



Article Study on Biomass Models of Artificial Young Forest in the Northwestern Alpine Region of China

Chunyan Mao^{1,2}, Lubei Yi³, Wenqiang Xu^{1,*}, Li Dai⁴, Anming Bao¹, Zhengyu Wang¹ and Xueting Zheng⁵

- State Key Laboratory of Desert and Oasis Ecology, Xinjiang Institute of Ecology and Geography, Chinese Academy of Sciences (CAS), Urumqi 830011, China
- ² Guiyang Geographic Information Big Data Center, Guiyang 550002, China
- ³ Qinghai Forestry Carbon Sequestration Service Center, Xining 810001, China
- ⁴ School of geography and Environmental Sciences, Guizhou Normal University, Guiyang 550025, China
- ⁵ Qinghai University, Xining 810000, China
 - Correspondence: xuwq@ms.xjb.ac.cn

Abstract: The artificial young forest is an important component of ecosystems, and biomass models are important for estimating the carbon storage of ecosystems. However, research on biomass models of the young forest is lacking. In this study, biomass data of 96 saplings of three tree species from the southern foot of the Qilian Mountains were collected. These data, coupled with allometric growth equations and the nonlinear joint estimation method, were used to establish independent, component-additive, and total-control compatible models to estimate the biomass of artificial young wood of Picea crassifolia (Picea crassifolia Kom.), Sabina przewalskii (Sabina przewalskii Kom.), and Pinus tabulaeformis (Pinus tabuliformis Carr.). The distribution characteristics of the biomass components (branch, leaf, trunk, and root biomass) and the goodness of fit of the models were also analyzed. The results showed that (1) the multiple regression models with two independent variables (MRWTIV) were superior to the univariate models for all three tree species. Base diameter was the best-fitting variable of the univariate model for Picea crassifolia and Pinus tabulaeformis, and the addition of base diameter and crown diameter as variables to the MRWTIV can significantly improve model accuracy. Tree height was the best-fitting variable of the univariate model of Sabina przewalskii, and the addition of tree height and crown diameter to the MRWTIV can significantly improve model accuracy; (2) the two independent variable component-additive compatible model was the best-fitting biomass model. The compatible models constructed by the nonlinear joint estimation method were less accurate than the independent models. However, they maintained good compatibility among the biomass components and enabled more robust estimates of regional biomass; and (3) for the young wood of Picea crassifolia, Sabina przewalskii, and Pinus tabulaeformis, the aboveground biomass ratio of each component to total biomass was highest for leaf biomass (26%-68%), followed by branch (10%-46%) and trunk (11%–55%) biomass, and the aboveground biomass was higher than the underground biomass. In conclusion, the optimal biomass model of artificial young forest at the sampling site is a multivariate component-additive compatible biomass model. It can well estimate the biomass of young forest and provide a basis for future research.

Keywords: northwest alpine zone; young plantation forest; biomass model; allocation characteristics of component biomass

1. Introduction

Forest is the largest carbon stock of terrestrial ecosystems, accounting for approximately 80% of aboveground biomass carbon and 40% of belowground biomass carbon in terrestrial ecosystems [1]. Forest, thus, plays a vital role in maintaining the global carbon balance and mitigating climate changes, and research on the forest carbon stock has received increased attention [1,2]. Forest biomass, one of the most important features



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Copyright: © 2022 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). of ecosystems, is an important factor underlying ecosystem productivity [3,4]. Accurate estimation of biomass in different ecosystems is important for estimating carbon stocks in terrestrial ecosystems [5]; however, young trees are often neglected in forest inventories and carbon stock estimations.

According to the report of the ninth forest resource inventory (2014–2018), the forest area of China is 220 million hm². The area of plantation forest is 80 million km², which accounts for 36% of the total forest area [6]. Moreover, plantation forests in China are mainly middle-aged forests and young forests, which have high carbon sequestration potential [1,7]. Young plantations are an important component of ecosystems, and biomass models of such plantations provide the basis for estimating the carbon storage of ecosystems. However, research on biomass models of young plantations with diameter at breast height (DBH) less than 5 cm is lacking, and the carbon-neutralizing capacity of forest ecosystems is often underestimated [7]. Biomass models can be used to establish the relationships between easily measurable plant factors (e.g., tree height and crown diameter) and biomass through regression analysis [8]. This method can provide relatively simple and accurate biomass estimates with fewer labor requirements; it is, thus, the most commonly used method for estimating the biomass of vegetation [8-12]. However, all biomass models established in previous studies are for trees with DBH larger than 5 cm; few studies on the biomass models of trees with DBH less than 5 cm have been conducted by comparison, and this has resulted in the underestimation of the carbon stock capacity of China's forest ecosystems [7].

To quantitatively study the distribution characteristics and growth patterns of trees, trees have been divided into different biomass components (branches, leaves, trunks, and roots), and independent biomass models have been established for each of these components [13–16]. Traditional independent biomass models typically establish separate regressions between biomass components and tree factors (such as DBH and tree height), which makes the models incompatible. The nonlinear simultaneous equation method has been proposed to overcome this problem [17], wherein the biomass of each component is calculated using total-control and hierarchical-combined-control methods. This approach of overcoming the incompatibility of biomass models has been widely used [12,18]. However, many biomass regression models that have been developed to date have been based on trees with DBH greater than 5 cm [8–23]; biomass models for young trees from which DBH cannot be collected have not been developed.

In this study, saplings of the three main tree species in the southern foot of Qilian Mountains in the alpine region of northwestern China (*Picea crassifolia, Pinus tabulaeformis,* and *Sabina przewalskii*) were sampled [24,25]. Parameters such as base diameter, tree height, and crown diameter of trees were measured, and biomass models of the young wood of the different tree species were established. Our findings fill a research gap in the development of biomass models of artificial young forest in the northwestern alpine region of China. Our results also have implications for climate change studies and for enhancing carbon dioxide neutralization in the northwestern alpine region of China.

2. Study Area

Our study site was located in the transition zone between the western Loess Plateau and the Qinghai–Tibet Plateau (Figure 1). Because it occurs on an arid plateau, variation in altitude, temperature, and moisture are substantial. The solar radiation in this region is strong, and the average temperature is low (3–6 °C). The average annual precipitation is 450-592 mm, and the distribution of precipitation throughout the year is uneven [24]. The forest coverage rate is relatively high (the alpine vegetation and shrub area of Qinghai–Tibet Plateau is over 250,000 km²) [1,25], and the vegetation types are mainly cold-temperate evergreen coniferous forest and deciduous broad-leaved forest [25]. The soil types include mainly cinnamon soil, chestnut soil, chernozem soil, gray cinnamon soil, and meadow soil [24,25].



Figure 1. Location of the sampling site.

3. Methods

3.1. Data Collection

The DBH of young trees less than 5 cm cannot be measured. Therefore, base diameter is measured to characterize the growth of such trees [26]. Theoretically, the base diameter of a tree refers to the diameter at the boundary between the trunk and the root system of the tree. However, in actual forestry work, the diameter at the surface is often measured because part of the trunk is buried in the soil [27].

Young trees in this study were defined as trees with DBH less than 6 cm. Because the height of some young trees was less than 1.3 m, the DBH for these trees could not be measured. Therefore, the base diameter was measured instead of DBH. Sampling was conducted in the forest at the southern foot of the Qilian Mountains in the alpine region of northwestern China, which runs through Datong County, Huangyuan County, and Huzhu County in Qinghai Province. From July to October 2021, a total of 10 sample plots with an area of 30 m \times 30 m were established at the sampling site, and terrain factors such as altitude, slope gradient, and slope position were measured. Growth factors of each of the trees sampled such as height and base diameter were also measured [28]. Trees in the sample plot were graded according to their diameters and heights. The whole plants of 41 *Picea crassifolia*, 28 *Sabina przewalskii*, and 27 *Pinus tabulaeformis* trees were harvested. The different components (trunk, branches, leaves, and roots) were numbered and stored for later analysis and processing. A total of 96 whole plant samples were collected (Table 1).

Table 1. Statistical characteristics of the sample data.

	Ţ.	Picea crassifoli	a	Pi	nus tahuliforn	nis	Sahina nrzezvalskij				
Variable Name		-									
	AVG	Range	SD	AVG	Range	SD	AVG	Range	SD		
Base Diameter (D)/cm	4.71	0.82-10.5	2.66	4.33	0.87-9.0	2.26	4.62	0.62-10.9	3.09		
Crown Diameter (C)/m	1.07	0.16-2.67	0.66	0.95	0.29-2.88	0.66	3.90	1.55-7.75	1.66		
Tree Height (H)/m	1.70	0.30 - 4.45	1.04	1.62	0.46-3.48	0.81	1.38	0.39-3.47	0.81		
Leaf Biomass/kg	1.57	0.008-6.0	1.76	0.62	0.026-3.2	0.83	0.60	0.005 - 2.3	0.67		
Branch Biomass/kg	1.20	0.004 - 6.4	1.46	0.47	0.01 - 2.8	0.69	0.37	0.002-2.2	0.51		
Trunk Biomass/kg	0.85	0.005-4.2	1.08	0.68	0.013-3.6	1.02	0.36	0.003 - 2.4	0.51		
Root Biomass/kg	0.88	0.006-3.9	0.98	0.59	0.02 - 3.04	0.86	0.57	0.004-2.8	0.71		

All plants sampled were well grown; samples were not taken from trees in areas that were severely disturbed or in special habitats to ensure consistency among samples. Before sampling, the base diameter (D, cm), tree height (H, m), and crown diameter (C, m) of the samples (east–west and north–south directions) were measured. Biomass was obtained by the whole plant harvesting method, and the total amount of trunk, branch, leaf, and root biomass was determined. After all the roots were excavated, all non-root impurities were removed, and the fresh weights were taken. After weighing, the samples were stored in a cloth bag, and information such as the location, tree species, weight, and date was taken. In the laboratory, samples were subjected to a de-enzyming treatment at 105 °C for two hours. Finally, the samples were dried at a constant temperature of 85 °C until a constant weight was achieved, and the oven-dried weight of the sample was measured.

3.2. Biomass Model Establishment

The structure of the allometric growth equations is relatively simple, and the parameters are relatively stable. In this study, the allometric growth equations of LY/T 2258-2014 were used to establish the biomass models [29]. The general structure is shown in Equation (1)

$$y = \beta_0 \times 1^{\beta_1} x_2^{\beta_2} \dots x_j^{\beta_j} + \varepsilon$$
⁽¹⁾

where y is the stand-level total biomass or biomass of each component; x_j is the independent variable (e.g., D, H, and C); β_j is the model parameter; and ε is the error. Based on the multivariate nonlinear joint estimation method, compatible models of *Picea crassifolia*, *Pinus tabulaeformis*, and *Sabina przewalskii* were established using the component-additive method and total-control method, and the fitting accuracy of each model was determined.

In addition to the tree factors measured in the sample plot, the interaction between crown diameter and tree height was also taken into account when selecting independent variables. The parameters with strong correlations with the biomass of each component and showing significant differences according to correlation analysis (IBM SPSS 19, Armonk, NY, USA) and double-screening stepwise regression (ForStat 3.0, China) were used as independent variables in the models. Independent and compatible models of the branches, leaves, trunk, roots, and total biomass were established.

3.2.1. Independent Models

Models of each component and total biomass were established, and univariate and multivariate models were fitted. The common structure of the univariate and multivariate nonlinear biomass models is shown in Equations (2) and (3):

$$M = a_0 D^{a1} + \varepsilon \tag{2}$$

$$M = a_0 D^{a1} H^{a2} + \varepsilon \tag{3}$$

where M is the biomass; D is the base diameter; H is the tree height; a_0 , a_1 , and a_2 are model parameters; and ε is the error.

3.2.2. Compatible Models

Compatible models satisfy the requirement that the total biomass of a single tree is equal to the sum of the biomass of each component, which requires the compatibility of the equations of each component and the total biomass. The multivariate nonlinear joint estimation is based on ordinary least squares regression, and the parameters of the equation set were fitted through joint estimation. The total biomass models and biomass models of each component were established by the component-additive method and total-control method, respectively.

Component-Additive Method

The component-additive method is based on the independent model of each component, which combines the biomass of each component and the total biomass into an equation set. The regression equation of each component includes its own independent variables, and the total biomass is a function of all independent variables, which ensures that the sum of each component is equal to the total amount. The expression of the model system is as follows:

where W_1 , W_2 , W_3 , W_4 , and W_5 are the estimated values of the trunk, branch, leaf, root, and total biomass, respectively; $f_1(x_1)$, $f_2(x_2)$, $f_3(x_3)$, and $f_4(x_4)$ are the independent models of the trunk, branch, leaf, and root biomass, respectively; the general structure of the independent model is shown in equation (1): $f_i(x_i) = a_i x_i^{b_i} x_j^{m_i} \cdots x_k^{n_i} + \varepsilon_i$, where X is the independent variable; and ε_1 , ε_2 , ε_3 , ε_4 , and ε_5 are the errors in the equations of trunk, branch, leaf, root, and total biomass, respectively.

Total-Control Method

In the total-control method, the total biomass is directly divided into four components (trunk, branches, leaves, and roots) to ensure that the sum of each component is equal to the total biomass. Assuming that the relative proportion of the trunk to total biomass is 1, the functions of branch, leaf, and root biomass to total biomass are $g_1(x)$, $g_2(x)$, and $g_3(x)$, respectively, and the total biomass model is $f_0(x)$. The expression of the model system is as follows:

$$\begin{cases} y_1 = \frac{1}{1+g_1(x)+g_2(x)+g_3(x)} \times f_0(x) \\ y_2 = \frac{g_1(x)}{1+g_1(x)+g_2(x)+g_3(x)} \times f_0(x) \\ y_3 = \frac{g_2(x)}{1+g_1(x)+g_2(x)+g_3(x)} \times f_0(x) \\ y_4 = \frac{g_3(x)}{1+g_1(x)+g_2(x)+g_3(x)} \times f_0(x) \end{cases}$$
(5)

where y_1 , y_2 , y_3 , and y_4 are the trunk, branch, leaf, and root biomass, respectively. To establish the univariate and multivariate total-control model system, $g_1(x)$, $g_2(x)$, and $g_2(x)$ need to be determined according to the biomass data. The general structure is shown in Equation (1), and the estimated value of each parameter was determined. On the basis of these estimated values, the parameter values of the model system (equation 5) were obtained by calculating the error-in-variable simultaneous equations. The aboveground biomass model $f_0(x)$ was obtained based on the independent model.

Nonlinear seemingly unrelated regression is considered the most reliable method for estimating the parameters of a compatible biomass model system [30], as it not only takes into account the correlation between the sub-equations but also ensures the compatibility between the models and the validity of the parameter estimates. The biomass model is a heteroscedastic model, and eliminating heteroscedasticity for both independent fitting and nonlinear simultaneous equation fitting is essential. The commonly used methods are logarithmic regression or weighted regression [31,32]. Weighted regression makes use of the residual squared error to obtain a weight function by ordinary regression fitting. Its fitting effect is comparable to that of a specific general weight function $W = 1/f^2(x)$. Some researchers have adjusted the general weight function to $W = 1/f^n(x)$ to improve the adaptability of the model to different biomass data [31]. In this study, $1/\sqrt{f(x)}$ was used as the weight function to perform weighted regression on the biomass equation, and the model parameters were fitted and evaluated using ForStat 3.0.

3.3. Model Evaluation and Accuracy Tests

The coefficient of determination (R^2), standard deviation of estimated values (*SEE*), total relative error (*TRE*), average systematic error (*ASE*), average prediction error (*MPE*),

average percentile standard error (*MPSE*), and six other parameters were used to evaluate the accuracy of the model [33]:

$$R^{2} = 1 - \sum (y_{i} - \hat{y}_{i})^{2} / \sum (y_{i} - \overline{y})^{2}$$
(6)

$$SEE = \sqrt{\sum (y_i - \hat{y}_i)^2 / (n - p)}$$
 (7)

$$TRE = \sum (y_i - \hat{y}_i) / \sum \hat{y}_i \times 100\%$$
(8)

$$ASE = \sum (y_i - \hat{y}_i) / \hat{y}_i / n \times 100\%$$
(9)

$$MPE = t_a.(SEE/\overline{y})/n \times 100 \tag{10}$$

$$MPSE = \sum |(y_i - \hat{y}_i) / \hat{y}_i| / n \times 100\%$$
(11)

where y_i is the actual observed value; \hat{y}_i is the model-estimated value; y is the average value of the samples; n is the number of samples; p is the number of parameters; and t_{α} is the t-value at the confidence level α . The model simulation and accuracy tests were conducted in SPSS 19 and ForStat 3.0, and the photos were processed in Origin 2019b.

4. Results

4.1. Correlation Analysis between Modeling Variables and The Biomass of Each Component

All samples of the three species (*Picea crassifolia, Sabina przewalskii*, and *Pinus tabulae*formis) were used to establish the models, and single factors or interaction factors with good fit were identified. There were highly significant differences among the variables (Table 2). For *Pinus tabulaeformis* and *Picea crassifolia*, base diameter (correlations greater than 0.85) and the interaction between tree height and base diameter (correlations greater than 0.9) had a significant effect on the biomass of each component. For *Sabina przewalskii*, base diameter had no significant effect on the biomass of each component, and tree height had a significant effect on the biomass of each component. According to the results of stepwise regression analysis, base diameter and the interaction between tree height and other forest factors were the modeling variables used for *Picea crassifolia*; tree height and the interaction between tree height and other forest factors were the modeling variables used for *Sabina przewalskii*.

Table 2. Correlation analysis between modeling variables and the biomass of each component.

Releva	ance	D	С	Н	СН	DH	D ² H	C ² H	D ² C
	Leaves	0.893 **	0.887 **	0.913 **	0.910 **	0.944 **	0.928 **	0.842 **	0.888 **
Dicea	Branches	0.888 ^{**}	0.903 **	0.828 **	0.885 **	0.904 **	0.931 **	0.856 **	0.968 **
crassifolia	Trunk	0.891 **	0.904 **	0.900 **	0.945 **	0.965 **	0.984 **	0.911 **	0.972 **
crussijonu	Root	0.877 **	0.860 **	0.825 **	0.829 **	0.877 **	0.884 **	0.762 **	0.889 **
	Sum	0.934 **	0.935 **	0.915 **	0.941 **	0.972 **	0.980 **	0.888 **	0.975 **
Dinne	Leaves	0.866 **	0.918 **	0.813 **	0.929 **	0.902 **	0.925 **	0.907 **	0.960 **
	Branches	0.847 **	0.936 **	0.808 **	0.953 **	0.895 **	0.919 **	0.950 **	0.966 **
1 mus tabuliformic	Trunk	0.888 **	0.904 **	0.850 **	0.943 **	0.952 **	0.988 **	0.908 **	0.980 **
lubulijorniis	Root	0.806 **	0.905 **	0.770 **	0.890 **	0.838 **	0.853 **	0.866 **	0.896 **
	Sum	0.883 **	0.946 **	0.840 **	0.960 **	0.930 **	0.956 **	0.937 **	0.984 **
	Leaves	0.859 **	0.908 **	0.938 **	0.950 **	0.924 **	0.865 **	0.916 **	0.874 **
Sahina	Branches	0.789 **	0.860 **	0.917 **	0.963 **	0.922 **	0.876 **	0.965 **	0.903 **
Saoina przewalskii	Trunk	0.737 **	0.840 **	0.884 **	0.949 **	0.888 ^{**}	0.845 **	0.970 **	0.877 **
	Root	0.803 **	0.825 **	0.896 **	0.916 **	0.904 **	0.845 **	0.904 **	0.886 **
	Sum	0.837 **	0.896 **	0.949 **	0.984 **	0.950 **	0.923 **	0.975 **	0.895 **

** Significant correlations at the 0.01 level (two-sided). Bold indicates the highest correlation per line.

4.2. Establishment of an Independent Biomass Model for Young Trees

Table 3 shows the estimated parameter values and evaluation indicators of the unaryweighted independent regression model, which can be used to estimate the biomass of each component and the aboveground biomass of *Picea crassifolia*, *Sabina przewalskii*, and *Pinus tabulaeformis*.

Base diameter was used as the independent variable of the univariate independent model of *Picea crassifolia* and *Pinus tabulaeformis*, and tree height was used as the independent variable of the univariate independent model of *Pinus tabulaeformis*. When tree height was added to the univariate model of *Picea crassifolia* as an independent variable, or when crown diameter was added to the univariate model of *Pinus tabulaeformis* and *Sabina przewalskii* as an independent variable, the R² of each component increased by varying degrees. The other evaluation indicators decreased by varying degrees when these variables were added, and the goodness of fit and accuracy of the models were higher than those of the univariate models.

For the trunks of *Picea crassifolia* and *Pinus tabulaeformis*, independent models with tree height as an independent variable were generally better than the independent models with crown diameter as independent variables; for the leaves and branches of *Picea crassifolia* and *Pinus tabulaeformis*, independent models with crown diameter as an independent variable were generally better than independent models with tree height as an independent variable. When crown diameter was added as an independent variable for *Pinus tabulaeformis*, the R² of the leaves and branches increased from 0.867 and 0.842 to 0.925 and 0.954, respectively, and the SEE of the estimated values decreased by 0.007 kg and 0.14 kg, respectively. The other indicators also decreased by varying degrees, and the model accuracy was significantly improved. However, model accuracy only slightly improved after tree height was added as an independent wariable. For each biomass component of *Sabina przewalskii*, the independent model with crown diameter as an independent variable was significantly improved compared with the independent model with base diameter as an independent variable. The R² was significantly higher, and the MPE and the standard deviation of the estimated value were lower, especially for branch and trunk biomass.

The R² values of the independent models for the total biomass of the three tree species were above 0.9, the SEE of the estimated value was below 1 kg, and the MPE was less than 15%. Overall, the bestfitting independent model for *Picea crassifolia* was a two independent variable model with base diameter and tree height as independent variables; the best-fitting independent model for *Pinus tabulaeformis* was a two independent variable model for *Sabina przewalskii* was a two independent variable model with tree height and crown diameter as independent variables. Therefore, the best-fitting independent biomass models of the three tree species were as follows: *Picea crassifolia*: M total = $0.098 \times D^{2.048} \times H^{0.403}$; *Pinus tabulaeformis*: M total = $0.213 \times D^{1.369} \times C^{1.067}$; and *Sabina przewalskii*: M total = $0.0484 \times C^{0.261} \times H^{1.923}$. The fitting accuracy of independent biomass models for each component was highest for total biomass, followed by trunk, branch, leaf, and root biomass.

4.3. Establishment of Compatible Biomass Models for Young Trees

On the basis of the model systems (4) and (5), multiple regression with two independent variables (MRWTIV) model and univariate models were established by the component-additive method and total-control method (Tables 4 and 5). For all three tree species, the MRWTIV were generally a better fit than the univariate models, and the best-fitting factors for each component of the univariate and MRWTIV model were consistent with the independent models. Specifically, the goodness of fit of the MRWTIV with crown diameter as an independent variable was generally better for *Sabina przewalskii* and *Pinus tabulaeformis;* for *Picea crassifolia*, the goodness of fit and prediction accuracy of the MRWTIV with tree height as an independent variable were generally better than the MRWTIV with crown diameter as an independent variable. The R² was increased by 0.031 and 0.032 for the

component-additive models and total-control models, respectively, when crown diameter was added as an independent variable, and this increase was particularly pronounced for the trunk biomass of *Sabina przewalskii*; the SEE of the estimated value decreased by 0.033 kg and 0.034 kg, respectively. The MPE was also reduced by 3.57% and 3.62% in the component-additive and total-control models, respectively. For the three tree species, the goodness of fit was higher for both of the compatible biomass models, with R² higher than 0.9 (for *Picea crassifolia* and juniper, R² was higher than 0.95), and the SEE of the estimated values was less than 1.18 kg for all models.

Both compatible biomass models have high fitting accuracy. The goodness of fit of the two compatible biomass models for *Picea crassifolia* and *Sabina przewalskii* using the same variable estimation algorithm was highest for total biomass, followed by trunk, branch, leaf, and root biomass; the goodness of fit of the two compatible biomass models of the *Pinus tabulaeformis* component was highest for trunk biomass, followed by total, branch, leaf, and root biomass.

There were no significant differences in the biomass of each component and the total biomass calculated by the component-additive models and total-control models for the three tree species, and \mathbb{R}^2 was less than 0.03 for all models. Overall, the component-additive models were slightly better than the total-control models, and the performance of each component of the three tree species differed. For the branch, trunk, and total biomass of *Picea crassifolia*, the component-additive models were slightly better than the total-control models; for the leaf and root biomass of *Picea crassifolia*, the total-control models were slightly better than the component-additive models. For Pinus tabulaeformis, the componentadditive models of leaf, root, branch, trunk, and total biomass were slightly better than the total-control model, with the exception of the MRWTIV of leaf and root biomass; for the trunk and root biomass of Sabina przewalskii, the component-additive models were slightly better than the total-control model; for the leaf and total biomass of *Sabina przewalskii*, the total-control models were slightly better than the component-additive models. The R^2 and SEE of the estimated values and the MPE of the total-control models of *Picea crassifolia* total biomass with tree height and base diameter as independent variables were reduced by 0.0009, 0.015, and 0.108%, respectively. Therefore, the best-fitting multivariate componentadditive models with the best-fitting parameters of each component of the three tree species were as follows:

Piceacrassifolia : •	$\begin{cases} M_L = 0.088D^{1.292} \times H^{0.957} \\ M_B = 0.043D^{1.762} \times C^{0.882} \\ M_T = 0.0087D^{2.15} \times H^{0.944} \\ M_R = 0.036D^{1.866} \times C^{0.235} \\ M_S = 0.088D^{1.292} \times H^{0.957} + 0.043D^{1.762} \times C^{0.882} \\ + 0.0087D^{2.15} \times H^{0.944} + 0.036D^{1.866} \times C^{0.235} \end{cases}$
Pinustabulaeformis	$ \begin{array}{l} M_L = 0.076 D^{1.172} \times C^{1.158} \\ M_B = 0.146 D^{0.549} \times C^{1.723} \\ M_T = 0.0032 D^{3.041} \times H^{0.268} \\ M_R = 0.378 D^{0.193} \times C^{1.665} \\ M_S = 0.076 D^{1.172} \times C^{1.158} + 0.146 D^{0.549} \times C^{1.723} \\ + 0.0032 D^{3.041} \times H^{0.268} + 0.378 D^{0.193} \times C^{1.665} \end{array} $
Sabinaprzewalskii :	$\begin{cases} M_L = 0.0932 C^{1.017} \times H^{0.99} \\ M_B = 0.0298 C^{1.204} \times H^{1.449} \\ M_T = 0.0102 C^{1.877} \times H^{1.255} \\ M_R = 0.145 D^{0.373} \times H^{1.643} \\ M_S = 0.0932 C^{1.017} \times H^{0.99} + 0.0298 C^{1.204} \times H^{1.449} \\ + 0.0102 C^{1.877} \times H^{1.255} + 0.145 D^{0.373} \times H^{1.643} \end{cases}$

			Evaluation Indicators											
Tree Species	Component	Models	D ²	SEE	MPE	TRE	ASE	MPSE						
			K	(kg)	(%)	(%)	(%)	(%)						
		$M = 0.0292D^{2.3167}$	0.832	0.73	14.7	-0.03	-7.8	27.8						
	Leaves	$M = 0.0736D^{1.4174} \times H^{0.8874}$	0.888	0.6	12.18	-0.02	-5.97	26.68						
		$M = 0.0566 D^{1.8808} \times C^{0.400}$	0.838	0.73	14.66	-0.04	-8.25	27.66						
		$M = 0.0133D^{2.5840}$	0.911	0.44	11.55	0.00	-3.41	27.39						
	Branches	$M = 0.0105 D^{2.8034} \times H^{-0.2157}$	0.913	0.44	11.55	0.00	-3.39	27.58						
		$M = 0.0488D^{1.7228} \times C^{0.7957}$	0.936	0.38	9.9	0.00	-3.16	27.44						
D: (6.1)		$M = 0.0056 D^{2.8441}$	0.929	0.29	10.79	0.00	10.29	23.51						
Picea crassifolia	Trunk	$M = 0.0101D^{2.0347} \times H^{1.0277}$	0.969	0.2	7.23	2.16	17.19	25.93						
n = 41		$M = 0.0172D^{2.1072} \times C^{0.6717}$	0.948	0.25	9.36	0.00	0.68	20.43						
		$M = 0.021 D^{2.198}$	0.827	0.41	14.78	0.00	-6.7	38.92						
	Root	$M = 0.021 D^{2.18} \times H^{0.018}$	0.827	0.42	14.98	0.00	-6.70	38.93						
		$M = 0.035D^{1.8491} \times C^{0.322}$	0.828	0.42	14.95	0.00	-6.60	38.80						
		$M = 0.064 D^{2.458}$	0.960	1.02	7 14	0.00	-3.95	18 42						
	Sum	$M = 0.098 D^{2.048} \times H^{0.403}$	0.972	0.86	6.02	0.00	-3.63	17.89						
	oun	$M = 0.159D^{1.853} \times C^{0.557}$	0.972	0.86	6.06	0.00	-4.12	18.07						
		$M = 0.0106 D^{2.5002}$	0.867	0.21	10.64	0.02	8 52	22.12						
	Loguos	$M = 0.0121 D^{2.2799} \times H^{0.2271}$	0.007	0.31	20.3	0.03	6.3Z	52.15 20.11						
	Leaves	$M = 0.0572 D^{1.4129} \times C^{0.8408}$	0.000	0.32	15.08	0.07	1 13	23.47						
		NA 0.004ED ² 8083	0.925	0.20	22.00	0.00	7.50	41.17						
	Prop choo	$M = 0.0045D^{-10000}$ $M = 0.0068D^{2.3661} \times H^{0.4915}$	0.835	0.29	23.88 23.93	0.00	7.52	41.17						
	branches	$M = 0.0068D^{1.0731} \times C^{1.3120}$	0.042	0.29	12.95	_0.00	_3.19	27 14						
Pinus			0.004	0.15	12.00	0.01	0.02	27.14						
tabuliformis	T 1	$M = 0.0038D^{3.0000}$	0.974	0.17	9.79	0.04	-9.83	33.66						
n = 27	Irunk	$M = 0.0072D^{-0.0211} \times H^{-0.0021}$ $M = 0.0112D^{2.3979} \times C^{0.5109}$	0.982	0.14	8.36	0.01	-0.21	28.35						
		M = 0.0112D	0.977	0.10	9.50	0.05	14.70							
	D	$M = 0.007 D^{2.003}$	0.733	0.45	30.63	0.00	7.9	66.38						
	Root	$M = 0.015D^{1.050} \times H^{0.014}$	0.729	0.47	31.56	0.03	-0.69	52.53						
		M = 0.239D**** × C****	0.85	0.57	24.74	-0.07	-10.90	39.30						
		$M = 0.024 D^{2.766}$	0.92	0.97	16.36	0.01	13.35	39.88						
	Sum	$M = 0.043D^{2.161} \times H^{0.053}$	0.92	0.99	16.72	0.04	7.62	31.23						
		$M = 0.213D^{1.509} \times C^{1.007}$	0.97	0.54	9.15	0.00	-0.35	24.13						
		$M = 0.2467 H^{1.9446}$	0.866	0.25	16.1	-0.13	-15.36	39.1						
	Leaves	$M = 0.1432D^{0.4502} \times H^{1.5075}$	0.878	0.24	15.74	-0.14	-15.97	36.92						
		$M = 0.0635C^{1.1437} \times H^{1.1830}$	0.881	0.24	15.51	-0.16	-14.83	37.7						
		$M = 0.1040 H^{2.4482}$	0.918	0.15	15.52	-0.03	-15.14	39.93						
	Branches	$M = 0.0867 D^{0.1533} \times H^{2.2986}$	0.919	0.15	15.81	-0.04	-15.62	39.4						
		$M = 0.0348C^{0.9302} \times H^{1.8203}$	0.932	0.14	14.46	-0.05	-14.78	38.82						
Sabina		$M = 0.1081 H^{2.3846}$	0.909	0.16	16.8	-0.01	-7.78	-38.42						
przewalskii	Trunk	$M = 0.1030 D^{0.0495} \times H^{2.3212}$	0.907	0.16	17.32	0.06	-8.55	39.08						
n = 28		$M = 0.0225 C^{1.3266} \times H^{1.4931}$	0.94	0.13	13.95	0.03	-6.34	37.66						
		$M = 0.036 H^{1.666}$	0.682	0.41	27.85	-0.02	-8.33	64.59						
	Root	$M = 0.148 D^{0.274} \times H^{1.856}$	0.846	0.29	19.81	-0.02	-15.51	46.46						
		$M = 0.195 C^{0.059} \times H^{2.067}$	0.84	0.29	20.18	-0.05	-15.88	47.57						
		$M = 0.113 H^{1.698}$	0.73	1.21	24.71	0.00	-8.96	56.44						
	Sum	$M = 0.030 D^{0.548} \times H^{2.157}$	0.90	0.75	15.33	0.07	-13.59	40.48						
		$\mathbf{M} = 0.484 \mathbf{C}^{0.261} \times \mathbf{H}^{1.923}$	0.95	0.52	10.63	-0.03	-14.32	32.94						
]	Roughening represents the best mod	el for each bi	iomass comp	oonent.									

 Table 3. Independent biomass models of the young wood of three tree species.

Tree	Models	Variables					Ev	aluation	Indicato	rs				
Species	mouch	vullubico -	a1	b1	m1	a2	b2	m3	a3	b3	m3	a4	b4	m4
Picea crassifolia	(4) (5)	D D,H D,C D D,H D,C	0.042 0.092 0.102 0.068 0.093 0.183	2.139 1.244 1.548 2.425 2.023 1.764	1.005 0.540 0.490 0.625	$\begin{array}{c} 0.009\\ 0.008\\ 0.044\\ 1.466\\ 0.943\\ 2.197\end{array}$	$\begin{array}{r} 2.749\\ 2.918\\ 1.759\\ -0.03\\ 0.747\\ -0.21\end{array}$	-0.20 0.858 -1.10 -0.03	$\begin{array}{c} 0.005\\ 0.009\\ 0.021\\ 8.089\\ 10.25\\ 4.853\end{array}$	$\begin{array}{r} 2.935\\ 2.123\\ 1.945\\ -0.75\\ -0.86\\ -0.40\end{array}$	0.969 0.881 0.007 -0.34	0.021 0.023 0.029 3.265 2.673 1.479	$\begin{array}{r} 2.187\\ 2.136\\ 1.990\\ -0.59\\ -0.04\\ 0.010\end{array}$	0.014 0.160 -0.89 -0.72
Pinus tabu- liformis	(4) (5)	D D,H H,C D D,H H,C	$\begin{array}{c} 0.007\\ 0.005\\ 1.151\\ 0.017\\ 0.015\\ 2.123\end{array}$	$2.693 \\ 2.744 \\ -1.70 \\ 2.932 \\ 2.655 \\ -0.27$	0.228 2.996 0.715 2.099	$\begin{array}{c} 0.004 \\ 0.004 \\ 0.848 \\ 1.764 \\ 0.948 \\ 2.788 \end{array}$	$\begin{array}{r} 2.847\\ 2.269\\ -1.84\\ -0.47\\ -0.42\\ -2.37\end{array}$	1.139 3.328 0.472 1.485	$\begin{array}{c} 0.002\\ 0.003\\ 0.300\\ 3.097\\ 1.247\\ 3.464 \end{array}$	3.359 2.782 0.933 -0.63 0.039 -2.10	0.762 1.331 -0.48 1.103	$\begin{array}{c} 0.007\\ 0.006\\ 1.760\\ 3.019\\ 1.352\\ 10.48 \end{array}$	$2.665 \\ 2.474 \\ -2.51 \\ -0.65 \\ -0.21 \\ -4.30$	$0.589 \\ 3.545 \\ -0.10 \\ 2.605$
Sabina przewalskii	(4) (5)	H D,H H,C H D,H H,C	0.299 0.206 0.094 0.713 0.575 0.209	$\begin{array}{c} 1.710 \\ 0.306 \\ 0.993 \\ 2.080 \\ 0.172 \\ 1.309 \end{array}$	1.420 1.012 1.924 1.078	$\begin{array}{c} 0.118\\ 0.107\\ 0.029\\ 1.409\\ 1.104\\ 2.952 \end{array}$	$\begin{array}{c} 2.308 \\ 0.080 \\ 1.438 \\ -0.33 \\ 0.199 \\ 0.177 \end{array}$	2.232 1.220 -0.52 -0.67	$\begin{array}{c} 0.085\\ 0.100\\ 0.010\\ 3.651\\ 2.208\\ 9.498\end{array}$	$\begin{array}{r} 2.624 \\ -0.13 \\ 1.251 \\ -0.95 \\ 0.409 \\ -0.31 \end{array}$	2.736 1.886 -1.33 -0.86	0.232 0.162 0.129 2.805 1.727 13.02	$\begin{array}{c} 1.977\\ 0.287\\ 1.616\\ -0.67\\ 0.387\\ 0.353\end{array}$	$1.718 \\ 0.513 \\ -1.02 \\ -1.38$

Table 4. Parameter values of the two compatible models estimating the total biomass and biomass of each component of three tree species.

In sum, the fitting accuracy of the compatible models for estimating total biomass and the biomass of each component for all three tree species was high, especially for the MRWTIV. The component-additive models were slightly better than the total-control models. The most appropriate models can be selected based on one's needs to accurately estimate regional biomass.

4.4. Biomass Distribution Characteristics of Each Component of Young Trees

Figure 2 shows the proportion of biomass of each component relative to the total biomass. When the base diameter was 0–11 cm, the proportion of leaf biomass (26%–62%) was highest for young Pinus tabulaeformis, followed by trunk (15%–55%) and branch (15%– 38%) biomass. As the base diameter increased, the proportion of leaf biomass decreased significantly, and the proportion of trunk biomass increased. The proportion of aboveground biomass was much higher than that of root (belowground) biomass. The proportion of root (belowground) biomass was approximately 22%, and changes in root biomass were small. The proportion of leaf biomass (33%–67%) was highest for *Picea crassifolia*, followed by branch (14%–47%) and trunk (11%–39%) biomass. As the base diameter increased, the proportion of leaf biomass decreased, the proportion of branch and trunk biomass increased, the proportion of root (belowground) biomass decreased significantly, and the proportion of aboveground biomass increased significantly. When the base diameter was 6–11 cm, the proportion of aboveground biomass was 80%–81%. The proportion of the biomass of leaves (33%–0.68%) was highest for Sabina przewalskii, followed by trunk (13%– 43%) and branch (10%–42%) biomass. In Sabina przewalskii, the proportion of leaf biomass decreased significantly, and the proportion of branch biomass increased significantly as the base diameter increased; changes in the biomass of different components as the base diameter were similar in Sabina przewalskii and Pinus tabulaeformis, and the proportion of aboveground biomass was approximately 70%.

In sum, the biomass of the leaves in the three species was highest (26%–68%), followed by branch (10%–46%) and trunk (11%–55%) biomass. As the diameter of the ground increased, the proportion of leaf biomass decreased significantly, and the proportion of branch and trunk biomass increased significantly; this pattern was especially pronounced for *Pinus tabulaeformis* trunk biomass, which was as high as 55%.

Tree	N 11 X	X7 · 11	R^2						SEE					MPE				TRE				
Species	Models	variables -	Leaves	Branches	Trunk	Root	Sum	Leaves	Branches	Trunk	Root	Sum	Leaves	Branches	Trunk	Root	Sum	Leaves	Branches	Trunk	Root	Sum
Picea crassifo- lia	(4) (5)	D D,H D,C D D,H D,C	$\begin{array}{c} 0.838 \\ 0.891 \\ 0.844 \\ 0.840 \\ 0.891 \\ 0.844 \end{array}$	0.913 0.915 0.938 0.912 0.912 0.937	0.928 0.969 0.948 0.929 0.968 0.948	0.827 0.827 0.829 0.827 0.828 0.829	0.960 0.974 0.972 0.960 0.973 0.972	0.72 0.59 0.70 0.71 0.59 0.70	$\begin{array}{c} 0.45 \\ 0.44 \\ 0.38 \\ 0.45 \\ 0.45 \\ 0.38 \end{array}$	0.31 0.20 0.26 0.31 0.21 0.26	$\begin{array}{c} 0.45 \\ 0.45 \\ 0.45 \\ 0.45 \\ 0.45 \\ 0.45 \\ 0.45 \\ 0.45 \end{array}$	$1.14 \\ 0.93 \\ 0.95 \\ 1.14 \\ 0.94 \\ 0.95$	14.46 11.88 14.19 14.37 11.85 14.17	11.75 11.64 9.94 11.79 11.82 9.97	11.49 7.58 9.73 11.39 7.69 9.75	16.16 16.17 16.10 16.19 16.14 16.10	8.10 6.56 6.75 8.05 6.67 6.73	-1.34 0.24 -1.17 -2.31 0.16 -0.43	1.55 1.30 0.93 2.11 1.72 1.01	1.05 2.24 0.98 -0.42 2.25 1.42	$\begin{array}{c} 0.11 \\ -0.5 \\ -0.3 \\ 0.99 \\ 0.09 \\ -0.2 \end{array}$	$\begin{array}{c} 0.16 \\ 0.75 \\ 0.0 \\ -0.1 \\ 0.97 \\ 0.35 \end{array}$
Pinus tabuli- formis	(4) (5)	D D,H H,C D D,H H,C	0.870 0.867 0.860 0.870 0.863 0.883	0.836 0.842 0.932 0.836 0.838 0.947	0.977 0.987 0.877 0.977 0.987 0.987 0.888	$\begin{array}{c} 0.733\\ 0.729\\ 0.864\\ 0.732\\ 0.724\\ 0.864\end{array}$	0.912 0.917 0.918 0.961 0.916 0.915 0.932	0.30 0.31 0.32 0.30 0.31 0.29	0.30 0.29 0.19 0.30 0.30 0.17	0.17 0.13 0.40 0.17 0.13 0.38	0.52 0.52 0.37 0.52 0.53 0.37	$ \begin{array}{c} 1.17\\ 1.16\\ 0.80\\ 1.17\\ 1.18\\ 1.06 \end{array} $	19.38 19.64 20.09 19.39 19.94 18.40	24.99 24.50 16.12 24.99 24.83 14.16	10.10 7.73 23.42 10.13 7.74 22.30	35.71 35.96 25.47 35.73 36.28 25.44	20.14 20.01 13.73 20.17 20.32 18.19	1.66 6.51 9.41 2.38 8.95 2.49	0.31 7.10 8.58 1.08 9.86 1.78	2.38 3.26 3.78 2.40 3.40 1.73	0.55 6.66 1.99 1.54 9.50 0.42	1.32 5.73 0.83 1.92 7.67 1.61
Sabina prze- walskii	(4) (5)	H D,H H,C H D,H H,C	0.880 0.891 0.899 0.883 0.893 0.903	0.922 0.922 0.938 0.922 0.922 0.922 0.938	$\begin{array}{c} 0.911 \\ 0.913 \\ 0.944 \\ 0.910 \\ 0.911 \\ 0.943 \end{array}$	$\begin{array}{c} 0.842 \\ 0.848 \\ 0.846 \\ 0.842 \\ 0.848 \\ 0.845 \end{array}$	0.953 0.956 0.968 0.953 0.956 0.969	0.23 0.22 0.22 0.23 0.22 0.21	$\begin{array}{c} 0.15 \\ 0.15 \\ 0.13 \\ 0.15 \\ 0.15 \\ 0.13 \end{array}$	$\begin{array}{c} 0.17\\ 0.17\\ 0.13\\ 0.17\\ 0.17\\ 0.17\\ 0.14 \end{array}$	0.33 0.32 0.32 0.33 0.32 0.32	$\begin{array}{c} 0.61 \\ 0.59 \\ 0.50 \\ 0.61 \\ 0.59 \\ 0.49 \end{array}$	15.22 14.54 13.99 15.04 14.42 13.73	15.86 15.83 14.13 15.83 15.82 14.09	$18.18 \\ 18.05 \\ 14.49 \\ 18.34 \\ 18.23 \\ 14.61$	22.69 22.24 22.44 22.70 22.27 22.45	12.72 12.33 10.43 12.67 12.36 10.32	$\begin{array}{r} -3.30 \\ -3.26 \\ -4.47 \\ -3.05 \\ -2.87 \\ -4.54 \end{array}$	$-1.43 \\ -1.43 \\ -2.50 \\ -0.97 \\ -0.90 \\ -2.06$	4.72 4.56 2.62 5.39 5.40 3.31	-1.5 -1.2 -1.9 -1.1 -0.7 -1.2	$\begin{array}{r} -0.9 \\ -0.8 \\ -2.0 \\ -0.5 \\ -0.3 \\ -1.6 \end{array}$

Table 5. Evaluation indicators of two compatible models estimating the total biomass and biomass of each component of three tree species.



Figure 2. Changes in the proportion of biomass of each component relative to the total biomass of the three tree species.

5. Discussion

For Pinus tabulaeformis and Picea crassifolia, the fitting accuracy and prediction accuracy of the MRWTIV model with tree height and crown diameter as independent variables to the independent model and the compatible models of each component were better than those of the univariate model with base diameter as an independent variable. Moreover, the univariate model with base diameter as the independent variable had the best fitting effect; when tree height and crown diameter were added to make it a MRWTIV, the fitting effect of each component did not significantly change, which is consistent with the results of previous studies [18,19,34,35]. Cai Huide et al. showed that the accuracy of the binary biomass model was better than that of the monobasic biomass model for Horsetail pine plantations in the construction of a standing wood biomass model for the major tree species in Guangxi [34]; Li Yufeng et al. found that the best general model for each organ was the binary model, and its goodness of fit and prediction accuracy were both higher and better suited to the sample sites studied [35]. When tree height was used as the best-fitting variable in the univariate models for Sabina przewalskii, and tree height and crown diameter were used as the best-fitting variables, model accuracy was significantly improved. This might be related to the biological characteristics of Sabina przewalskii (Figure 3). The tendency of young Sabina przewalskii to have more than one trunk might have resulted in errors in the collection of base diameter data.



Figure 3. Young Sabina przewalskii samples.

The compatible models built using the nonlinear joint estimation method were less accurate compared with the independent models. However, they maintained good compatibility among the components and enable estimations of regional biomass. The R² values of the compatible models were slightly smaller than those of the independent model, and the TRE, MPE, and root-mean-square error of the compatible models were slightly larger than those of the independent models.

There were no significant differences in the fitting accuracy of the compatible models constructed by the component-additive and total-control methods, but the componentadditive models were slightly superior in general, especially the MRWTIV, which had the best fitting effect, and root biomass, which had poor fitting accuracy. The componentadditive method first establishes independent equations of each component and then integrates the independent equations of each component to form an equation set for joint estimation. The total-control method is based on the independent models of total biomass. The proportional function of each component was first calculated, and then the equation set was formed by adjusting the total biomass for joint estimation. Therefore, the component-additive model involves controlling the total amount while ensuring that the estimation of each component is accurate. The estimation accuracy of each component was higher with the component-additive models compared with the total-control models. Because the total is the sum of the components, the total estimation was also more accurate. Therefore, for tree roots with poor fitting accuracy, the fitting effect of the componentadditive models was better. For the MRWTIV with the best fitting effect, the R^2 values of the total aboveground amount were generally above 0.9, which highlights the advantage of the component-additive models for accurately estimating each component.

In their study, Kim et al. emphasized that the site-specific allometric models are more accurate in predicting the forest biomass estimates on the local level, as they take into account the site effects [36]. The study found that there was no significant difference in the explanatory power of diameter at different heights on volume and biomass changes, but in terms of the biomass model, 0.5 m diameter (base diameter) may be more suitable than DBH [12]. However, most biomass models are based on DBH variables [8–13]. In this study, three young tree biomass models were developed based on field sampling data in the Qinghai alpine region, and the best model fit accuracy and prediction accuracy were good. Few studies have been conducted on young forest biomass models. The biomass model for samples below 6 cm obtained in this study was compared with the standing tree biomass model (*Picea crassifolia* and *Pinus tabulaeformis*) published by the National Forestry Industry Standard of China Forestry and Grassland Administration [37,38]. It was found that the biomass model of forestry standard mainly used the DBH and tree height variables

and did not add the model results of variables such as crown width. The accuracy of forest standard biomass model is applicable to the whole country, slightly lower than that of the northwest alpine region model obtained in this study, especially the leaf components. The relatively low coefficient of determination of leaf biomass is consistent with the findings of existing studies [39], likely due to the fact that leaves are more influenced by biotic and abiotic factors and, thus, show some variation [40], while leaf and branch biomass sizes are uncertain due to a combination of factors such as depression and stand conditions [39].

In conclusion, the optimal biomass model of artificial young forest at the sampling site is a multivariate component-additive compatible biomass model. When calculating the amount of biomass of individual trees, the independent biomass model has high accuracy; when calculating the biomass of the sample wood area (whole plant and each component), the nonlinear joint estimation of the compatibility model is more compatible error than the independent model error. Although error is slightly large, the model maintains good compatibility between each component, and it can effectively predict the biomass of the area. Although there was no significant difference in fitting accuracy of the compatibility models constructed by the component-additive and total-control methods, the componentadditive models were slightly superior in general, especially the MRWTIV, which had the best fitting effect, and leaf and root biomass, which had poor fitting accuracy.

6. Conclusions

On the basis of biomass data taken from 96 saplings of *Picea crassifolia, Sabina przewalskii,* and Pinus tabulaeformis, independent, component-additive, and total-control compatible models were established using allometric growth equations and nonlinear joint estimation method. The goodness of fit and the estimation accuracy of the models were also analyzed. The main results are detailed below.

- (1) Multiple regression with two independent variables was superior to univariate models for all three tree species. For *Pinus tabulaeformis* and *Picea crassifolia*, base diameter was the best-fitting variable of the univariate model, and when the base diameter and crown diameter were used as multivariate model variables, model accuracy was significantly improved. For *Sabina przewalskii*, tree height was the best-fitting variable of the univariate model; when tree height and crown diameter were used as multivariate model variables, model accuracy was significantly improved, which might be related to the biological characteristics of *Sabina przewalskii* (namely, their tendency to have multiple trunks).
- (2) The optimal biomass models were those in which the multivariate components were added to the compatibility models. When calculating the amount of single wood biomass, the independent biomass model has high accuracy; when calculating the biomass of the sample wood area (whole plant and each component), the nonlinear joint estimation of the compatibility model is more compatible with the independent model error. Although error is slightly large, the model maintains good compatibility between each component, and it can effectively predict the biomass of the area. Although there were no significant differences in the fitting accuracy of compatibility models constructed using the component-additive and total-control methods, the component-additive models were slightly superior in general, especially the multiple regression with two independent variables, which had the best fitting effect, and leaf and root biomass, which had poor fitting accuracy.
- (3) The largest biomass component of the three tree species was the leaves (26%–68%), followed by the branches (10%–46%) and trunks (11%–55%). As the base diameter increased, the proportion of leaf biomass decreased significantly, and the proportion of branch and trunk biomass increased significantly, especially for the proportion of *Pinus tabulaeformis* trunk, which was as high as 55%. Aboveground biomass was higher than root (belowground) biomass. As the base diameter increased from 0 to 11 cm, the proportion of aboveground biomass of *Picea crassifolia* increased, and

the proportion of aboveground biomass of *Pinus tabulaeformis* and *Sabina przewalskii* decreased slightly.

In this study, biomass models were established for three important young plantations in the southern foot of the Qilian Mountains. Based on field sampling data and comparison of multiple models, the model accuracy was high. However, limited to research resources and time, the author keenly realized that there is still much room for improvement in the number of plots and the depth of research. In the future, it is necessary to increase the number of survey plots and sampling sites on the basis of the completed plots, improve the accuracy of relevant parameters and models, and continually improve the accuracy of biomass estimation.

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