



## MODELING ABOVE-GROUND BOLE BIOMASS OF SELECTED TREE SPECIES WITHIN THE FORESTRY RESEARCH INSTITUTE OF NIGERIA (FRIN)

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### ABSTRACT

*The objective of this study was to develop species-specific allometric models and pooled above-ground bole biomass models for selected tree species within the Forest Research Institute of Nigeria (FRIN). The objective was met by obtaining, Diameter at Breast Height (DBH), Diameter at Top (DT) and Bole Height (BH) of tree species. The collected variables were used and two selected species in terms of their basal area coverage: *Khaya senegalensis* and *Pinus caribaea* were selected for biomass modeling. The allometric models were developed from a two-step stratified sampling approach. Population dimensions were determined from sample plots, where-after trees were sampled for biomass representing the collected dimensions. The dry mass of the sampled components were used in a regression modeling approach to develop a set of species-specific and combined species linear models. The best models were selected based on goodness-of-fit model evaluation criteria and a two-step upscaling process was used to upscale samples to tree level and from tree to stand level. DBH and basic density were significant predictors of total above-ground bole biomass (AGBB) and diameter as single predictor produced consistently good results. Diameter was used throughout the up scaling process to determine the biomass per ha. The  $R^2$  fit for the models were high (0.99). Models 5 and 10 had low RMSE (9.38 and 7.55) and BIC values of 83.4 and 77.1. The parameter  $p$ -values of all models were significant ( $p < 0.05$ ). Future research can investigate remote sensing applications with field data to estimate forest biomass over larger areas.*

**Keywords:** *Khaya senegalensis*, *Pinus caribaea*, species-specific models, combined-species models, diameter, basic density.

### INTRODUCTION

Forests play an important role in the global carbon cycle and in the mitigation of carbon dioxide emissions and as a result, the need to accurately measure carbon stored in forests has increasingly gained recognition (Brown 2002; IPCC 2006). During the process of photosynthesis trees sequester carbon which is stored as part of the structural biomass, thus making them carbon sinks (Goicoa *et al.*, 2011). Considering the above, the estimation of above-ground tree biomass by using allometric equations (Henry *et al.*, 2010) or biomass expansion factors (IPCC, 2006; Dovey, 2009) is an essential aspect of the evaluation of carbon stocks (Goicoa *et al.*, 2011).

Biomass equations are developed for industrial and scientific purposes. These models evaluate tree characteristics that are relatively difficult to measure, like crown and stem mass, from easily collected data like diameter at breast height, height and basic density (Saint-André *et al.*, 2005; Chave *et al.*, 2005; Parresol, 1999) or tree volume (Dovey, 2009). Information on carbon stocks is important for studying forest productivity; nutrient cycling and quantities of fuel wood (Terakunpisut *et al.*, 2007). Forests can be influenced by natural or human causes that can lead to forest degradation. In cases of severe disturbance, forests can become sources of CO<sub>2</sub> where the net primary production

(NPP) is exceeded by oxidation and respiration. As the problem of CO<sub>2</sub> emissions continues, part of the mitigation efforts rely on the development and availability of accurate environmentally benign and cost-effective techniques for measuring the quantity and quality of carbon sequestered. Although, conventional techniques for the estimation of biomass may be very precise, their usage in carbon sequestration quantification is inadequate.

Therefore, very few general allometric equations have been developed to assess the biomass of single tropical and temperate forest tree species and for combinations of tree species. Since tropical forests consist of a variety of species, generic multi-species equations are often used to estimate total biomass per ha of all species. Information on species-specific equations that require fewer trees to be sampled as compared to multi-species equations has not yet been documented. However, limited allometric equations exist for forest species of sub-Saharan Africa and generalized equations developed for forests in other continents are often applied to the forests of sub-Saharan Africa. Therefore, This study is aimed at developing above-ground bole biomass models for two selected tree species and pooled above-ground bole biomass models for the mixed forest ecosystem in Forestry Research Institute of Nigeria (FRIN), thus contribute towards better resource use and environmental management practices.

**MATERIALS AND METHODS**

**Study Area**

The zone of FRIN mixed forest ecosystem lies at longitudes 30° 53' 30"E and latitudes 70° 55' 0"N. It has approximately 215 m altitude in the city of Ibadan. Ibadan lies in the transition zone between equatorial rainforest to the south and savanna to the north. The mean annual rainfall is approximately 1420.106 mm with average monthly rainfall being lowest in January and highest in June and September. The mean annual temperature ranges between 18.7° C and 34.4° C having its minimum as 22.7° C as a result of the position of the area falling within the high temperature zone of south west Nigeria.

**Location of Sample Plots**

Reconnaissance survey was first undertaken in the mixed forest ecosystem to obtain preliminary first-

hand information of the situation in the mixed forest ecosystem. There was a total enumeration of tree species in the mixed forest ecosystem, trees species with a diameter at breast height (DBH) ≥ 10 cm at 1.3m above the surface level were measured. The trees species within the area were measured for Diameter at Breast Height (DBH), Diameter at the Top (DT) and Bole Height (BH). A botanist and local people were engaged for the identification of botanical names and local names of tree species respectively.

**Estimation of Tree Volume**

Frequently used volume equations include, Smalian, Huber and Newton functions. Volume of stem sections are often calculated using Smalian’s formula, or alternatively by using the geometric formula for the truncated cone (Seifert and Seifert 2014).The above-ground bole biomass models was computed as a product of tree volume. The volume of trees species was estimated using geometric formula for truncated cone as shown below:

$$V = \frac{\pi l}{3} (R^2 + Rr + r^2) \dots\dots\dots (1)$$

Where:

V= Volume of the tree (m<sup>3</sup>)

l = length of stem sections (m)

R,r = the diameters at the thick and the thin end (cm)

π = 3.143.

**Trees sampled for Above-Ground Bole Biomass Sampling of bole wood for volume and density**

Since whole tree destructive sampling will not be used, basic density determination was restricted to the collection of core samples at breast height of sample trees in each of the diameter at breast height distribution classes (0 – 25 cm, 25 – 50 cm, 50 – 75 cm, 75-100 cm and 100 -125 cm). Core samples of 5 mm diameter was collected from sampled tree at diameter at breast height level to determine the bole density, making sure to reach the pith of the tree using a device called an increment borer. The bole diameters (cm) were recorded at the specific point where the core sample was taken. The bole samples were collected for later processing in the laboratory to determine basic density.

**Laboratory procedures**

**Determining the volume and basic density of the core samples**

To determine the volume (cm<sup>3</sup>) of the core samples, three methods were tested and the standard deviations (SD) of the measurements were compared: (1) Water displacement, with measuring the displaced water volume (2) water displacement with a balance and, (3) multiplying the basal area (mm<sup>2</sup>) and length (mm) of core samples measured with Vernier calliper. The best method was selected with the lowest SD. Method three (3) is mathematically express as follows:

$$V = \frac{\pi}{4} D^2 TL \dots\dots\dots (2)$$

To determine the dry weight in grams for the core samples, the cores were oven dried at 103±2 °C (American Society for Testing and Materials 2008) until constant weight. The basic density was determined by dividing the total dry weight of the core sample by the total volume determined. To determine the basic density for each sample tree, the densities obtained from the core samples at diameter at breast height level of the tree was calculated by Equation 3.

$$\rho = \frac{BM}{V} \dots\dots\dots (3)$$

Therefore,  
AGBB = V · ρ ..... (4)

**Where:** ρ = basic wood density of bole sample (kg/m<sup>3</sup>), AGBB = oven-dry biomass (kg), V = volume of core sample (m<sup>3</sup>), TL = total length of the core sample (m), D = diameter of core sample (cm), π = pi (3.143) (Chave, 2005).

**Estimation of AGBB within the mixed Forest Ecosystem**

The mean AGBB for each tree species in the mixed forest ecosystem were computed and then multiplied by 10,000m<sup>2</sup> to acquire the AGBB per hectare. However half of the value gave the carbon stock per hectare for the forest ecosystem (Aghimien et al., 2015).

**Species-specific Above-Ground Bole Biomass Estimation**

Species-specific above-ground bole biomass models were developed to estimate the bole biomass on the individual tree level for each of the two selected

species. Independent predictor variables included in the models were diameter at breast height (DBH), height (TH) and wood density (WD). The bole biomass models were evaluated and models based on their compliance with the assumptions of linear regression. The same approach was adopted for estimation of the pooled above-ground bole biomass. The mathematical models are stated below:

Model 1: AGBB = α (DBH) ..... (5)

Model 2: ln(AGBB) = c + αln(DBH) ... (6)

Model 3: ln(AGBB) = c + αln(DBH) + βln(TH)...(7)

Model 4: ln(AGBB) = c + αln(DBH) + βln(WD) ...(8)

Model 5: ln(AGBB) = c + αln(DBH) + βln(WD) + χln(TH) .....(9)

**Where:** AGTB = Above-ground bole biomass (kg)  
DBH = Diameter at breast height; TH = height  
WD = Wood density; ln= The natural logarithm  
The values c, α, β and χ are best fit parameters (Aghimien et al., 2015).

**Data Analysis**

For statistical analysis and upscaling of above-ground bole biomass, R-Statistical software was used in R Studio. Various models were tested with various combinations of independent variables for above-ground bole biomass. Models were evaluated for compliance to the assumptions of linear modeling and by model evaluation criteria.

**Evaluation of Selected Models**

The evaluation of the model was based the goodness of fit statistics such as Coefficients of determination (R<sup>2</sup>), Root mean square error (RMSE) and Bayesian information criterion (BIC).

- Coefficient of determination (R<sup>2</sup>): It provides a measure of how observed outcomes are replicated by the model, as the proportion of total variation of outcomes explained by the

Model  

$$R^2 = 1 - \left( \frac{\sum_{i=1}^n (y_i - \hat{y}_i)^2}{\sum_{i=1}^n (y_i - \bar{y})^2} \right) \dots\dots\dots (10)$$

- Root mean square error (RMSE): It represents the sample standard deviation of the differences between predicted and observed values. It estimates must be low as much as possible in order to reduce biased.

$$RMSE = \sqrt{\frac{1}{n} \sum_{i=1}^n (y_i - \hat{y}_i)^2} \dots\dots\dots (11)$$

The significant differences between estimated and actual values were calculated to identify the best estimator.

$$S_{\bar{X}_1, \bar{X}_2} = \sqrt{\frac{1}{2}(S_{\bar{X}_1}^2 + S_{\bar{X}_2}^2)} \dots \dots \dots (12)$$

Where:

$\bar{X}$  = Means for predicted and observed data respectively

$S_{\bar{X}_1, \bar{X}_2}$  = Pooled standard deviation

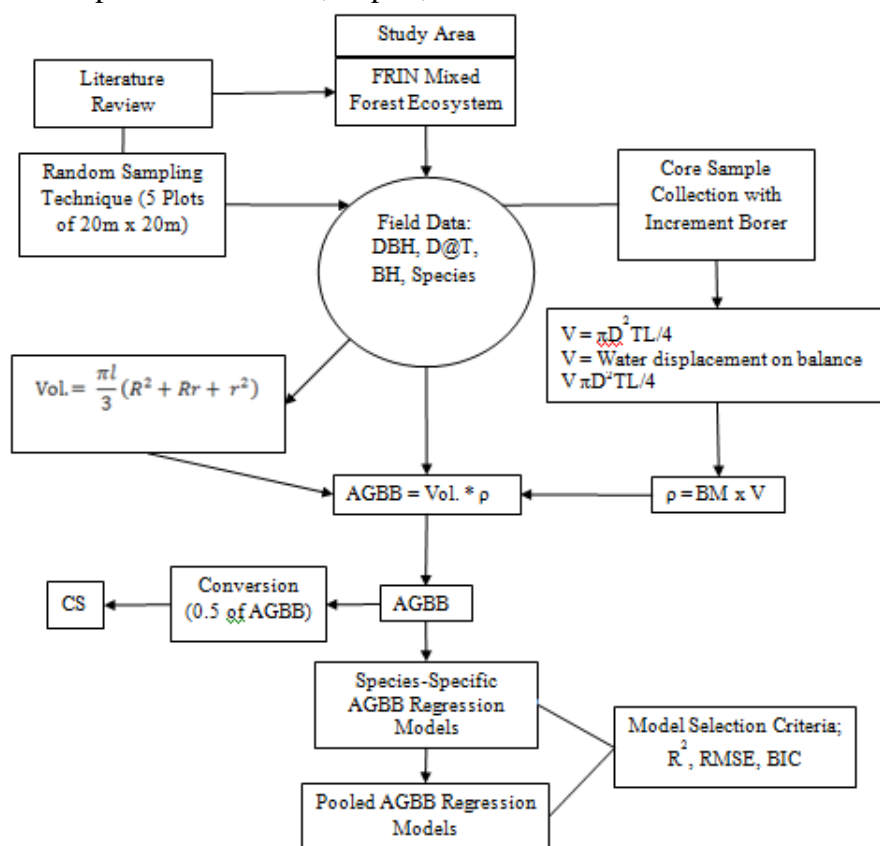
**Bayesian information criterion (BIC):** It is a criterion for equation selection among a finite set of equations; the model with the lowest BIC is preferred for model development. It is based, in part,

on the likelihood function and it is closely related to the Akaike information criterion (AIC). The mathematical expression for comparing maximum likelihood equations is defined as:

$$BIC = -2 * \ln \left( \sum_{i=1}^n (y_i - \hat{y}_i) / 2/n \right) + \ln(N) * K \dots \dots (13)$$

Where:

$y_i$  = observed value,  $\hat{y}_i$  = predicted value, N = number of observations and K = number of parameters estimated. Root Mean Square Error (RMSE) value fitting of criteria to estimate evaluation is most important and forecasts are increasingly accurate with lower RMSE values (Sileshi, 2014).



**Figure 1: Methodology Flow Chart**

**RESULTS**

**Forest Composition and Tree Dimensions**

A total of three hundred and twenty one (321) individual species were found in the mixed forest ecosystem from forty nine (49) tree species including one (1) unknown. The dominant tree

species in the study site included *Pinus caribae* (84), *Khaya senegalensis* (32), *Triplochyton scelexylon* (19), *Eucalyptus camandolensis* (15), *Albizia lebbek* (13), *Gmelina arborea* (13), respectively as recorded (Table 1). The two most dominated tree species were calibrated to develop allometric equations.

**Table 1: Tree species composition Within the Forestry Research Institute of Nigeria (FRIN)**

Species	Frequency	Percentage (%)
<i>Acacia spp</i>	3	0.93
<i>Afzelia africana</i>	1	0.31
<i>Albizia lebek</i>	15	4.67
<i>Annogeuseus leocarpus</i>	3	0.93
<i>Antiaris africana</i>	2	0.62
<i>Azardirecta indica</i>	9	2.80
<i>Balanitesae gyptiaca</i>	1	0.31
<i>Blighia spida</i>	2	0.62
<i>Brystegia spp</i>	1	0.31
<i>Cassia astula</i>	1	0.31
<i>Casuarina spp</i>	1	0.31
<i>Cesicepanaeca spp</i>	1	0.31
<i>Chrysophyllum albedum</i>	2	0.62
<i>Ciba pentadra</i>	1	0.31
<i>Cola gigantia</i>	1	0.31
<i>Cordia spp</i>	10	3.12
<i>Dacryodis edulis</i>	3	0.93
<i>Delonix regia</i>	2	0.62
<i>Entadrophregma angolense</i>	5	1.56
<i>Eucalyptus camandulensis</i>	18	5.61
<i>Gliricidia sepium</i>	5	1.56
<i>Gmelina arborea</i>	13	4.05
<i>Hidegardia barteri</i>	1	0.31
<i>Irvingia gabonensis</i>	4	1.25
<i>Khaya senegalensis</i>	32	9.97
<i>Lagerstroemia speciosa</i>	3	0.93
<i>Leucinia lecocephala</i>	1	0.31
<i>Margrateria celosoidis</i>	1	0.31
<i>Melalo calucanidiscus</i>	1	0.31
<i>Milicia excelsa</i>	1	0.31
<i>Monodora spp</i>	2	0.62
<i>Morindalucida</i>	6	1.87
<i>Nauclea diderichii</i>	3	0.93
<i>Newbuldia leavis</i>	8	2.49
<i>Parkia biglobosa</i>	4	1.25
<i>Pericopsis alata</i>	5	1.56
<i>Pinus caribaea</i>	84	26.17
<i>Pterocacarus spp</i>	6	1.87
<i>Shorea spp</i>	4	1.25
<i>Spondia mombin</i>	2	0.62
<i>Tectona grandis</i>	1	0.31
<i>Terminalia superba</i>	8	2.49
<i>Terocarpus spp</i>	2	0.62
<i>Tetraplera teprapetra</i>	5	1.56
<i>Treculia africana</i>	9	2.80
<i>Trichinia arborea</i>	3	0.93
<i>Triplochiton scleroxylon</i>	19	5.92
<i>Zylia zylocapa</i>	3	0.93
<i>Unknown</i>	3	0.93

**Diameter distribution of all species**

A test of kurtosis performed on the DBH distribution (Figure 2), indicated a leptokurtic

distribution with values >3 (5.50) with a high probability for extreme values. A test of skewness performed indicated a value >0 (2.03) where the

distribution is skewed to the right and that most values are concentrated left of the mean with extreme values to the right. Thus, most of the recorded smaller DBH range of between 5 - 15cm while the highest DBH value range from 45 and above (Figure 2). The highest bole height were recorded in the range of between 10 - 15m while boles with lowest value range from 20 - 25m (Figure 3).

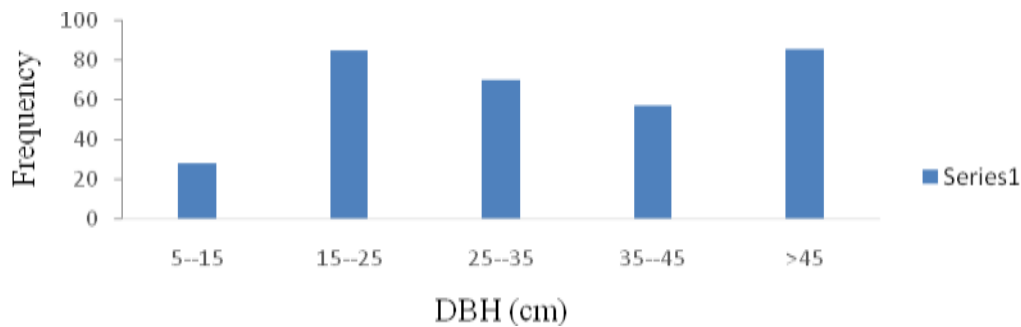
**Basal area coverage for all recorded species**

Forty seven (47) of the recorded species contributed to 63.86% of the total basal area. *Pinus caribaea* had the highest basal area contribution of 26.17% followed by *Khaya senegalensis* and *Triplochiton*

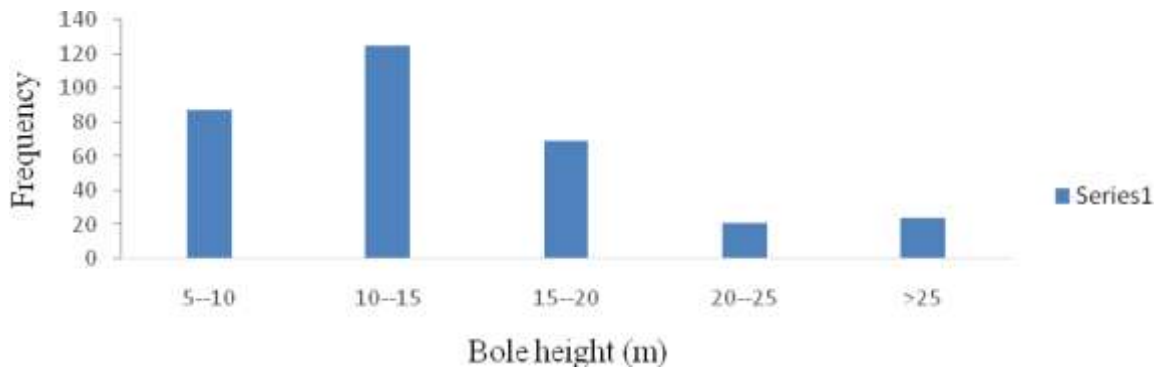
*scleroxylon*, each contributing to 9.97% and 5.92% (Table 2).

**Diameter distribution of *Pinus caribaea* with a total of 84 boles**

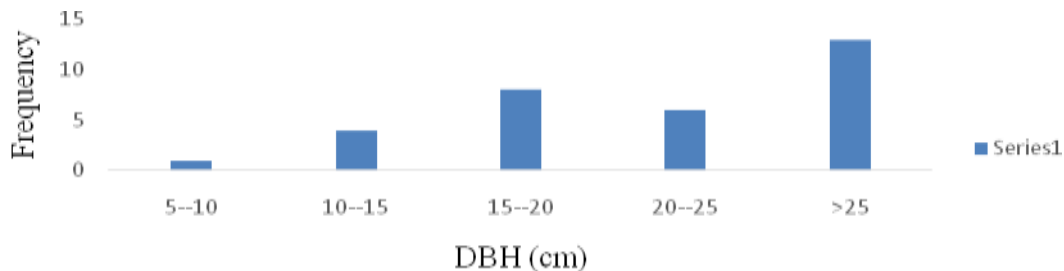
The majority of the recorded DBH for *P. caribaea* were above 30 cm. No boles were recorded for the DBH range of between 5 – 10 cm. However, the lowest DBH value ranges from 10-15cm (Figure 6). The highest boles were recorded in the range of between 15 – 20 m while the lowest bole heights were recorded in the range of between 25 – 30m. However, there was no bole height recorded in 30m and above (Figure 7).



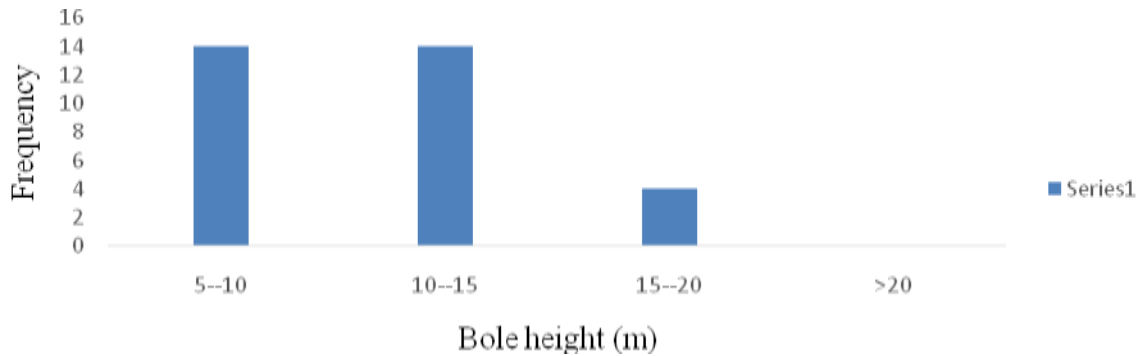
**Figure 2: Diameter distribution of all species with a total of 321 boles**



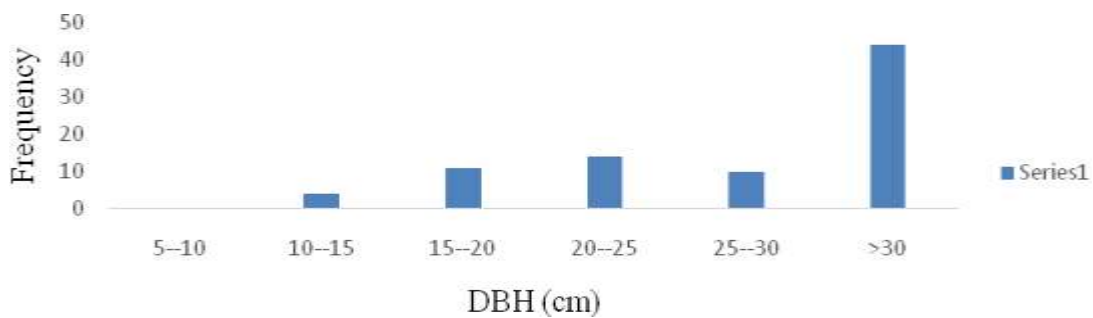
**Figure 3: Bole height distribution of all species with a total of 321 boles**



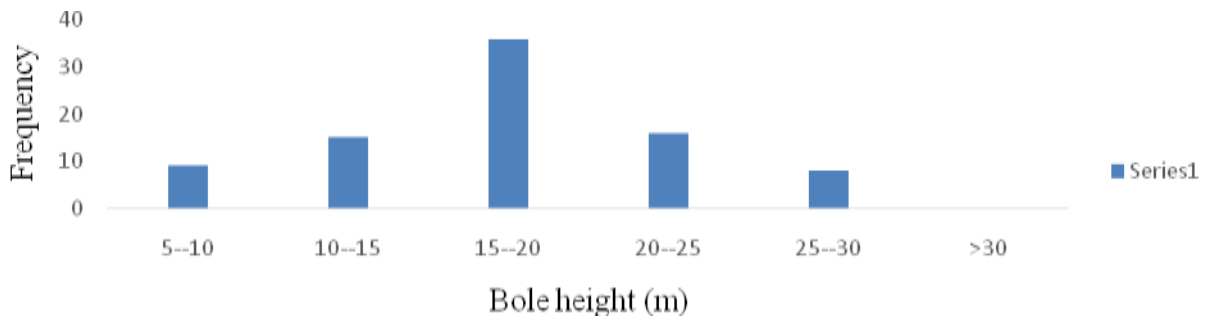
**Figure 4: Diameter distribution of *Khaya senegalensis* with a total of 32 boles**



**Figure 5: Bole height distribution of *Khaya senegalensis* with a total of 32 boles**



**Figure 6: Diameter distribution of *Pinus caribaea* with a total of 84 boles**



**Figure 7: Bole height distribution of *Pinus caribaea* with a total of 84 boles**

**Table 2: Measured DBH and bole height of all the species, *K. senegalensis* and *P. caribaea*.**

Species	Measured DBH (cm)					Measured bole height (m)			
	n	Min	Max	Mean	SD	Min	Max	Mean	SD
All species	321	7.00	168.00	37.27	21.59	4.50	33.00	14.52	6.17
<i>K. senegalensis</i>	32	10.00	110.00	31.75	22.97	5.500	18.00	10.98	3.46
<i>P. caribaea</i>	84	11.00	106.00	33.69	15.26	6.00	33.00	18.52	5.88

**Key:** n = Number of observation; Min. = Minimum; Max. = Maximum; SD = Standard Deviation' cm = centimeter  
m = meter

**Diameter distribution of *Khaya senegalensis* with a total of 32 boles**

Most of the measured DBH classes were found in 25 cm and above while the lowest DBH classes

value range from 5-10cm (Figure 4). The highest bole height distribution was ranged between 5 – 15m while the lowest bole height classes range between 15-20m. However, there were no boles

recorded in 20m and above. The inventory results in Table 2 indicate that the maximum recorded DBH for *Khaya senegalensis* is higher than the maximum value for *Pinus caribaea*, but the standard deviation from the measured bole height is higher for *Pinus caribaea* than for *Khaya senegalensis*. Mean calculated boles per ha were also higher for *Pinus caribaea* than for *Khaya senegalensis*.

**Species Specific Biomass Models to Scale up from Sample**

When an untransformed DBH of Models 1, and 6 were fitted for *K. senegalensis* and *P. caribaea* (Table 3). Models include ln-transformed models (Models 2, and 7), and models incorporating DBH and lnDBH variables. The untransformed models (Models 1, and 6) hold R<sup>2</sup> values of 0.80 and 0.77 with Bayesian information criterion (BIC) of 63.9 and 65.5 for *K. senegalensis* and *P. caribaea* respectively, while the transformed models (Models 2, and 7) hold R<sup>2</sup> values of 0.99 and 0.99 with BIC of 25.5 and 32.7 respectively.

The parameter values for all models were significant (p <0.05), except for the intercept values of Models 2 and 7 which were not significantly

different from 0 (p>0.05). The models without significant intercept values were all re-fitted without the intercept. The RMSE values were the lowest for the ln-transformed models (Models 2, and 7) and highest for Models 3 and 8. Model 2 and 7 were selected as the best performing models since the models having relatively good R<sup>2</sup> values and low RMSE values. Although the intercept of model 2 proved to be not significant and refitted without the intercept, the model was not rejected.

The predicted DBH values for the two selected models plotted against the residuals; show that there was no clear pattern and that there was visually no obvious heteroscedicity (Figure 8 - 10). A Shapiro-Wilk test performed on the residuals confirmed that the residuals were normally distributed (p >0.05). There was some indication that some certain points may have exerted excessive leverage, but excluding these points from the model made no difference to the parameter estimates and Cook's test indicated that this was not the case.

**Table 3: Diameter and height distribution of *K. senegalensis* and *P. caribaea* measured for height and biomass**

Species	Model	Dependent variable	Independent variable	Parameter estimates (with p-values in parentheses)				R <sup>2</sup>	RMSE	BIC
				b <sub>0</sub>	b <sub>1</sub>	b <sub>2</sub>	b <sub>3</sub>			
<i>K. senegalensis</i>	1	AGBB	DBH	3.07	7.74			0.80	2.5	63.9
	2	lnAGBB	lnDBH	-	2.79			0.99	0.09	25.5
	3	lnAGBB	lnDBH and lnBH	-1.49	2.00	1.00		0.99	9.38	85.3
	4	lnAGBB	lnDBH and lnWD	0.95	2.38	-		0.72	0.25	47.8
	5	lnAGBB	lnDBH, lnWD and lnBH	-1.49	2.00	1.00	1.00	0.99	9.38	83.4
<i>P. caribaea</i>	6	AGBB	DBH	9.5	2.72			0.77	3.28	65.5
	7	lnAGBB	lnDBH	-	8.60			0.99	0.10	32.7
	8	lnAGBB	lnDBH, lnBH	-1.24	2.00	-		0.99	6.34	68.7
	9	lnAGBB	lnDBH and lnWD	1.09	2.47	-		0.93	0.29	49.2
	10	lnAGBB	lnDBH, lnBH and lnWD	-1.24	2.00	1.00	1.00	0.99	7.55	77.1

**Key:** AGBB = Above ground bole biomass; ln = Log normal; DBH = Diameter at breast height; BH = Boleheight; WD = Wood density; R<sup>2</sup> = Coefficient of determination; RMSE = Root mean square error; BIC = Bayesian information criterion; b<sub>0</sub>, b<sub>1</sub>, b<sub>2</sub> and b<sub>3</sub> = Coefficients



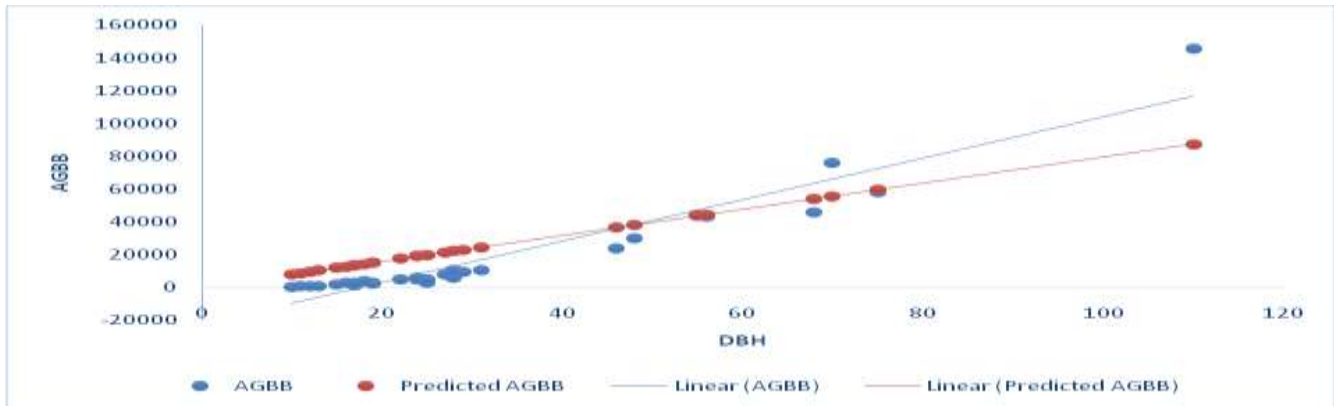
Two models were formulated for predicting the bole height of both *K. senegalensis* and *P. caribaea* (Table 3). Models 3 and 8 were ln-transformed models with lnDBH and lnBH as independent variables while two-predictor variable models (models 2 and 4). The ln-transformed models (models 3 and 8) were superior with regards to their R<sup>2</sup> (0.99% and 0.99%) and had higher RMSE values than models 2 and 7. All the model parameters were highly significant (p <0.05).

Model 4 and 9 were selected for the purpose of this study since both models have significant parameters, both models have high R<sup>2</sup> values (0.72% and 0.93%) and because of the simplicity of the models using lnDBH and lnWD as predictor variable, making them immediately applicable to all trees without a modeling step of bole height in between. When three parameters (lnDBH, lnBH and lnWD) were fitted for *K. senegalensis* and *P. caribaea* to estimate the AGBB. Three predictor variable models (Models 5 and 10). The R<sup>2</sup> fit for the models were high (0.99). Models 5 and 10 had

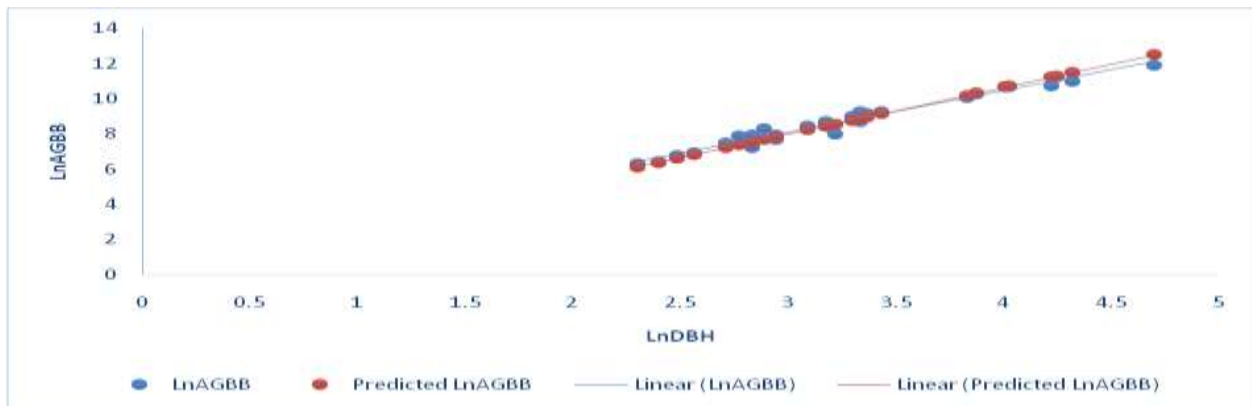
low RMSE (9.38 and 7.55) and BIC values of 83.4 and 77.1. The parameter p-values of all models were significant (p <0.05).

**Combined Species Models**

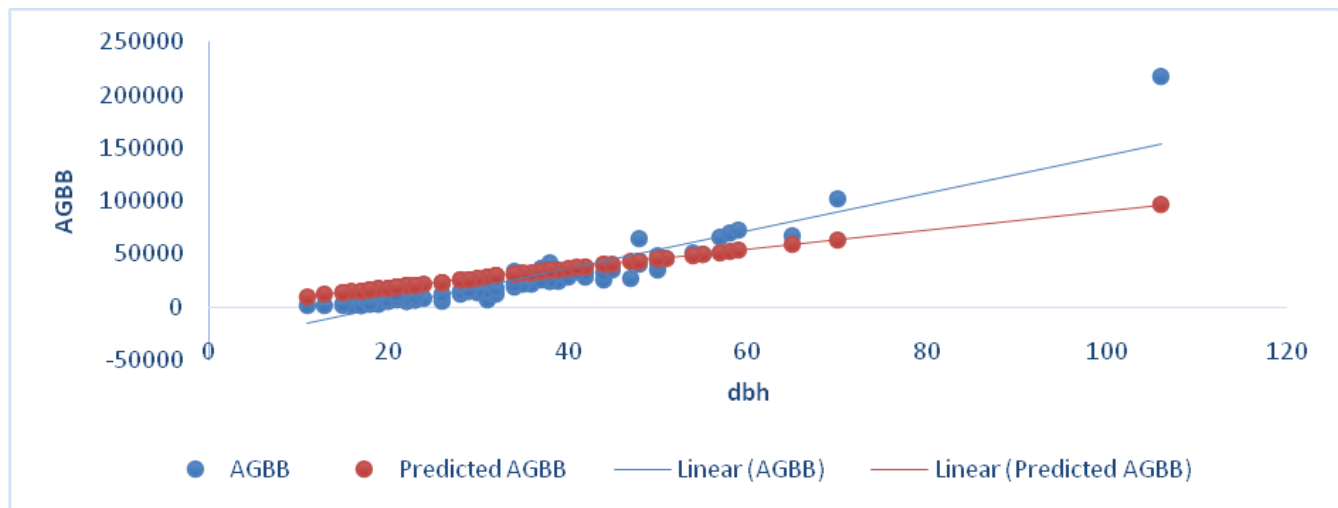
Table 4 revealed that the pearson correlation between AGBB and WD is 0.11, which indicates that there is a low positive relationship between the variables because the point fall outside the line. The relationship between these variables is positive because as AGBB increases, the WD also increases. The p-values for the correlation between AGBB and WD is higher than the significance level at  $\alpha = 0.05$ , which indicates that the correlation coefficients is not significant. The pearson correlation between AGBB and DBH is 0.92, which revealed that there is a high positive relationship between the variables. The relationship between these variables is positive because as AGBB increases, the DBH also increases. The p-values for the correlation between AGBB and DBH is less than the significance level at  $\alpha = 0.05$ , which indicates that the correlation coefficients is significant as presented in Figure 5.



**Figure 8: Diameter and linear models for *K. senegalensis***



**Figure 9: Diameter and linear models for *K. senegalensis***



**Figure 10: Diameter and linear models for *P.caribaea***

The Pearson correlation between AGBB and BH is 0.44, which shows that there is a moderate positive relationship between the variables. The relationship between these variables is positive because as AGBB increases, the BH also increases. The p-values for the correlation between AGBB and BH is higher than the significance level at  $\alpha = 0.05$ , which indicates that the correlation coefficients is not significant as presented in Figure 5.

Five AGBB models have been formulated to estimate the AGBB of the combined species model (Table 5). The predictor variables that have been used include DBH (Model 11), lnDBH (Model 12), lnDBH and lnBH (Model 13), lnDBH and lnWD (Model 14) and a combination of lnDBH, lnWD and lnBH (Models 15). The parameters were first fitted in the logarithmic form but exhibit a good fit. The  $R^2$  fit of some models were the same (0.99). Model 13 had the lowest RMSE value followed by model 14 and 12. Model 13 had the lowest BIC value and model 15 the highest.

The p-values of all parameters and models were significant ( $p < 0.05$ ). Model 13 was the superior model, having a high  $R^2$  value and low BIC and RMSE values. The ln-transformed model having lnDBH and lnBH as predictor variable, was selected to estimate AGBB, since the model has a high  $R^2$  fit

and all the parameter values are significant ( $p < 0.05$ ). Model 13 is also a more parsimonious model since it has two independent variables and complies with the concept of parsimony. The predicted AGBB values of the best performing model 13.

Five models were developed to estimate the AGBB of the combined model (Table 5). Models having single (Model 11 – 12), two (models 13, and 14) and three predictor variables (Model 15) have been fitted. Predictor variables include DBH, BH and WD. All models had  $R^2$  values of 0.99, except for models 11 and 14 having  $R^2$  values of 0.77 and 0.95. Model 13 had the lowest RMSE value, followed by model 14, 12 and 11. Model 13 had the lowest BIC value followed by models 14, 12 and 11.

All the parameter and model p-values were significant ( $p < 0.05$ ), except for the DBH parameter in model 12 having a not significant ( $p < 0.05$ ) value. Model 13 was the best performing model, having low RMSE and BIC values. Model 13 having the ln-transformed DBH and BH as predictor variables were selected since it has a high  $R^2$  value and because of the simplicity of the model using two as a predictor variables.

**Table 4: Pearson correlation Matrix**

	WD	DBH	BH	DT	BA	VOL	AGBB
WD	1						
DBH	0.049394	1					
BH	0.536997	0.399972	1				
DT	0.049394	0.999999	0.399972	1			
BA	-0.03886	0.949008	0.250549	0.949008	1		
VOL	0.099103	0.926814	0.432001	0.926814	0.951657	1	
AGBB	0.106644	0.924449	0.43646	0.924449	0.94807	0.999906	1

**Key:** WD = Wood density; DBH = Diameter at breast height; BH = Bole height; DT = Diameter at top; BA = Basal area; Vol. = Volume; AGBB = Above-ground bole biomass

**Table 5: Pooled diameter and height distribution of *K. senegalensis* and *P. caribaea* measured for height and biomass**

Species	Model	Dependent variable	Independent variable	Parameter estimates (with p-values in parentheses)				R <sup>2</sup>	RMSE	BIC
				b <sub>0</sub>	b <sub>1</sub>	b <sub>2</sub>	b <sub>3</sub>			
Pooled	11	AGBB	DBH	1.25	3.54			0.77	3.08	44.9
	12	lnAGBB	lnDBH	-	15.85			0.99	0.37	32.8
	13	lnAGBB	lnDBH and lnBH	-0.16	1.99	1.02		0.99	0.009	23.4
	14	lnAGBB	lnDBH and lnWD	8.42	2.44	18.62		0.95	0.28	27.3
	15	lnAGBB	lnDBH, lnWD and lnBH	2.61	2.00	1.00	1.00	0.99	8.49	82.5

**Key:** AGBB = Above ground bole biomass; ln = Log normal; DBH = Diameter at breast height; BH = Bole height WD = Wood density; R<sup>2</sup> = Coefficient of determination; RMSE = Root mean square error; BIC = Bayesian information criterion; b<sub>0</sub>, b<sub>1</sub>, b<sub>2</sub>, b<sub>3</sub> = Coefficients

**DISCUSSION**

**Sample Size and Variability of Sampled Trees**

The sample size of trees selected for AGBB sampling is dependent on the variability of the resource and higher accuracies are associated with higher costs (Kunneke *et al.* 2014). Fewer sample trees are necessary for species-specific models than for generic multi-species models (Picard *et al.* 2012). Steward *et al.* (1992) tested the variability in stand biomass of Central American dry zone species using three site and species-specific allometric models developed from three different sample sizes of 16, 12 and eight sample trees respectively. They found that estimates using allometric models developed from 16 sample trees were as accurate as models developed from 12 trees, but that the

biomass estimates became more variable when eight trees were used. Considering the findings above, the sample size used in this study to develop site and species-specific allometric models are sufficient to estimate the biomass of the selected species with reasonable accuracy. Yavasli (2013) and Samalca (2007) recommended that trees sampled for AGBB should follow an even distribution of size classes covering all size classes measured during the plot sampling and that allometric equations should not be applied beyond the valid regression range from which it was developed (Chave *et al.* 2005). Trees sampled for biomass were sampled following a stratified approach to cover an even distribution of DBH and height variation (Kunneke *et al.* 2014).

## CONCLUSION

Diameter was used throughout the up scaling process to determine the biomass per ha. The R<sup>2</sup> fit for the models were high (0.99). Models 5 and 10

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