

# Estimation of stem and tree level biomass models for *Prosopis juliflora/pallida* applicable to multi-stemmed tree species

Emil Cienciala · Alex Centeio · Petr Blazek ·  
Maria da Cruz Gomes Soares · Radek Russ

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**Abstract** The aim of this paper is to develop biomass models for commonly multi-stemmed *Prosopis juliflora/pallida* trees. The data were collected on three of the Cape Verde islands (Maio, Santiago and Santo Antao). The dataset covers 240 trees containing 1,882 stems with stem diameter at breast height over 2 cm; of that 255 individual tree stems were sampled destructively. These calibration data were used to construct stem and tree-level models for estimation of total aboveground biomass and its fine and course fractions with diameter threshold of 5 cm. A set of parameterized biomass models for multi-stemmed *Prosopis* spp. trees suited for biomass estimation at tree and stem levels using appropriate set of independent variables, commonly available in forest inventory programs, was created. The effect of site (island) on tree allometry was not detected. The two-phase construction of tree biomass models based on destructive sampling limited to individual stems combined with a routine field measurement of entire multi-stemmed tree specimen represents a practicable approach leading to biomass and carbon assessment that may be generally suited for tree species with complex multi-stemmed growth form similar to that of *Prosopis* spp.

**Keywords** Aboveground biomass · Carbon · Allometric equations · Inventory · Woody resources

## Introduction

The Cape Verde islands are relatively small in terms of surface area, but with remarkably wide spectrum of growth conditions that determine occurrence of diverse terrestrial ecosystems. A large part of the land surface is rather warm and dry, representing challenging conditions for most tree species of the tropical zone. In this respect, the outstandingly important woody genus is *Prosopis*, which has been successfully used in afforestation programs to combat desertification, restore degraded locations and promote sustainable use of land on Cape Verde. This applies also for other arid regions in Asia, Sub-Saharan Africa and Latin America, although on some of these locations *Prosopis* spp. is also reported to be highly invasive with negative impacts to local ecosystems (Muturi et al. 2010; Zachariades et al. 2011). It should be noted that the taxonomy of *Prosopis* is rather difficult, because leaves vary in size and *Prosopis* may also create hybrid populations (Pasiecznik et al. 2003). This also applies to Cape Verde islands, where the most common *Prosopis* species is *P. juliflora*, although it may actually also include *P. pallida* species or any hybrids *P. juliflora* × *P. pallida*. To distinguish the particular *Prosopis* species is yet to be addressed by more advanced genetic techniques as demonstrated recently (Sherry et al. 2011; Palacios et al. 2012). In this material, we make no further distinction between these species and use the name *Prosopis* spp. for the *P. juliflora/pallida* complex.

Since 2008, the Republic of Cape Verde has been conducting its first statistical National Forest Inventory (NFI) survey. Data on tree abundance and tree dendrometric data

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E. Cienciala (✉) · P. Blazek · R. Russ  
Institute of Forest Ecosystem Research (IFER),  
Areal 1. jilovske a.s., 254 01 Jílové u Prahy, Czech Republic  
e-mail: emil.cienciala@ifecr.cz

A. Centeio · M. d. Cruz Gomes Soares  
Ministry of Rural Development, Directorate General  
for Agriculture, Forestry and Animal Industry (DGASP),  
Achada São Felipe—Praia, C.P.278,  
Santiago Island, Cape Verde

are collected across the Cape Verde islands. To enable estimation of volume, biomass and carbon stock held in trees, suitable local volume and biomass models need to be developed, which would use the specific information from the NFI survey. Unlike single stem trees, *Prosopis* spp. most commonly grow as poly-stemmed individuals, although trees with one or two clear trunks may also occur. Hence, their tree form varies from more erect to shrubby. The plasticity of tree forms of *Prosopis* spp. is reflected in corresponding measurement methodology adopted in the NFI program.

The published literature on *Prosopis* spp. allometry remains scarce and the estimation procedures largely differ. This is due to the extremely variable tree form with multiple stems originating often close to the ground or from the ground. Hence, a determination of tree basal area is problematic and the published literature show different approaches to address this issue. Some authors use the measurement of tree basal area at a prescribed height close to the ground or at the conventional breast height (Padrón and Navarro 2004; Muturi et al. 2011), while others use stem measurements directly at the ground and estimate the equivalent tree basal area by summing up basal area of individual stems (Alvarez et al. 2011a). These approaches may not always be optimal as the tree stems may originate close to the ground and the accuracy of stem or tree diameter measurements may be affected by a large heterogeneity in stem shape at a prescribed reference position close to the ground, which also makes the field work challenging.

The aim of this study is to construct effective biomass models and describe practicable approach of developing such models for *Prosopis juliflora/pallida* complex, typical representatives of tree species with multi-stemmed growth form, suitable for aboveground biomass and carbon stock estimation based on conventionally measured data collected in statistical forest inventory survey programs.

## Methods

### Sampling sites

The sampling sites of *Prosopis* spp. used for this study were scattered across the three major islands of Cape Verde, namely Maio, Santiago and Santo Antao (Fig. 1). The specific locations of trees used in this study were selected randomly including 11–19 sites on each island. All sampling sites were located in the very arid or arid zone according to the agro-ecological site classification currently used in Cape Verde (Diniz and de Matos 1988, 1999). The sampling sites covered vertical gradients between 17 and 57 m above sea level (a.s.l.) in Maio,

17–406 m a.s.l. in Santiago and 282–1,319 m a.s.l. in Santo Antao.

### Measurement and sampling procedures

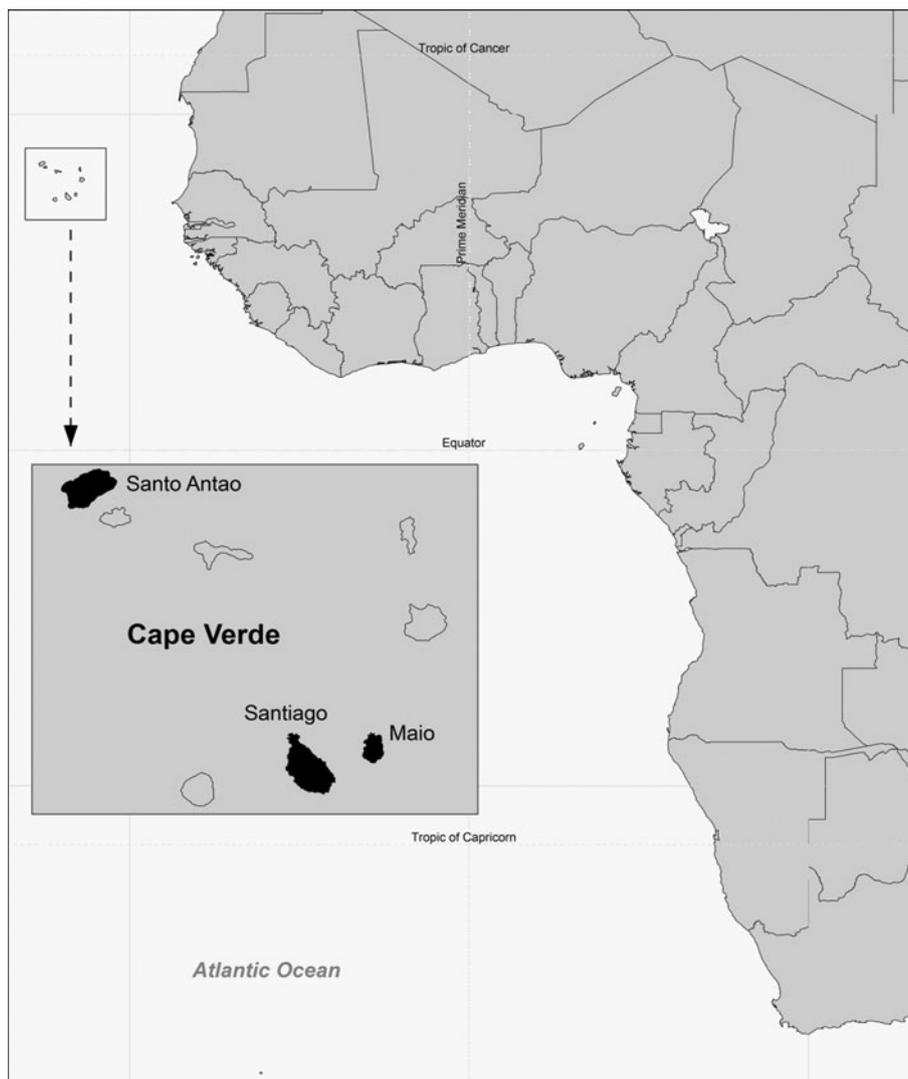
The measurement and sampling of *Prosopis* spp. stems and trees for this study was conducted during September 2011 on Maio, August 2011 on Santiago and June 2011 on Santo Antao.

The measurement methodology of standing *Prosopis* trees was linked to the standard measurement procedures of the National Forest Inventory (NFI) of Cape Verde. NFI treats *Prosopis* biometry in the following way: (i) stem diameter at breast height ( $DBH_s$ ) is measured for all stems with  $DBH_s$  of 5 cm and larger, (ii) all stems with  $DBH$  between 2 and 5 cm are counted and their  $DBH_s$  assessed and recorded as one mean value applicable for all such stems of a tree, (iii) tree height (maximum) is measured, and (iv) tree crown projection is measured using at least five projected points. The biomass sampling program used in this study used identical measurement procedure. One exception was point (ii), when  $DBH_s$  of each sample stem was specifically measured also for the dimensions between 2 and 5 cm. All field measurement and mapping was done using the Field-Map technology setup (<http://www.fieldmap.cz>), consisting of laser rangefinder (Impulse, Laser Technology, Inc., USA), electronic compass (Map-Star, Laser Technology, Inc., USA), electronic caliper (DigiTech, Haglof, Sweden), GPS and field computer equipped with Field-Map ver. 12 software solution (IFER-MMS, Czech Republic), facilitating measurement and mapping of this particular *Prosopis* spp. biomass sampling project.

The measurement procedure in the field covered altogether 240 trees of *Prosopis* spp., containing totally 1,882 stems. Of that number, 1,481 stems had  $DBH_s$  of at least 5 cm, while the  $DBH$  for 401 stems ranged between 2 and 5 cm. At least one stem was sampled destructively from each tree as described below. The summary information on sampled material on each of the three islands is given in Table 1.

The destructively sampled stems were selected randomly from each tree. The suitable sample trees were also selected randomly from the population at each actual sample site. Most commonly, one stem was sampled per one tree, occasionally two stems of different dimensions were taken from identical trees. The destructively sampled stems were cut at breast height using chain or hand saw and processed on the ground into a woody component with stem diameter of at least 5 cm, while the rest of the stem biomass represented the fine fraction including leaves, small branches and woody parts up to 5 cm in diameter. These two components were effectively distinguished

**Fig. 1** Location of the study—three of the Cape Verde islands, namely Santo Antao, Santiago and Maio



**Table 1** Overview of the empirical tree material collected and used in the analysis of this study; dimensions of sample stem diameter at breast height (DBH<sub>s</sub>) concern only the destructively sampled stems and include minimum (MIN), average (AVG) maximum (MAX) values

| Island      | No. trees measured | No. stems measured | No. stems destructively sampled <sup>a</sup> | Sample DBH <sub>s</sub><br>MIN AVG<br>MAX (cm) |
|-------------|--------------------|--------------------|----------------------------------------------|------------------------------------------------|
| Maio        | 75                 | 657                | 78                                           | 4.5, 8.8, 16.0                                 |
| Santiago    | 88                 | 604                | 89                                           | 2.5, 7.9, 18.8                                 |
| Santo Antão | 77                 | 621                | 88                                           | 2.9, 8.9, 18.6                                 |
| Totally     | 240                | 1,882              | 255                                          | 2.5, 8.5, 18.8                                 |

<sup>a</sup> Each sample stem was subdivided into fine and coarse component using a diameter threshold of 5 cm

using 5-cm metal fork to label the woody spots to be cut and separated. Both biomass components were weighted in the field using a field balance to obtain total fresh weight

for each of the two stem biomass components. Of each component, a small sample of about 250–600 g was taken for each felled stem for estimating a component-specific dry weight (DW; kg) to fresh weight (FW; kg) ratio (DW/FW; –). Sample weight was measured at the field station on a balance with resolution of grams on the same day as sampled in the field. Sample DW was estimated later after oven-drying at 105 °C in the laboratory until a constant weight was achieved. DW/FW was used to convert FW data collected at the level of the two stem biomass components into the corresponding (oven) dry weight.

#### Two-phase biomass model estimation concept

Generally, biomass models were constructed using the most commonly form, namely that of power functions (Zianis and Mecuccini 2004). However, as often preferred in allometric studies, we used the approach of linearization in order to avoid non-linear parameterization, stabilize

variance and facilitate a more straightforward comparison of models between the islands. In this way, the general power function relating the dependent variable  $Y$  to independent variables  $X_0$ – $X_n$

$$Y = p_0 \times X_1^{p_1} \times X_2^{p_2} \dots X_n^{p_n} \quad (1)$$

with parameters  $p_0, p_1$ – $p_n$  to be fitted, is transformed to

$$\ln Y = p_0 + p_1 \times \ln X_1 + p_2 \times \ln X_2 \dots + p_n \times \ln X_n + \varepsilon \quad (2)$$

where  $\varepsilon$  represents the additive error term. It should be noted, however, that such transformation produces a bias that must be statistically treated (Sprugel 1983). Here, we used the correction as applied by Marklund (1987), who calculated a model specific correction factor  $\lambda$  from the data as follows:

$$\lambda = \frac{\sum_{i=1}^n Y_i}{\sum_{i=1}^n e^{\ln \hat{Y}_i}} \quad (3)$$

where  $n$  is number of samples and  $Y_i, \hat{Y}_i$  represent the observed and fitted values. This approach ensures that the mean predicted value is equal to the mean observed value. Hence, an unbiased estimate of  $Y$  is given as

$$\hat{Y} = \lambda \times \exp(p_0 + p_1 \times \ln X_1 + p_2 \times \ln X_2 \dots + p_n \times \ln X_n) \quad (4)$$

The mean relative prediction error (MPE, %) was calculated as follows (Nelson et al. 1999):

$$\text{MPE} = \frac{100}{n} \sum_{i=1}^n \left| Y_i - \hat{Y}_i \right| / Y_i \quad (5)$$

The creation of biomass models for *Prosopis* spp. trees followed a two-phase estimation concept. In this, stem biomass ( $AB_s$ ; kg) models are formulated and parameterized first and thereon the appropriate functional form is used in combination with entire tree-level input data to seek the appropriate effective models for estimating tree aboveground biomass ( $AB_t$ ; kg) and other desired characteristics to be quantified at tree level. Utilizing the statistical approach of linear regression on linearized power functions as described in Eqs. 1–4 above, stem-level biomass model utilizes fundamentally stem diameter at breast height ( $DBH_s$ ; cm) as an independent variable. However, the effect of including stem height ( $H_s$ ; m) and sampling site elevation ( $Z$ ; m a.s.l.) was also tested. Note that  $AB_s$  represents dry mass of entire stem excluding the part below breast height (1.3). That fraction is included only at tree level as described below.

The tree-level biomass models for estimating total aboveground biomass tested several independent variables collected (directly or derived) in the field during the

National Forest Inventory program. The most fundamental one is tree equivalent diameter at breast height (EDBH<sub>*t*</sub>; cm), conceptually identical as tree diameter used, e.g., by Alvarez et al. (2011a). It was calculated for each sample tree using the formula

$$\begin{aligned} \text{EDBH}_t &= 2 \times \sqrt{(\text{DBH}_{s1}/2)^2 + (\text{DBH}_{s2}/2)^2 + \dots + (\text{DBH}_{sn}/2)^2} \\ & \quad (6) \end{aligned}$$

where  $DBH_{s1}, DBH_{s2}, \dots, DBH_{sn}$  is the stem breast height diameter of  $n$ -stems of a given tree (in cm). Besides EDBH<sub>*t*</sub>, other independent variables tested for tree-level model construction included crown projection area (CPA; m<sup>2</sup>), crown width (CW; m), tree height ( $H_t$ ; m), number of tree stems (SN) that reached diameter of at least 5 cm at breast height (1.3 m) and sampling site elevation ( $Z$ ). With exception of  $Z$ , the above mentioned tree level data are shown in Fig. 2.

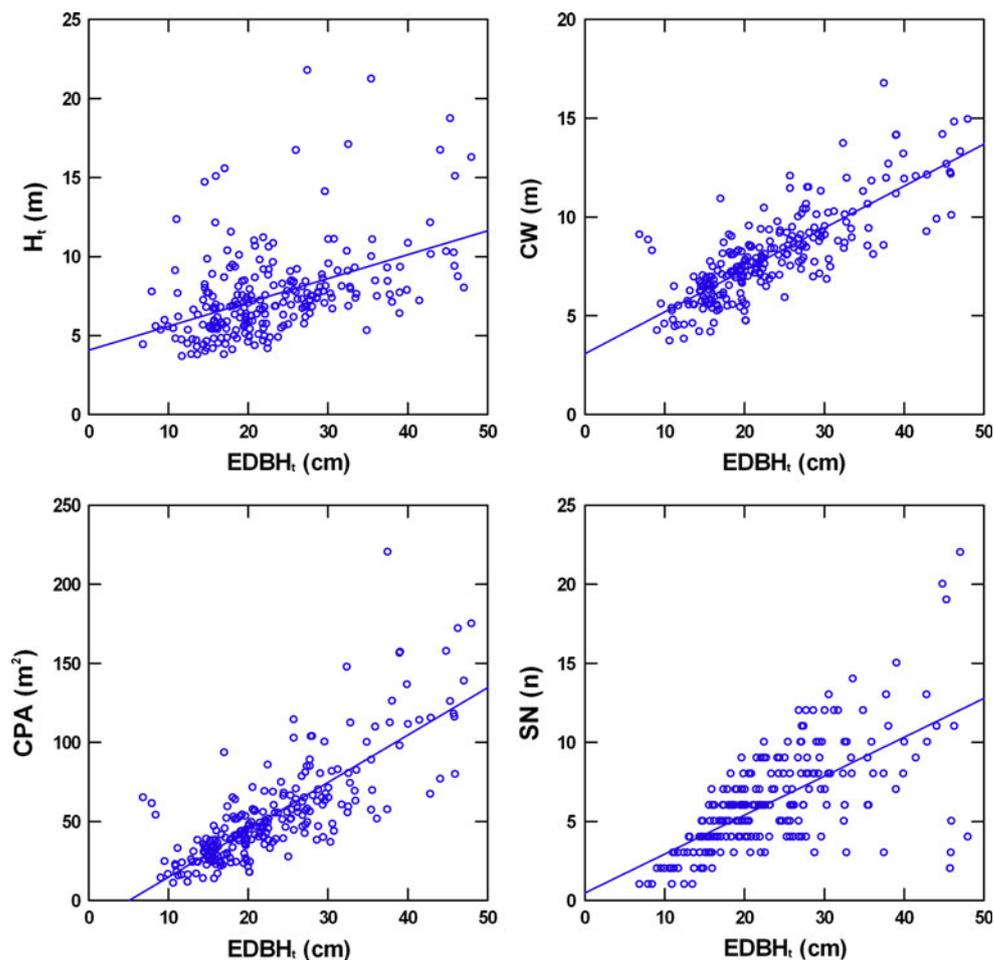
EDBH<sub>*t*</sub> was also used to calculate the tree equivalent “single-stem” woody part volume from ground to the breast height, using cylinder volume formula and length of 1.3 m, corresponding to breast height. This tree volume fraction was converted to biomass using a conventional density of 800 kg/m<sup>3</sup>, a conservative value for *P. juliflora* wood (Little and Wadesworth 1964; Chave et al. 2009; Zanne et al. 2009). This fraction combined with the stem biomass estimated and summed up for all stems of a tree gives a tree above-ground biomass ( $AB_t$ ) that was used to parameterize tree-level models. Herewith,  $AB_t$  in this study represents dry mass of entire tree and its parts from the ground (in kg), but excluding small stems with DBH under 2 cm, the contribution of which was neglected.

The models for estimating biomass at stem ( $AB_s$ ) and tree ( $AB_t$ ) level are provided exclusively for dry mass. Hence, they can be directly used for estimating carbon content when adopting a conventional ratio of 0.5 for carbon content held in woody mass as recommended by IPCC (2003).

To facilitate estimation of woody (parts with diameter 5 cm and larger) and fine biomass (up to diameter threshold of 5 cm) components separately at tree level, a suitable model for fine biomass share estimation was identified. It basically followed the logic of Eq. 1, testing the available independent data on EDBH<sub>*t*</sub>, CPA, CW,  $H_t$ , and SN. Similarly, suitable functional forms to estimate EDBH<sub>*t*</sub> on the basis of solely tree-level independent variables were analyzed.

All models were estimated and evaluated on the basis of linear and nonlinear regression statistics, taking into account the classical criteria such as coefficient of determination (adjusted  $R^2$ ) and standard error of estimate (SEE). The decisive criterion for judging model

**Fig. 2** Data at tree level including tree height ( $H_t$ ), crown width (CW), crown projection (CPA) and number of stems (SN) with diameter larger than 5 cm, plotted against tree equivalent diameter at breast height (EDBH<sub>*t*</sub>)



performance when comparing different models was Schwarz's Bayesian information criterion (BIC; Schwarz 1978), as implemented in SYSTAT (version 13) statistical software (SYSTAT Software, Inc. 2009). BIC is a similar criterion as Akaike information criterion (AIC) or Corrected Akaike Information Criterion, which were also consulted. However, only BIC is explicitly reported together with the regression results here. To compare model regression lines to identify the effect of location (island), the analysis of covariance (ANCOVA) as implemented within GLM in SYSTAT (version 13) was used. It includes the Tukey's Honestly-Significant-Difference Test to identify the possible effects between each pair of islands.

## Results

### Stem-level biomass models

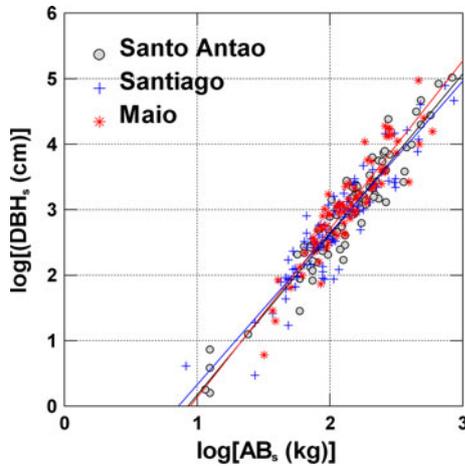
Stem biomass ( $AB_s$ ) model parameterized in its linearized form 2 for data by individual islands using solely  $DBH_s$  as independent variable resulted in the fits explaining

85–91 % variability in the observed biomass values when analyzed for individual islands and 88 % for the full dataset (Fig. 3; Table 2).

The regression lines in Fig. 3 mostly overlap and are barely discernible for individual islands. It suggests insignificant effect of location (islands) on the stem biomass model. Testing the regression lines for similarity, the ANCOVA analysis revealed no statistically significant difference among individual islands ( $p = 0.080$ ). The pairwise comparison of  $AB_s$  models using Tukey's Honestly-Significant-Difference Test (SYSTAT 13) revealed the closest match between the data from Santiago and Santo Antao ( $p = 0.913$ ). On the contrary, the relatively weakest correspondence was attributed between data from Maio and Santo Antao ( $p = 0.080$ ), which actually determines the above reported ANCOVA result for the entire data set including all three islands.

Adding stem height ( $H_s$ ) as a second independent variable had no significant effect on the fit of the observed stem biomass. Using a step-wise regression procedure, the only marginal improvement of the regression statistics for the  $AB_s$  model combining both  $DBH_s$  and  $H_s$  was detected in

the case of Santiago island sub-sample. In this case,  $R^2$  increased from 0.850 to 0.860 and BIC decreased from 57.9 to 53.7. For Maio and Santo Antao islands, the



**Fig. 3** Linear regression of log-transformed stem biomass ( $AB_s$ ) model with  $DBH_s$  as the only independent variable for the individual islands

**Table 2** Regression statistics for the parameterized stem biomass models ( $AB_s$ ; kg) according to 2–4 using  $DBH_s$  as independent variable: correction factor  $\lambda$ , fitted parameters  $p_0$ ,  $p_1$ , coefficient of determination  $R^2$ , number of observations ( $n$ ), mean prediction error (MPE; %) and Schwarz’s Bayesian Information Criterion (BIC) are shown for the data from individual islands and totally

| Island      | Regression statistics |        |       |       |                  |      |       |
|-------------|-----------------------|--------|-------|-------|------------------|------|-------|
|             | $\lambda$             | $p_0$  | $p_1$ | $R^2$ | $n$              | MPE  | BIC   |
| Maio        | 1.031                 | -2.435 | 2.568 | 0.848 | 76 <sup>a</sup>  | 25.6 | 40.8  |
| Santiago    | 1.047                 | -1.988 | 2.316 | 0.850 | 89               | 27.9 | 57.9  |
| Santo Antão | 1.048                 | -2.281 | 2.451 | 0.914 | 88               | 23.1 | 26.6  |
| Totally     | 1.042                 | -2.216 | 2.437 | 0.877 | 253 <sup>a</sup> | 25.5 | 112.6 |

Model form:  $AB_s = \lambda \times \exp(p_0 + p_1 \times \ln(DBH_s))$

<sup>a</sup> Two identified outliers were excluded from the regression

**Table 3** Parameterized models for tree-level biomass ( $AB_t$ ; kg) and their performance assessed by linear regression on the log-transformed relations (Eq. 2) including the fitted parameters  $p_0$ – $p_3$ , coefficient of determination ( $R^2$ ), number of included observations ( $n$ ), standard error of estimate (SEE) and Schwarz’s Bayesian Information Criterion (BIC)

| Variables         | Regression statistics |        |       |       |        |       |       | $R^2$ | $n^a$ | SEE  | BIC |
|-------------------|-----------------------|--------|-------|-------|--------|-------|-------|-------|-------|------|-----|
|                   | $\lambda$             | $p_0$  | $p_1$ | $p_2$ | $p_3$  | $p_4$ |       |       |       |      |     |
| $EDBH_t$          | 1.011                 | -1.804 | 2.272 | –     | –      | –     | 0.988 | 239   | 0.091 | -452 |     |
| $EDBH_t, H_t$     | 1.009                 | -1.863 | 2.231 | 0.095 | –      | –     | 0.989 | 239   | 0.087 | -468 |     |
| $EDBH_t, SN$      | 1.002                 | -1.995 | 2.419 | –     | -0.153 | –     | 0.993 | 238   | 0.068 | -586 |     |
| $EDBH_t, H_t, SN$ | 1.002                 | -2.018 | 2.386 | 0.056 | -0.145 | –     | 0.993 | 238   | 0.066 | -593 |     |
| $H_t, CW$         | 1.098                 | -0.230 | –     | 0.528 | –      | 2.159 | 0.729 | 237   | 0.417 | 276  |     |
| $H_t, SN, CW$     | 1.092                 | -0.099 | –     | 0.541 | 0.353  | 1.787 | 0.764 | 237   | 0.388 | 248  |     |

Model form:  $AB_t = \lambda \times \exp(p_0 + p_1 \times \ln(EDBH_t) + p_2 \times \ln(H_t) + p_3 \times \ln(SN) + p_4 \times \ln(CW))$

Additionally, a correction factor  $\lambda$  is included to facilitate use of the parameterized models according to (Eq. 4)

<sup>a</sup> Outliers excluded if  $n < 240$

biomass model for utilizing both  $DBH_s$  and  $H_s$  yielded always somewhat weaker statistics as compared to model with one single independent variable  $DBH_s$ . This also applies for the full data set combining all islands, for which most effective model was that using solely  $DBH_s$  as independent variable (Table 2). Thereby, this model was used in combination with tree-level independent variables to analyze the biomass models at tree level.

Effect of site elevation ( $Z$ ) on  $AB_s$  models was not detected and  $Z$  was always reported as superfluous in the regression models. This applies both when using total data set and data of individual islands.

### Tree level biomass models

The most effective models for estimating tree level biomass ( $AB_t$ ) are shown in Table 3. The tree biomass model analysis identified the best combinations of independent variables  $EDBH_t$ ,  $CPA$ ,  $CW$ ,  $H_t$ , and  $SN$  analyzed using the regression analysis on log-transformed data. The strongest model for  $AB_t$  using only one independent variable was that using  $EDBH_t$  that explained 98.8 % variability in the observed  $AB_t$ . Any other single variable model had a significantly weaker performance. Of these,  $CPA$  and  $CW$  ranked second explaining 69.0 % of the variability in  $AB_t$ .

The analysis of the  $AB_t$  models utilizing a combination of several independent variables revealed that the most effective additional variable was  $SN$ . The  $AB_t$  model using a combination of  $EDBH_t$  and  $SN$  was by all metrics significantly better than the combination of  $EDBH_t$  and  $H_t$  (cf. Table 3). However, the best overall result was obtained for the  $AB_t$  model using a combination of the three independent variables, namely  $EDBH_t$ ,  $SN$ , and  $H_t$ . It explained 99.3 % of the variability in the observed data, identically as the two-variable model with  $EDBH_t$  and  $SN$ , but it was as marginally better as assessed by other indicators (SEE, BIC, cf. Table 3). Including crown parameter as the fourth

independent variable either in the form of CW or CPA did not improve the fit and was found superfluous ( $p = 0.213$ ). Similarly, there was no effect of site elevation ( $Z$ ) in any of the combined regression models.

Besides the  $AB_t$  models utilizing  $EDBH_t$ , it was important to identify the performance of the  $AB_t$  models based on other tree characteristics when the explicit measurement of stem diameters is not available. The best tree biomass model identified combined  $H_t$ , SN, and CW, explaining 76 % variability in the observed data. Once the model used only  $H_t$ , CW that have the potential of being assessed remotely, the model was slightly weaker explaining 72.9 % of the variability in the observed data (Table 3).

#### Estimating the share of fine and woody components

Assessing the components of fine and coarse woody fraction (threshold diameter 5 cm) followed the logic of the two-phase model estimation. First, stem fine fraction biomass ( $AB_{sD<5}$ ) was parameterized as a single-variable model utilizing  $DBH_s$ , using the approach of 1–4. It resulted in the fitted stem model with  $p_0 = -1.532$ ,  $p_1 = 1.847$ ,  $R^2 = 0.677$ ,  $SEE = 0.411$ ,  $n = 254$  and  $\lambda = 1.091$ . Secondly, tree-level estimation of biomass model applicable to fine fraction ( $AB_{tD<5}$ ) was carried out using the observed data for the sampled stems complemented with the stem-level model assessment for all remaining stems within a particular tree, which was summed up at a tree level. The result of tree level biomass model parameterization for  $AB_{tD<5}$  is listed in Table 4.

The best model found for estimating  $AB_{sD<5}$  was that combining three independent variables, namely  $EDBH_t$ ,  $H_t$ , and SN (Table 4). However, basically equally good was the model combining  $EDBH_t$  and SN only, while adding  $H_t$  was barely justifiable by the regression statistics ( $p = 0.003$ ). Adding crown information using either CW or CPA had no positive effect on the  $AB_{sD<5}$  model and hence considered superfluous ( $p = 0.113$ ).

Optionally,  $AB_{tD<5}$  can also be assessed using a model calculating the share of fine biomass relative to entire tree biomass, i.e., using the known quantity of  $AB_t$  and the fraction  $AB_{tD<5}/AB_t$ . This fraction was found to be best estimated using a combination of  $EDBH_t$ , SN and  $H_t$  as independent variables. Such model explained 75.3 % of the variability in  $AB_{tD<5}/AB_t$ . This result is, however, significantly weaker than the estimates based on the parameterized models that assess  $AB_{tD<5}$  directly as reported in Table 4. This observation is also reflected graphically: the ratio of  $AB_{tD<5}/AB_t$  shows a considerable larger scatter as compared to the estimates of both  $AB_{tD<5}$  and  $AB_t$  (using the corresponding best biomass models) when plotted jointly (on different y-axes) against  $EDBH_t$  in Fig. 4.

#### Discussion

The fundamental importance for a successful model construction is the strength of the model fit to available independent variables. As proven in many allometric studies, stem diameter is the most powerful variable that always explains most of the variability in observed tree biomass (Marklund 1988; Zianis et al. 2005). This is also confirmed here for *Prosopis* spp., where the  $AB_s$  model based on  $DBH_s$  explained 85–91 % of the observed variability, whereas the additional contribution of  $H_s$  was marginal (for one of the islands) or none (elsewhere). This is easy to understand, as the also the dependence between  $DBH_s$  and  $H_s$  for *Prosopis* spp. with exceptionally complex growth form is weak: a commonly used exponential dependence 1 between  $DBH_s$  and  $H_s$  explained only 21 % of the observed values (data not shown here). This is fundamentally different than observed for single-stem tree species, where such relationship is commonly rather strong (e.g., Cienciala et al. 2006, 2008).

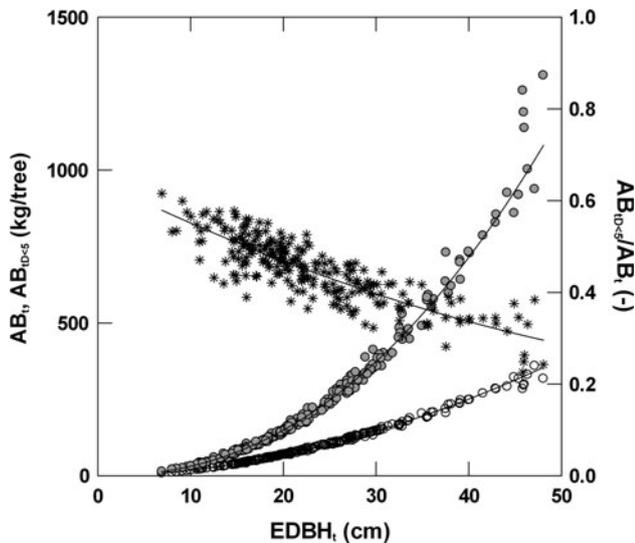
At a tree level, the contribution of tree height ( $H_t$ ) was found statistically significant, but also weak: it improved

**Table 4** Parameterized models for tree-level fine fraction biomass component ( $AB_{tD<5}$ ) and their performance assessed by linear regression on the log-transformed relations (Eq. 2) including the fitted parameters  $p_0$ – $p_3$ , coefficient of determination ( $R^2$ ), number of included observations ( $n$ ), standard error of estimate (SEE) and Schwarz's Bayesian Information Criterion (BIC)

| Variables                                                                                                              | Regression statistics |        |       |        |       |       |       |       |      |
|------------------------------------------------------------------------------------------------------------------------|-----------------------|--------|-------|--------|-------|-------|-------|-------|------|
|                                                                                                                        | $\lambda$             | $p_0$  | $p_1$ | $p_2$  | $p_3$ | $R^2$ | $n^a$ | SEE   | BIC  |
| $EDBH_t$                                                                                                               | 1.002                 | −1.401 | 1.876 | –      | –     | 0.984 | 237   | 0.086 | −477 |
| $EDBH_t, H_t$                                                                                                          | 1.003                 | −1.352 | 1.908 | −0.075 | –     | 0.985 | 237   | 0.083 | −487 |
| $EDBH_t, SN$                                                                                                           | 1.004                 | −1.286 | 1.795 | –      | 0.080 | 0.986 | 237   | 0.080 | −504 |
| $EDBH_t, H_t, SN$                                                                                                      | 1.005                 | −1.262 | 1.827 | −0.055 | 0.071 | 0.986 | 237   | 0.079 | −507 |
| Model form: $AB_{tD<5} = \lambda \times \exp(p_0 + p_1 \times \ln(EDBH_t) + p_2 \times \ln(H_t) + p_3 \times \ln(SN))$ |                       |        |       |        |       |       |       |       |      |

Additionally, a correction factor  $\lambda$  is included to facilitate use of the parameterized models according to (Eq. 4)

<sup>a</sup> Outliers excluded if  $n < 240$



**Fig. 4** The graphical representation of biomass models for entire tree ( $AB_t$ ; filled symbols) and fine fraction ( $AB_{D<5}$ ; open symbols) and the ratio of  $AB_{D<5}/AB_t$  (eight-star symbol) plotted against  $EDBH_t$ ; exponential and quadratic smoothers are overimposed for enhancing clarity in data trends

the fit only marginally. On the contrary, considering stem number (SN) was found more effective in explaining variability in tree biomass (cf. Table 3). This contradicts the observation made for commonly multi-stemmed *Prosopis flexuosa* in Argentina by Alvarez et al. (2011b), who found SN to be superfluous in their tree biomass model. We suspect that this contradiction may simply reflect the barely adequate tree sample size ( $n = 39$ ) used by Alvarez et al. for detecting the contribution of SN in their biomass models for *Prosopis flexuosa*, a tree species with inherently large growth form variability.

Considering the fact that  $AB_s$  model relies solely on  $DBH_s$ , the estimated MPE of about 25 % at a single-stem level is considered adequate. MPE was estimated and reported only for  $AB_s$  models, whereas such estimate would be biased at tree level because  $AB_t$  models used the calibration data represented both by the direct observations for stems that were cut, and by  $AB_s$  model estimates for all other stems within each tree. However, it should be understood that MPE of  $AB_t$  models is expected to be significantly lower as compared to that reported for  $AB_s$  models. This is because there are multiple stems forming each tree. Once this is considered, the sample size effectively increases, which reduces the expected scatter of residuals at tree level and hence also the resulting error of  $AB_t$  estimation. This effect was indicatively tested on our data set that was used for estimating the  $AB_s$  model ( $n = 253$ ) using bootstrapping. In this resampling exercise, identically large ( $m = 1,000$ ) samples of mean residuals and corresponding observations were generated from the original dataset using different sample size (1, 2, 5, 10)

representing number of stems (SN) per tree. The MPE calculated from these bootstrapped samples confirmed successively decreasing errors. The 95 % confidence interval of arithmetic mean MPE reached 34.6, 9.9, and 6.4 % relative to that for single-stem tree for SN of 2, 5, and 10, respectively. In other words, the MPE estimated as 25.4 % for the  $AB_s$  model would correspondingly decrease at  $AB_t$  to 8.8, 2.5, and 1.7 % for the multi-stemmed trees with 2, 5, or 10 stems each, respectively. Since the real number of stems (SN) with DBH of at least 5 cm in our data ranged from 1 to 22 with a median value of six stems per tree, the expected relative MPE for  $AB_t$  estimation should be around 2.5 %. Note, however, that this estimate represents only a model error and does not include the contribution of measurement and sampling error.

It is interesting to observe that the effect of location (islands) on the biomass models was found insignificant. In general, the effect of island on stem and tree allometry was indeed expected to be negligible because all sampling locations across the islands belong to very arid or arid ecological zones according to the local ecological classification (Diniz and de Matos 1988, 1999). That anticipation should, however, also apply to DW/FW, but somewhat different DW/FW was estimated for samples from individual islands (not shown here). Trying to reveal the reasons for the observed differences in DW/FW, we identified some effect of elevation ( $Z$ ) for Santo Antao. In this island, the only one with a pronounced elevation gradient, DW/FW for coarse biomass fraction was decreasing with increasing  $Z$ . This effect was weak, but statistically significant (adj.  $R^2 = 0.20$ ,  $p < 0.001$ ) and may at least partly explain the observed DW/FW of 0.651 observed for Santo Antao, which was significantly lower than DW/FW of 0.714 and 0.742 observed for Maio and Santiago, respectively (ANOVA,  $p < 0.001$ ). It can be expected that within the altitudinal gradient of the sampling locations on Santo Antao, there will be a pronounced temperature gradient and to a lesser extent also a precipitation gradient (only the arid and semi-arid regions of the island as identified by Diniz and de Matos 1999 were sampled). This may have affected the observed elevation trend for DW/FW. No further analysis of DW/FW was conducted here as this was not the primary goal of this study and no suitable data on local climatic gradient were available. However, it may be concluded that a specific estimation of DW/FW ratio for the biomass samples contributes to increased accuracy and reliability of biomass model parameterization and hence an appropriate attention should be paid to this issue.

A quantitative comparison with other biomass models estimated for *Prosopis* spp. published in the literature is uneasy. This is mostly because the limited literature mostly does not offer adequately representative biomass studies for *Prosopis* spp. and/or use different tree indices as

independent variables. Our tree level model compares favorably to the parameterized tree biomass model utilizing DBH recently published by Muturi et al. (2011) for naturally established *Prosopis* trees in Kenya, specifically once stemming is suppressed in the equation by setting  $SN = 1$ , which corresponds best to the material analyzed by these authors. However, their sampling size is limited to be conclusive, which also applies to another published study on *Prosopis pallida* allometry from Peru by Padrón and Navarro (2004). The latter study is also unclear in terminology and a suitable equation for dry biomass could not be clearly identified from the text.

A different comparison of the parameterized biomass models offers the analysis made by Zianis and Mecuccini (2004). They, among others, tested the validity of the generic theoretical exponential relationship between tree biomass and tree diameter as suggested by West et al. (1999) on the basis of the fractal model for tree allometry. For this, examined on a “global” dataset containing 279 allometric equations, Zianis and Mecuccini (2004) found a mean empirical value of the scaling parameter (exponent)  $b$  (corresponding to  $p_1$  in our general 1) of 2.368. This was significantly lower than the theoretical value of 2.67 from the proposed relationship of West et al. (1999). Our estimate of scaling parameter  $b$  for *Prosopis* spp. derived from our samples at stem ( $n = 255$ ) and tree ( $n = 240$ ) level gives 2.368 and 2.382, respectively, i.e., both basically matching the empirical estimate of Zianis and Mecuccini (2004). This tight coherence gives further confidence in the biomass models for *Prosopis* spp., specifically when considering their complex growth form and occurrence on ecologically marginal locations.

We conclude that the presented equations at stem and tree level are sufficiently robust to be applicable across the islands of Cape Verde and very likely also elsewhere, which is, however, to be verified yet. The presented approach of deriving tree-level biomass models for multi-stemmed tree species is effective in terms of biomass sampling required and results achieved, which makes us to recommend it for *Prosopis* spp. and other tree species with similarly complex growth form.

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