB$ = exp(-1.7692+2.1666*ln(D)) Equation (Es-1)

$tAGB$ = exp(-3.0385+1.5705*ln(D)+1.1214*ln(H)) Equation (Es-2) = Optimal equation (SP-02)

$tAGB$ = exp(5.1394+0.8603*ln(D^2H)) Equation (Es-3)

The models from Brown (1997) and Chave et al., (2005) were used for comparison for these two main species.

The Table 3-31is the result of percentage error for each equation (details in Annex A.19).

Table 3-31Relative error of biomass equations per plant family

Equations	No. of control samples	Min Δ%	Max Δ%	$\bar{\Delta}$%	No. of +Δ%	No. of -Δ%
Vatiaca odorata species						
(Vo-1)	4	1.61	8.91	5.76	2	2

(Vo-2)	4	1.47	8.55	4.74	3	1
(Vo-3)	4	1.38	8.42	4.65	3	1
Brown	4	4.10	-9.25	7.34	3	1
Chave	4	0.19	-18.40	8.90	2	2
Endospermum sinensis species						
(Es-1)	4	-0.79	25.62	8.49	3	1
(Es-2)	4	7.64	-20.62	12.63	2	2
(Es-3)	4	-4.76	-17.66	9.16	2	2
Brown	4	-36.89	-56.17	48.98	0	4
Chave	4	-11.71	33.45	20.17	2	2

The results indicate that the average deviations for two main species of the validated models are consistently smaller than that of the previously published models. In *Vatica odorata* species, prediction of *tAGB* based on validated equations resulted in average deviation ranging from 4.65% to 5.76%. On the other hand, the previously published models gave the average deviation of lower than 10%. This means that all equations can be used to estimate the total tree biomass of this species.

For the *Endospermum sinensis* species, the previously published models have poor estimation of tAGB with average deviation of 20.17% and 48.98% for the equations of Chave et al (2005) and Brown (1997), respectively. The validated equations gave average deviation ranging from 8.49% to 12.63%.

Figure 3.9shows the observed values and the predicted lines using Power model and models of the previously publications.

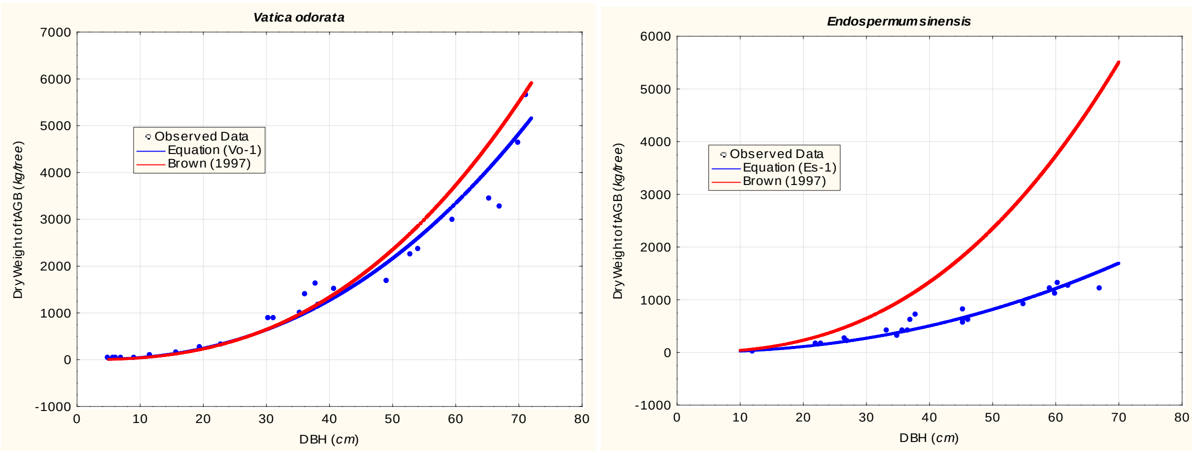

Figure 3.9 DBH and dry weight of the tAGB for V. odorata and E. sinensis species from the observed data and the predicted lines using Power model and previously published models

3.4 Result 4: BEF and BCEF

3.4.1 BCEF

The following table is the analysis of BCEF of sample trees in each sample plot.

Table 3-32 Result of BCEF (Mg m^{-3}) analysis per sample plot

Plot ID	n_i	Mean	Min	Max	Std.Err.	Coef.Var.
HT00	50	0.5983	0.3099	1.2829	0.2036	34.03
HT01	50	0.7091	0.3926	1.2502	0.1962	27.66
HT02	51	0.6469	0.3230	1.3444	0.2089	32.28
NA01	50	0.4870	0.2901	0.9583	0.1691	34.72
Average	201	0.6105	0.2901	1.3444	0.2100	34.40

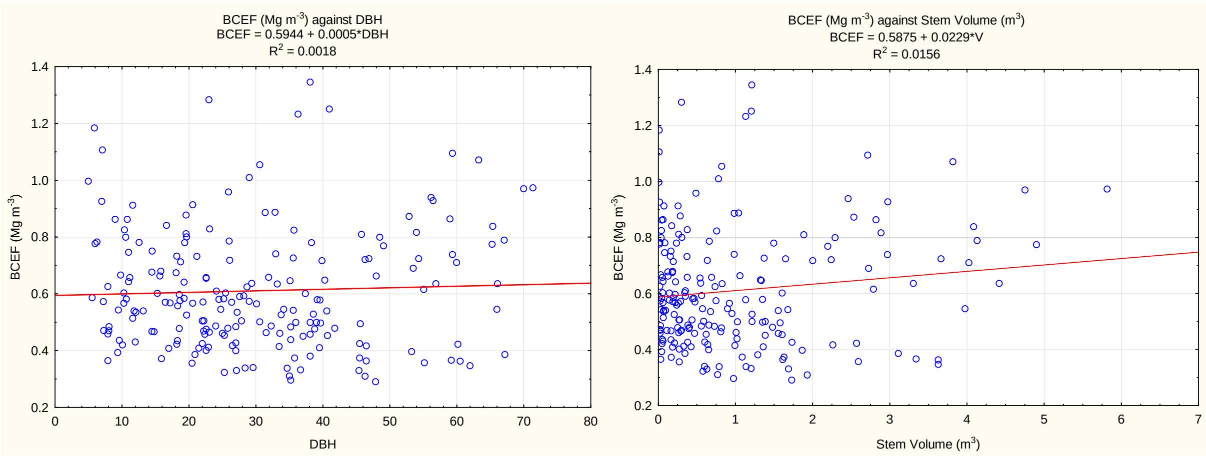

Figure 3.10 Scatter plot and linear regression of BCEF versus DBH and Stem volume

The result in the above figure shows that the R^2 values are very small indicates that the BCEF do not depend on DBH and stem volume.

3.4.2 BEF

The following table is the analysis of BEF of sample trees in each sample plot.

Table 3-33 Result of BEF analysis per sample plot

Plot ID	n_i	Mean	Min	Max	Std.Err.	Coef.Var.
HT00	50	1.3019	1.0455	1.9704	0.1872	14.38
HT01	50	1.2303	1.0416	1.7671	0.1367	11.11
HT02	51	1.2581	1.0558	2.0311	0.1698	13.50
NA01	50	1.1862	1.0832	1.9025	0.1251	10.55
Average	201	1.2442	1.0416	2.0311	0.1612	12.96

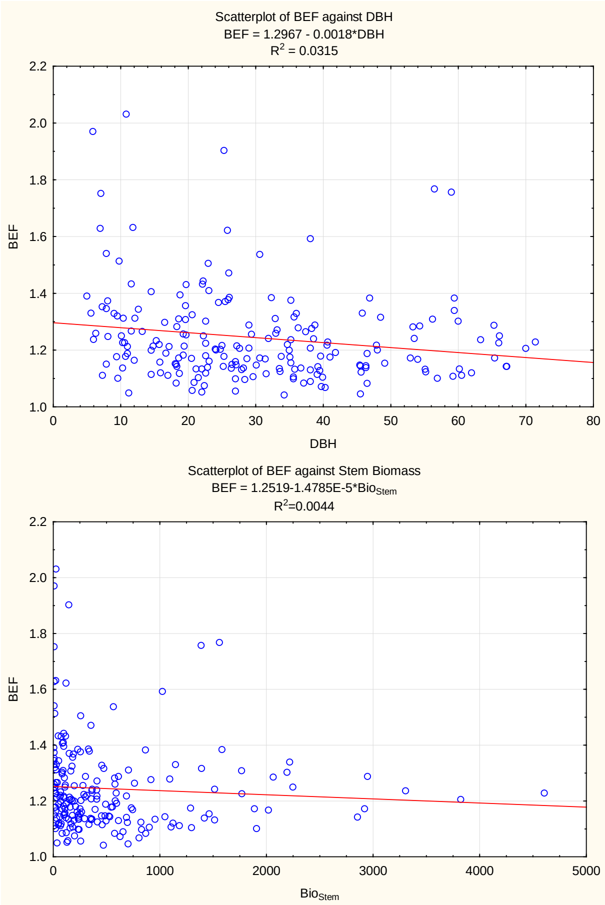

Figure 3.11 Scatter plot and linear regression of BEF versus DBH and Stem biomass

The result in the above figure shows that the R^2 values are very small indicates that the BEF do not depend on DBH and stem biomass.

4 RESULTS FOR BAMBOO FORESTS (*Dendrocalamus barbatus*)

4.1 Result 1: forest and trees characteristics

4.1.1 Forest characteristics: species composition and forest structure

Forest structure

Table 4-1is the statistic of number of bamboo trees per bamboo cluster in sample plot.

Table 4-1 Statistics of number of bamboo trees per cluster

Cluster No.	N	Cluster No.	N	Cluster No.	N	Cluster No.	N
1	11	23	12	45	11	66	11
2	8	24	6	46	6	68	13
3	10	25	12	47	9	69	10
4	10	26	8	48	7	70	8
5	7	27	9	49	13	71	12
6	10	28	18	50	13	72	9
7	12	29	11	51	8	73	11
8	8	30	8	52	7	74	11
9	11	31	10	53	11	75	10
10	15	32	8	54	11	76	10
11	10	33	11	55	10	77	11
12	9	34	12	56	12	78	8
13	12	35	8	57	9	79	9
14	9	36	15	58	9	80	13
15	11	37	14	59	10	81	7
16	18	38	15	60	12	82	10
17	14	39	12	61	12	83	8
18	11	40	9	62	8	84	11
19	11	41	14	63	11	85	15
20	11	42	10	64	10	86	12
21	15	43	14	65	13		
22	11	44	7	Total number of bamboo tree			922

The total number of cluster in sample plot is 86 and the total number of bamboo tree per plot is 922.

In each bamboo cluster, all bamboo trees was measured DBH and classified into 3 age classes (I-young, II-medium, and III-old). The age class of bamboo was determined based on the following characteristics:

Young: bamboo age 1-2 years and have adequate development of branches and foliage. The stem is deep blue, with hair and no lichen on stem. The stem contains much water, is soft and white color inside. The sheaves of bamboo shoot remain on the stem.

Medium: bamboo age 3-4 years. There are no sheaves on the stem and dense branches distribute mainly on the top of the stem. The color of stem and main branch skin is deep blue mixed with brownish-yellow and there is spotted lichen on the stem.

Old: bamboo is 5 years or more. The leaves are light blue and stems are bluish-yellow or spotted whitish-grey caused by strong development of lichen (70-80 %) and the deep blue color of the stem skin has almost disappeared.

The diameter distribution of sample plots by age classes is illustrated in Table 4-2:

Table 4-2 Diameter distribution of bamboo by plots and age classes

Diameter range (cm)	DBH_i (cm)	Number of tree			
		Total	A=I	A=II	A=III
2.0-4.0	3	3	1	2	-
4.0-6.0	5	81	27	16	38
6.0-8.0	7	285	70	80	135
8.0-10.0	9	399	117	122	160
10.0-12.0	11	148	32	40	76
12.0-14.0	13	6	1	1	4
Total		922	248	261	413

Note: A = age class, A=I (young), A=II (mediate) and A=III (old)

Because the stem form of *D. barbatus* is curved in the form of a question mark, physical measurement of the total of tree height cannot be taken without felling. Therefore height was estimated based on the result of regression between height and diameter which was established from data of the felled sample bamboo trees.

The result of details inventory of sample bamboo clusters are shown in Annex B.1.

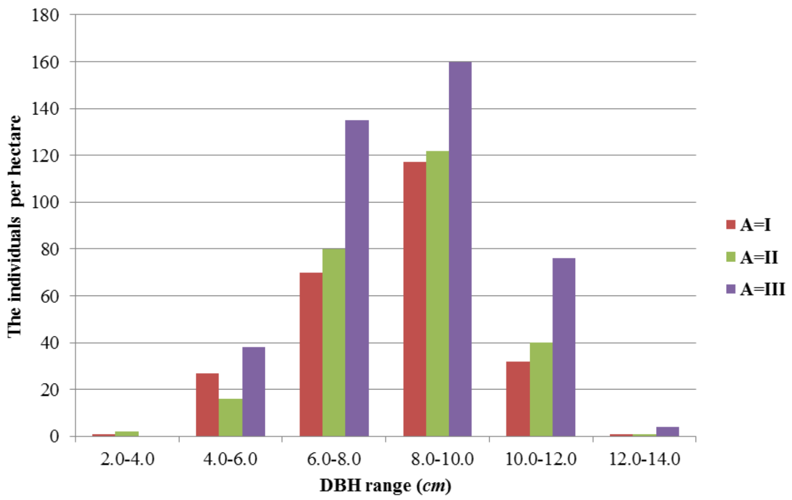

Figure 4.1 The diameter distribution of bamboo forest by age classes

4.1.2 Relation between H and diameter

The relationship between bamboo tree height (H) and DBH was established based on the dataof100 sample bamboo trees. Three models bellow were chosen to establish this regression.

$H = b_1 + b_2*DBH$ Model (3.12)

$H = b_1 + b_2*log(DBH)$ Model (3.13)

$H = b_1*DBH^{b2}$ Model (3.14)

Table 4-3presents the results of correlation analysis for the above equations (details in AnnexB.3):

Table 4-3 The regression coefficients, R-square SSE and AIC of candidate equations

Models	N	b_1	b_2	$\bar{R}^2$	SSE
(3.12)	100	4.8822^{***}	0.9271^{***}	0.6417^{***}	132.4
(3.13)	100	-2.0558^{ns}	16.0659^{***}	0.6243^{***}	138.8
(3.14)	100	3.5913^{***}	0.5946^{***}	0.6227^{***}	134.0

Note: The statistical analyses are significant at 95% confidence interval. ***$p<0.001$; **$p<0.01$; *$p<0.05$; and non-significant, $^{ns}p>0.05$.

The result above shows that, the adjusted coefficient of determination ($\bar{R}^2$) of the equations are high, ranging from 0.6227 to 0.6417. Thus, the relationship between the bamboo tree height and diameter in these models are strong and can be considered functional relations.

On comparison of $\bar{R}^2$ and *SSE* values model (3.12) has the smallest *SSE* value, therefore model (3.12) is selected as the optimal equation using for estimating total height of bamboo. The optimal equation is:

$H = 4.8822 + 0.9271*DBH$ $\bar{R}^2 = 0.6417$ Equation (H-05)

Based on these results the descriptive statistics for bamboo were generated (Table 4-4).

Table 4-4 Descriptive statistics of bamboo stand

Contents	Unit	Age = I	Age = II	Age = III	Total
Tree density	Tree per ha	248	260	414	922
Average DBH	cm	8.21	8.44	8.28	8.31
Min DBH	cm	2.6	3.9	3.8	2.6
Max DBH	cm	12.3	12.6	12.6	12.6
Std. Dev.	cm	1.72	1.51	1.72	1.66
Average H	m	12.49	12.71	12.56	12.59

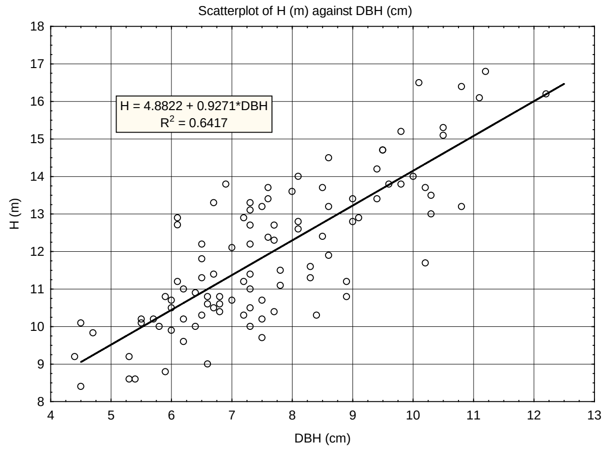

Figure 4.2 **The best fitted equation of H-DBH regression in bamboo forest**

4.1.3 Biomass of sample trees

To measure the fresh biomass of bamboo forests, 100 sample trees were randomly selected. The distribution of sample trees by age class is shown in Table 4-5(details in the Annex B.2).

Table 4-5Sample tree count for fresh biomass measurement of bamboo forests

DBH range (cm)	DBH_i (cm)	Sample tree count by age class			
		Sum	A=I	A=II	A=III
2.0-4.0	3	0	0	0	0
4.0-6.0	5	13	13	0	0
6.0-8.0	7	50	30	16	4
8.0-10.0	9	24	0	12	12
10.0-12.0	11	12	0	2	10
12.0-14.0	13	1	0	0	1
Total		100	43	30	27

Note: A = age class, A=I (young), A=II (mediate) and A=III (old)

After felling, the sample trees were separated into stems, branches and foliage and then weighed for fresh biomass (Annex B.2). To estimate the total fresh biomass of bamboo, the average fresh weight per component of sample tree per age class was first calculated (Table 4-6).

Table 4-6 **Average fresh biomass estimation per bamboo component by age class**

Age class	n_i	Average fresh biomass of a bamboo sample (kg)							
		Stem	%	Branch	%	Foliage	%	Total	%
I	43	12.08	68.2	3.20	18.1	2.43	13.7	17.71	100
II	30	19.95	70.2	4.79	16.9	3.67	12.9	28.41	100
III	27	29.63	72.9	6.48	15.9	4.54	11.2	40.64	100
Average	-	19.18	70.7	4.56	16.8	3.37	12.4	27.11	100

The results indicate that the average fresh biomass per bamboo tree is27.11 kg, of which the stem is19.18 kg (or 70.7%), branch is4.56 kg (16.8 %) and foliage is3.37 kg (12.4 %). Greater values of fresh biomass were observed with increase in age class.

Results from Table 4-1were employed to estimate the total fresh biomass of bamboo (Table 4-7).

Table 4-7 Calculation of total fresh biomass of bamboo stand by age classes

Age class	N_i	Total fresh biomass of bamboo stand per ha (kg)							
		Stem		Branch		Foliage		Total	
		Aver.	Per ha	Aver.	Per ha	Aver.	Per ha	Aver.	Per ha
I	248	12.08	2995	3.20	795	2.43	603	17.71	4392
II	261	19.95	5206	4.79	1250	3.67	959	28.41	7415
III	413	29.63	12,236	6.48	2675	4.54	1875	40.64	16,786
Total	922	19.18	20,437	4.56	4720	3.37	3437	27.11	28,593

The results indicate that total fresh biomass of bamboo is about 28.593 ton/ha, of which fresh biomass of stem is20.437 ton/ha (or 71.5 %), branch is4.72 ton/ha (16.5 %) and fresh biomass of foliage is3.437 ton/ha (12.0 %).

For dry biomass analysis, from 100 sample bamboo trees, 51 sample trees were randomly selected (Table 4-8, details in Annex B.4).

Table 4-8 Sample bamboo tree count for dry biomass analysis

DBH range (cm)	DBH_i (cm)	Sample tree count for dry biomass analysis by age class			
		Sum	A=I	A=II	A=III
2.0-4.0	3				
4.0-6.0	5	9	9		
6.0-8.0	7	23	8	11	4
8.0-10.0	9	10		5	5
10.0-12.0	11	9		1	8
12.0-14.0	13				
Total		51	17	17	17

Note: A = age class, A=I (young), A=II (mediate) and A=III (old)

In each sample tree, six samples were taken, of which four samples were for stems, one sample for branches and one sample for foliage. These samples (306 in total) were analyzed in the laboratory, and the dry biomass of each bamboo component was calculated (Annex B.5).

To estimate the dry biomass of sample trees dry-fresh mass ratio (p_j) was calculated (Table 4-9, details in Annex B.5).

Table 4-9 Calculation of dry-fresh biomass ratios for sample tree by age classes

Age class	n_i	Dry-fresh mass ratio of each bamboo components		
		Stem	Branch	Foliage
I	17	0.3972	0.3968	0.2987
II	17	0.4552	0.4287	0.3338
III	17	0.4822	0.4622	0.3786
Average		0.4449	0.4292	0.3370

The average dry biomass of a sample bamboo tree in each age class is shown in the Table 4-10(details in Annex B.6).

Table 4-10 Calculation of average dry biomass for bamboo components by age class

Age class	n_i	Average dry biomass of a bamboo sample (kg)							
		Stem	%	Branch	%	Foliage	%	Sum	%
I	17	3.75	67.1	1.22	21.8	0.62	11.0	5.59	100
II	17	8.73	74.0	1.86	15.8	1.20	10.2	11.79	100
III	17	13.52	73.1	3.19	17.3	1.78	9.6	18.49	100
Average		8.67	71.4	2.09	18.3	1.20	10.3	11.96	100

The results indicate that the average dry biomass per bamboo is11.96 kg, of which the stem accounts for 8.67 kg (or 71.4%), the branch is 2.09 kg (18.3 %) and the foliage is1.20 kg (10.3 %). Greater values of dry biomass were observed with increase in age class.

4.2 Result 2: Modeling of Aboveground biomass

4.2.1 Modeling per tree compartments

To develop the allometric equation for biomass estimation, some formulae were tested:

$$y = b_1 * \exp(b_2 * D) \quad (3.15)$$

$$y = b_1 * (D)^{b2} \quad (3.16)$$

$$y = b_1 + b_2 * (D^2H) \quad (3.17)$$

$$y = b_1 + b_2 * \log(D^2H) \quad (3.18)$$

$$y = b_1 * (D^2H)^{b2} \quad (3.19)$$

where: *y* is dependent variable (total dry biomass, dry biomass of stem, branch, foliage; in *kg*); *D* is diameter at breast height (*cm*); D^2H is in m^3; b_1, $b_2$are regression coefficients

For stem biomass, all candidate models were tested, first through graphic exploration using scatter plots (Figure 4.3) and then through correlation analysis (Table 4-11, details in Annex B.7).

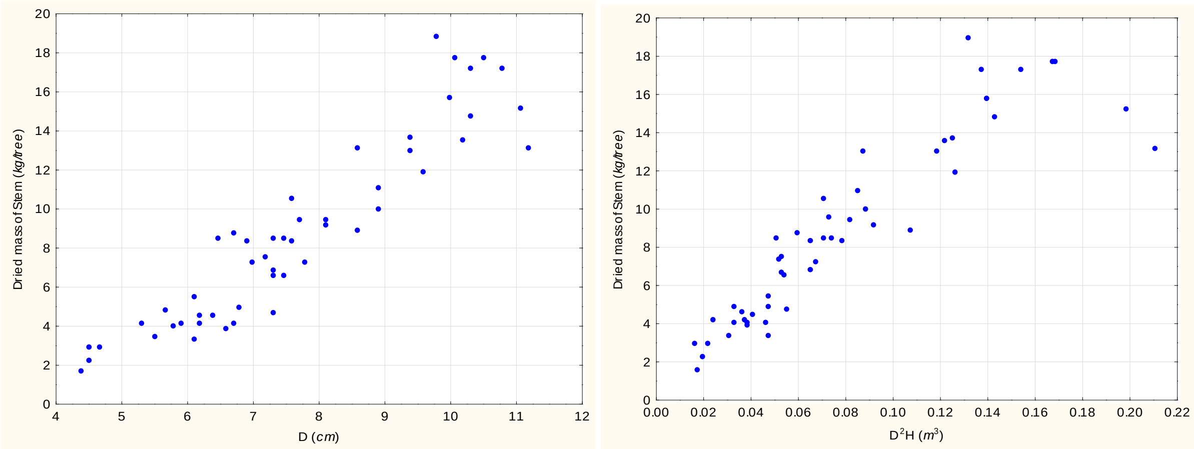

Figure 4.3 **Scatter plots of stem biomass and variables D and D^2H in bamboo forests**

Table 4-11 Correlation analysis of stem biomass equations in bamboo forests

Age class	Equation	N	b_1	b_2	$\bar{R}^2$	SSE
I	(3.15)	17	1.0629**	0.2148***	0.6025***	5.43
	(3.16)	17	0.4006^{ns}	1.2712***	0.6431***	4.93
	(3.17)	17	1.6076**	60.3328***	0.5679***	5.58
	(3.18)	17	10.5228***	4.5882***	0.6239***	4.86
	(3.19)	17	23.0174*	0.5390***	0.5966***	5.21
II	(3.15)	17	3.0865***	0.1317***	0.6714***	12.48
	(3.16)	17	0.8343**	1.1427***	0.6780***	12.31
	(3.17)	17	5.3960***	40.3977***	0.7258***	13.83
	(3.18)	17	19.9701***	10.0689***	0.7780***	11.20
	(3.19)	17	27.0126***	0.4447***	0.7084***	11.78
III	(3.15)	17	1.9640*	0.2028***	0.7613***	67.09
	(3.16)	17	0.1889^{ns}	1.9021***	0.7805***	61.32
	(3.17)	17	4.1994*	78.0882***	0.7306***	60.73
	(3.18)	17	32.6175***	20.0212***	0.8118***	42.43
	(3.19)	17	54.5535***	0.6481***	0.8304***	52.97
General	(3.15)	51	1.1909***	0.2469***	0.8576***	181.57
	(3.16)	51	0.1132**	2.1018***	0.8833***	151.80
	(3.17)	51	1.5928**	89.4100***	0.8267***	190.06
	(3.18)	51	27.3598***	15.8138***	0.8375***	178.25
	(3.19)	51	65.8565***	0.7843***	0.8910***	167.88

Note: The statistical analyses are significant at 95% confidence interval. ***$p < 0.001$; **$p < 0.01$; *$p < 0.05$; and non-significant, $^{ns}p > 0.05$.

The results indicate that the values for the adjusted coefficient of determinations ($\bar{R}^2$) of the candidate models are medium to high, ranging from 0.5679 in model (3.17) in age class I to 0.8910 in model (3.19) for the general category. Thus, the relationship between the stem biomass of bamboo forest with variables *D* or D^2H in these equation forms is strong and can be considered functional relations.

The results also indicate that all candidate models have significant values of coefficients b_2 at $p<0.001$.

On comparing $\bar{R}^2$ and *SSE* values, model (3.16) is selected as the optimal equation for estimating stem biomass of bamboo forest, for the general category. For estimations per each age class, model (3.18) is the optimal model. Optimal equations for respective age classes are:

Age class I:	$y = 10.5228 + 4.5882*\log(D^2H)$	$\bar{R}^2 = 0.6239$	Equation (S-05)
Age class II:	$y = 19.9701 + 10.0689*\log(D^2H)$	$\bar{R}^2 = 0.7780$	Equation (S-06)
Age class III:	$y = 32.6175 + 20.0212*\log(D^2H)$	$\bar{R}^2 = 0.8118$	Equation (S-07)
General:	$y = 0.1132*D^{2.1018}$	$\bar{R}^2 = 0.8833$	Equation (S-08)

For branch biomass, models (3.15), (3.16), (3.18) and (3.19) were tested firstly through graphic exploration on scatter plots (Figure 4.4) and then through correlation analysis between branch biomass and variables *D* and D^2H (

Table 4-12, details in Annex B.8).

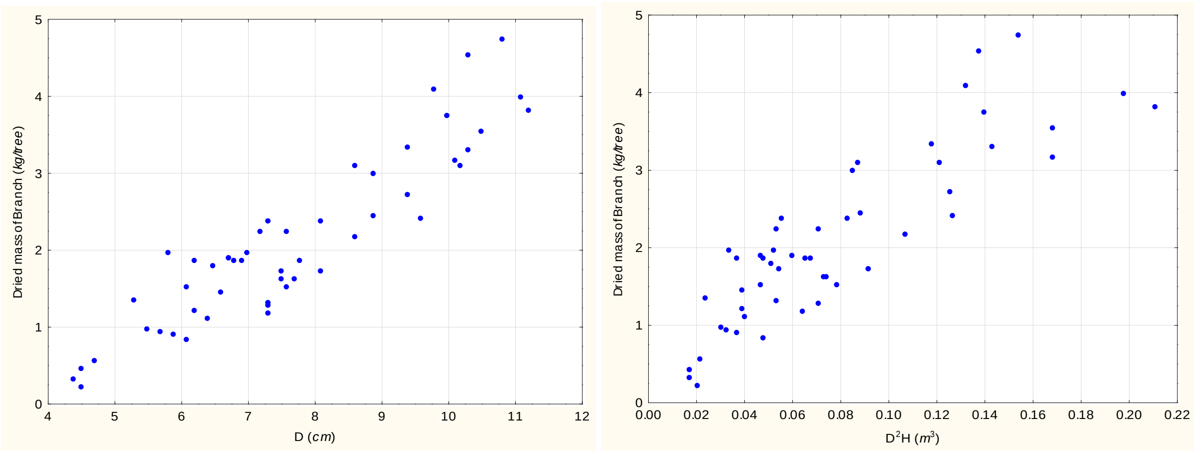

Figure 4.4 Scatter plots of branch biomass and variables D and D^2H in bamboo forests

Table 4-12Correlation analysis of branch biomass equations in bamboo forests

Age class	Equation	N	b_1	b_2	$\bar{R}^2$	SSE
I	(3.15)	17	0.0606^{ns}	0.5039^{***}	0.7523^{***}	1.78
	(3.16)	17	0.0055^{ns}	3.0420^{***}	0.7817^{***}	1.69
	(3.18)	17	5.7005^{***}	3.0352^{***}	0.5826^{***}	2.51
	(3.19)	17	67.1869^{ns}	1.2040^{*}	0.6487^{***}	2.57
II	(3.15)	17	0.3439^{***}	0.2121^{***}	0.5842^{***}	1.75
	(3.16)	17	0.0403^{ns}	1.8570^{***}	0.5776^{***}	1.86
	(3.18)	17	5.6144^{***}	3.3600^{***}	0.6412^{***}	2.41

Age class	Equation	N	b_1	b_2	$\bar{R}^2$	SSE
	(3.19)	17	10.9103^{***}	0.7020^{***}	0.5360^{***}	2.05
III	(3.15)	17	0.4883^{*}	0.1973^{***}	0.7492^{***}	3.36
	(3.16)	17	0.0535^{ns}	1.8207^{***}	0.7535^{***}	3.29
	(3.18)	17	6.9877^{***}	3.9799^{***}	0.6268^{***}	4.21
	(3.19)	17	10.4740^{**}	0.5507^{***}	0.6892^{***}	4.51
General	(3.15)	51	0.3007^{***}	0.2411^{***}	0.7529^{***}	10.03
	(3.16)	51	0.0326^{**}	2.0177^{***}	0.8079^{***}	9.30
	(3.18)	51	6.1831^{***}	3.4611^{***}	0.7469^{***}	14.87
	(3.19)	51	13.8942^{***}	0.7312^{***}	0.7409^{***}	13.78

Note: The statistical analyses are significant at 95% confidence interval. ***$p < 0.001$; **$p < 0.01$; *$p < 0.05$; and non-significant, $^{ns}p > 0.05$.

The results indicate that the adjusted coefficient of determinations ($\bar{R}^2$) of the validated models are medium to high, ranging from 0.5360 (3.19) in age class II to 0.8079 (3.16) in the general category. Thus, the relationship between the branch biomass of bamboo forest with variables D or D^2H in these equation forms is strong and can be considered functional relations.

The results also indicate that in age class I, all of the models have non-significant values of coefficient b_1 at $p<0.05$, with the exception of model (3.18), therefore in age class I, model (3.18) is selected as the optimal model. Based on the significance of coefficients and on comparing $\bar{R}^2$ and *SSE* values, model (3.15) is selected as the optimal model to estimate branch biomass of bamboo forest age classes II and III; and in general category the optimal is model (3.16). Optimal equations for respective age classes are:

Age class I:	$y = -5.7005 + 3.0352*\log(D^2H)$	$\bar{R}^2 = 0.5826$	Equation (B-05)
Age class II:	$y = 0.3439*\exp(0.2121*D)$	$\bar{R}^2 = 0.5842$	Equation (B-06)
Age class III:	$y = 0.4883*\exp(0.1973*D)$	$\bar{R}^2 = 0.7492$	Equation (B-07)
General:	$y = 0.0326*D^{2.0177}$	$\bar{R}^2 = 0.8079$	Equation (B-08)

For foliage biomass, models (3.15), (3.16), (3.18) and (3.19) were tested, firstly through graphic exploration using scatter plots (Figure 4.5) and then through correlation analysis between foliage biomass and variables D and D^2H(Table 4-13, details in Annex B.9).

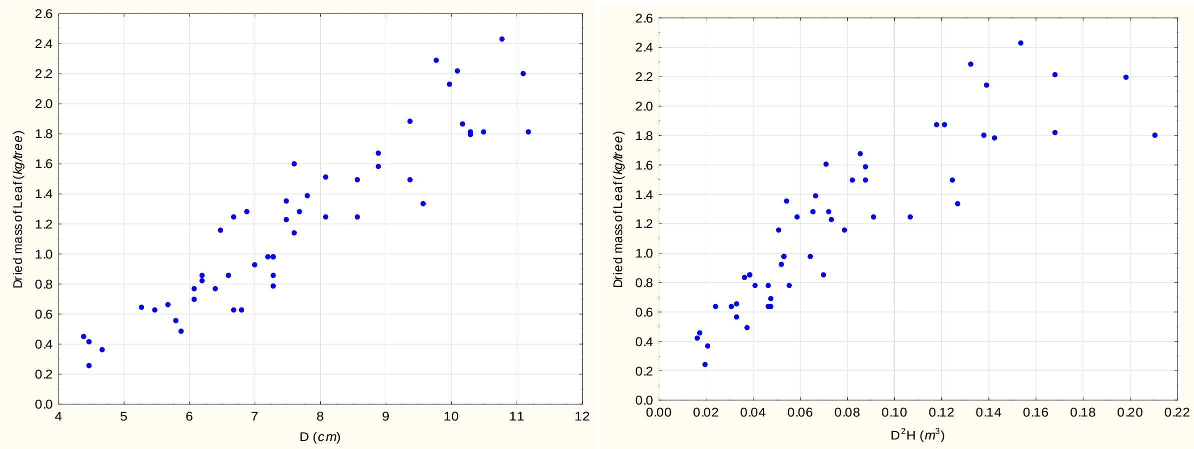

Figure 4.5 Scatter plots of foliage biomass and variables D and D^2H in bamboo forests

Table 4-13Correlation analysis of foliage biomass equations in bamboo forests

Age class	Equation	N	b_1	b_2	$\bar{R}^2$	SSE
I	(3.15)	17	0.1479*	0.2429**	0.5853***	0.22
	(3.16)	17	0.0479^{ns}	1.4506***	0.6166***	0.20
	(3.18)	17	1.8067***	0.8383***	0.5204***	0.23
	(3.19)	17	4.2735^{ns}	0.5756**	0.5109***	0.25
II	(3.15)	17	0.4429***	0.1263***	0.5097***	0.48
	(3.16)	17	0.1256*	1.0986***	0.5271***	0.47
	(3.18)	17	2.6552***	1.3040***	0.5681***	0.49
	(3.19)	17	3.4670***	0.4175***	0.5047***	0.50
III	(3.15)	17	0.4319**	0.1494***	0.6790***	0.77
	(3.16)	17	0.0828^{ns}	1.3691***	0.6888***	0.76
	(3.18)	17	3.5153***	1.8174***	0.6667***	0.74
	(3.19)	17	4.7899***	0.4572***	0.6904***	0.77
General	(3.15)	51	0.2207***	0.2119***	0.8270***	2.71
	(3.16)	51	0.0314***	1.7720***	0.8653***	2.28
	(3.18)	51	3.3778***	1.8387***	0.8243***	2.69
	(3.19)	51	6.7131***	0.6613***	0.8383***	2.83

Note: The statistical analyses are significant at 95% confidence interval. ***$p < 0.001$; **$p < 0.01$; *$p < 0.05$; and non-significant, $^{ns}p > 0.05$.

The results indicate that the adjusted coefficient of determinations ($\bar{R}^2$) of the candidate models are medium to high, ranging from 0.5047 (3.19) in age class II to 0.8653 (3.16) in the general category. Thus, the relationship between the foliage biomass of bamboo forests with variables D or D^2H in these equation forms is strong and can be considered functional relations.

The results also show that in age class I, all models generate non-significant coefficient values b_1 at $p<0.05$ with the exception of models (3.15) and (3.18), therefore for age class I, model (3.15) is selected as the optimal model due to the smaller *SSE* value between the models(3.15) and (3.18). For age class II and in the general category, based on the significance of coefficients and comparing $\bar{R}^2$ and *SSE* values, model (3.16) is selected as the optimal model for estimating foliage biomass. For age class III, model (3.18) is selected. Optimal equations for respective age classes are:

Age class I:	$y = 0.1479*\exp(0.2429*D)$	$\bar{R}^2 = 0.5853$	Equation (L-05)
Age class II:	$y = 0.1256*D^{1.0986}$	$\bar{R}^2 = 0.5271$	Equation (L-06)
Age class III:	$y = 3.5153 + 1.8174*\log(D^2H)$	$\bar{R}^2 = 0.6667$	Equation (L-07)
General:	$y = 0.0314*D^{1.7720}$	$\bar{R}^2 = 0.8653$	Equation (L-08)

4.2.2 Modeling of total aboveground biomass

For total above ground biomass (*tAGB*) of bamboo forests, all candidate models were tested, firstly through graphic exploration on scatter plots (Figure III.12) and then through correlation analysis between *tAGB* and variables *D* and D^2H (Figure 4.6, details in Annex B.10).

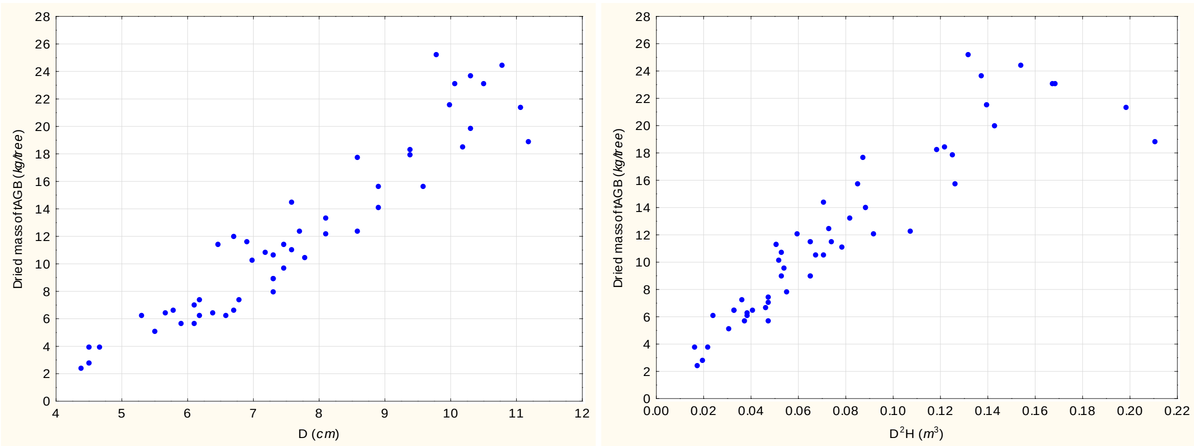

Figure 4.6 Scatter plots of tAGB and variables D and D^2H in bamboo forests

Table 4-14 Correlation analysis of tAGB equations in bamboo forests

Age class	Equation	N	b_1	b_2	$\bar{R}^2$	SSE
I	(3.15)	17	1.0733^{**}	0.2801^{***}	0.7594^{***}	9.37
	(3.16)	17	0.3001^{*}	1.6582^{***}	0.7978^{***}	8.06
	(3.17)	17	1.5956^{*}	112.3811^{***}	0.6840^{***}	11.98
	(3.18)	17	18.0333^{***}	8.4321^{***}	0.7286^{***}	10.29
	(3.19)	17	54.4177^{*}	0.6778^{***}	0.7073^{***}	11.32
II	(3.15)	17	3.7710^{***}	0.1442^{***}	0.6844^{***}	23.60
	(3.16)	17	0.8992^{**}	1.2517^{***}	0.6886^{***}	23.78
	(3.17)	17	6.8355^{***}	60.0720^{***}	0.7502^{***}	27.03
	(3.18)	17	28.2397^{***}	14.7329^{***}	0.7763^{***}	24.21
	(3.19)	17	40.1493^{***}	0.4829^{***}	0.6964^{***}	24.26
III	(3.15)	17	2.8418^{**}	0.1969^{***}	0.7936^{***}	94.67
	(3.16)	17	0.2982^{ns}	1.8385^{***}	0.8103^{***}	86.46

	(3.17)	17	6.4463**	100.9292***	0.7400***	96.77
	(3.18)	17	43.1205***	25.8184***	0.8181***	67.71
	(3.19)	17	69.3722***	0.6137***	0.8396***	83.16
General	(3.15)	51	1.7042***	0.2424***	0.8811***	264.62
	(3.16)	51	0.1726***	2.0545***	0.9150***	215.61
	(3.17)	51	2.5101***	119.4117***	0.8385***	311.60
	(3.18)	51	36.9280***	21.1241***	0.8498***	289.90
	(3.19)	51	86.2110***	0.7633***	0.9040***	269.65

Note: The statistical analyses are significant at 95% confidence interval. ****p < 0.001*; ***p < 0.01*; **p < 0.05*; and non-significant, $^{ns}p > 0.05$.

The results also indicate that the adjusted coefficients of determination ($\bar{R}^2$) of the candidate models are very high, ranging from 0.6840 in model (3.17) for age class I to 0.9150 in model (3.16) for the general category. Thus, the relationship between the *tAGB* of bamboo forests with variables *D* or D^2H in these equation forms is very strong and can be considered functional relations.

The results also indicate that all candidate models have significant values of coefficients b_2 at $p<0.05$ with the exception of model (3.16) for age class III.

On comparing $\bar{R}^2$ and *SSE* values, model (3.16) is selected as the optimal equation for estimating *tAGB* of bamboo forests for the general category. Optimal equations for respective age classes are:

Age class I:	$y = 0.3001*D^{1.6582}$	$\bar{R}^2 = 0.7978$	Equation (T-05)
Age class II:	$y = 0.8992*D^{1.2517}$	$\bar{R}^2 = 0.6886$	Equation (T-06)
Age class III:	$y = 43.1205+25.8184*\log(D^2H)$	$\bar{R}^2 = 0.8181$	Equation (T-07)
General:	$y = 0.1726*D^{2.0545}$	$\bar{R}^2 = 0.9150$	Equation (T-08)

Using the results of diameter distribution, *tABG* equations developed, *tAGB* per hectare was calculated (Table 4-15).

Table 4-15 Calculation of total above ground biomass per ha of bamboo forests

Age class	N (tree/ha)	DBH (cm)	H (m)	D^2H (m^3)	tAGB (ton/ha)
I	248	8.21	12.49	0.0842	2.44
II	260	8.44	12.71	0.0905	3.35
III	414	8.28	12.56	0.0861	6.47
Total	922	8.31	12.59	0.0869	12.33

4.2.3 Validation of equations

Twenty sample trees were also felled as the control data (Annex B.11). Only equations for stand level were evaluated. Deviation (relative error, Δ%) calculated as formula (1.3) was employed to validate the accuracy of the selected models (Table 4-16, details in Annex B.12).

For stem biomass, the following equations were validated:

$Y = 1.1909*\exp(0.2469*D)$ (S-3.15)

$Y = 0.1132*D^{2.1018}$ (S-3.16) = Equation (S-08)

$Y = 1.5928+89.41*(D^2H)$ (S-3.17)

$Y = 27.36+15.814*\log(D^2H)$ (S-3.18)

$Y = 65.856*(D^2H)^{0.7843}$ (S-3.19)

Table 4-16 Percentage error of stem biomass equations

Equation	No. of control samples	Min Δ%	Max Δ%	$\overline{\Delta}$%	No. of +Δ%	No. of -Δ%
(S-3.15)	20	0.20	-20.64	10.06	10	10
(S-3.16)	20	0.25	-18.13	9.83	10	10
(S-3.17)	20	0.22	22.07	9.46	11	9
(S-3.18)	20	1.54	32.03	15.89	12	8
(S-3.19)	20	-1.53	25.61	10.12	10	10

The maximum error of stem biomass estimation ranges from -18.13% in equation (S-3.16) to32.03% in equation (S-3.18). The average deviation ranges from 9.46% in equation (S-3.17) to 15.89% in equation (S-3.18). This result is entirely consistent with the results for optimal models selection. The errors are at acceptable levels for the estimation of stem biomass of standing trees in bamboo forests.

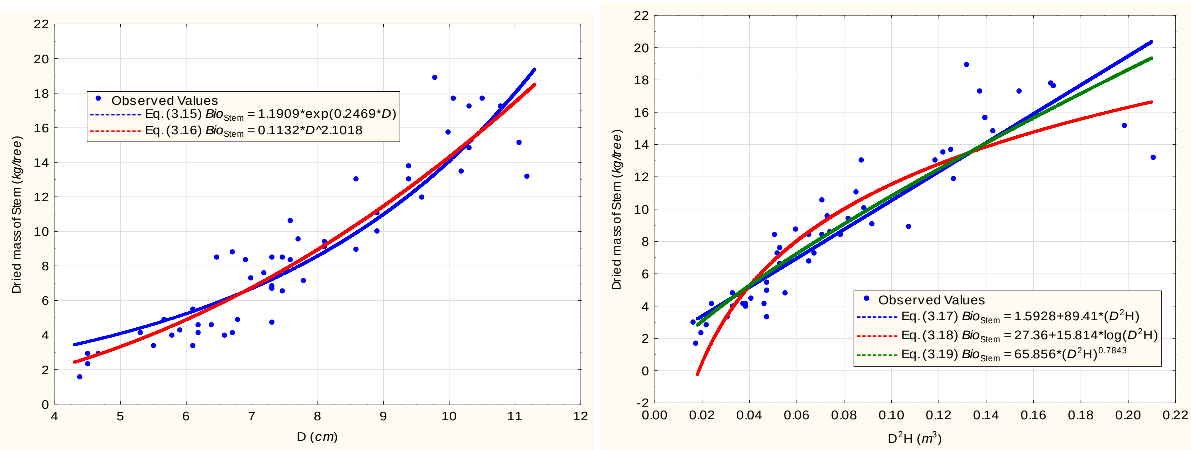

Figure 4.7 The regression lines of validated models for estimating stem biomass of bamboo forests

For branch biomass, the following equations were validated:

$Y = 0.3007*\exp(0.2411*D)$ (B-3.15)

$Y = 0.0326*D^{2.0177}$ (B-3.16) = Equation (B-08)

$Y = 6.1831+3.4611*\log(D^2H)$ (B-3.18)

$Y = 13.894*(D^2H)^{0.7312}$ (B-3.19)

Table 4-17is the result of the deviation for each equation (details in Annex B.13).

Table 4-17 Relative error of branch biomass equations

Equation	No. of control samples	Min Δ%	Max Δ%	$\bar{\Delta}$%	No. of +Δ%	No. of -Δ%
(B-3.15)	20	-1.01	19.89	9.45	10	10
(B-3.16)	20	-2.30	21.45	10.25	10	10
(B-3.18)	20	3.37	31.84	14.81	17	3
(B-3.19)	20	-0.59	-28.23	12.29	14	6

The results indicate that the maximum error of branch biomass estimation ranges from 19.89% for equation (B-3.15) to 31.84% for equation (B-3.18). The average deviation ranges from 9.45% for equation (B-3.15) to 14.81% for equation (B-3.18). This result is entirely consistent with previous results of optimal models selection. These error levels are acceptable for branch biomass estimation of standing trees in bamboo forests.

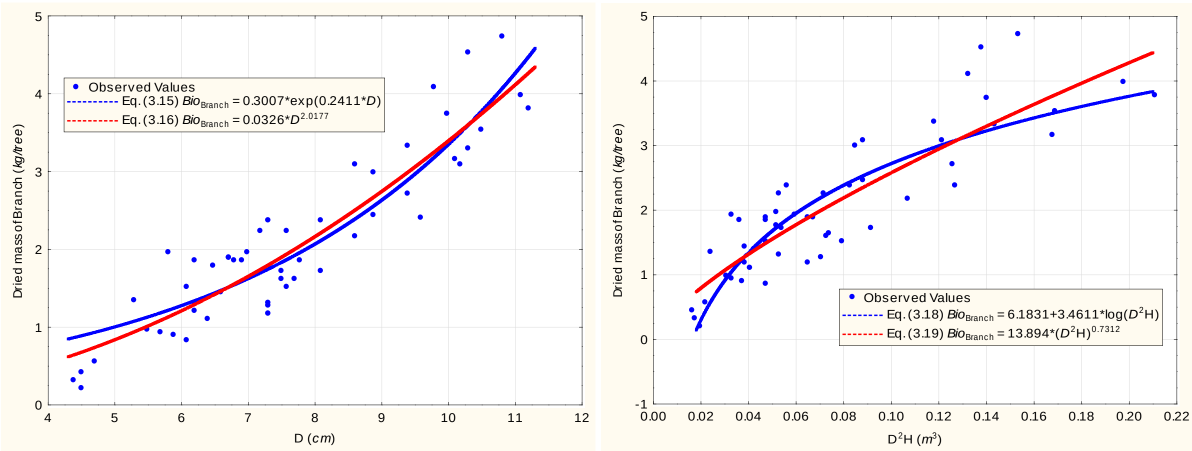

Figure 4.8 The regression lines of validated models to estimate branch biomass of bamboo forests

For foliage biomass, the following equations were validated:

$Y = 0.2207*\exp(0.2119*D)$ (L-3.15)

$Y = 0.0314*D^{1.7720}$ (L-3.16) = Equation (L-08)

$Y = 3.3778+1.8387*\log(D^2H)$ (L-3.18)

$Y = 6.7131*(D^2H)^{0.6613}$ (L-3.19)

Table 4-18 is the result of relative error for each equation (details in Annex B.14).

Table 4-18 Relative error of foliage biomass allometric equations

Equation	No. of control samples	Min Δ%	Max Δ%	$\bar{\Delta}$%	No. of +Δ%	No. of -Δ%
(L-3.15)	20	-0.42	27.96	11.63	11	9
(L-3.16)	20	1.28	20.75	10.55	13	7
(L-3.18)	20	2.29	30.05	14.60	16	4
(L-3.19)	20	0.56	-30.83	12.80	16	4

The results indicate that the maximum error of foliage biomass estimation ranges from 20.75% for equation (L-3.16) to -30.83% for equation (L-3.19). The average deviation ranges from 10.55% for equation (L-3.16) to 14.60% for equation (L-3.18). This result is entirely consistent with previous results of optimal models selection. The error levels are acceptable for foliage biomass estimation of standing trees in bamboo forests.

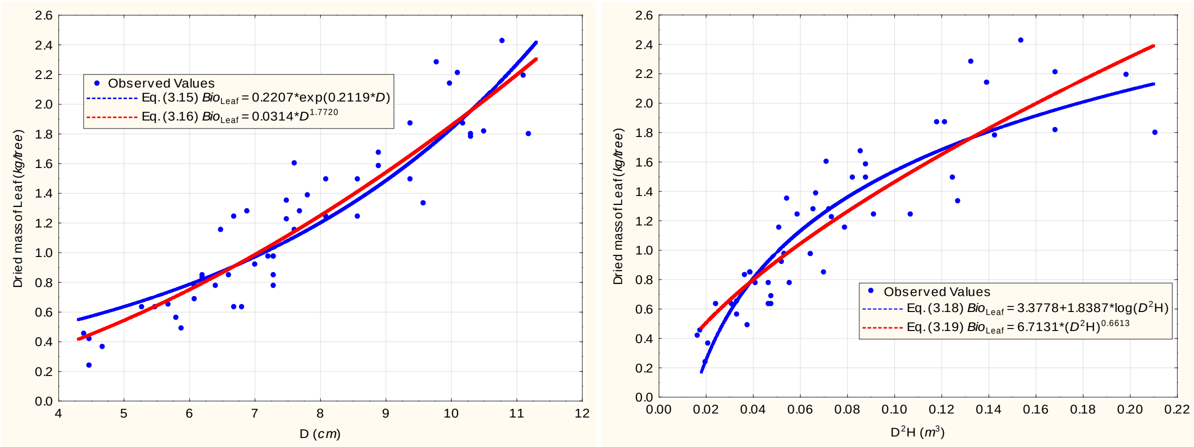

Figure 4.9 The regression lines of validated models for estimating foliage biomass (Bio_{Leaf}) of bamboo forests

For total above ground biomass (tABG), the following equations were validated:

$Y = 1.7042*\exp(0.2424*D)$ (T-3.15)

$Y = 0.1726*D^{2.0545}$ (T-3.16) = Equation (T-08)

$Y = 2.5101+119.41*(D^2H)$ (T-3.17)

$Y = 36.928+21.124*\log(D^2H)$ (T-3.18)

$Y = 86.211*(D^2H)^{0.7633}$ (T-3.19)

Table 4-19is the result of relative error for each equation (details in Annex B.15).

Table 4-19 Percentage error of total tree aboveground biomass equations

Equation	No. of control samples	Min Δ%	Max Δ%	$\overline{\Delta}$%	No. of +Δ%	No. of -Δ%
(T-3.15)	20	1.11	-18.54	7.81	10	10
(T-3.16)	20	-0.17	-16.54	7.41	10	10
(T-3.17)	20	-0.10	-17.89	8.72	11	9
(T-3.18)	20	4.15	29.66	14.19	11	9
(T-3.19)	20	-0.27	19.81	9.09	11	9

The maximum error of total biomass estimation ranges from -16.54% for equation (T-3.16) to 29.66% for equation (T-3.18). The average error ranges from 7.41% for equation (T-3.16) to 14.19% for equation (T-3.18). These error levels are acceptable for estimation of total aboveground biomass of standing trees in bamboo forests.

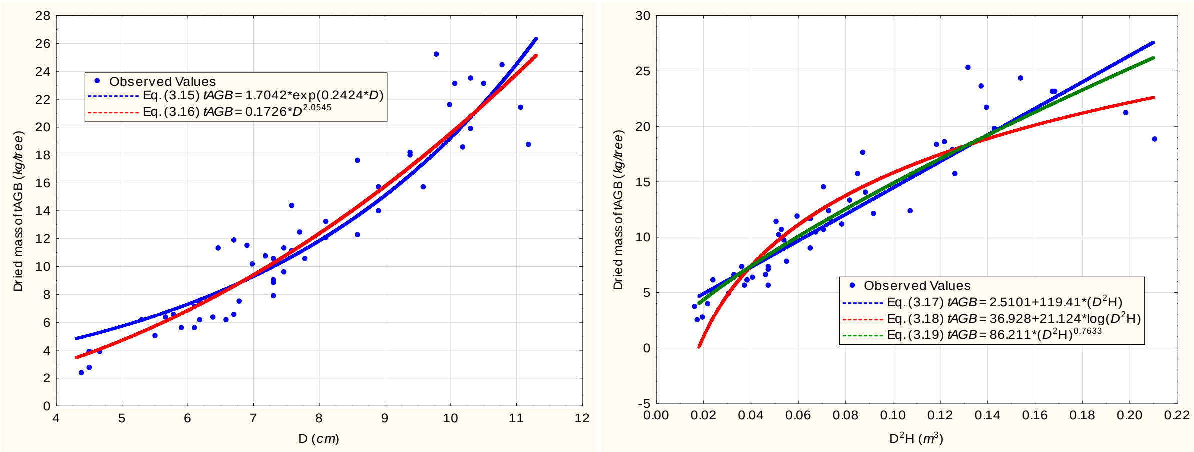

Figure 4.10 The regression lines of validated models for estimating total above ground biomass (tAGB) of bamboo forests

5 CONCLUSIONS AND RECOMMENDATIONS

5.1 Evergreen broadleaf (EB) forests

The main purpose of this study is to develop allometric equations for tree biomass estimation. Five models, in linear and non-linear forms, were employed for the estimation of total tree above ground biomass (*tAGB*) and biomass of tree components. The independent variables used are DBH, H and WD. The optimal equations selected for estimating tree biomass are:

Bole	$y = 0.2270*D^{2.3519}*WD^{1.2211}$	$\bar{R}^2 = 0.9751$	$\bar{\Delta}\% = 8.15\%$	(S-04)
Branch	$y = 0.0637*D^{2.2738}*WD^{1.8007}$	$\bar{R}^2 = 0.8465$	$\bar{\Delta}\% = 17.79\%$	(B-04)
Foliage	$y = 0.1114*D^{1.5122}*WD^{0.9124}$	$\bar{R}^2 = 0.6616$	$\bar{\Delta}\% = 18.05\%$	(L-04)
tAGB	$y = 0.3429*D^{2.3028}*WD^{1.2901}$	$\bar{R}^2 = 0.9723$	$\bar{\Delta}\% = 5.74\%$	(T-04)

On comparing these equations with previously published models of Brown (1997) and Chave et al., (2005), the developed optimal model for *tAGB* estimation generated higher accuracy than those of Brown (1997) and Chave et al (2005). The models from Brown (1997) and Chave et al., (2005) may lead to overestimation when applied to the data from this study.

Equations for some main plant families and tree species were also developed. The selected optimal equations are as follows:

Dipterocarpaceae:	$y = 0.0860*D^{1.9869}*H^{0.7157}$	$\bar{R}^2 = 0.9941$	$\bar{\Delta}\% = 4.14\%$	(F-01)
Euphorbiaceae:	$y = 0.0409*D^{1.5860}*H^{1.1584}$	$\bar{R}^2 = 0.9822$	$\bar{\Delta}\% = 9.75\%$	(F-02)
Fagaceae:	$y = 0.0414*D^{1.6357}*H^{1.2475}$	$\bar{R}^2 = 0.9368$	$\bar{\Delta}\% = 5.33\%$	(F-03)
Vatica odorata:	$y = 0.0860*D^{1.8646}*H^{0.9434}$	$\bar{R}^2 = 0.9945$	$\bar{\Delta}\% = 4.65\%$	(Sp-01)
Endospermum sinensis:	$y = 0.0409*D^{1.5705}*H^{1.1214}$	$\bar{R}^2 = 0.9777$	$\bar{\Delta}\% = 9.16\%$	(Sp-02)

On comparing with previous studies, these selected models also generate higher accuracy than models of Brown (1997), Chave et al (2005) and/or Basukiet al., (2009). The model of Brown (1997) overestimated the *tAGB* for plant families and tree species. In contrast, the model of Basuki et al., (2009) underestimated the *tAGB* for Dipterocarpaceae family.

5.2 Bamboo forests

Five forms, linear and non-liner were developed for biomass estimation in bamboo forest. The dependent variables are total above ground biomass (*tAGB*) and the biomass of tree components (stem, branch, foliage). The independent variables are DBH and H. The selected optimal models are:

Bole	$y = 0.1132 * D^{2.1018}$	$\bar{R}^2 = 0.8833$	$\bar{\Delta}\% = 9.83\%$	(S-08)
Branch	$y = 0.0326 * D^{2.0177}$	$\bar{R}^2 = 0.8079$	$\bar{\Delta}\% = 10.25\%$	(B-08)
Foliage	$y = 0.0314 * D^{1.7720}$	$\bar{R}^2 = 0.8653$	$\bar{\Delta}\% = 10.55\%$	(L-08)
tAGB	$y = 0.1726 * D^{2.0545}$	$\bar{R}^2 = 0.9150$	$\bar{\Delta}\% = 7.41\%$	(T-08)

5.3 Recommendations

For further application of the selected equation for biomass estimation in North Central Coastal region, following are some recommendations:

- Sites for data collection should be expanded to collect more biomass data
- The independent data used to validate the developed models should be expanded, especially in the models developed for families and species.
- For EB forests, the equations may reach higher accuracy with WD as additional independent variable. Therefore, we recommend generating the equations of *tAGB* with DBH, H and WD at 1.3 m. WD at 1.3 m can easily generated by using increment borer to take samples.
- In bamboo forests, the developed equations should be compared with results of other researches.

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