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Early growth evaluation and biomass allocation differences of *Cupressus funebris* clones and families

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Abstract

Clonal forestry offers the opportunity to increase yields, enhance uniformity and improve wood characteristics. Evaluation of growth differences between clones and families has rarely been studied in slow-growing *Cupressus funebris* species, and whether such growth differences are related to biomass allocation patterns remains to be revealed and is essential for assessing the genetic selection potential and carbon sink capacity of superior species. We studied the genetic variation, heritability (replication power) and gain levels of 36 clones and 33 families of superior trees and analysed their biomass allocation patterns. The results showed that the early growth of *Cupressus funebris* was dominated by high growth, and the clones grew rapidly, with 253.36% and 51.77% higher diameter at breast height and height at 8 years old than the family lines, respectively. However, the genetic variation of growth traits in the families was higher than that of the clones. The clone repeatability and family heritability levels were evaluated. According to the 10% selection rate, the genetic gains of DBH and tree height of clones were 39.53% and 24.23%, respectively, 5.22 times and 2.05 times the genetic gains of families. The ratio of narrow and broad heritability of each trait was estimated to be 0.55-0.68, with an average value of 0.63, indicating that clones obtained higher additional genetic gains through nonadditive effects. The growth advantage of the clones was to increase the biomass of the aboveground part (86.03%) at the expense of the belowground biomass allocation, which was mainly reflected by the proportion of branch and leaf biomass allocation. The branches and leaves of the clones were dominated by the middle and upper layers, which accounted for 180.64% and 60.14%, respectively, while the middle and lower layers of the branches and leaves of the family lines accounted for a higher percentage. The model $\ln W = k_0 + k_1 \ln D + k_2 \ln H + k_3 \ln C$ has the best prediction of biomass and could be used for early genetic evaluation of *Cupressus funebris*. In general, *Cupressus funebris* clones are fast growing and will help to improve the productivity and carbon storage of stands through genetic selection and utilization.

Keywords: Clone, family, genetic selection, biomass allocation, allometric growth, genetic gain

Early growth evaluation and biomass allocation differences of *Cupressus funebris* clones and families

1、 Introduction

Family and clone are currently the main silvicultural tree species of good seed promotion methods. Cloning is the use of individuals with outstanding growth and other traits in the population to rapidly form commercial forests through asexual propagation, such as grafting, cuttings, and tissue culture, to improve the productivity of forest trees and wood products, which has become a major trend in current forestry development [1]. Clones have advantages that cannot be matched by family forestry. First, they can make better use of additive genetic variance because the differences between the participating clones contain all additive variance, while the differences between full-sib families and half-sib families contain only 1/2 and 1/4 of the additive variance, respectively. Second, the clones obtain the full nonadditive genetic variance because the promoted clones lines maintain their full genetic values [2, 11]. During production, it was found that the family limits the reselection of superior forest tree varieties due to high genetic heterozygosity, and heterozygous advantage is maintained only in the first generation, while the clones have stable and consistent growth trait performance, facilitate intensive management, and can significantly improve forestry management efficiency [1]. In addition, coniferous trees usually have a very long childhood, and clonal afforestation avoids the production problems restricting breeding, such as too long of a seed orchard construction time, low selection efficiency and unstable seed setting [3, 4, 10].

The success of clonal forestry depends on the biological characteristics of tree species to a large extent. Due to the age and position effects, most of them carry out large-scale vegetative reproduction when reaching the early selection age. For example, Eucalyptus, Poplar, Willow and their hybrids have achieved true clonal breeding, with the most remarkable results in poplar, including natural hybrids that have been used on a large scale [5, 13]. Eucalyptus clone forestry has also been used very successfully in broad-leaved trees with genetic gains of 25-50% [6, 7]. Among coniferous trees, Baltunis et al. tested young clones of Loblolly pine and showed that the best clone had almost twice the genetic gain of the family lines and 40-60% higher productivity [8]. The application of Radiata pine clones in volume, wood hardness, wood density and other aspects also has good performance, and the genetic gain is as high as 10-25% [9].

The study of plant biomass allocation is a way to explore intrinsic plant growth patterns and how these growth patterns and biomass allocation change under the influence of various factors. Biomass allometric growth models, which combine simple and readily available predictor variables with tree biomass, provide a general and reliable approach to forest growth and carbon balance [12]. A useful feature of the allometric approach to biomass partitioning is that it implicitly accounts for differences in plant size. The other approach to biomass partitioning is based on taking the fractions of total plant mass constituted by particular organs—leaves (leaf mass fraction), stem (stem mass fraction), and roots (root mass fraction). Because the strength of the allometric relationships (R^2) depends on the range of plant sizes compared, it has been advocated to combine both approaches in studies of plant biomass partitioning [14]. Genetic differences in biomass allocation patterns have been confirmed at the provenance and family levels of Norway spruce, White spruce, White birch and other tree species, which also implies that genetic differences in plant growth and biomass allocation may be revealed by comparing allometric growth relationships at the family or clonal level [16-18]. When intercepts and

not slopes of the allometric relationships vary, it reflects variation in biomass distribution at a given plant size but not in growth rates. In contrast, variation in slopes may reflect genetic differences in the growth rate of an organ relative to the other or to total plant mass.

If the slope difference between families and clones persists, it indicates that the biomass distribution pattern will lead to the difference in plant growth rate. There is still an important problem here, whether the biomass distribution pattern of fast- and slow-growing genotypes remains fixed in the population at the family level or the clone level, which will significantly affect the allometric growth index [18]. At the intraspecific level, there may be significant differences between the interpretation of biomass allocation patterns (ontogenetic trend) by allometric growth equation and the wide interspecific level [15, 19, 24].

Cypress (*Cupressus funebris* Endl.) is a major ecological restoration species in rocky desertification areas and barren forest areas [22]. *Cupressus funebris* is an important branch for making cypress essential oil and research shows that cypress essential oil can relieve pressure [42]. However, *Cupressus funebris* has excellent material and adaptability, but compared to coniferous species in the same region as Masson pine and China fir, it grows slowly. Through the first-generation seed garden built, it was found that the low seed yield of *Cupressus funebris*, the difficulty of hybrid seed production and the slow genetic improvement process restricted the improvement of the productivity of artificial forests [23]. Through top-pruning, sprouting promotion and juvenile technology, many healthy cuttings can be formed every year, and the cutting rooting rate of the 5-year-old *Cupressus funebris* female parent can reach more than 85% [21]. Therefore, there is significant potential to carry out clonal forestry of *Cupressus funebris*, but the growth evaluation of clones has yet to be revealed.

In the genetic population, the difference in biomass allocation to specific organs will affect the growth of trees, which will also determine the genetic improvement strategy of tree species. Therefore, this study attempts to test the following hypotheses by using *Cupressus funebris* clones and family test forests with the same planting location and tree age: 1) Regardless of the level of clone and family, the variation in the early growth of *Cupressus funebris* is higher, and clones show a higher growth advantage than families; 2) the distribution patterns of biomass in different organs of clones and families are distinct, especially the distribution of underground and aboveground biomass; and 3) to establish and evaluate the allometric growth relationship between biomass and growth, which is suitable for predicting the early productivity and genetic gain level of *Cupressus funebris*. Testing these hypotheses will allow us to better understand the patterns of genetic variation for early growth traits in *Cupressus funebris* and explain the pattern of biomass allocation for rapid growth of superior genotypes, which is important for productivity and enhancement of *Cupressus funebris*.

2 Materials and methods

2.1 Experimental materials and planting

The 8-year-old *Cupressus funebris* clone and family determination forest are from the forest farm of Kaihua County, Zhejiang Province. The geographical coordinates are 118°24′24″E and 29°8′17″N. The region experiences a subtropical monsoon climate. The average annual temperature is 16.4 °C, the average temperature difference between day and night is 10.5 °C, the average annual rainfall is 1814 mm, the average annual sunshine hours are 1679.8 hours, and the frost-free period is 252 days.

Among them, there were 36 clones in the test materials of the clonal test forest, including 35 clones (4-year-old cutting orchard) and 1 control (local common single plant, CK1). Ten-micrometer-long semilignified cuttings were selected and cut in the nursery. There were 33 families in the materials

of the family test forest, including 32 families (seeds collected in the seed garden of the first-generation clone) and 1 control (local common single-plant collected seeds, CK2). The seedlings were sown in March and cut in May 2012, and the experimental forest was built in 2013. The two experimental forests adopt completely random block groups, and three experimental block groups are set. The 10 plots are arranged in a single row, and the row spacing is 2 m × 2 m.

2.2 Growth survey and biomass sampling

2.2.1 Growth measurement

At the age of 3 years, the height and crown width of the whole forest were investigated. At the age of 8 years, the tree height, DBH, branch height and crown width were investigated. The estimation formula of a single tree volume is V=0.000057173591*$D_{1.3}^{1.8813305}$*$H^{0.99568845}$ [31], where V, D and H are the volume, DBH and tree height, respectively.

2.2.2 Biomass measurements

The clone and family were ranked separately according to the TOPSIS comprehensive evaluation method [25], and three grades of excellent, good and poor were selected, three clones and families were selected for each grade, three plants were selected for each zone group, and 81 sample trees were felled for the clones and families. In addition, controls with the same number of plants were selected in each test stand for comparison.

For the analysis tree sampling method reference [18], biomass measurements were made at the tree and root levels. After the tree was felled, the height of the tree was measured. The stem was cut into 1 m sections and weighed. Afterwards, a 5 cm disc was removed from the middle of each section, and the fresh weight of each disc (with skin) was measured separately. The live crown was divided into three equal sections. The fresh weight of the branches (including needles) was recorded by section. From each section, three representative branches were sampled; the branches and needles were separated, and their fresh weights were recorded. The branch/needle ratio was used to calculate the fresh weights of the sectional branch and needle weight. At the root level, the root system was divided by size into root components of coarse roots (>2 cm in diameter, contains the root pile) and fine roots (<2 cm). All samples were brought back to the laboratory and baked at 80 °C in an oven to a constant weight, and the dry weight was measured. The dry biomass of all tree components was calculated by multiplying the fresh weight of each component by the dry/fresh weight ratio.

2.3 Data processing and analysis

2.3.1 Analysis of variance and genetic parameters

One-way analysis of variance (ANOVA) of SPSS 26.0 (SPSS Inc., Chicago, IL, USA) software was used to analyse the growth differences of each trait at the clone and family levels and the differences between clones and families. The linear model of variance analysis is:

$$X_{ijk} = \mu + F_i + B_j + F_iB_j + e_{ijk}$$

Where: μ is the overall average, F_i is the effect between clones or families, B_j is the intergroup effect, e_{ijk} is a random error.

The TYPE1 method in the VARCOMP process of SAS 9.4 (SAS Institute, 2009) was used to calculate the following genetic parameters:

Phenotypic variation coefficient: (CV)： $CV=\frac{\delta_p}{\bar{X}}\times 100\%$

Where: CV is the coefficient of variation, δ_p is the standard deviation, $\bar{X}$ is the average value of traits.

Clone repeatability: $R=\frac{\sigma_A^2}{\sigma_A^2+\frac{\sigma_{AB}^2}{b}+\frac{\sigma_e^2}{nb}}$

Where: R is the repetitive force, σ_A^2 is the variance component of clones, σ_{AB}^2 is the variance component of the interaction between clone and block, σ_e^2 is the variance component of the random error, n is the harmonic value of the number of individual plants in the plot, and b is the number of block.

Family heritability: $h^2 = \frac{\sigma_F^2}{\sigma_F^2+\frac{\sigma_{FB}^2}{b}+\frac{\sigma_e^2}{nb}}$

Where: σ_F^2 is the variance component of the family, σ_{FB}^2 is the variance component of the interaction between family and block.

The real gain (G) was calculated as follows: $G=\frac{x_i-\bar{X}}{\bar{X}}$

The genetic gain (ΔG) was calculated as follows: $\Delta G = \frac{i\delta_p h^2}{\bar{X}}$

Where: x_i is the average value of the characters of the selected clones, $\bar{X}$ is the average value of clone or family traits, i is the selection strength, δ_p is the standard deviation and h^2 is the heritability of the family.

TOPSIS (technique for order of preference by similarity to ideal solution) was used to comprehensively assess the growth traits and quality prioritization of the clones and families with the DPS V7.05 statistical software package (Hangzhou Information Ruifeng Technology, Co., Ltd., Hangzhou, China) [26, 27].

2.3.2 Establishment of the anisotropic growth model

Due to heteroscedasticity in the biomass model, a log-transformed form ($\ln Y = a + b \ln X$) of the power function ($Y = aX^b$) was used to model relative biomass growth and eliminate heteroscedasticity [28, 29]. The following five heteroscedastic growth models were selected:

$$\ln W = k_0 + k_1 \ln D \quad (Eq\ 1)$$
$$\ln W = k_0 + k_1 \ln D + k_2 \ln H \quad (Eq\ 2)$$
$$\ln W = k_0 + k_1 \ln D + k_2 \ln H + k_3 \ln C \quad (Eq\ 3)$$
$$\ln W = k_0 + k_1 \ln D^2 H \quad (Eq\ 4)$$
$$\ln W = k_0 + k_1 \ln D^2 H + k_2 \ln C \quad (Eq\ 5)$$

Where: W is the biomass of each component, k_0、k_1、k_2、k_3 are the fitting coefficient, D is the diameter at breast height, H is the height of the tree, and C is the height under the branch. $Eq\ 2$, $Eq\ 3$ and $Eq\ 5$ use the variance expansion coefficient (*VIF*) to measure the degree of multicollinearity [30]; The Coefficient of determination (R^2) and root mean square error (*RMSE*) were used to evaluate and optimize the model effect.

3. Results and analysis

3.1 Growth difference analysis of clones and families

The average tree height of 3-year-*old Cupressus funebris* clones was 1.51 m, and the coefficient of variation was 28.58%. The average tree height of the family was 0.95 m, and the coefficient of variation was 46.10%. At the age of 8 years, the average tree height, DBH, under branch height and crown width of the clones were 4.32 m, 3.87 cm, 40.13 cm and 1.06 m, respectively, with 21.26%-43.24% variation; the average tree height, DBH, under branch height and crown width of the family were 2.82 m, 1.81 cm, 39.48 cm and 0.75 m, respectively, with a variation range of 20.92% - 59.31% (Table 1). The DBH and tree height of the clones were 253.36% and 51.77% higher than those of the family, respectively. The height diameter ratio of the family was 1.10, while that of the clone was 2.56. The height growth of the *Cupressus funebris* clone was significantly higher than that of the family.

3.2 Analysis of genetic differences in growth traits

There were highly significant differences (P<0.01) in all growth traits between clones or families, both at 3 and 8 years of age. The clones with the highest tree height and diameter at breast height were 91.78% and 39.12% higher than the lowest clones and 80.76% and 23.74% higher than the control CK, respectively; the family with the highest tree height and diameter at breast height were 46.11% and 37.84% higher than the lowest family and 19.47% and 12.03% higher than the control CK2, respectively.

The range of replication power of clones at 3 and 8 years of age ranged from 0.372 to 0.554 and 0.651 to 0.756, respectively. The range of heritability of the families at 3 and 8 years of age ranged from 0.498 to 0.606 and 0.132 to 0.322, respectively (Table 2). Based on the 10% selection rate, the genetic gains of 8-year-old clones were 39.53%, 24.23 and 82.21% for DBH, height and wood volume, respectively, and 7.58%, 11.82% and 35.38% for families.

The TOPSIS method was used to rank the superior and inferior clones of *Cupressus funebris* clones and families (Table 3). The superior clones were selected as C6, C9, and C14, the intermediate clones were C1, C5, and C11, and the inferior clones were C10, C20, and C34. The DBH and height of the good clones were 132.28% and 118.15% of the medium clones and 146.17% and 122.88% of the poor clones, respectively. The excellent families were selected as F8, F18 and F24, the medium families were F5, F10 and F22, and the poor families were F11, F26 and F32, where the DBH and height of the good families were 112.98% and 112.28% of the medium families, respectively, and 122.67% and 116.16% of the poor families.

3.3 Biomass distribution pattern

3.3.1 Distribution proportion of biomass of each organ

The clones had 8.9% more biomass allocation in the aboveground part than the families and the highest percentage of trunk biomass allocation. The clones had a 23.5% lower percentage of trunk biomass than the families, but the percentage of branch and leaf biomass allocation was higher than that of the families at 180.64% and 60.14%, respectively. The proportion of belowground biomass allocation was 33.16% more in the family line than in the clone, and the proportion of coarse and fine root biomass to total biomass was 27.31% and 47.16% higher than in the clone, respectively (Table 4). The biomass of branches and leaves in the middle layer of the crown was the highest. At the clone level, the percentage of branches and leaves in the middle layer was 55.48% and 54.02%, respectively, and the biomass of branches and leaves in the upper layer was 7.24% and 14.4% higher than that in the lower layer; at the family level, the percentage of branches and leaves in the middle layer was 45.56% and 47.64%, respectively, and the biomass of branches and leaves in the upper layer was 5.24% and 7.18% lower than that in the lower layer (Fig. 1). Regression equations of aboveground and underground biomass, trunk and leaf biomass and branch biomass were established, respectively, with a significant linear relationship. The slope difference between clones and families was not significant, but the intercept difference was significant ($P < 0.05$) (Fig. 2).

3.3.2 Biomass allometric growth model

The allometric growth models of total biomass, aboveground biomass, belowground biomass and growth traits are shown in Table 4. The worst fit was achieved with DBH as a single variable (*Eq*. 1), and when tree height was added to the model as a second independent variable (*Eq*. 2), the accuracy of the model fitted with DBH alone as an independent variable was improved, but to a limited extent. When DBH, tree height, and under branch height were used as independent variables (*Eq*. 3), the coefficient of determination R^2 reached the maximum, *RMSE* was small, the model fit was good, and the variance expansion factors (*VIFs*) were 2.442 and 3.106, respectively, indicating that there was no multicollinearity. When tree height *H* in the form of D^2H and *D* was integrated into one parameter as an

independent variable (*Eq.* 4), the fitting degree of single plant total biomass and aboveground and underground biomass of clones decreased, R^2 decreased by 15.47%, 17.11% and 6.83%, respectively, while the accuracy of the family model decreased slightly, and R^2 decreased by 1.24%, 2.49% and 1.43%, respectively. Compared with the *Eq.* 4 model, the fitting degree of the *Eq.* 5 model increased when the under branch height was added as an independent variable. Generally, the under branch height is added to the model as an independent variable, which has a significant impact on the fitting degree of the biomass model. Based on R^2, *RMSE* and *VIF*, *Eq.* 3 was selected as the best fitting model of *Cupressus funebris* biomass.

Biomass estimates for all tested clones and families using the *Eq.* 3 model to assess the level of gain in early productivity of *Cupressus funebris* were 29.54% to 54.13% for clones and 20.24% to 50.48% for families at selection intensities of 5%-45% (Fig. 3). When the selection intensity was less than 30%, the realistic gain in biomass of the clones was greater than that of the families, and as the selection intensity increased, the level of biomass gain shown for the family gradually exceeded that of the clone.

4. Discussion

4.1 Evaluation of clonal and family forestry

Estimates of genetic gain from clonally replicated trials in conifers were initially started in the 1980s, but there are rather few reliable estimates. Genetic variance and broad-sense heritability are expected to be higher than the corresponding additive variance and narrow-sense heritability if there is significant nonadditive genetic variance. A valid comparison of relative genetic control must therefore use datasets that come from the same trial with comparable pedigrees. The genetic gain of *Cupressus funebris* clone forestry compared with that of the family was obvious, and the growth traits of the clone were significantly higher than those of the family line after measurement, with the DBH, height and wood volume being 253.36%, 51.77% and 534.95% higher than those of the family line, respectively. In a study of clone tests of Black spruce at 10 years of age, it was shown that additional genetic gain through dominant and epistatic effects was almost equal to that obtained by full- and half-sib selection [32]. Similarly, in the White spruce clone test assay, the predicted nonadditive genetic variance at 6 years of age was approximately 50% larger than the additive variance, but the nonadditive genetic variance at 14 years of age was approximately 20% of the additive variance [36].

One of most extensive studies of clone trials was in radiate pine, where $h^2 = 0.26$ for DBH was substantially higher than $h^2 = 0.14$, resulting in the nonadditive variance being just slightly less than the additive variance. The top 5% of clones was estimated to yield 24% genetic gain, an improvement of more than 100% over family forestry at the same selection intensity, indicating that there is considerable nonadditive genetic variance that should be exploited in breeding and deployment programs for P. radiata [9, 33]. The volume gain over the family mean by choosing the best clones from each family was estimated to be 12.6% in another loblolly pine clone trial. The top clone of the 45 clones tested yielded 39.8% more volume than the grand mean. The top five and the top ten clones had 30% and 23% more volume gain than the grand mean, respectively. Young clone testing in loblolly pine estimated that genetic gain from the best clones selected from the ten best families was almost double (20%) than selection based on the best families (10%) [8]. The study estimated that the ratio of narrow and broad heritability for each trait in 8-year-old clones ranged from 0.55 to 0.68, with a mean value of 0.63, indicating that the nonadditive effect was greater, and with the advancement of generations or increase in selection intensity, the clones not only made better use of additive genetic variance but also obtained more nonadditive genetic variance and maintained the genetic value of good traits, and the clones utilized greater genetic benefits [11], which can greatly advance clone forestry for slow-growing *Cupressus*

funebris species by implementing asexual breeding techniques such as cuttings and group culture [23].

4.2 Biomass distribution mode

The biomass of *Cupressus funebris* clones and families was mainly distributed in the aboveground part, among which the trunk biomass accounted for the largest proportion, and the branch and leaf biomass of clones were 2.83 and 1.60 times that of families, respectively. Combined with the growth of 8-year-old *Cupressus funebris* trees, the branch and leaf biomass of clones accounted for a larger proportion, and the crown was dominated by the upper middle layer, while the growth of families was dominated by the lower middle layer, which made the clone growth have a larger photosynthetic area for photosynthesis. Usually, the upper layer of the crown intercepts 70% of the photosynthetic radiation, and only 3% ~10% reaches the ground cover layer, and the light received by the crown gradually decreases with increasing canopy depth [34]. Many factors place a role in the interaction between these plants and light, including the vertical structure of the canopy determining the intensity of photosynthesis, the leaf biomass being highly sensitive to light; the distribution of leaves being influenced by the location of branches on the trunk, stand height and crown density, and their growth being closely related to light intensity. Physiologically, trees of fast-growing provenances absorb more sunlight for photosynthesis and accumulate more organic substances aboveground [18].

Early studies focused on the response of tree biomass to environmental changes (i.e., water, light and nutrients) [35]. The findings from these studies were in response to improved growing environments; fast-growing trees tend to allocate proportionally less biomass to needles and branches but more to stems than slower-growing trees. However, this study was conducted to compare biomass allocation between clones and families under similar growth conditions, and the fast-growing clone lines showed more allocation of organic matter to needles and branches (Table 4). This finding differs from the results in different environments, where *Cupressus funebris* prefers to grow in calcareous soils with infertile soils; additionally, the balanced growth hypothesis suggests that to meet the rapid growth demands that require more efficient access to resources in the environment, plants allocate resources to the organs that need them most, which is likely the branch and leaf organs of *Cupressus funebris* clones because allocate more energy [38]. It can be expected that clones with high growth potential can achieve higher productivity or carbon storage capacity than those with slow growth . Stovall et al. (2013) concluded that physiological processes other than biomass partitioning were responsible for clonal differences in growth. At the root level, the fast-growing genotypes had relatively less allocation of fine root biomass and more allocation of coarse root biomass, which was confirmed in this study (Table 4).

The study also showed that there was a significant linear relationship between aboveground and underground biomass and between trunk and branch and leaf biomass. Although the slopes of clones and families did not show significant differences, the ratios of aboveground and underground biomass were 6.15:1 and 3.76:1, the ratios of trunk to branch biomass were 2.40:1 and 8.91:1, and the ratios of trunk to leaf biomass were 1.91:1 and 4.0:1, respectively. In terms of biomass allocation strategy, the results show that the fast-growing clones are not only at the expense of underground biomass but also because the branches and leaves of the clones have stronger competitive ability. Sufficient branches and leaves are important factors for clones to show rapid growth.

4.3 Establishment of allometric growth relationship

Generally, an allometric function is suitable for genotypes with various growth rates [36]. In this study, the prediction accuracy could be improved by fitting the characteristic parameters of clones and families (Table 5), which is consistent with the results of biomass allocation in genetic experimental forests of different provenances of *Picea koraiensis* and white birch [18, 39].Therefore, we considered

the inclusion of genetic effects in the prediction of biomass. This inclusion seems to be particularly important for traits such as total aboveground biomass and whole-tree biomass. DBH, as the easiest to measure accurately, is the most widely used in biomass models to obtain high fitting accuracy; however, *Cupressus funebris* is a slow-growing species, and in this study, with $D_{1.3}$ as the single independent variable, the R^2 of the model was lower, the *RMSE* was higher, and it was slightly less accurate, while the estimation accuracy was improved when the tree height trait was added to the biomass model as the second parameter, which may be related to the predominance of high growth in the early years of *Cupressus funebris*. Some studies have shown that the inclusion of *H* in the biomass model can counteract area effects [40]. When the under branch height is included in the model as the second independent variable, the estimation accuracy can be significantly improved, there is no significant correlation between *D* and the under branch height, and there is no multicollinearity problem in the model. It shows that the height, $D_{1.3}$ and the under branch height of *Cupressus funebris* can have a strong internal correlation with the biomass, which is the key parameter of the biomass model. *Cupressus funebris* is easy to branch. The height of the tree crown is determined by the under branch height, which determines the height of the tree crown that receives photosynthesis and thus has an impact on the growth variation of *Cupressus funebris* [41]. In this study, the under branch height R^2 is introduced to reach the maximum value, which improves the accuracy of model fitting.

Through the simulation study, it was found that from the perspective of growth, the application of genetic selection can improve the growth characteristics and aboveground biomass of plants, indicating that planting fast-growing clones can indirectly improve the productivity of biomass. At present, most of the trees are based on genetic selection of excellent families and clones. Paying attention to the potential of genetic selection is the direction of future plantation production and carbon storage capacity. During the early growth stage, it is more practical to select superior lines by considering the DBH, tree height and under branch height and to evaluate the genetic potential of biomass. To further understand the interaction between biomass al location and genetic selection in growth and development, it is important to study heritability and genetic correlation [18].

Simulation studies showed that the application of genetic selection can improve plant growth traits and aboveground biomass from a growth perspective, indicating that planting fast-growing clones can indirectly improve biomass productivity. Currently, most forest trees are based on genetic selection of good families and clones, and emphasis on genetic selection potential is the direction of concern for future plantation forest production and carbon storage capacity. In the early growth stage, it is more relevant to assess the genetic potential of biomass by considering the DBH, tree height and under branch height to select the superior. To further understand the interaction between biomass allocation and genetic selection in growth and development, it is important to study heritability and genetic correlation [18].

In this study, the gain level of clones and families was evaluated according to the selection intensity. It was found that when the selection rate was less than 30%, the realistic gain of biomass of clones was greater than that of families. With the increase in selection intensity, the biomass gain level of families gradually exceeded that of clones. It is suggested in Harry's risk assessment of clonal forestry that the number of clonal genotypes in the clonal plantation is related to the genetic gain and risk of the plantation. To reduce the risk of clonal forestry and ensure high genetic gain, it is particularly important to determine the "safe" number of clonal genotypes in the clonal artificial forest. First, the deployment of 5-30 clones in the clonal artificial forest can effectively ensure the "safety" of clonal forestry. Second, the optimal diversity level and genetic gain balance of the clonal artificial forest population may be approximately 18 clones, or at least approximately 6 clones [1]. Therefore, in our work on clonal forestry of *Cupressus*

funebris and other slow-growing trees, it is suggested to evaluate the interaction effect of genotype and environment in family/clonal experiments in multiple climatic regions and estimate their additive and nonadditive genetic variance to predict the stability and genetic gain of clonal forestry.

5 Conclusion

The genetic gain of DBH and tree height estimated by the test of *Cupressus funebris* clones were 39.08% and 14.86% higher than those of the family test forest. To implement the clone and family forestry in *Cupressus funebris*, it is suggested to estimate the additive and nonadditive genetic variance from the existing test forest to effectively predict the additional genetic gain of the clone forestry compared with the family forestry, which is related to the selection intensity and population size. At the level of genetic selection, both clones and families were selected for their benefits on biomass production capacity. Above-and underground biomass and the distribution between them were among the factors affecting their fast and slow growth, where clones showed fast growth characteristics that improved the biomass distribution in the aboveground part, mainly reflected by the proportion of branch and leaf biomass distribution. The choice of fitting tree height, DBH and under branch height as specific parameters to the biomass prediction function to reflect growth differences can effectively improve the prediction accuracy of the model for assessing the biomass production potential of different strains.

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Statements and Declarations

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

CRediT authorship contribution statement

All authors contributed to the study conception and design. **Tao Yang:** Formal analysis, Writing - Original Draft. **Zhen Zhang:** Conceptualization, Methodology, Writing - Review & Editing, Project administration. **Pengcheng Wang**: Supervision, Review & Editing. **Wenyue Wang**: Investigation, Data curation. **Guoqing Jin:** Investigation, Data curation. **Yongbin Qiu**: Investigation**. Han Shen:** Investigation. **Zhichun Zhou:** Supervision. All authors read and approved the final manuscript.

Figures

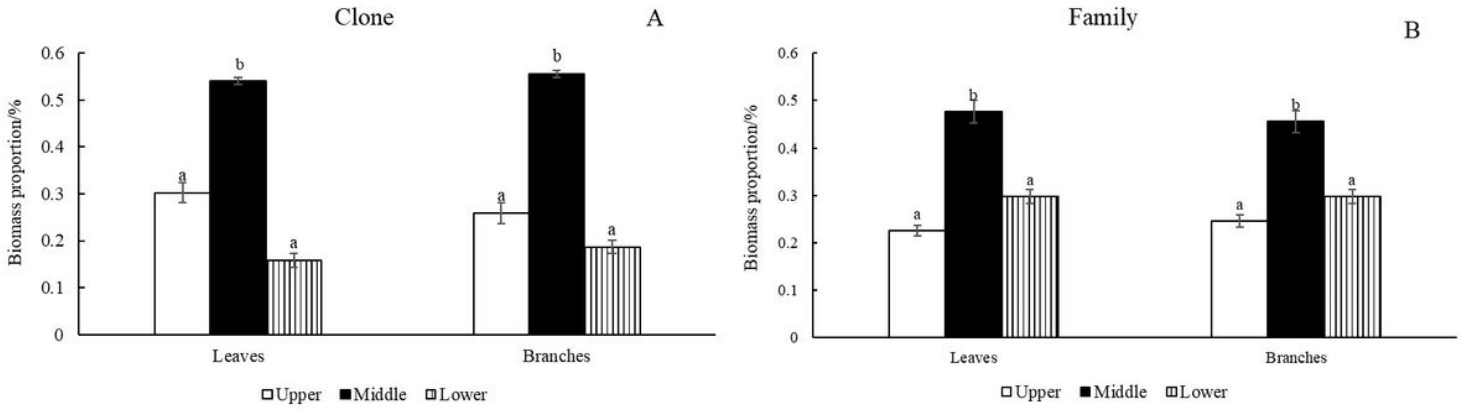


Figure 1

Distribution ratio of branch and leaf biomass of cypress clones(A) and families(B)

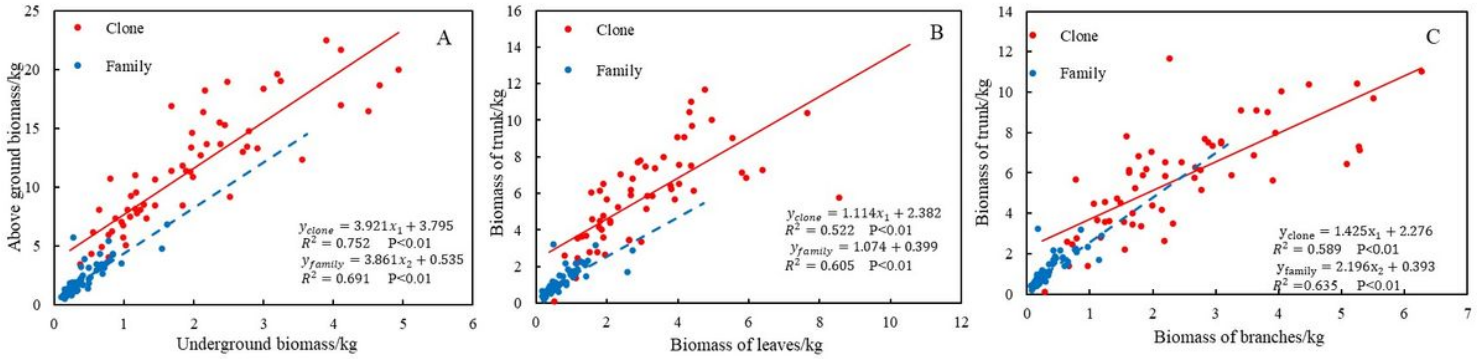


Figure 2

Fitted regression equation. Red dots represent the clones. Blue dots represent the families.

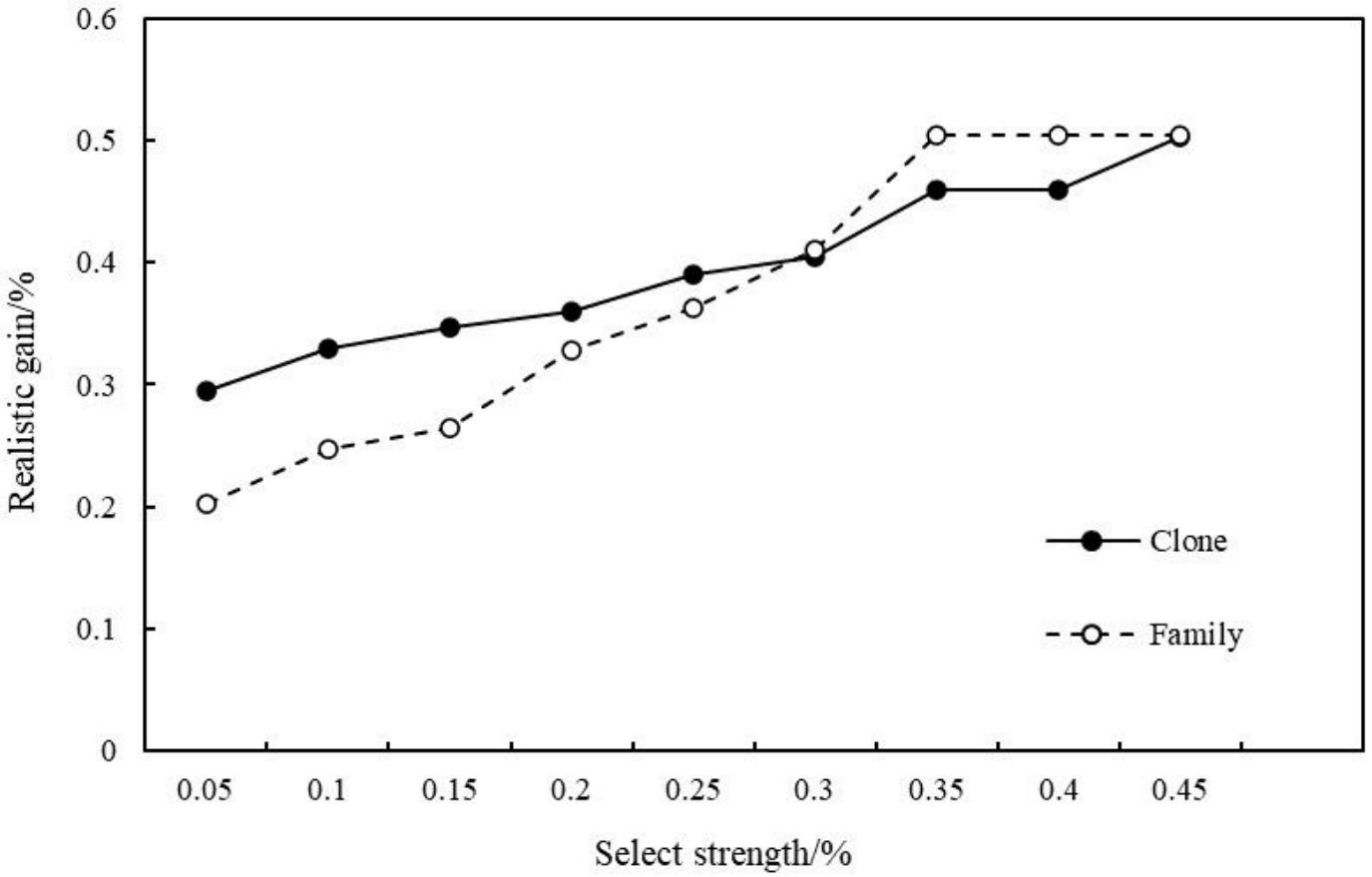


Figure 3

Estimating the actual gain level of biomass of cypress clones and families. Solid line represent the clone. Dashed line represent the family.

Supplementary Files

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