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Allometric biomass equations for tree species used in agroforestry systems in Uganda

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Abstract Estimates of above-ground biomass are required for better planning, sustainable management and monitoring of changes in carbon stocks in agroforestry systems. The objective of this study was to develop and compare biomass equations for *Markhamia lutea, Casuarina equisetifolia, Maesopsis eminii* and *Grevillea robusta* grown in a linear simultaneous agroforestry system in Uganda. These species were established in single rows in the middle of fields in 1995 from four-month old seedlings. A total of 57 trees were sampled for this study, 13 for *M. lutea,* 12 for *C. equisetifolia,* 16 for *M. eminii* and 16 for *G. robusta*. Biomass values of the various tree components (stem, branches and foliage) as well as the total above-ground biomass were fitted to linear and non-linear allometric models using total height, diameter-at-breast height (DBH), crown width as predictor variables. Although both DBH and height are typically used as independent variables for predicting above-ground biomass, the addition of height in biomass equations did not significantly improve model performance for *M. eminii*, *M. lutea* and *G. robusta*. However, addition of height significantly increased the proportion of variation explained in above-ground biomass for *C. equisetifolia*, while DBH did not significantly improve the prediction of biomass. The study confirmed the need for developing species-specific biomass equations.

Keywords Agroforestry · Allometric biomass equations · *Maesopsis eminii* · *Markhamia lutea* · *Grevillea robusta* · *Casuarina equisetifolia*

Introduction

Allometric equations to predict above-ground biomass of trees have been widely developed in forestry and agroforestry for both industrial and scientific purposes. Biomass estimates have been used to assess forest structure and condition (Saint-Andre et al. 2005), to estimate forest productivity and carbon fluxes (Chambers et al. 2001; Zianis et al. 2005), and to assess carbon (C) sequestration in wood, leaves, and roots (Cooper 1983; Specht and West 2003). Several studies have developed biomass models for various tree species (Araujo et al. 1999; Fuwape et al. 2001; Onyekwelu 2004; Rapp et al. 1999; Specht and West 2003; Wang et al. 2000) and shrubs (Verwijst and Telenius 1999). Most biomass equations utilize diameter breast height

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at 1.37 m above ground (DBH) alone or in combination with height as independent variables because they are easy to measure and provide reliable predictions (Onyekwelu 2004; Rapp et al. 1999; Wang et al. 2000).

Biomass equations have been developed for mixtures of tropical species (Chambers et al. 2001; Chave et al. 2005; Cole and Ewel 2006; Ketterings et al. 2001). Almost all of these relationships, whether intended for application to individual species, mixed-species forests, specific biogeographical regions, or climate-related biomes, are based on the allometric model. However, application of allometric equations to dicotyledonous trees is difficult because woody dicotyledonous trees have complicated branching patterns, and a large portion of the above-ground biomass consists of non-living xylem. These factors complicate form-function relationships and both factors change with tree age, tree spacing, height and site conditions (Cole and Ewel 2006).

The wealth of allometric equations that relate the biomass of individual tree components to DBH and/or to tree height has been summarized for European (Zianis et al. 2005), North American (Arevalo et al. 2007; Jenkins et al. 2003; Ter-Mikaelian and Korzukhin 1997), Australian tree species (Eamus et al. 2000; Keith et al. 2000) and woodland tree species of West Africa (Sawadogo et al. 2010). Studies conducted on tropical tree species are often site specific, for instance, Brazil (Araujo et al. 1999; Keller et al. 2001), India (Mani and Parthasarathy 2007) and Costa Rica (Cole and Ewel 2006). The few studies conducted in Africa were either based on savanna woodlands (Tietema 1993; Sawadogo et al. 2010) or tropical moist forest of Cameroon (Deans et al. 1996), containing different species from those of Uganda. Existing biomass equations for tropical species currently used in agroforestry systems in Uganda have not been evaluated.

Knut (1993) noted that in tropical areas, where hundreds of species occur within relatively small areas, it is impracticable to establish functions for every species. For such situations, he recommended using a pooled equation with a logarithmic model of the form;

$$ln(\mathrm{WSUM}) = ln(\mathrm{DBH}) + ln(CW) + ln(\mathrm{HT}) + \varepsilon \qquad (1)$$

where, WSUM is the whole dry fresh biomass (kg), DBH (cm), CW is crown width (cm) and HT is tree height (m). That model was parameterized by pooling all the tree species data and grouping by DBH class. This modelling approach has been used in Uganda for all ecosystems (plantations, tropical forest, woodlands and agroforestry systems) by Drichi (2003) to estimate biomass. Such generalization for tropical forests, however, may not be suitable for species growing in a plantation or agroforestry systems since differences in management practices will influence the allocation of biomass to the various tree components. In addition, the model included independent variables, which are correlated; this is likely to result in biased ordinary least squares estimates. Although the predictive ability of the model is not affected, high adjusted R^2 obtained due to multicollinearity complicates assessment of performance of the individual independent variables.

The objective of the current study was to develop and compare above-ground component biomass equations for *Grevillea robusta, Casuarina equisetifolia, Maesopsis eminii* and *Markhamia lutea* trees that are growing in linear simultaneous or similar agroforestry systems in central Uganda.

Materials and methods

Study area

This study was conducted at Kifu National Forestry Resources Research Institute (NaFORRI) (latitude 0°48′N, longitude 32°46′E, elevation 1,250 m above mean sea level [amsl]) in Mukono district in Central Uganda. Kifu is located approximately 30 km east of Kampala, the capital city of Uganda. Rainfall is distributed bimodally, with long rains starting in March and ending in June while short rains start in August and end in November. Data from the metrological station at the site show that between 2002 and 2006, the average annual rainfall was 1,560 mm. The annual minimum and maximum temperatures at Kifu are 20.8 and 25.2 °C, respectively.

The vegetation in this region is characterized by elephant grass (*Pennisetum purpureum*) and remnants of high tropical forest and eucalyptus woodlots (Wajj-Musukwe 2003). Swamps are covered by papyrus reeds (*Cypresus papyrus*) and sedges are found in several valley bottoms. The soil is a sandy loam ferralsol averaging 14 % clay, 30 % silt and 57 % sand, with a pH of 6.2 and an organic matter concentration of

11.3 g kg^{-1} in the top 0–0.45 m (Okorio 2000). The soils are slightly acidic sandy loams (Okorio 2000) with bulk densities in the range of 0.49 in the surface to 2.38 Mg m^{-3} in th subsoil (Tumwebaze 2008).

Description of the tree species

Four tree species were utilized in this study. *C. equisetifolia* L. is an evergreen with a finely branched and open crown that attains heights of 6–35 m tall and DBH up to 100 cm (MacDicken 1994). The altitudinal range where this species grows naturally is from 0 to 1,400 m asl with a mean annual temperature of 10–35 °C and mean annual rainfall of 200–3,500 mm. The species prefers deep well-drained coarse textured soils (MacDicken 1994). It grows in association with actinorhizal bacteria, through which it fixes atmospheric nitrogen. The tree has proteoid roots and forms association with vesicular arbuscular mycorrhizae.

Grevillea robusta A. Cunn. is a deciduous tree, which grows up to 12–25 m tall and 80 cm DBH. The crown is conical and fairly open with moderate competition to crops. The tree trunk is straight and branches up to 15 m (Harwood and Booth 1992). The species grows at an altitudinal range of 0–2,300 m asl, requires a mean annual rainfall of 600–1,700 mm, mean annual temperature of 14–31 °C and prefers medium texture soils, but establishes well in alluvial soils. The species occurs naturally in Australia, and has been introduced into sub-tropical highland regions of the world and is widely planted in Africa (Harwood and Booth 1992).

Maesopsis eminii Engl. is a leafy semi-deciduous tree, which grows up to 10-30 m in height with a clear bole of up to 100 cm DBH. The umbrella-like dense crown competes with annual crops but is compatible with shade tolerant perennials. The species grows at an altitudinal range of 700–1,500 m, requires mean annual rainfall of 1,200–1,300 mm and mean annual temperature of 22–27 °C. It grows best on deep moist fertile sandy loam soils but tolerates a wide range of site conditions. It occurs naturally in Uganda, East, Central and West Africa (Katende and Brinie 1995). Because of its dense canopy, it has been used as a shade tree for coffee in Uganda, cocoa in the Democratic Republic of Congo and Cardamom plantations in southern India.

Markhamia lutea K. Schum. is an evergreen tree, growing to 15 m in height, with a narrow irregular crown and deep long tap root. Highly competitive to crops, this species is found within an altitudinal range of 900–2,000 m, requiring a mean annual rainfall of 800–2,000 mm and a mean annual temperature of 12–27 °C. It grows best on red loam soils but can tolerate well-drained acidic clay loams. It occurs naturally in lake basins and highlands of East Africa with high rainfall including Uganda (Katende and Brinie1995). *M. lutea* grows rapidly in forest soils and the tree can attain a height growth rate of 2 m per year. The tree can be pruned and pollarded to reduce shading and can be coppiced at 1.7 m in height.

Methods of data collection

Above-ground biomass measurements

The four tree species were established in September, 1995 in randomized block design, where trees were planted in the field as four- month seedlings from the nursery. The seedlings were planted in the middle of the plot (25 m by 30 m) along a east–west axis at 1 m spacing, resulting into 24 trees per plot (Wajj-Musukwe 2003). After three years of growth, the trees were thinned by removing every other tree and crown pruning was done to reduce shade by removing one-third of the crown before planting of the crops (Okorio 2000; Wajj-Musukwe 2003).

Before destructive sampling of above-ground biomass, total tree height was measured using a Sunto clinometer, DBH measured using a Caliper (average of two perpendicular measurements) and crown width measured using a distance meter tape (average of two perpendicular readings) were recorded for all the trees in the study area. These data were used to establish the stratified sampling frame for the selection of sample trees for biomass measurements. Trees were grouped according to DBH, with the number of bins varying for each species. Four DBH classes were chosen for *C. equisetifolia* and three DBH classes were selected for *G. robusta, M. eminii* and *M. lutea* to cover the range of DBH for each species. For *G. robusta, M. eminii* and *M. lutea*, five trees were randomly selected in each diameter class and for *C. equisetifolia,* four trees were randomly selected in each diameter class. The sampled trees were selected irrespective of tree vigor and form; DBH class was the sole selection criterion.

Each sample tree was felled, total height and bole lengths (up to a 10 cm top) were measured. Branches, defined as woody material <10 cm in diameter, were cut from the bole (>10 cm) and placed on a plastic sheet (Briggs et al. 1989). All the foliar material (leaves, twigs and fruits collectively referred to as foliage) was collected from the felled trees and packed in plastic labeled bags. The fresh weights of the foliage were recorded and the foliage was removed from the bags and placed in the sun for drying. Branches were tied with sisal ropes and suspended from 300 kg hanging scale to determine their fresh weight. A subsample of ten branches representing each branch size was randomly selected for estimating the dry- to fresh-weight ratios. These subsamples were labeled, tied with sisal ropes and weighed in the field at the end of the day. The bole of each sample tree was divided into three sections of equal length (Briggs et al. 1989). The three bole sections were weighed in the field to record the fresh weight and three sample discs of 5 cm thickness were randomly taken from each bole section. The fresh weight of each disc was recorded in field at the time when the discs were cut off from the bole and taken to the laboratory for drying.

Small branches (<10 cm diameter), foliage and sample discs were dried to constant weight in the oven at 105 °C for 48 h (Briggs et al. 1989). Subsample dry weight was recorded immediately after drying. For branch, foliage and disc samples, a ratio of oven-dry to fresh-weight was calculated and an average ratio obtained. Total fresh weight of each component and the corresponding average oven-dry to fresh weight ratio were multiplied to obtain an estimate of dry-weight. Total above-ground biomass (TAGB) was computed as the sum of all component (bole, branches and foliage) weights (kg)..4

Data analysis

Three sets of biomass equations were used to select the best model for each of the four biomass components. The first two sets of equations employed all species' data pooled together, while the third set of equations was fitted to each species individually. The first set of equations consisted of six separate biomass models, with each model using the logarithm of biomass regressed against the logarithm of either DBH, height and crown width, either in combination or alone.

$$\text{Model 1A}: ln(\mathrm{Y}) = \beta_0 + \beta_1\, ln(\mathrm{DBH}) + \varepsilon \qquad (2)$$

$$\text{Model 1B}: ln(\mathrm{Y}) = \beta_0 + \beta_2\, ln(\mathrm{H}) + \varepsilon \qquad (3)$$

$$\text{Model 1C}: ln(\mathrm{Y}) = \beta_0 + \beta_3\, ln(\mathrm{CW}) + \varepsilon \qquad (4)$$

$$\text{Model 1D}: ln(\mathrm{Y}) = \beta_0 + \beta_1\, ln(\mathrm{DBH}) + \beta_2\, ln(\mathrm{H}) + \varepsilon \qquad (5)$$

$$\text{Model 1E}: ln(\mathrm{Y}) = \beta_0 + \beta_1\, ln(\mathrm{DBH}) + \beta_3 ln(\mathrm{CW}) + \varepsilon \qquad (6)$$

$$\text{Model 1F}: ln(\mathrm{Y}) = \beta_0 + \beta_1\, ln(\mathrm{DBH}) + \beta_2 ln(\mathrm{H}) + \beta_3\, ln(\mathrm{CW}) + \varepsilon \qquad (7)$$

where *ln* is the natural logarithm, Y the dry weight of the specific biomass component (bole, branches, foliage and total above-ground biomass), DBH is diameter breast height (cm), H is total tree height (m), CW is crown width (m), and β_0, β_1, β_2, and β_3, are parameters to be estimated. Separate equations were developed for each above-ground biomass component. Model 1F was recommended by (Knut 1993) for use in tropical forests of Uganda because these forests have hundreds of species in a small area with different ages, size and morphology.

The second set of models incorporated dummy variables to test for differences in slope and intercept among species. This was conducted to assess the need for developing species-specific equations in agroforestry systems. Separate biomass equations were developed for each above-ground biomass component.

$$\text{Model 1A}: ln(\mathrm{Y}) = \beta_0 + \beta_1 ln(\mathrm{DBH}) + \varepsilon \qquad (2)$$

$$\text{Model 2A}: ln(\mathrm{Y}) = \beta_0 + \beta_1 ln(\mathrm{DBH}) + \alpha_1 \mathrm{Z}_1 + \alpha_2 \mathrm{Z}_2 + \alpha_3 \mathrm{Z}_3 + \varepsilon \qquad (8)$$

$$\text{Model 2B}: ln(\mathrm{Y}) = \beta_0 + \beta_1 ln(\mathrm{DBH}) + \alpha_4 \mathrm{Z}_1 ln(\mathrm{DBH}) + \alpha_5 \mathrm{Z}_2 ln(\mathrm{DBH}) + \alpha_6 \mathrm{Z}_3 ln(\mathrm{DBH}) + \varepsilon \qquad (9)$$

$$\text{Model 2C}: ln(\mathrm{Y}) = \beta_0 + \beta_1 ln(\mathrm{DBH}) + \alpha_1 \mathrm{Z}_1 + \alpha_2 \mathrm{Z}_2 + \alpha_3 \mathrm{Z}_3 + \alpha_4 \mathrm{Z}_1 ln(\mathrm{DBH}) + \alpha_5 \mathrm{Z}_2 ln(\mathrm{DBH}) + \alpha_6 \mathrm{Z}_3 ln(\mathrm{DBH}) + \varepsilon \qquad (10)$$

where Z_1, Z_2 and Z_3 are dummy variables used to represent the four tree species (Table 4), β_0, β_1, α_1–α_6 are regression parameters to be estimated, all other variables as defined previously.

The third set of models used data for each species individually, and consisted of the following equations:

$$\text{Model 3A}: ln(\mathrm{Y}) = \beta_0 + \beta_1\, ln(\mathrm{DBH}) + \varepsilon \qquad (2)$$

$$\text{Model 3B}: ln(\mathrm{Y}) = \beta_0 + \beta_2\, ln(\mathrm{H}) + \varepsilon \quad (3)$$

$$\text{Model 3C}: ln(\mathrm{Y}) = \beta_0 + \beta_1\, ln(\mathrm{DBH}) + \beta_2 ln(\mathrm{H}) + \varepsilon \quad (5)$$

where all variables are as defined previously.

Comparisons among the regression models were based on their residual plots, model mean squared error, coefficient of determination (R^2), standard error of estimates and the predicted residual sum of squares (PRESS). This was possible because the dependent and independent variables of the equations were similarly transformed (Onyekwelu 2004). The PRESS statistic can be used to select predictor variables and also validate the chosen model (Draper and Smith1966). To correct for bias in biomass estimation due to the natural logarithmic transformation, a correction factor (CF) for each equation was computed using the method suggested by (Sprugel 1983).

The biomass of the above-ground woody component of this agroforestry system was calculated by obtaining average biomass of the sampled trees (bole, branch, foliage and TAGB) in each plot and respective DBH class. The average plot biomass was multiplied by the number of trees in DBH classes to which the sampled trees belonged to obtain the total biomass in each DBH class; total plot biomass was obtained for each tree component and TAGB. Plot biomass was expressed on a unit area basis by dividing the plot component biomass (bole, branch, foliage and TAGB) by plot area (0.075 ha).

Results

Descriptive statistics of sampled trees

Among the four species, *M. eminii* and *G. robusta* had the largest trees with respect to DBH and crown width. *C. equisetifolia* was the tallest with the smallest DBH, producing the most cylindrical boles, while *M. lutea* had the shortest trees with the narrowest crowns (Table 1).

Maesopsis eminii and *G. robusta* had a higher correlation between TAGB and DBH, while *C. equisetifolia* and *M. lutea* had the poorest correlation (Fig. 1). The figure suggests a curvilinear relationship for *M. eminii.* Logarithmic transformation linearized the relationship between TAGB and DBH for all species (Fig. 2). Clustering of the data by species reinforces the need for individual models for each species.

Biomass equations

DBH alone (Model 1A) explained between 20 and 48 % of the variation in each of the tree biomass components (foliage, branch and bole), as well as the total above-ground biomass for most models (Table 2). Height alone (Model 1B) is the poorest predictor of individual component and TAGB biomass data; no more than 16 % of variation in component biomass was explained by height (Table 2). When crown width alone is regressed on tree component biomass for the pooled data, no more than 35 % of the variation is explained by the relationship (Model 1C), though the model is highly significant (Table 2). Models 1D (DBH, HT) and 1F (DBH, HT, CW) have lower PRESS statistics compared to other models and would be better for predicting foliage and branch biomass, respectively. PRESS and MSE for model 1A are lower compared to other models, indicating better prediction for bole and TAGB (Table 2). DBH is the best predictor variable, and HT and CW contribute little much to predicting component biomass when species are combined. Pooling across species does not generate reliable biomass equations.

Species differences in allometric relationships

Three dummy variables were included in the analysis to determine if there was a need to develop species-specific biomass equations. The regression model included DBH and three dummy variables (Z_1, Z_2 and Z_3) to represent separate intercepts (Model 2A), the interaction between DBH and each dummy variable to represent separate slopes for each species (Model 2B), and both components (Model 2C). The inclusion of dummy variables for separate intercepts (Model 2A), improved the proportion of variation explained by 13 % for foliage biomass, 7.3 % for branch biomass, 5.1 % for bole biomass and 6.4 % for TAGB compared to model 1A (DBH alone) (Table 3). Similar amount of variation was explained by regressing tree component biomass and TAGB with DBH and dummy variables representing separate slopes.

Comparing results of Model 1A (with DBH only) and Models 2A, 2B and 2C (that have the dummy variables, Table 3), there is an improvement in the

Table 1 Descriptive statistics of sampled trees used in developing biomass equations for a linear agroforestry system in central Uganda

Variable	Species	Number tree harvested	Mean	StDev	Minimum	Maximum
DBH (cm)	*C. equisetifolia*	12	18.95	5.04	11.4	26.2
	G. robusta	16	31.08	5.76	21.8	41.6
	M. eminii	16	29.28	7.54	16.3	43.9
	M. lutea	13	23.93	5.38	14.0	33.3
Height (m)	*C. equisetifolia*	12	20.59	5.67	11.2	27.3
	G. robusta	16	19.89	1.94	16.6	23.1
	M. eminii	16	20.41	3.82	11.9	25.2
	M. lutea	13	16.24	3.16	11.2	22.4
Crown width (cm)	*C. equisetifolia*	12	6.10	1.16	4.6	7.8
	G. robusta	16	7.54	0.95	5.8	9.0
	M. eminii	16	8.65	3.17	5.2	14.7
	M. lutea	13	5.16	1.20	3.2	6.6
Branch dry biomass (kg)	*C. equisetifolia*	12	28.14	13.38	12.9	50.9
	G. robusta	16	167.70	107.00	21.7	387.0
	M. eminii	16	100.80	107.40	11.7	420.5
	M. lutea	13	45.5	51.60	5.4	197.8
Foliage biomass (kg)	*C. equisetifolia*	12	22.80	11.54	7.6	40.0
	G. robusta	16	35.97	18.78	11.6	84.0
	M. eminii	16	27.23	18.65	5.7	78.0
	M. lutea	13	18.89	14.32	4.4	55.0
Bole biomass (kg)	*C. equisetifolia*	12	198.50	164.60	25.0	538.1
	G. robusta	16	287.00	133.40	89.4	673.1
	M. eminii	16	219.50	131.70	37.5	471.4
	M. lutea	13	119.40	76.30	42.1	287.2
Total individual tree above ground dry biomass (kg)	*C. equisetifolia*	12	249.50	182.90	49.0	621.0
	G. robusta	16	490.70	230.20	201.8	1,138.6
	M. eminii	16	347.60	232.40	54.9	900.9
	M. lutea	13	183.80	104.50	61.7	332.7

proportion of variation explained for total above ground biomass by 12.6 %. For foliage, branch and stem, improvement attained by including the dummy variable ranged from 11.1 to 17.8 %. Results of TAGB indicate that dummy variables Z_2 and Z_2*DBH representing the *M. eminii* relative to *C. equisetifolia* species are significant at $\alpha = 0.05$. Separate biomass equations should be developed for individual species growing in agroforestry systems.

Model 2A, with separate intercepts for some species, has low PRESS and MSE and higher adjusted R^2, hence being a better model for predicting foliage biomass compared to all other models. For branch biomass, Model 2C has a lower MSE and PRESS plus a higher adjusted R^2, indicating a need for separate intercepts and slopes in predicting branch biomass. Bole biomass and TAGB is better predicted by either Model 2A or 2B, which have lower PRESS and MSE and higher adjusted R^2 (Table 3). Therefore, there is a need for either separate intercepts or slopes in predicting foliage, branch, bole biomass and TAGB. Apart from bole biomass, all other tree component models and TAGB should include either different intercepts, slopes or both (Table 4). Better equations result when dummy variables are used to differentiate intercepts and slopes for the four species.

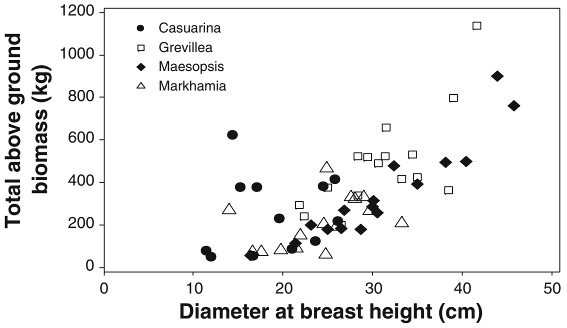

Fig. 1 Scatter plot of total above ground biomass against diameter at breast height (pooled data)

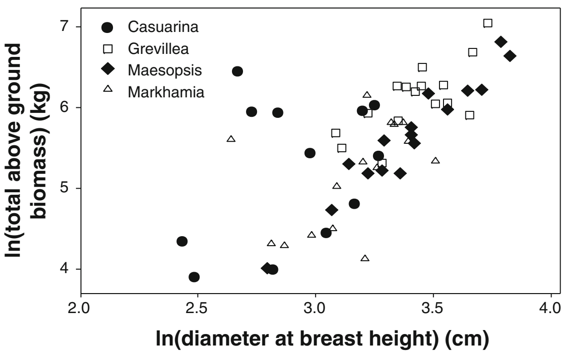

Fig. 2 Scatter plot of total above ground biomass against diameter at breast height (after logarithmic transformation of pooled data)

Species-specific allometric relationships

Allometric relationship for C. equisetifolia

The use of DBH only (Model 3A) does not explain more than 30 % variation in biomass of any of the tree components or the total above-ground biomass for *C. equisetifolia* (Table 5). The slope is not significantly ($P < 0.05$) different from zero for branch, stem and TAGB, except for foliage biomass. For all tree components and TAGB, model 3A has higher PRESS and MSE statistics. When height is included (model 3C), the regression coefficient for DBH is non-significant ($P > 0.05$) but that of height is significant at $\alpha = 0.05$ and 0.001 (Table 5). There is an improvement in the proportion of variability explained in biomass for all the tree components ranging from 40 to 78 %. A model with height alone (Model 3B) explains almost the same amount of variation as model 3C, except in the case of branch biomass where the adjusted $R^2 = 27.5$ %. On the other hand, the PRESS statistic and MSE for Model 3B is lower than that of 3C, and so foliage biomass is better predicted by a model with height as the only independent variable (Table 5). In predicting biomass for branch, bole and the total above-ground biomass, model 3C is superior, with lower PRESS, MSE and higher adjusted R^2. Model 3C was chosen as the final model for *C. equisetifolia* since it explains more than 70 % of the variation for all the tree components and TAGB, except foliage. DBH is of limited or no use for this species; HT is the better predictor.

Allometric relationship for G. robusta

The biomass model with DBH explains more 50 % of the variation for all tree components except for bole biomass, which had an explained variation of 35.8 % (Table 6). Model 3A has lower values of PRESS, MSE and higher adjusted R^2compared to other models. This model (3A) is better for predicting all the tree components biomass and TAGB, except foliage (Table 6). For predicting foliage biomass, Model 3C would be better because it has lower PRESS, MSE and higher adjusted R^2, but it should be noted that this model requires two predictor variables and the gains in predictive power are comparatively small.

Allometric relationship for M. lutea

The biomass model with DBH alone explains more 20 % of the variation for all tree components and TAGB (Table 7). Model 3A, with lower values of PRESS, MSE and higher adjusted R^2compared to the others, is chosen as the final model for *M. lutea*.

Allometric relationship for M. eminii

DBH is highly correlated with all the biomass components and the total above-ground biomass for *M. eminii* (Table 8). The amount of variation explained by DBH in total above-ground biomass was 92.7 % and for all other components this ranged from 30 to 70 %. For TAGB and foliage biomass, Model 3A is a better predictor because 3A has lower PRESS, MSE and higher adjusted R^2, while branch and bole biomass require the addition of height to DBH as another independent variable. Unlike bole biomass, height as predictor variable in Model 3C is non-significant

($P < 0.005$) and there little gain in using 3C for predicting branch biomass, hence 3A is better for predicting branch biomass.

Final models with corresponding correction factor for total above-ground biomass (TAGB)

Tree species	Model	CF
C. equisetifolia	$\ln TAGB = -2.99 - 0.79\ln(\mathrm{DBH}) + 3.27\ln(\mathrm{H})$	1.099
M. eminii	$\ln TAGB = -2.29 + 2.38\ln(\mathrm{DBH})$	1.019
M. lutea	$\ln TAGB = -2.59 + 2.42\ln(\mathrm{DBH})$	1.043
G. robusta	$\ln TAGB = 0.01 + 1.81\ln(\mathrm{DBH})$	1.024

No systematic pattern was observed in the residuals plots for *M. eminii* and *G. robusta,* C. *equisetifolia* and *M. lutea.* The normal probability plots for residuals of final model for all the species show that the residuals are normally distributed ($P > 0.05$).

Discussion

Both DBH and height are often used as independent variables for predicting above-ground biomass. The addition of height did not significantly improve the performance of the allometric biomass models for *M. eminii*, *M. lutea* and *G. robusta*, which is in agreement with previous studies (Carvalho and Parresol 2003; Onyekwelu 2004; Peichl and Arain 2007). Contrary to these results, the addition of height significantly improved the prediction in above-ground biomass for *C. equisetifolia*, while DBH was not significantly correlated to biomass prediction. *C. equisetifolia* has a conical crown shape with straight bole and very small branches with needles. Height contributes more to biomass prediction than any other variable for this species. Although no study was found in the literature that has used height as the only independent variable to explain variation in biomass, some studies have included height as a secondary variable in addition to DBH and have noted an improvement in the predictability of the models (Cienciala et al. 2006; Wagner and Ter-Mikaelian 1999).

Furthermore, Ketterings et al. (2001) indicated that tree height was more time consuming, and thus, costly to measure and while it may not explain more of the variance at the site where the data originated, its incorporation has the advantage of increasing the equation's potential applicability to different sites. When Model 1F (Table 2) was fitted to the data, only DBH was significant, and there was only 2–3 % improvement in variation explained with the addition of height and crown width as compared to Model 1A (DBH alone) (Table 2). This suggests that the three variable model used for other Ugandan tree species may not be suitable for trees growing within agroforestry systems. We also noted the amount of variation explained by the models in Table 2 ranges between 30 and 50 %, indicating either weak allometric relationships between tree components for Ugandan tree species in the agroforestry systems or a need to include a different set of predictor variables.

On the other hand, with the exception of *M. eminii,* the adjusted R^2 and their corresponding P values of *C. equisetifolia, M. lutea and G. robusta* are not typical of allometric equations reported in the literature for plantation, grassland and forest trees. This may be due to different impacts of management practices (thinning, root and branch pruning) applied to trees in a linear simultaneous agroforestry system to reduce competition between crops and trees. These practices may impact biomass allocation within a tree and also reduce the strength of the relationship between DBH, height and crown. It has been noted (Lott et al. 2000) that allometric equations developed for closed canopy natural or plantation forests may not be suitable for agroforestry systems because trees within an agroforestry system are more open-grown and are not sensitive to the competition between crops and trees. Unlike the other species in this study, *M. eminii* is self pruning and this may result in the high correlation between DBH and height with the biomass for each tree component and TAGB.

Another issue with this study that may have resulted in low R^2 for our allometric equations is the relatively small sample size for each species (i.e., $n < 30$). However, conducting another study may be next to impossible given the limited number of available sample trees at the study site and how the direct method used is destructive, very expensive and time consuming. Lott et al. (2000) suggested that despite the influence of management practices applied in the agroforestry systems, estimates of above-ground biomass and leaf area could be obtained by measuring diameter of all branches and trunk cross-sectional area immediately

Table 2 Regression equations for data pooled for four different tree species (*Casuarina equisetifolia, Grevillea robusta, Maesopsis eminii* and *Markhamia lutea*) grown in a linear agrofrestry system in central Uganda

Biomass component	Model[1,2]	Regression parameters estimates				MSE	R-sq (adj.) (%)	PRESS[9] Statistic
		β_0	β_1	β_2	β_3			
Foliage	1A[3]	−1.120	1.280***			0.343	31.5	21.14
	1B[4]	−1.240		1.460***		0.398	20.6	24.27
	1C[5]	0.777			1.200***	0.369	26.4	22.83
	1D[6]	−2.172	1.013**	0.6571		0.334	33.4	21.00
	1E[7]	−0.905	0.899**		0.5462	0.334	33.2	21.15
	1F[8]	−1.880	0.694*	0.593	0.489	0.328	34.6	21.22
Branch	1A	−4.120	2.490***			0.717	45.8	43.71
	1B	−0.470		1.510*		1.227	7.3	74.77
	1C	−0.282			2.240***	0.851	35.7	51.13
	1D	−3.020	2.780***	0.686		0.713	46.2	43.80
	1E	−3.770	1.860***		0.894	0.690	47.8	42.27
	1F	−2.440	2.140***	0.813	0.972	0.679	48.7	41.78
Bole	1A	0.321	1.470***			0.419	33.2	26.30
	1B	0.700		1.500***		0.521	17.1	32.27
	1C	2.420			1.410***	0.443	29.5	27.03
	1D	−0.472	1.269***	0.4945		0.417	33.4	26.68
	1E	0.597	0.976**		0.704	0.402	35.9	26.35
	1F	−0.070	0.836***	0.408	0.665	0.404	35.7	27.04
TAGB	1A	0.230	1.640***			0.326	44.6	20.39
	1B	1.450		1.400***		0.496	15.7	30.50
	1C	2.710			1.500***	0.377	35.9	22.92
	1D	−0.010	1.580***	0.148		0.331	43.8	20.97
	1E	0.480	1.190***		0.637	0.321	47.0	20.23
	1F	0.370	1.170***	0.066	0.630	0.318	46.1	20.93

[1] Models are provided in the body of the text, β_0–β_3 are estimated regression parameters, *MSE* mean squared error, * means that the coefficient is significant at 0.1, ** significant at $\alpha = 0.05$, and *** significant at $\alpha = 0.001$ level, *R-sq(adj.)* adjusted coefficient of multiple determination

[2] All models have $P < 0.001$

[3] Model 1A (DBH only)

[4] Model 1B (HT only)

[5] Model 1C (CW only)

[6] Model 1D (DBH & HT)

[7] Model 1E (DBH & CW)

[8] Model 1F (DBH, HT & CW)

[9] PRESS statistics used to validate the models (small is better)

below the first branch of the crown. However, the suggested methods are time-consuming and are generally only easily applied to trees younger than four years.

Generally, height is not required for predicting foliage, branch or TAGB biomass for most agroforestry tree species we studied in this paper, although it does improve the predicted value of bole biomass for *Maesopsis eminii*. However, height is not useful in predicting any tree component or TAGB for *M. lutea* and *G. robusta*. For *C. equisetifolia*, data on height and DBH are required to estimate foliage, branch, bole and TAGB biomass. Therefore, for all the species, except *C. equisetifolia*, when DBH data are available, biomass can be predicted. When *C. equisetifolia*

Table 3 Testing for differences in intercepts and/or slopes for component biomass equations among four tree species

Biomass component	Model[1,] [2]No	Regression parameters estimates								MSE	R-sq (adj.) (%)	PRESS[3] statistic
		β_0	β_1	α_1	α_2	α_3	α_4	α_5	α_6			
Foliage	1A[4]	−1.12	1.28***							0.343	31.5	21.14
	2A[5]	−1.60	1.58***	−0.35	−0.70**	−0.77**				0.278	44.5	17.92
	2B[6]	−2.00	1.71				−0.12	0.22**	−0.25**	0.282	43.8	18.23
	2C[7]	−0.52	1.21**	−1.96	−2.34	−2.17	0.525	0.537	0.47	0.291	41.9	20.02
Branch	1A	−4.12	2.49***							0.717	45.8	43.71
	2A	−3.23	2.22***	0.54	−0.21	−0.41				0.621	53.1	39.92
	2B	−3.06	2.14**				0.19	−0.03	0.10	0.624	52.8	40.21
	2C	3.18	0.02	−7.54	−10.4**	−8.90**	2.61**	3.31**	2.87**	0.533	59.8	34.72
Bole	1A	0.32	1.47***							0.419	33.2	26.30
	2A	0.22	1.60**	−0.11	0.46	−0.56*				0.387	38.3	25.78
	2B	0.01	1.67***				−0.04	−0.13	−0.18*	0.389	38.1	25.65
	2C	1.05	1.31**	−0.12*	−3.96	0.49	0.046	1.071	−0.31	0.389	43.8	29.17
TAGB	1A	0.23	1.64***							0.326	44.6	20.39
	2A	0.29	1.69***	0.03	0.40	0.22*				0.289	51.0	19.11
	2B	0.17	1.73***				0.01	−0.11	−0.15*	0.291	50.6	19.17
	2C	2.16	1.05*	−1.76	−5.10**	−1.11	0.62	1.47**	0.25	0.280	52.4	20.70

[1] Models are provided in the body of the text, β_0–$\beta 1$ and α_1–α_6 are estimated regression parameters, *MSE* mean squared error, * means that the coefficient is significant at 0.1, ** significant at $\alpha = 0.05$, and *** significant at $\alpha = 0.001$ level, *R-sq(adj.)* adjusted coefficient of multiple determination

[2] All models have $P < 0.001$

[3] PRESS statistics used to validate the models (small is better)

[4] Model 1A (DBH only)

[5] Model 2A (DBH, separate intercepts & slopes)

[6] Model 2B (HT, separate intercepts & slopes)

[7] Model 2C (DBH, HT, separate intercepts & slopes)

Table 4 Contribution of intercepts and/or slopes for component biomass equations among four tree species

Component biomass (kg)		Sum of squares error of reduced model	Sum of squares error of full model	Mean square error full model	F-values from data	Degrees of freedom	F-values from statistical table at 5 %	Calculated *P* values
Foliage	Intercepts	19.568	15.036	0.278	4.070	4, 54	2.548	0.005
	Slopes	19.568	15.215	0.282	3.862	4, 54	2.548	0.007
	Both	19.568	14.856	0.291	2.311	7, 51	2.197	0.039
Branch	Intercepts	40.861	33.525	0.621	2.953	4, 54	2.548	0.028
	Slopes	40.861	33.706	0.624	2.867	4, 54	2.548	0.032
	Both	40.861	27.159	0.533	3.676	7, 51	2.197	0.003
Bole	Intercepts	23.899	20.921	0.387	1.922	4, 54	2.548	0.120
	Slopes	23.899	21.001	0.389	1.863	4, 54	2.548	0.130
	Both	23.899	19.834	0.389	1.493	7, 51	2.197	0.191
TAGB	Intercepts	18.595	15.579	0.289	2.613	4, 54	2.548	0.045
	Slopes	18.595	15.725	0.291	2.464	4, 54	2.548	0.056
	Both	18.595	14.296	0.280	2.191	7, 51	2.197	0.050

Reduced model includes DBH only as the dependent variable and full model has DBH, intercepts and/or slopes

R-sq(adj.) adjusted coefficient of multiple determination

Table 5 Biomass regression equations for *Casuarina equisetifolia*

Biomass component	Model[1]	Regression parameters			MSE	R-sq (adj.) (%)	Model *P* value	PRESS[2] Statistic
		β_0	β_1	β_2				
Foliage	3A[3]	−0.52	1.21**		0.213	32.7	0.030	2.92
	3B[4]	−2.39		1.82***	0.069	78.2	0.000	1.06
	3C[5]	−2.71	0.29	1.64***	0.071	77.6	0.000	1.17
Branch	3A	3.18	0.02		0.255	0.0	0.971	3.63
	3B	0.23		1.02**	0.168	27.5	0.046	2.21
	3C	1.14	−0.84	1.53***	0.139	40.0	0.041	2.16
Bole	3A	1.05	1.31		1.106	3.8	0.258	15.32
	3B	−5.10		3.37***	0.311	73.0	0.000	3.99
	3C	−4.14	−0.88	3.91***	0.293	74.5	0.001	4.03
TAGB	3A	2.16	1.05		0.761	3.0	0.274	10.55
	3B	−3.04		2.79***	0.208	73.9	0.000	2.68
	3C	−2.19	−0.79	3.27***	0.189	75.9	0.000	2.65

[1] Models are provided in the body of the text, β_0–β_2 are regression parameters, *MSE* mean squared error, ** significant at $\alpha = 0.05$, and *** significant at $\alpha = 0.001$ level, *R-sq(adj.)* adjusted coefficient of multiple determination

[2] PRESS statistics used to validate the models (small is better)

[3] Model 3A (DBH only)

[4] Model 3B (HT only)

[5] Model 3C (DBH & HT)

Table 6 Biomass regression equations for *Grevillea robusta*

Biomass component	Model[1]	Regression parameters			MSE	R-sq (adj.) (%)	Model *P* value	PRESS[2] Statistic
		β_0	β_1	β_2				
Foliage	3A[3]	−5.00	2.50***		0.047	81.0	0.000	0.84
	3B[4]	−4.72		2.73**	0.149	44.4	0.006	2.44
	3C[5]	−7.22	2.05***	1.24*	0.032	88.0	0.000	0.52
Branch	3A	−5.50	3.06**		0.268	53.7	0.002	4.67
	3B	0.51		1.47	0.587	0.0	0.378	5.21
	3C	−3.67	3.43***	−1.02	0.277	52.3	0.007	10.94
Bole	3A	1.06	1.32**		0.096	35.8	0.014	1.68
	3B	2.84		0.93	0.147	2.5	0.270	2.57
	3C	1.22	1.33*	−0.04	0.105	30.0	0.056	1.99
TAGB	3A	0.01	1.81***		0.047	70.4	0.000	4.67
	3B	3.10		1.02	0.152	4.0	0.238	10.94
	3C	0.73	1.95***	−0.39	0.049	69.2	0.001	5.21

[1] Models are provided in the body of the text, β_0–β_2 are regression parameters, *MSE* mean squared error, * means that the coefficient is significant at 0.1, ** significant at $\alpha = 0.05$, and *** significant at $\alpha = 0.001$ level, R-*sq(adj.)* adjusted coefficient of multiple determination

[2] PRESS statistics used to validate the models (small is better)

[3] Model 3A (DBH only)

[4] Model 3B (HT only)

[5] Model 3C (DBH & HT)

Table 7 Biomass regression equations for *Markhamia lutea*

Biomass component	Model[1]	Regression parameters			MSE	R-sq (adj.) (%)	Model *P*-value	PRESS[2] Statistic
		β_0	β_1	β_2				
Foliage	3A[3]	−1.93	1.49*		0.273	23.4	0.064	4.03
	3B[4]	0.86		0.71	0.371	0.0	0.470	4.89
	3C[5]	−1.36	1.81*	−0.80	0.789	17.4	0.171	4.42
Branch	3A	−4.91	2.63*		0.726	27.0	0.048	10.33
	3B	−0.33		1.38	1.016	0.0	0.400	15.18
	3C	−4.11	3.07*	−0.80	0.789	20.7	0.143	13.50
Bole	3A	−3.08	2.43**		0.127	68.5	0.001	1.80
	3B	−0.39		1.83	0.302	24.7	0.057	4.14
	3C	−3.26	2.33***	−0.18	0.139	65.2	0.003	2.11
TAGB	3A	−2.59	2.42***		0.083	76.9	0.000	1.29
	3B	0.16		1.80*	0.262	27.4	0.047	3.67
	3C	−2.73	2.35***	−0.139	0.092	74.5	0.001	1.69

[1] Models are provided in the body of the text, β_0–β_2 are regression parameters, *MSE* mean squared error, * means that the coefficient is significant at 0.1, ** significant at $\alpha = 0.05$, and *** significant at $\alpha = 0.001$ level, *R-sq(adj.)* adjusted coefficient of multiple determination

[2] PRESS statistics used to validate the models (small is better)

[3] Model 3A (DBH only)

[4] Model 3B (HT only)

[5] Model 3C (DBH & HT)

Table 8 Biomass regression equations for *Maesopsis eminii*

Biomass component	Model[1]	Regression parameters			MSE	R-sq (adj.) (%)	Model *P*-value	PRESS[2] Statistic
		β_0	β_1	β_2				
Foliage	3A[3]	−2.86	1.75***		0.363	35.9	0.000	6.81
	3B[4]	−0.56		1.20	0.536	5.3	0.196	10.49
	3C[5]	−2.62	1.82**	0.161	0.390	31.1	0.035	8.31
Branch	3A	−7.02	3.33***		0.369	68.6	0.000	6.48
	3B	0.22		1.29	1.176	0.0	0.341	22.8
	3C	−4.52	4.17***	−1.84	0.280	76.1	0.000	4.70
Bole	3A	−2.90	2.38***		0.111	78.9	0.000	1.89
	3B	−2.17		2.44**	0.274	48	0.002	4.85
	3C	−4.35	1.92***	0.994**	0.085	83.8	0.000	1.66
TAGB	3A	−2.93	2.52***		0.037	92.7	0.000	0.65
	3B	−0.48		2.03**	0.345	32.4	0.013	6.63
	3C	−3.24	2.43***	0.211	0.039	92.5	0.000	0.75

[1] Models are provided in the body of the text, β_0–β_2 are regression parameters, *MSE* mean squared error, ** significant at $\alpha = 0.05$, and *** significant at $\alpha = 0.001$ level, *R-sq(adj.)* adjusted coefficient of multiple determination

[2] PRESS statistics used to validate the models (small is better)

[3] Model 3A (DBH only)

[4] Model 3B (HT only)

[5] Model 3C (DBH & HT)

biomass stocks are to be estimated, DBH and height data are necessary.

In this study, Sprugel's (1983) method was used to calculate the correction factors for the models, even though some researchers use no correction, since the difference in biomass estimates is considered negligible (Malimbwi et al. 1994). It is advisable, however, to analyze each case individually to ascertain the need for the correction factor in biomass estimates. Methods for estimating stand biomass often involve prediction of individual tree biomass and summation to obtain stand biomass (Parresol 1999). Biomass additivity is a desirable feature of tree component regression equations as well as for total tree biomass (Carvalho and Parresol 2003; Parresol 1999; Bi et al. 2004). The additivity property eliminates inconsistency between the sum of predicted values for components, such as stem, bark, branch and leaf, and the prediction for total tree. Besides logical consistency, a system of additive biomass equations, when estimated by taking into account the inherent correlation among the biomass components, has greater statistical efficiency than separately estimated equations for individual components (Bi et al. 2004). In this study, additivity is recognized but was not addressed; mean biomass for individual biomass components does not add up to the TAGB for any species, which indicates lack of logical consistency among the components equations (Bi et al. 2004; Carvalho and Parresol 2003; Parresol 1999). We recommend that in predicting total above-ground biomass for a linear simultaneous or similar agroforestry system, the use of an additive model which incorporates both individual component biomass equations as well as TABG be used (Bi et al. 2004; Parresol 1999).

Although it is sometimes recommended that models used for prediction purposes be validated with independent data (Chiyenda and Kozak 2004), only a limited amount of tree data were available and collected at the study site. As a result, regression equation performance could not be validated using independent data. However, the predictive sum of squares statistic (PRESS) provide adequate methodology to validate the chosen models.

Conclusion

This study demonstrates the importance of developing individual site specific biomass equations. The results also suggest that biomass equations developed for natural forests may not be adequate for an agroforestry, managed plantation or woodland ecosystems.

In addition, the study showed the need to develop separate biomass equations for individual species growing in agroforestry system. The inclusion of height improves the predictive ability of the model for bole biomass for only *M. eminii*, but does not improve the predictability of biomass models for *M. lutea* and *G. robusta*, nor other tree components of *M. eminii*. Height data are important in predicting all the tree components and total above-ground biomass for *C. equisetifolia*. In general, DBH is the best independent variable for predicting above-ground biomass components in *M. lutea, G. robusta* and *M. eminii*, with height not contributing any significant predictive power, except for *M. eminii* bole biomass. Above-ground biomass components in *C. equisetifolia*, in contrast, are better predicted by height, with DBH contributing no predictive power.

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