



## Article

# Genetic Parameter Estimates and Genotype $\times$ Environment Interactions of Growth and Quality Traits for *Betula alnoides* Buch.-Ham. ex D. Don in Four Provenance-Family Trials in Southern China

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**Abstract:** *Betula alnoides* is a valuable timber species with wide ecological adaptability in Southeast Asia and southern China. There are more than 150,000 ha of *B. alnoides* plantations in China until now. However, heavy differentiation in growth and quality traits with low productivity are usually seen in the practice. Elite germplasm are thus urgently needed for this species. Here growth and quality traits for 199 families of 25 provenances were assessed at four sites when 10–15 years old to estimate genetic parameters and reveal genotype by environment ( $G \times E$ ) interaction, and screen out superior provenances and families for plantation forestry of *B. alnoides*. The growth and quality performances of provenances varied with sites. Significant site, provenance, family and provenance-site effects were revealed for most growth and quality traits, while significant family-site effects were only observed in crown width (CW) and crown shape (CS), inferring that there existed significant  $G \times E$  interaction. The provenance repeatability ( $h_p^2$ ) and family heritability ( $h_f^2$ ) of all tested traits ranged from 0.026 to 0.636 and 0.148 to 0.578, respectively. Stem volume showed the highest genetic and phenotypic coefficients of variation (GCV, PCV) among all traits at each site. The diameter at breast height (DBH), tree height (H), height to live crown base (HCB) and CW were strongly correlated with other traits, and were also under relatively higher genetic control and had stronger discriminating ability on genotype differences. Through biplot analyses of main genotypic effect and  $G \times E$  interaction (GGE) for these traits, five provenances and 20 families were screened out with selection ratio of 20 % and 10% at provenance and family level, respectively. The genetic and realized gains at provenance level ranged from 0.25% to 2.01% and 2.43% to 14.84%, and those at family level ranged from 0.85% to 21.22% and 5.76% to 36.71%, respectively. The findings lay a foundation for subsequent study on genetic improvement and breeding of this species, and application of the superior provenances and families will greatly increase the productivity of its plantations in practice.

**Keywords:** *Betula alnoides*; genetic variation; genotypes by environments interaction; genotypic correlation; heritability

## 1. Introduction

*Betula alnoides* Buch.-Ham. ex D. Don is a multiple-ploidy tree species in the genus *Betula*, family Betulaceae, and is indigenous to the warm subtropical and tropical regions in Southeast Asia and southern China [1]. *B. alnoides* is a fast-growing valuable tree species, its wood is widely used for floor and furniture-making as well as house decoration due to its beautiful texture, middle density, and excellent processing characteristics [2], and its barks are of medicinal application due to their

anti-inflammatory and lipid-lowering properties [3,4]. In addition, *B. alnoides* is one of the pioneer tree species in evergreen broad-leaved secondary forests and its ecological values were also well recognized in water conservation, maintenance of biodiversity and soil fertility, and carbon sequestration [5]. This species has a wide adaptability to soil types, altitudes and climate conditions [6], and is becoming more and more popular in plantation forestry in southern China. Up to now, more than 150,000 ha of *B. alnoides* plantations have been established in Yunnan, Guangxi, Guangdong, and Fujian provinces [7]. However, heavy differentiation in growth and quality traits are usually observed in the practice due to the fact that plantations are mostly established with seedlings from unselected germplasms of this species. This leads to low productivity of the plantations. Consequently, the excellent germplasms have become in urgent need of plantation forestry of *B. alnoides*.

It is well-known that provenance or family tests are the foundation of selective breeding. Since 2000, many trial plantations have been established with provenances and families from natural distribution areas of Yunnan and Guangxi in order to screen out the excellent germplasm and broaden plantation scale of *B. alnoides* in southern China, which provide good support in genetic improvement and breeding of this species [5]. Based on early evaluations, many superior provenances and families were separately selected at each site in Yunnan, Guangxi, and Fujian [8–11]. These previous studies showed that the excellent provenances at one site might not maintain their good performance in other sites, which severely limits their application area. This difference may be attributed to the genotype by environment ( $G \times E$ ) interactions.

Genetic parameters like heritability, genetic correlation and genetic gain of traits are often used as a considerable basis for determining selection strategies and predicting selection effects, but  $G \times E$  interaction usually affects the estimation of heritability and genetic gain in the breeding program of a tree species [12].  $G \times E$  interaction also reflects the adaptability of tree species to environmental factors such as air temperature, rainfall, soil, pests, etc. [13], and it has been reported for growth and quality traits as well as wood property of many important timber species. For example, significant  $G \times E$  interactions were observed in tree height, diameter at breast height and volume for *Betula pendula* Roth, *Betula kirghisorum* Sav.-Rydzg, *Betula pubescens* Ehrh., *Pinus densiflora* Sieb. et Zucc. and *Pinus taeda* L. [14–16], in branchiness, straightness and wood density for *Eucalyptus regnans* F. Muell., *Pinus radiata* D. Don and *Eucalyptus grandis* W. Hill ex Maiden [17–19]. For *B. alnoides*, it is also essential to explain the pattern and range of  $G \times E$  interaction by combined trials in multiple sites. This is useful to select germplasms which stably perform well across sites.

In the present study, four trial plantations of *B. alnoides* provenances and families are involved, which were established in Mengla and Changning, Yunnan, Pingxiang, Guangxi and Hua'an, Fujian, respectively. Parts of these plantations were evaluated in the previous studies when one to four years old, and it was indicated that the variations among provenances and families were unstable and increased with age [9]. Now the ages of these plantations are 10 to 15 years old. The mean annual increments of tree height and diameter at breast height are the highest nearly in 15 years old which is about half a rotation and is also the appropriate age for combination test at multiple sites in terms of excellent germplasm selection [5]. The objectives of the present study were thus to (1) describe the variation of growth and quality traits in different sites; (2) estimate the genetic variation and heritability for these traits, and examine the genetic relationship among traits; (3) reveal the genotype by environment interactions for these traits; and (4) select the superior and stable provenances and families across sites. The findings will be helpful to improve the understanding of  $G \times E$  interaction and promote the process of genetic improvement of this species.

## 2. Materials and methods

### 2.1. Materials

The Provenance-family trials of *B. alnoides* were conducted at four sites: Mengla, Yunnan; Pingxiang, Guangxi; Hua'an, Fujian; and Changning, Yunnan, where 400, 386, 280 and 250 half-sib

families of all 25 provenances were involved, respectively. Only 199 half-sib families of 25 provenances existed in all four trials and were mainly analyzed in the present study. All the germplasms were collected from Yunnan and Guangxi, China. Table 1 shows the information of the four trials, and Table A1 shows the localities of 25 provenances. Randomized complete block design was used in each trial with single tree plots and 12 to 19 replicates. The seedlings were planted with 2 m × 3 m spacing.

**Table 1.** Locations, climatic conditions, and tree age of four trials.

Site	Latitude N	Longitude E	Altitude (m)	Mean Annual Air Temperature (°C)	Rainfall (mm·Year <sup>−1</sup> )	Tree Age (Year)
Mengla, Yunnan	21°31′39″	101°29′23″	1161	21.70	1350	15
Pingxiang, Guangxi	22°01′59″	106°51′01″	550	20.20	1350	15
Hua'an, Fujian	24°56′19″	117°30′59″	275	20.80	1643	14
Changning, Yunnan	24°49′23″	99°56′54″	1250	18.50	1260	10

## 2.2. Measurement of Tree Growth and Quality Traits

Stem diameter at breast height (DBH) was measured using diameter tape with a precision of 0.1cm, tree height and height to live crown base (HCB) were measured using Vertex IV Altimeter (Haglöf Sweden AB, Västernorrland, Sverige) with a precision of 0.1 m, and crown width (CW) was measured using sliding staff with a precision of 0.1m. Stem volume (VOL) was calculated with the following equation [20]:

$$VOL = \frac{0.45}{4} \times \pi D_{1.3}^2 H \quad (1)$$

where  $D_{1.3}$  and  $H$  were stem diameter at breast height (DBH) and tree height, respectively.

Quality traits including stem form (SF), crown shape (CS) and branchiness (BRA) were evaluated and standardized according to Wang et al. [21].

## 2.3. Statistical Models and Genetic Analysis

Variance analyses (ANOVA) and Duncan's multiple range tests were performed to estimate the variance of traits using univariate restricted maximum likelihood (REML) model in the Genstat 18th software. The following linear mixed models were used for individual site analysis (2) and multi-site analysis (3) at provenance level, respectively [22,23]:

$$y_{ijk} = \mu + B_i + P_j + PB_{ij} + e_{ijk} \quad (2)$$

$$y_{ijkl} = \mu + S_i + B(S)_{ij} + P_k + PS_{ik} + PB(S)_{ijk} + PYS_{ikl} + PYB(S)_{ijkl} + e_{ijklm} \quad (3)$$

where  $y$  is the observations of traits,  $\mu$  is the overall mean,  $S$  and  $B(S)$  are the fixed effects of site and block within site,  $P$ ,  $PS$ ,  $PB(S)$ ,  $PYS$  and  $PYB(S)$  are the random effects of provenance, and provenance-site, provenance-block within site, provenance-year-site, provenance-year-block within site interactions, respectively, and  $e$  is residual error. The fixed effects of year and site-year and year-block within site interactions and the random effects of provenance-year interaction were excluded from the models (3) due to non-significant difference.

Provenance repeatability ( $h_p^2$ ) and variance components of phenotypic ( $\sigma_{ph}^2$ ) in individual and joint site analyses were estimated using Equations (4) and (6) as well as (5) and (7), respectively. Phenotypic coefficient of variation (PCV, %) and genetic coefficient of variation (GCV, %) were calculated with Equations (8) and (9), respectively [24]:

$$h_p^2 = \frac{\sigma_p^2}{\sigma_p^2 + \frac{\sigma_{pb}^2}{n_s n_b} + \frac{\sigma_e^2}{n_s n_b}} \quad (4)$$

$$h_p^2 = \frac{\sigma_p^2}{\sigma_p^2 + \frac{\sigma_{ps}^2}{n_s} + \frac{\sigma_{pb}^2}{n_s n_b} + \frac{\sigma_{pys}^2}{n_s n_y} + \frac{\sigma_{pyb}^2}{n_s n_b n_y} + \frac{\sigma_e^2}{n_s n_b n_y}} \quad (5)$$

$$\sigma_{ph}^2 = \sigma_p^2 + \sigma_{pb}^2 + \sigma_e^2 \quad (6)$$

$$\sigma_{ph}^2 = \sigma_p^2 + \sigma_{ps}^2 + \sigma_{pb}^2 + \sigma_{pys}^2 + \sigma_{pyb}^2 + \sigma_e^2 \quad (7)$$

$$GCV = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100\% \quad (8)$$

$$PCV = \frac{\sqrt{\sigma_{ph}^2}}{\bar{X}} \times 100\% \quad (9)$$

where  $\sigma_p^2$ ,  $\sigma_{ps}^2$ ,  $\sigma_{pb}^2$ ,  $\sigma_{pys}^2$ ,  $\sigma_{pyb}^2$ ,  $\sigma_e^2$ ,  $\bar{X}$  are the estimates of variance components for provenance, and provenance-site, provenance-block within site, provenance-year-site and provenance-year-block within site interactions, residual error and mean of traits; and  $n_s$ ,  $n_y$ ,  $n_b$  are the number of sites, year and the harmonic mean of blocks within sites.

Family models for individual site analysis (10) and multiple sites joint analysis (11) were listed in the following [22,23]:

$$y_{ijk} = \mu + B_i + P_j + PB_{ij} + F(P)_{jk} + F(P)B_{ijk} + e_{ijkl} \quad (10)$$

$$y_{ijk} = \mu + S_i + B(S)_{ij} + P_k + PS_{ik} + PB(S)_{ijk} + PYS_{ikl} + PYB(S)_{ijkl} + F(P)_{km} + F(P)Y_{klm} + F(P)YS_{iklm} + F(P)YB(S)_{ijklm} + e_{ijklmn}, \quad (11)$$

where  $y$  is the observations of traits;  $\mu$  is the overall mean;  $S$  and  $B(S)$  are the fixed effects of site and block within site;  $P$ ,  $F(P)$ ,  $PS$ ,  $PB(S)$  and  $F(P)S$  are the random effects of provenance, family, and provenance-site, provenance-block within site and family-site interactions, respectively;  $F(P)B(S)$ ,  $PYS$ ,  $PYB(S)$ ,  $F(P)YS$  and  $F(P)YB(S)$  are the random effects of family-block within site, provenance-year-site, provenance-year-block within site, family-year-site and family-year-block within site interactions; and  $e$  is residual error.

The fixed effects of year, and site-year and year-block within site interactions as well as the random effects of provenance-year, family-site and family-block within site interactions were excluded from the models due to non-significant difference.

Family heritability ( $h_f^2$ ) in individual site and multi-site analysis were estimated with the following Equations (12) and (13), respectively [24]:

$$h_f^2 = \frac{\sigma_f^2}{\sigma_f^2 + \frac{\sigma_{fb}^2}{n_s n_b} + \frac{\sigma_e^2}{n_s n_b}} \quad (12)$$

$$h_f^2 = \frac{\sigma_f^2}{\sigma_f^2 + \frac{\sigma_{fy}^2}{n_y} + \frac{\sigma_{fys}^2}{n_s n_y} + \frac{\sigma_{fyb}^2}{n_s n_b n_y} + \frac{\sigma_e^2}{n_s n_b n_y}} \quad (13)$$

where  $\sigma_f^2$ ,  $\sigma_{fy}^2$ ,  $\sigma_{fys}^2$ ,  $\sigma_{fyb}^2$ ,  $\sigma_e^2$  are variance components of family, and family-year, family-year-site and family-year-block within site interactions, and residual error of trait, respectively; and  $n_s$ ,  $n_y$ ,  $n_b$  are the number of sites, year and the harmonic mean of blocks within sites.

Genetic correlations ( $r_G$ ) among traits were calculated using the Equation (14) [25]:

$$r_G = \frac{Cov_G(x, y)}{\sqrt{\sigma_G^2(x) \times \sigma_G^2(y)}} \quad (14)$$

where  $Cov_G(x, y)$  is the genotypic co-variances between trait  $x$  and  $y$ ;  $\sigma_G^2(x)$  and  $\sigma_G^2(y)$  are the genotypic variances of trait  $x$  and  $y$ .

The breeding values of provenances and families were estimated using the method of best linear unbiased prediction (BLUP), and were then used in biplot analysis for main genotypic effects and  $G \times E$  interaction (GGE) by Genstat 18th software [26]. As described in detail, the breeding values of 25 provenances or 199 families in four sites could be displayed by a rank-two matrix. After the main environmental effects were removed through ANOVA, the main genotypic effect ( $G$ ) and interaction effect ( $G \times E$ ) were retained in the new matrix. The matrix was then decomposed into its component matrices using the method of singular-value decomposition. The first two principal components (PC1 and PC2) that explained about 85% of the total variation were used to build the biplot [27].

The superiority of provenances and families could be intuitively seen in the biplot graph according to their position in concentric circles, smaller concentric circle referred to better superiority. The superiority could also be ranked by superiority coefficients, smaller coefficients represented better superiority [12]. Based on the ranks of superiority, the desired provenances were then selected with the ratio being 20%, and the excellent families were done with the ratio being 10% regardless of provenances.

Genetic gains ( $\Delta G$ ) and realized gains ( $\Delta G_r$ ) were calculated as follows [25]:

$$\Delta G = \frac{ih_i^2 \sqrt{\sigma^2}}{\bar{X}} \times 100\% \quad (15)$$

$$\Delta G_r = \frac{\bar{x} - \bar{X}}{\bar{X}} \times 100\% \quad (16)$$

where  $i$  is selection intensity (the selection rate is 20% and 10% at levels of provenance and family, respectively);  $h_i^2$  is heritability of trait;  $\sqrt{\sigma^2}$  is standard deviation;  $\bar{x}$  is mean of traits for selected provenances or families; and  $\bar{X}$  is mean of traits for all provenances or families.

### 3. Results

#### 3.1. Variation of Growth and Quality Traits among Sites and Provenances

Table 2 showed the means and ranges of growth and quality traits in each of the four trials. The trees at Mengla site showed the highest levels in the mean annual increment of tree height (MAH), crown width (CW) and branchiness (BRA), which indicated that Mengla was the most suitable for *B. alnoides* among the four sites. The mean annual increment of diameter at breast height (MABDH), mean annual increment of tree height (MAH), rate of height to live crown base to tree height (HCB·Height<sup>-1</sup>), CW and mean annual increment of stem volume (MAVOL) were the lowest at Changning site. The trees at Hua'an site had the highest MADBH and MAVOL, but had the lowest stem form (SF) and BRA.

**Table 2.** Growth and quality performance of *Betula alnoids* at four trial sites.

Sites	Values	MADBH (cm·Year <sup>-1</sup> )	MAH (m·Year <sup>-1</sup> )	HCB-Height <sup>-1</sup>	CW (m)	MAVOL (m <sup>3</sup> ·Year <sup>-1</sup> )	SF	CS	BRA
Mengla	Mean (SE)	1.34 (0.01) b	1.22 (0.01) a	0.57 (0.00) b	4.71 (0.04) a	0.0196 (0.0003) a	0.63 (0.02) c	0.65 (0.01)	0.77 (0.01) a
	Range	0.3–2.5	0.4–1.8	0.1–0.9	0.6–9.9	0.000–0.069	0.1–1.0	0.1–1.0	0.1–1.0
Pingxiang	Mean (SE)	1.04 (0.01) c	0.94 (0.01) c	0.61 (0.01) a	4.49 (0.06) b	0.0098 (0.0004) b	0.69 (0.02) b	0.64 (0.01)	0.75 (0.01) ab
	Range	0.3–2.5	0.4–1.9	0.2–0.9	0.7–9.2	0.000–0.071	0.1–1.0	0.1–1.0	0.1–1.0
Hua'an	Mean (SE)	1.50 (0.01) a	1.18 (0.01) b	0.56 (0.00) c	3.09 (0.05) c	0.0204 (0.0003) a	0.52 (0.01) d	0.64 (0.01)	0.65 (0.01) c
	Range	0.3–2.5	0.2–1.9	0.2–1.4	0.5–7.5	0.000–0.078	0.1–1.0	0.1–1.0	0.1–1.0
Changning	Mean (SE)	0.78 (0.01) d	0.83 (0.01) d	0.51 (0.01) d	2.34 (0.07) d	0.0020 (0.0005) c	0.77 (0.03) a	0.64 (0.02)	0.73 (0.01) b
	Range	0.3–2.4	0.4–1.9	0.2–0.9	0.6–6.7	0.000–0.072	0.1–1.0	0.1–1.0	0.1–1.0

**Notes:** MADBH, mean annual increment of diameter at breast height; MAH, mean annual increment of tree height; HCB-Height<sup>-1</sup>, rate of height to live crown base to tree height; CW, crown width; MAVOL, mean annual increment of stem volume; SF, stem form; CS, crown shape; BRA, branchiness. Means with standard error (SE) in parenthesis were of significant difference at 0.05 level according to Duncan's multiple range tests if followed by wholly different small letters in the same column.

Performance of growth and quality traits of 25 provenances were shown in Table 3, which were presented as means of all four sites for each trait. Significant differences were observed in all traits among provenances. MADBH, MAH, CW and MAVOL of provenance A were nearly the lowest in all 25 provenances, but its SF and BRA were the highest. The highest MAH and CW were observed in provenance P.

The growth and quality performance of 25 provenances differed among four sites (see Tables A2–A5). The lowest MAH, SF, CS, and BRA were observed in provenance O at the Mengla site. MADBH, MAH, MAVOL showed the best performance in provenance V, while the poorest in provenance L at Pingxiang site. At Hua'an and Changning sites, the highest MADBH and MAVOL were seen in provenance P, and the lowest MAH, MAVOL and SF in provenance S.

### 3.2. Genetic Variance, Heritability, and Genotypic Correlation

It was shown from the estimation of variances and genetic parameters for all tested traits at each site (Table 4) that provenance effects were significant in most of the traits at four sites except SF and BRA at Pingxiang site as well as CS and BRA at Changning site. While significant family effects were mainly observed in growth traits at Mengla and Pingxiang sites. As a whole, the highest provenance repeatability ( $h_p^2$ ) of all tested traits were observed at Hua'an site (mean: 0.332), and the highest family heritability ( $h_f^2$ ) at Mengla site (mean: 0.164). The genetic (GCV) and phenotypic (PCV) coefficient for variation of all traits at Hua'an site ranged from 3.15% to 15.93% and 20.30% to 70.44%, with their means (9.83% and 44.21%) being the highest in four sites. Volume and quality traits showed higher PCV than most of the other growth traits at each site.

The variances of sources, variance components, and genetic parameters were estimated at four sites together. Significant differences were observed only in CW and CS for family-site interaction, while for other sources of variances, significant differences were seen in most of the traits (Table 5).  $h_p^2$  and  $h_f^2$  of all traits ranged from 0.026 to 0.636 and 0.148 to 0.578, respectively (Table 6).  $h_p^2$  of HCB, SF and BRA showed higher levels than that of other traits.  $h_f^2$  of growth traits were higher than that of quality traits. GCV and PCV of variation ranged from 0.58% to 5.99% and 21.09% to 66.78%, respectively. On the whole, GCV and PCV for quality traits were higher than those for most growth traits.

The genotypic correlation coefficients among all sorts of traits were shown in Table 7. There were moderate to strong positive genotypic correlations between DBH, height, and volume. Strong positive genotypic correlations were observed between SF, HCB, and BRA, while strong negative correlations were seen between these traits and CW.

**Table 3.** Growth and quality performance for 25 provenances of *Betula alnoids*.

Provenances	MADBH (cm·Year <sup>-1</sup> )	MAH (m·Year <sup>-1</sup> )	HCB-Height <sup>-1</sup>	CW (m)	MAVOL (m <sup>3</sup> ·Year <sup>-1</sup> )	SF	CS	BRA
A	1.04 (0.05) j	1.02 (0.05) f	0.60 (0.02) ab	3.16 (0.25) c	0.0096 (0.0013) f	0.77 (0.04) a	0.66 (0.05) bc	0.83 (0.04) a
B	1.29 (0.05) abcde	1.08 (0.04) bcdef	0.57 (0.02) bcdefgh	3.80 (0.23) ab	0.0158 (0.0017) abcde	0.67 (0.04) bcde	0.66 (0.04) bc	0.73 (0.04) bcdef
C	1.19 (0.03) bcdefghi	1.12 (0.02) abcde	0.61 (0.01) a	3.68 (0.14) ab	0.0148 (0.0011) abcde	0.63 (0.03) cdefg	0.63 (0.03) bc	0.77 (0.02) abcdef
D	1.12 (0.04) ij	1.04 (0.03) ef	0.59 (0.01) abcde	3.72 (0.18) ab	0.0122 (0.0011) def	0.68 (0.03) bcde	0.67 (0.03) bc	0.76 (0.03) bcdef
E	1.27 (0.03) abcdefg	1.10 (0.02) bcdef	0.55 (0.01) defgh	3.86 (0.13) ab	0.0151 (0.0008) abcde	0.62 (0.03) defg	0.71 (0.02) b	0.67 (0.02) def
F	1.15 (0.06) fghij	1.05 (0.04) def	0.58 (0.02) bcdef	3.28 (0.22) bc	0.0133 (0.0018) cdef	0.75 (0.04) abc	0.63 (0.04) bc	0.82 (0.03) ab
G	1.18 (0.07) cdefghi	1.13 (0.05) abcde	0.60 (0.02) abcd	3.49 (0.25) abc	0.0183 (0.0023) a	0.70 (0.05) abcd	0.69 (0.05) bc	0.80 (0.04) ab
H	1.25 (0.04) abcdefgh	1.11 (0.03) abcde	0.58 (0.01) bcdefg	3.97 (0.18) a	0.0156 (0.0011) abcde	0.69 (0.03) bcde	0.66 (0.03) bc	0.77 (0.03) abcde
I	1.20 (0.05) bcdefghi	1.14 (0.03) abc	0.58 (0.01) abcdef	3.94 (0.18) a	0.0166 (0.0014) abcd	0.67 (0.03) bcdef	0.64 (0.04) bc	0.74 (0.03) bcdef
J	1.21 (0.03) bcdefghi	1.11 (0.02) abcde	0.60 (0.01) ab	3.84 (0.15) ab	0.0150 (0.001) abcde	0.64 (0.03) bcdefg	0.58 (0.03) c	0.79 (0.03) abc
K	1.31 (0.03) abcde	1.15 (0.02) ab	0.59 (0.01) abcde	3.99 (0.15) a	0.0173 (0.0009) ab	0.66 (0.03) bcdefg	0.65 (0.03) bc	0.78 (0.02) abcd
L	1.15 (0.04) fghij	1.07 (0.03) cdef	0.57 (0.01) bcdefgh	3.78 (0.15) ab	0.0141 (0.0012) abcde	0.75 (0.02) ab	0.62 (0.03) bc	0.79 (0.03) abc
M	1.17 (0.04) efghi	1.08 (0.03) bcdef	0.60 (0.01) abc	3.35 (0.18) abc	0.0137 (0.0012) bcdef	0.69 (0.03) bcde	0.59 (0.04) bc	0.78 (0.03) abcde
N	1.12 (0.04) hij	1.03 (0.03) ef	0.55 (0.01) cdefgh	3.72 (0.15) ab	0.0127 (0.0013) cdef	0.61 (0.03) defg	0.62 (0.03) bc	0.71 (0.03) bcdef
O	1.18 (0.03) defghi	1.06 (0.03) def	0.57 (0.01) bcdefgh	3.61 (0.14) ab	0.0128 (0.0008) cdef	0.60 (0.030) defgh	0.61 (0.030) bc	0.67 (0.03) cdef
P	1.33 (0.04) abc	1.16 (0.02) a	0.53 (0.01) h	3.91 (0.14) a	0.0186 (0.0013) a	0.66 (0.026) bcdefg	0.71 (0.03) b	0.69 (0.03) cdef
Q	1.25 (0.05) abcdefgh	1.07 (0.03) bcdef	0.53 (0.02) h	3.90 (0.20) ab	0.0140 (0.0013) bcdef	0.59 (0.04) efgh	0.86 (0.03) a	0.66 (0.05) ef
R	1.33 (0.03) ab	1.11 (0.02) abcde	0.53 (0.01) gh	3.85 (0.12) ab	0.0175 (0.0009) ab	0.58 (0.02) efgh	0.67 (0.02) bc	0.66 (0.02) f
S	1.15 (0.04) ghij	1.01 (0.04) f	0.57 (0.02) bcdefg	3.21 (0.21) bc	0.0116 (0.0011) ef	0.49 (0.05) h	0.64 (0.04) bc	0.70 (0.05) bcdef
T	1.26 (0.03) abcdefg	1.08 (0.02) bcdef	0.55 (0.01) efgh	3.61 (0.14) abc	0.0145 (0.0009) abcde	0.55 (0.03) fgh	0.64 (0.03) bc	0.67 (0.03) cdef
U	1.23 (0.03) bcdefgh	1.07 (0.02) bcdef	0.55 (0.01) efgh	3.76 (0.11) ab	0.0150 (0.0008) abcde	0.59 (0.02) defgh	0.65 (0.02) bc	0.66 (0.02) ef
V	1.28 (0.04) abcdef	1.07 (0.03) bcdef	0.54 (0.01) fgh	3.74 (0.18) ab	0.0149 (0.0011) abcde	0.63 (0.03) bcdefg	0.71 (0.03) bc	0.73 (0.03) bcdef
W	1.38 (0.02) a	1.12 (0.01) abcde	0.56 (0.01) cdefgh	3.92 (0.09) a	0.0180 (0.0007) ab	0.54 (0.02) gh	0.66 (0.02) bc	0.66 (0.02) ef
X	1.20 (0.03) bcdefghi	1.04 (0.02) def	0.54 (0.01) gh	3.72 (0.12) ab	0.0140 (0.0008) bcdef	0.62 (0.02) cdefg	0.62 (0.02) bc	0.67 (0.02) ef
Y	1.31 (0.02) abcd	1.13 (0.02) abcd	0.56 (0.01) bcdefgh	3.99 (0.10) a	0.0166 (0.0007) abc	0.60 (0.02) defg	0.71 (0.02) b	0.74 (0.02) bcdef
Means	1.25 (0.01)	1.09 (0.01)	0.56 (0.00)	3.78 (0.03)	0.0154 (0.0002)	0.62 (0.01)	0.66 (0.01)	0.72 (0.01)

**Notes:** A, Mengla; B, Yuanyang; C, Mojiang; D, Jinghong; E, Xichou; F, Zhenyuan; G, Tengchong; H, Jinggu; I, Ruili; J, Fengqing; K, Pingbian; L, Jiangcheng; M, Shuangjiang; N, Lancang; O, Lingyun; P, Longzhou; Q, Donglan; R, Tianlin; S, Debao; T, Tiane; U, Pingguo; V, Baise; W, Tianyang; X, Jingxi; Y, Napo; MADBH, mean annual increment of diameter at breast height; MAH, mean annual increment of tree height; HCB-Height<sup>-1</sup>, rate of height to live crown base to tree height; CW, crown width; MAVOL, mean annual increment of stem volume; SF, stem form; CS, crown shape; BRA, branchiness. Means with standard error in parenthesis were of significant difference at 0.05 level according to Duncan's multiple range tests if followed by wholly different small letters in the same column.



**Table 4.** Estimates of variances ( $\sigma_p^2$ ,  $\sigma_{pb}^2$ ,  $\sigma_f^2$ ,  $\sigma_{fb}^2$ ,  $\sigma_e^2$ ,  $\sigma_{ph}^2$ ) for provenance, provenance-block within site, family, family-block within site, residual error and phenotypic variance, provenance repeatability ( $h_p^2$ ), family heritability ( $h_f^2$ ), co-efficient of variation at genetic and phenotypic level (genetic coefficient of variation (GCV), phenotypic coefficient of variation (PCV)) for tested traits at each site.

Sites	Traits	F Value of $\sigma_p^2$	F Value of $\sigma_f^2$	$\sigma_p^2$	$\sigma_{pb}^2$	$\sigma_e^2$	$h_p^2$	$\sigma_f^2$	$\sigma_{fb}^2$	$\sigma_e^2$	$h_f^2$	$\sigma_{ph}^2$	GCV%	PCV%
Mengla	DBH	2.50 ***	1.30 *	0.647	0.287	23.530	0.230 (0.096)	1.297	NE	22.250	0.226 (0.079)	24.464	4.00	24.58
	Height	2.74 ***	1.34 **	0.392	0.283	12.560	0.252 (0.100)	0.592	NE	11.960	0.198 (0.084)	13.236	3.40	19.75
	HCB	4.03 ***	1.22 *	0.336	0.893	6.955	0.320 (0.114)	0.355	4.165	2.475	0.211 (0.084)	8.184	5.54	27.37
	CW	2.27 ***	1.29 *	0.042	0.102	2.191	0.169 (0.098)	0.127	0.833	1.232	0.235 (0.079)	2.335	4.35	32.29
	Volume	2.60 ***	1.36 **	0.001	0.001	0.030	0.236 (0.098)	0.002	NE	0.028	0.246 (0.079)	0.031	9.83	59.43
	SF	2.54 ***	1.20 ns	0.002	0.006	0.089	0.199 (0.108)	0.003	NE	0.086	0.160 (0.085)	0.097	7.32	49.34
	CS	2.62 ***	1.10 ns	0.003	0.008	0.095	0.211 (0.109)	0.001	0.004	0.091	0.029 (0.095)	0.105	7.62	49.48
	BRA	2.18 ***	0.86 ns	0.002	0.005	0.091	0.184 (0.105)	0.000	NE	0.091	0.006 (0.064)	0.098	5.73	40.42
Pingxiang	DBH	8.69 ***	1.33 *	3.084	2.773	13.080	0.609 (0.094)	0.435	13.000	0.285	0.090 (0.109)	18.937	11.17	27.67
	Height	5.50 ***	1.25 ns	0.620	3.018	7.069	0.330 (0.147)	0.124	7.318	0.045	0.048 (0.121)	10.707	5.59	23.23
	HCB	3.11 ***	1.50 ***	0.044	0.997	2.531	0.091 (0.154)	0.012	2.489	0.095	0.014 (0.121)	3.572	2.52	22.62
	CW	4.46 ***	1.60 ***	0.230	0.479	2.616	0.373 (0.128)	0.093	2.409	0.183	0.098 (0.116)	3.325	10.66	40.52
	Volume	5.45 ***	1.12 ns	0.001	0.002	0.009	0.480 (0.117)	0.000	0.009	0.000	0.093 (0.109)	0.012	23.39	72.69
	SF	0.78 ns	0.98 ns	0.000	0.007	0.082	0.001 (0.092)	0.002	0.080	0.006	0.055 (0.101)	0.088	0.46	42.92
	CS	4.67 ***	1.59 ***	0.008	0.013	0.084	0.384 (0.127)	0.002	0.081	0.005	0.072 (0.112)	0.104	13.46	50.12
	BRA	1.44 ns	1.11 ns	0.001	0.009	0.079	0.057 (0.114)	0.000	0.080	0.004	0.003 (0.106)	0.089	3.45	39.82
Hua'an	DBH	3.60 ***	0.94 ns	1.120	1.080	21.080	0.336 (0.107)	0.020	2.239	18.950	0.004 (0.071)	23.280	5.01	22.85
	Height	2.50 ***	1.14 ns	0.270	0.815	10.140	0.197 (0.112)	0.274	0.475	9.445	0.099 (0.075)	11.224	3.15	20.30
	HCB	3.19 ***	1.18 ns	0.296	0.326	5.581	0.334 (0.112)	0.005	0.643	4.959	0.003 (0.078)	6.203	6.07	27.79
	CW	3.52 ***	0.94 ns	0.106	0.081	1.943	0.343 (0.107)	0.002	0.187	1.768	0.003 (0.076)	2.129	10.28	46.16
	Volume	4.01 ***	1.10 ns	0.002	0.001	0.026	0.363 (0.105)	0.000	0.002	0.024	0.028 (0.076)	0.029	13.76	59.23
	SF	2.54 ***	0.97 ns	0.005	0.000	0.121	0.275 (0.104)	0.000	0.011	0.111	0.001 (0.070)	0.126	13.48	70.44
	CS	4.83 ***	1.41 ***	0.011	NE	0.109	0.509 (0.097)	0.004	0.025	0.082	0.119 (0.078)	0.121	15.93	51.96
	BRA	3.25 ***	1.00 ns	0.005	0.008	0.108	0.294 (0.109)	0.000	0.015	0.094	0.014 (0.069)	0.121	10.97	54.90
Changning	DBH	2.86 ***	1.02 ns	0.215	0.130	2.835	0.567 (0.126)	0.042	0.710	2.097	0.057 (0.143)	3.180	6.01	23.08
	Height	1.83 *	0.97 ns	0.096	0.064	2.695	0.386 (0.168)	0.132	NE	2.577	0.170 (0.123)	2.855	3.74	20.36
	HCB	1.58 *	1.09 ns	0.010	0.137	1.270	0.108 (0.256)	0.065	0.201	1.003	0.178 (0.125)	1.416	2.31	28.18
	CW	1.99 **	1.38 *	0.027	NE	0.653	0.425 (0.153)	0.059	NE	0.601	0.282 (0.104)	0.680	6.94	34.98
	Volume	2.21 *	0.97 ns	0.000	0.000	0.000	0.460 (0.154)	0.000	0.000	0.000	0.081 (0.139)	0.000	13.16	61.93
	SF	2.21 ***	0.97 ns	0.000	0.003	0.068	0.060 (0.122)	0.000	0.001	0.065	0.002 (0.112)	0.071	2.06	34.87
	CS	0.93 ns	0.85 ns	0.000	0.002	0.116	0.027 (0.229)	0.000	0.022	0.094	0.001 (0.105)	0.118	2.09	52.92
	BRA	0.69 ns	1.15 ns	0.000	NE	0.090	0.019 (0.151)	0.003	NE	0.087	0.116 (0.121)	0.090	0.43	41.11

**Notes:** DBH, diameter at breast height; HCB, height to live crown base; CW, crown width; SF, stem form; CS, crown shape; BRA, branchiness. Features in parentheses were standard errors. \*\*\*  $p < 0.001$ ; \*\*  $0.001 < p < 0.01$ ; \*  $0.01 < p < 0.05$ ; ns indicates not significant, level of significance of effects. NE, not estimated and assumed to be zero.



**Table 5.** *F* values and significance levels for variance from different sources of all traits in combined variance analysis of four sites.

Traits	Site (3)	Block within Site (48)	Provenance (24)	Provenance-Site (72)	Provenance-Block within Site (801)	Family (199)	Family-Site (388)
DBH	1517.82 ***	6.25 ***	3.71 ***	3.27 ***	1.10 *	1.35 **	0.93 ns
Height	1560.85 ***	6.98 ***	2.73 ***	2.66 ***	1.30 ***	1.46 ***	1.01 ns
HCB	1073.10 ***	13.06 ***	5.16 ***	1.90 ***	1.40 ***	1.39 ***	0.96 ns
CW	549.52 ***	5.72 ***	3.01 ***	3.03 ***	1.30 ***	1.41 ***	1.24 **
Volume	625.06 ***	4.93 ***	3.17 ***	2.60 ***	1.02 ns	1.39 ***	0.88 ns
SF	111.01 ***	6.12 ***	3.23 ***	1.20 ns	1.10 ns	1.16 ns	0.92 ns
CS	1.01 ns	6.22 ***	2.88 ***	3.06 ***	1.23 ***	1.34 **	1.24 **
BRA	45.03 ***	4.15 ***	3.45 ***	1.37 *	1.20 ***	1.05 ns	0.89 ns

**Notes:** DBH, diameter at breast height; HCB, height to live crown base; CW, crown width; SF, stem form; CS, crown shape; BRA, branchiness. The number in parentheses is the degree of freedom. \*\*\*  $p < 0.001$ ; \*\*  $0.001 < p < 0.01$ ; \*  $0.01 < p < 0.05$ ; ns indicates not significant, level of significance of effects.

**Table 6.** Estimates of variances ( $\sigma_p^2$ ,  $\sigma_{ps}^2$ ,  $\sigma_{pb}^2$ ,  $\sigma_{pys}^2$ ,  $\sigma_{pyb}^2$ ,  $\sigma_f^2$ ,  $\sigma_{fy}^2$ ,  $\sigma_{fys}^2$ ,  $\sigma_{fyb}^2$ ,  $\sigma_e^2$ ,  $\sigma_{ph}^2$ ) for provenance, provenance-site, provenance-block within site, provenance-year-site, provenance-year-block within site, family, family-year, family-year-site, family-year-block within site, residual error and phenotypic variance, provenance repeatability ( $h_p^2$ ), family heritability ( $h_f^2$ ), coefficient of variation at genetic and phenotypic level (GCV, PCV) for various traits in combined analysis of four sites.

Random Effect	DBH	Height	HCB	CW	Volume	SF	CS	BRA
$\sigma_p^2$	0.080	0.008	0.091	0.007	0.000	0.001	0.000	0.001
$\sigma_{ps}^2$	NE	NE	0.099	NE	0.001	0.001	0.005	NE
$\sigma_{pb}^2$	NE	0.885	NE	0.136	0.001	NE	0.005	NE
$\sigma_{pys}^2$	1.060	0.349	NE	0.085	NE	NE	NE	0.001
$\sigma_{pyb}^2$	0.900	NE	0.574	NE	NE	0.004	NE	0.006
$\sigma_e^2$	17.590	9.225	4.816	1.948	0.020	0.095	0.102	0.094
$h_p^2$	0.276	0.066	0.602	0.230	0.026	0.636	0.123	0.634
	(0.581)	(0.043)	(0.160)	(0.396)	(0.037)	(0.147)	(0.114)	(0.115)
$\sigma_f^2$	0.193	0.147	0.112	0.029	0.001	0.001	0.000	0.000
$\sigma_{fy}^2$	0.146	0.090	NE	NE	NE	NE	NE	NE
$\sigma_{fys}^2$	0.005	NE	0.041	0.037	NE	NE	0.002	NE
$\sigma_{fyb}^2$	1.393	4.730	1.133	0.558	0.002	0.018	0.035	0.022
$\sigma_e^2$	8.015	4.730	3.849	1.439	0.019	0.080	0.065	0.074
$h_f^2$	0.428	0.276	0.495	0.379	0.578	0.173	0.149	0.148
	(0.099)	(0.152)	(0.124)	(0.151)	(0.083)	(0.153)	(0.136)	(0.161)
$\sigma_{ph}^2$	19.630	10.467	5.580	2.176	0.022	0.100	0.112	0.102
GCV%	1.61	0.58	3.52	2.21	1.43	5.99	2.62	4.95
PCV%	25.19	21.09	27.60	39.02	66.78	51.06	50.75	44.39

**Notes:** DBH, diameter at breast height; HCB, height to live crown base; CW, crown width; SF, stem form; CS, crown shape; BRA, branchiness. The variance analysis at provenance level was estimated in all four sites, while that at family level was estimated in Mengla, Pingxiang and Huanan sites, and the values shown in parentheses were standard errors. NE, not estimated and assumed to be zero.

**Table 7.** Genotypic correlation coefficients among tested traits.

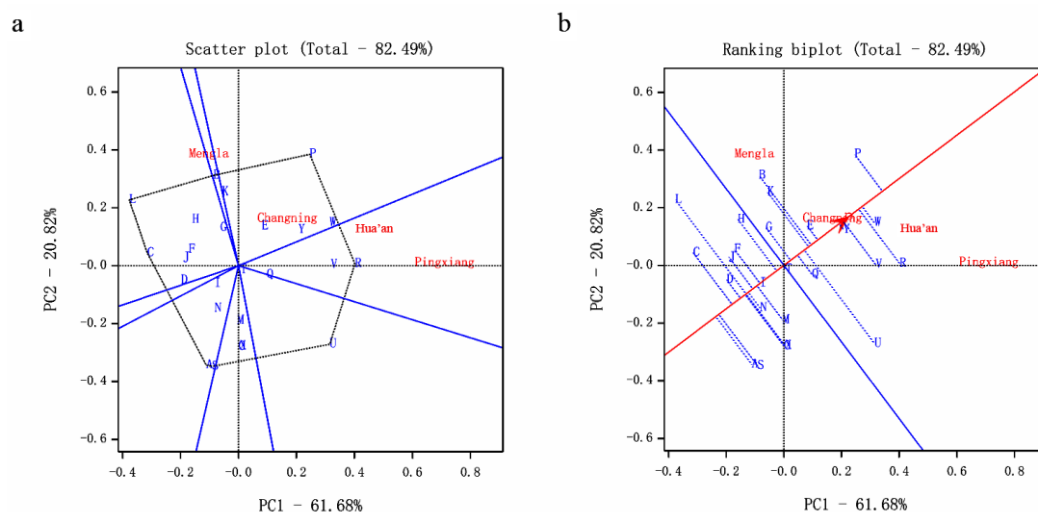
Traits	Height	HCB	CW	Volume	SF	CS	BRA
DBH	0.440 *	−0.386	0.765 **	0.732 **	−0.493 *	0.657 *	−0.520 *
Height		0.580 *	−0.117	0.521 *	0.386	0.028	0.430 *
HCB			−0.795 **	−0.088	0.705 **	−0.595 *	0.922 **
CW				0.482 *	−0.701 **	0.807 *	−0.776 **
Volume					0.006	0.547 *	−0.041
SF						−0.476 *	0.855 **
CS							−0.531 *

**Notes:** DBH, diameter at breast height; HCB, height to live crown base; CW, crown width; SF, stem form; CS, crown shape; BRA, branchiness. \*\*  $p < 0.01$ ; \*  $0.01 < p < 0.05$ , level of significance of correlation coefficients.

### 3.3. Genotype by Environment ( $G \times E$ ) Interaction

Provenance-site interactions were significant for all traits except SF, while family-site interaction was significant only for CW and CS (Table 5). There were significantly positive genetic correlations

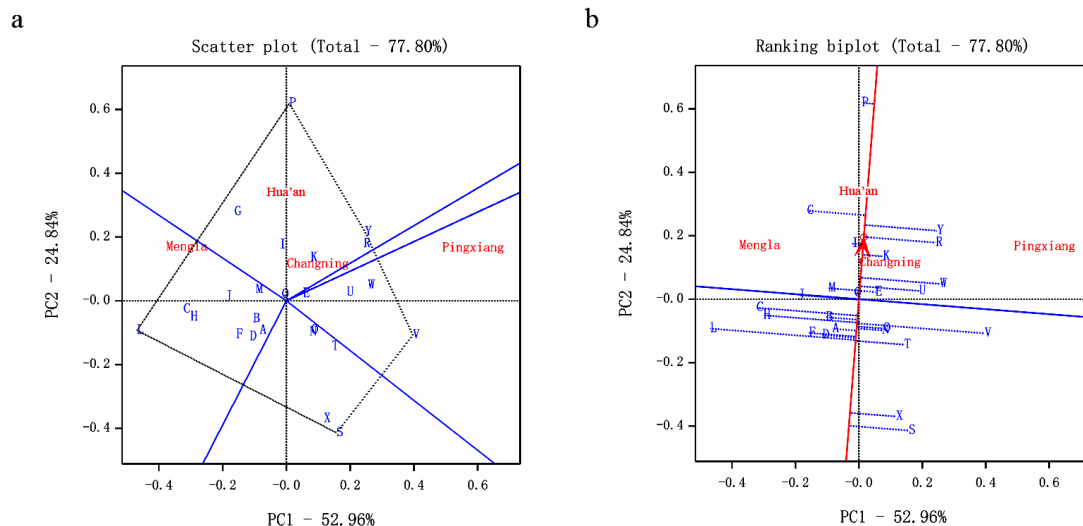
between DBH, Volume, CW and CS as well as between HCB, BRA and SF (Table 7). In addition, it was indicated from Figures 5 and 6 that abilities of DBH, HCB, height, and CW to discriminate provenances and families were stronger than those of other traits. DBH, HCB, and height were thus used to estimate provenance-site interactions by biplot analysis for main genotypic effects and GGE based on the predicted breeding values, and CW was used to estimate the family-site interactions. In the biplot of GGE, the cosine of the angle between the two environment segments indicated their correlations. Figure 1a showed the biplot of DBH for 25 provenances. There were sharp angles between segments of Changning, Hua'an and Pingxiang sites indicating positive correlations between them. Environment vector represented as an arrow vector joining center and co-ordinates of tested environment, its length indicated the discriminating ability on genotypic differences. Pingxiang showed the most discriminating ability for DBH in the present study. The biplot was divided into eight sectors in polygon view with provenances U, R, P, B, L, C, A and S as the vertexes. Vertex genotypes contributed overall most variation and demonstrated the best performance in each sector. From Figure 1a, it could be deduced that provenances L, B, and K were possible candidates for Mengla, and R and V for Pingxiang and Hua'an, and P for Changning based on DBH. In Figure 1b, the average environment axis (AEA) represented as an arrow vector joining the center and average coordinates of the tested site. Changning site was found to be the most representative environment for the growth of DBH as it has a smaller angle with AEA. The direction of AEA was the trend of the approximate mean for trait in all sites, it could be seen that provenance P showed the highest DBH, followed by W, R, V and Y, and the lowest DBH was observed in A and S. More variations in all four sites were observed in provenances L and U as it has longer perpendicular lines between their co-ordinates and AEX, and little variations for DBH were observed in provenances I, T and Y.



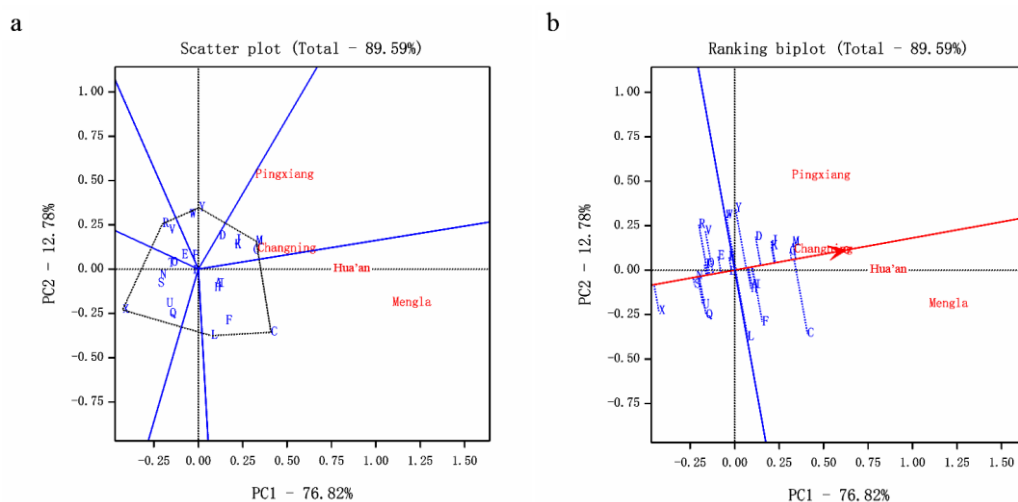
**Figure 1.** Biplot analysis based on diameter at breast height (DBH) data of 25 provenances. (a) Polygon view of genotype by environment (G×E) interaction (GGE) biplot—which is best for what, (b) genotypes of ranking provenances. A, Mengla; B, Yuanyang; C, Mojiang; D, Jinghong; E, Xichou; F, Zhenyuan; G, Tengchong; H, Jinggu; I, Ruili; J, Fengqing; K, Pingbian; L, Jiangcheng; M, Shuangjiang; N, Lancang; O, Lingyun; P, Longzhou; Q, Donglan; R, Tianlin; S, Debao; T, Tiane; U, Pingguo; V, Baise; W, Tianyang; X, Jingxi; Y, Napo.

Figure 2a showed the biplot for height, it was indicated that Changning and Hua'an had similar and higher environmental representativeness, and Pingxiang showed a higher ability to discriminate genotypic differences for tree height. Provenances L, C, and H were possible candidates for Mengla, and P for Changning and Hua'an, and V for Pingxiang based on height. Figure 2b showed that height of provenance P was the highest, followed by G, Y, R, I and K, and the lowest height was observed in provenances S and X. Little variations for height were observed in provenances G, I and P, and more variations were observed in L and V.

Figure 3a showed the biplot of HCB for 25 provenances. Provenance C, L, and F were possible candidates for Mengla and Hua'an, and M, G, J and K for Changning and Pingxiang based on HCB. It was indicated from Figure 3b that Changning and Hua'an had similar and higher environmental representativeness, and Mengla showed higher discriminating ability on genotypic differences. HCB of provenance M was the highest, followed by C, G, J, and K, and the lowest HCB was observed in provenance X. Little variations for height were observed in provenances N, S, L and G, and more variations in C and Y.



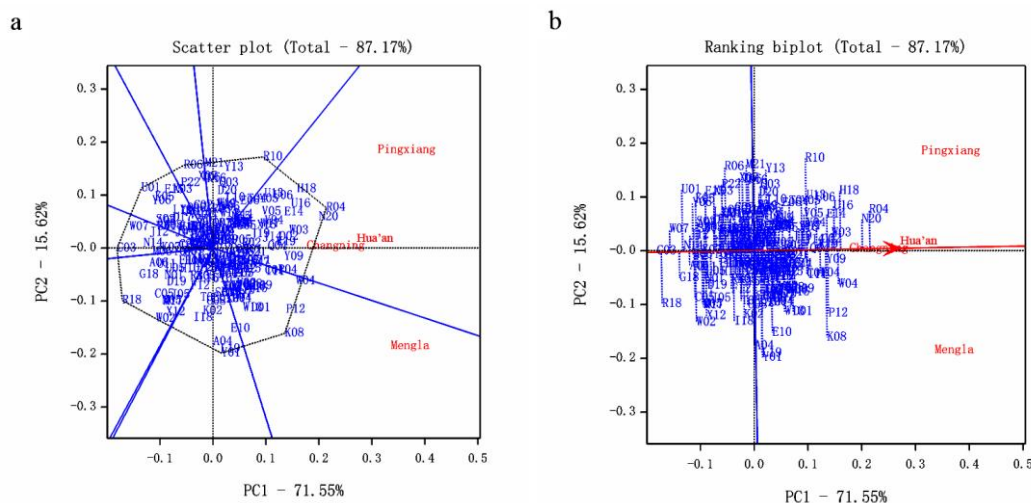
**Figure 2.** Biplot analysis based on the height of 25 provenances. (a) Polygon view of GGE biplot—which is best for what, (b) genotypes of ranking provenances. A, Mengla; B, Yuanyang; C, Mojiang; D, Jinghong; E, Xichou; F, Zhenyuan; G, Tengchong; H, Jinggu; I, Ruili; J, Fengqing; K, Pingbian; L, Jiangcheng; M, Shuangjiang; N, Lancang; O, Lingyun; P, Longzhou; Q, Donglan; R, Tianlin; S, Debao; T, Tiane; U, Pingguo; V, Baise; W, Tianyang; X, Jingxi; Y, Napo.



**Figure 3.** Biplot analysis based on HCB data of 25 provenances. (a) Polygon view of GGE biplot—which is best for what, (b) genotypes of ranking provenances. A, Mengla; B, Yuanyang; C, Mojiang; D, Jinghong; E, Xichou; F, Zhenyuan; G, Tengchong; H, Jinggu; I, Ruili; J, Fengqing; K, Pingbian; L, Jiangcheng; M, Shuangjiang; N, Lancang; O, Lingyun; P, Longzhou; Q, Donglan; R, Tianlin; S, Debao; T, Tiane; U, Pingguo; V, Baise; W, Tianyang; X, Jingxi; Y, Napo.

Figure 4a showed the biplot of CW for 199 families. Families K08, P12, and W04 were possible candidates for Mengla, and R04, N20 and H18 for Pingxiang, Hua'an and Changning based on CW. From Figure 4b it was indicated that Changning and Hua'an had similar and higher environmental

representativeness, and Mengla and Pingxiang showed higher discriminating ability on genotypic differences. Family R04 was the highest, followed by N20, H18, and W04, and the lowest CW was observed in C03. Little variations for CW were observed in families C03, K07 and Q04, and more variations in Y01, L19 and A04.

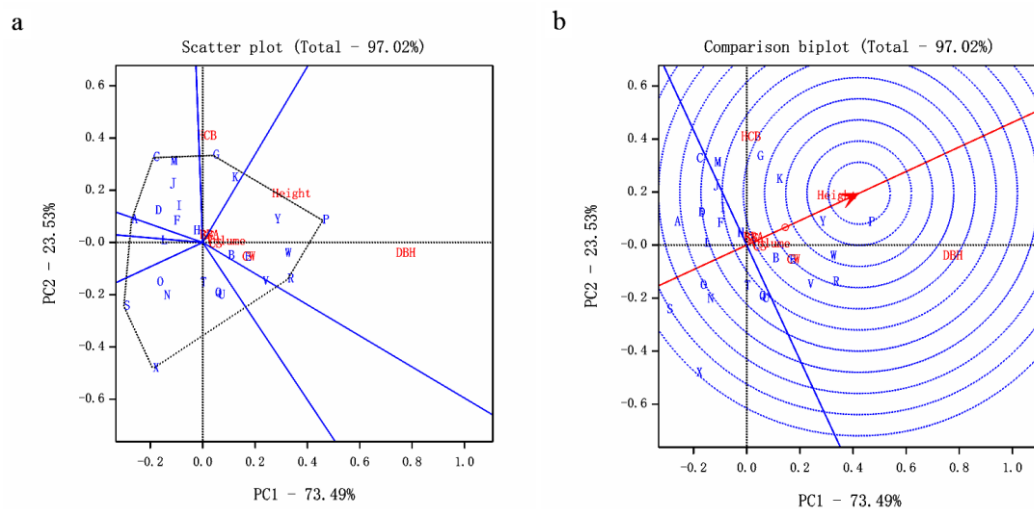


**Figure 4.** Biplot analysis based on CW data of 199 families. (a) Polygon view of GGE Biplot – which is best for what, (b) genotypes of ranking provenances. A, Mengla; B, Yuanyang; C, Mojiang; D, Jinghong; E, Xichou; F, Zhenyuan; G, Tengchong; H, Jinggu; I, Ruili; J, Fengqing; K, Pingbian; L, Jiangcheng; M, Shuangjiang; N, Lancang; O, Lingyun; P, Longzhou; Q, Donglan; R, Tianlin; S, Debao; T, Tiane; U, Pingguo; V, Baise; W, Tianyang; X, Jingxi; Y, Napo; Letters followed by numbers were the number of families.

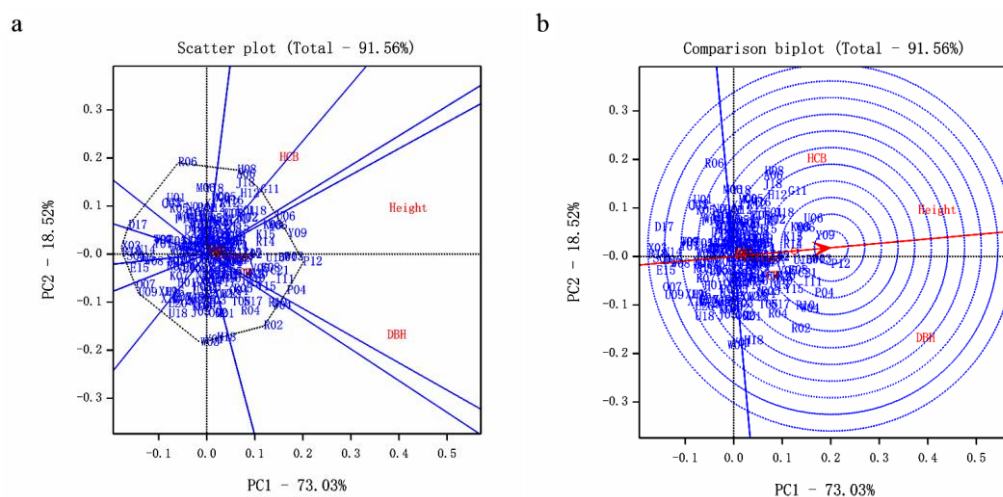
### 3.4. Superiority Rank and Selection for Provenances and Families

The GGE biplot of which-won-where view at provenance level was presented in Figure 5a. The provenances were divided into seven sectors, P and R were possible candidates for DBH, CW, CS, height and volume, and G and K were for HCB, BRA, and SF. In mean and stability view for trait performances of provenances (Figure 5b), DBH had the highest environmental representativeness, and height showed higher discriminating ability on genotypic differences. Provenances H, Y and L had little variations for traits, and more variations were seen in provenances X, C, and M. Additionally, provenance P performed the best for all traits, followed by Y and W, the poorest performances were observed in X and S. To rank the provenances based on their position in concentric circles, P was the most desirable provenance to be selected based on overall traits as it was located on the smallest concentric circle, follow by provenances Y, W, K, and R.

Figure 6a showed the GGE biplot at family level, families P12, P04 and Y09 were possible candidates for DBH, height, Volume, CW, and CS, and H08, A06, and G11 were possible candidates for HCB, BRA, and SF. Ranking the families in Figure 6b, P12 was the most desirable family to be selected based on overall traits. Y09, W03, D01, and U06 were also desirable families. To rank the provenances and families based on their superiority and stability, excellent provenances and families were then screened out with a selection rate of 20% and 10%, respectively. The means and realized gains of traits were presented in Table 8. It was inferred that not every trait could be positively selected. For example, the genetic and realized gains of  $\text{HCB} \cdot \text{height}^{-1}$  were negative, while HCB, height, and crown width showed positive genetic and realized gains. These meant longer clear-wood and frondent crown, which were targets of selection in the present study. The genetic and realized gains of all traits except  $\text{HCB} \cdot \text{height}^{-1}$  ranged from 0.25% to 2.01% and 2.43% to 14.84% at provenance level, and from 0.85% to 21.22% and 5.76% to 36.71% at family level, respectively.



**Figure 5.** Biplot analysis based on all traits of 25 provenances. (a) Polygon view of GGE biplot—which is best for what, (b) genotypes of ranking provenances. DBH, diameter at breast height; HCB, height to live crown base; CW, crown width; SF, stem form; CS, crown shape; BRA, branchiness; A, Mengla; B, Yuanyang; C, Mojiang; D, Jinghong; E, Xichou; F, Zhenyuan; G, Tengchong; H, Jinggu; I, Ruili; J, Fengqing; K, Pingbian; L, Jiangcheng; M, Shuangjiang; N, Lancang; O, Lingyun; P, Longzhou; Q, Donglan; R, Tianlin; S, Debao; T, Tiane; U, Pingguo; V, Baise; W, Tianyang; X, Jingxi; Y, Napo.



**Figure 6.** Biplot analysis based on all traits of 199 families. (a) Polygon view of GGE Biplot—which is best for what, (b) Genotypes of ranking families. DBH, diameter at breast height; HCB, height to live crown base; CW, crown width; SF, stem form; CS, crown shape; BRA, branchiness; A, Mengla; B, Yuanyang; C, Mojiang; D, Jinghong; E, Xichou; F, Zhenyuan; G, Tengchong; H, Jinggu; I, Ruili; J, Fengqing; K, Pingbian; L, Jiangcheng; M, Shuangjiang; N, Lancang; O, Lingyun; P, Longzhou; Q, Donglan; R, Tianlin; S, Debao; T, Tiane; U, Pingguo; V, Baise; W, Tianyang; X, Jingxi; Y, Napo; Letters followed by numbers were the number of families.

**Table 8.** Growth, quality traits and realized gains of the excellent provenances and families.

Provenances	DBH (cm)	Height (m)	HCb (m)	CW (m)	Volume (m <sup>3</sup> )	SF	CS	BRA	MADBH (cm·Year <sup>-1</sup> )	MAH (m·Year <sup>-1</sup> )	HCb·Height <sup>-1</sup>	MAVOL (m <sup>3</sup> ·Year <sup>-1</sup> )	Superiority Coefficient	Rank
P	18.58	16.12	8.42	3.91	0.27	0.66	0.71	0.69	1.33	1.16	0.53	0.02	0.0148	1
Y	18.60	16.00	8.86	3.99	0.24	0.60	0.71	0.74	1.31	1.13	0.56	0.02	0.0269	2
W	19.64	15.89	8.81	3.92	0.26	0.54	0.66	0.66	1.38	1.12	0.56	0.02	0.0378	3
K	18.97	16.72	9.65	3.99	0.26	0.66	0.65	0.78	1.31	1.15	0.59	0.02	0.0457	4
R	18.59	15.47	8.15	3.85	0.25	0.58	0.67	0.66	1.33	1.11	0.53	0.02	0.0578	5
Selected mean	18.88	16.04	8.78	3.93	0.25	0.61	0.68	0.71	1.33	1.14	0.55	0.02		
Total means	17.59	15.34	8.56	3.78	0.22	0.62	0.66	0.72	1.25	1.09	0.56	0.02		
Genetic gains (%)	2.01	0.30	1.55	0.90	0.39	1.59	0.42	0.80	1.88	0.25	-1.01	0.38		
Realized gains (%)	7.31	4.57	2.57	3.91	14.84	2.43	3.56	1.37	6.81	3.78	-1.68	14.55		
Families	DBH (cm)	Height (m)	HCb (m)	CW (m)	Volume (m <sup>3</sup> )	SF	CS	BRA	MADBH (cm·Year <sup>-1</sup> )	MAH (m·Year <sup>-1</sup> )	HCb·Height <sup>-1</sup>	MAVOL (m <sup>3</sup> ·Year <sup>-1</sup> )	Superiority Coefficient	Rank
P12	23.29	19.49	10.45	4.82	0.43	0.63	0.81	0.75	1.60	1.34	0.55	0.03	0.0092	1
Y09	19.49	17.33	9.72	4.63	0.31	0.64	0.84	0.85	1.39	1.24	0.57	0.02	0.0123	2
W03	21.88	18.37	9.88	4.90	0.35	0.67	0.82	0.81	1.50	1.25	0.55	0.02	0.0205	3
D01	18.48	15.48	9.68	4.20	0.22	0.77	0.80	0.92	1.32	1.13	0.58	0.01	0.0210	4
U06	20.46	18.89	10.86	5.00	0.33	0.66	0.76	0.72	1.39	1.28	0.58	0.02	0.0217	5
W06	19.33	16.59	9.74	3.85	0.29	0.56	0.59	0.70	1.37	1.19	0.58	0.02	0.0271	6
C21	22.69	19.37	11.69	4.78	0.41	0.84	0.86	0.89	1.53	1.31	0.61	0.03	0.0313	7
U16	19.11	16.14	8.87	4.33	0.26	0.60	0.74	0.73	1.36	1.16	0.55	0.02	0.0320	8
I11	22.24	19.78	10.06	5.00	0.37	0.88	0.82	0.82	1.50	1.34	0.51	0.03	0.0383	9
K08	20.68	18.81	10.53	4.78	0.32	0.80	0.75	0.68	1.41	1.28	0.57	0.02	0.0405	10
K15	21.81	18.00	11.54	4.09	0.33	0.49	0.70	0.77	1.48	1.22	0.64	0.02	0.0409	11
G11	20.22	19.08	11.49	4.33	0.31	0.68	0.79	0.84	1.39	1.32	0.61	0.02	0.0413	12
R14	19.28	16.52	9.02	4.00	0.26	0.49	0.65	0.76	1.37	1.18	0.56	0.02	0.0441	13
P04	22.03	18.95	8.92	4.59	0.41	0.77	0.75	0.65	1.52	1.31	0.50	0.03	0.0476	14
E08	20.81	17.56	9.20	4.22	0.29	0.63	0.78	0.66	1.44	1.21	0.55	0.02	0.0488	15
R10	22.37	17.72	8.85	4.63	0.35	0.72	0.69	0.69	1.55	1.22	0.50	0.02	0.0498	16
W04	23.50	18.21	8.82	4.69	0.38	0.57	0.72	0.65	1.64	1.27	0.48	0.03	0.0511	17
Y15	19.46	15.84	8.73	4.09	0.27	0.67	0.79	0.67	1.37	1.13	0.57	0.02	0.0516	18
V05	19.08	15.38	8.84	4.12	0.25	0.62	0.65	0.75	1.34	1.09	0.55	0.02	0.0527	19
I18	20.96	18.46	11.50	3.53	0.34	0.64	0.52	0.79	1.45	1.27	0.64	0.02	0.0533	20
Selected mean	20.86	17.80	9.92	4.43	0.32	0.66	0.74	0.75	1.45	1.24	0.56	0.02		
Total means	18.34	15.88	8.89	3.89	0.24	0.61	0.66	0.71	1.28	1.11	0.57	0.02		
Genetic gains (%)	5.87	5.17	5.73	5.21	21.22	1.46	1.92	0.85	5.43	4.67	-0.37	20.92		
Realized gains (%)	13.72	12.09	11.57	13.73	36.71	8.47	12.86	5.76	12.69	10.92	-0.76	36.20		

**Notes:** The excellent provenances and families were selected with 20% and 10 % selection rate, respectively. P, Daqingshan; Y, Napo; W, Tianyang; K, Pingbian; R, Tianlin; DBH, diameter at breast height; HCb, height to live crown base; CW, crown width; SF, stem form; CS, crown shape; BRA, branchiness; MADBH, mean annual increment of diameter at breast height; MAH, mean annual increment of tree height; HCb·Height<sup>-1</sup>, rate of height to live crown base to tree height; MAVOL, mean annual increment of stem volume.



#### 4. Discussion

Significant variances were observed for most growth and quality traits at levels of provenance and family, which showed good potential for elite germplasm selection of *B. alnoides*. The performances of growth traits were usually observed not consistent with those of quality traits for the same provenance. For example, the mean annual increment of diameter at breast height (MADBH), crown width (CW), height and volume were the lowest but stem form (SF) and branchiness (BRA) were the highest in provenance A. This discrepancy was also observed in other tree species like *Pinus radiata* [28], which make it difficult to take equally both growth and quality traits into consideration for selection of elite germplasms. A trade-off between growth and quality traits should thus be done according to the objective in the breeding program of *B. alnoides*.

Growth and quality traits of trees are mainly impacted by genotype, but also environment condition and physiological age [23]. Significant site effects were observed for all growth and quality traits tested except crown shape in the present study, indicating that *B. alnoides* trees had high phenotypic plasticity in these traits. Based on biplot analysis of GGE, Mengla and Pingxiang showed high discriminating ability of height, diameter at breast height (DBH), height to live crown base (HCB) and CW on genotypic differences, and similar environmental representativeness of Hua'an and Changning were observed in height, DBH, HCB and CW traits. Site effects reflect the comprehensive reactions of trees to edaphic status, local and regional climatic conditions, etc. [29]. In the present study, the growth performance did not show an obvious trend with such a large range of altitude (275–1250 m), this is closely dependent on geomorphic features in southern China. But anyhow, mean annual air temperature and rainfall may play important roles in growth performance and showed less difference among four trial sites (Table 1). The relatively poor growth performance of *B. alnoides* at Changning site may partially be attributed to its shallow soil thickness and low rainfall compared to other sites.

The growth and quality traits varied among provenances and trial sites, which usually could be interpreted from the significant provenance-site interaction [30]. In the previous studies, there existed significant interactions between genotype and environment in tree height, DBH and stem volume for *Larix kaempferi* (Lamb.) Carrière [25] and in SF for *Pinus radiata* [28]. In the present study, significant provenance-site and provenance-block within site interactions were observed in most growth and quality traits based on combined variance analysis, demonstrating strong interactions between environment and provenance. While significant family-site interactions were seen only in CW and crown shape (CS). These inferred that the provenance-site interactions were more significant than family-site ones, this was consistent with the study on DBH and SF for *Psuedotsuga menziesii* (Mirb.) Franco [31].

G × E interaction will usually reduce the genetic gain by reducing the heritability at multi-site trials [12], while there was no significant decline in the heritability of most traits in the present study, which was a foundation for enough genetic gains obtained through selection. Selecting superior and stable for application at different sites was an efficient strategy for dealing with its significant G × E effects, and was also the main breeding program for *B. alnoids*. The tested traits showed low-to-moderate heritability in multi-site genetic analysis. The estimates of provenance repeatability for SF, BRA, and HCB were higher than those for other traits, this was in accordance with many previous studies such as the high provenance repeatability of stem straightness and branch traits for *Pinus radiata* [32]. While the estimates of family heritability for growth traits were higher than those for quality traits in the present study. Growth traits were also under more substantial genetic control than quality traits at family levels in the study of *Pinus elliottii* Engelm., which might be caused by a strong environment effect [23].

The phenotypic and genetic coefficient of variation (GCV, PCV) of volume and DBH were higher than those of height at each site, which indicated that volume and DBH were more sensitive to environmental influence than tree height. This was consistent with the studies on *Populus deltoides* Bartr. ex Marsh. [33]. The PCV of stem volume and quality traits were higher than other growth traits in both multi-site and single-site analysis, which indicated that G × E interaction of quality traits was



stronger than that of most growth traits, and this was consistent with the above-mentioned result that growth traits were under stronger genetic control than quality traits. It was inferred that more genetic gains in terms of quality can be expected from selection at provenance level, and more genetic gains in terms of growth traits like volume can be expected from selection at family level for *B. alnoides*.

Significant correlations among traits indicated that growth and quality traits were not independent for *B. alnoides*. Moderate to strong positive genotypic correlations among DBH, height, and volume were observed. The correlations between DBH and volume were higher than those between height and volume, which showed the importance of DBH in selection for high stem volume [34]. The correlations between height with CW, SF and CS were not significant in the present study, while the previous study on clonal selection (3.5 years old unclosed forest) of *Betula alnoides* × *Betula. luminifera* H. Winkler hybrids showed that CW, SF, CS, and BRA were significantly correlated to height [21]. This difference could also be interpreted from the unstable growth performance and correlations between traits in the young plantations [20]. As stem volume and SF are the most concerned in plantation forestry of *B. alnoides*.

SF showed the highest while volume showed the lowest for provenance repeatability, indicating that genetic gain of SF was higher than that of volume in the selection for single trait. DBH, height, and HCB showed strong discriminating ability on provenance differences according to biplot analysis for GGE and were of moderate to strong genotypic correlations with most other traits. These inferred that it was possible to simplify the selected traits to DBH, HCB, and SF, and obtain good provenances with multi-trait. As to the family level, all growth traits had higher family heritabilities than quality traits. In particular, DBH, height, and HCB showed strong discriminating ability on family differences according to biplot analysis for GGE. In addition, moderate to strong correlations usually existed between growth and quality traits. These inferred that it was possible to simplify the selected traits to volume, DBH, height, and HCB, and obtain good families with multi-trait.

As to methods for the analysis of  $G \times E$  interaction and selection for excellent germplasms, variance analysis, principal coordinates analysis, and factor analysis as well as index selection and combined selection were widely used in the breeding process of trees [12,35,36]. However, these methods were usually applied to the analysis with a single site, population with simple genetic structure and non-visual form. The BLUP breeding value can be estimated for multi-trait in multi-site based on linear mixed models. Biplot analysis method can show the main genotypic effect (G) and interaction effect ( $G \times E$ ) of multi-site, and both superiority and stability of genotypes and the discriminating ability of traits can be visualized in biplot analysis for GGE according to the BLUP breeding value [26,36]. The present study also showed that the combination of BLUP breeding value and GGE biplot analysis is an appropriate method of multi-site selection for multiple traits.

For selection strategies in the present study, the desired provenances and families have been selected separately from provenances and families regardless of provenances. These germplasm can be applied in the practice. However, the trials were established with a single tree plot so as to evaluate more families. In the further study, multiple trees of a family will be arranged in each plot to reduce the environmental effect and improve the estimation of heritability and realized genetic gains, and these selected families and new families from the natural populations of the desired provenances will be involved in the progeny trials [37,38]. More superior families and individuals in families will thus be screened out for plantation forestry of *B. alnoides*.

## 5. Conclusions

Based on the combined analysis on growth and quality traits of 199 families of 25 provenances of *B. alnoides* at four sites when 10–15 years old, the genetic variance, heritability, correlation, and  $G \times E$  interaction were estimated and the provenances and families were ranked. The results showed that there existed a remarkable site, provenance, family, and provenance-site effects for tested traits, indicating the significance of  $G \times E$  interaction. The provenance repeatability of HCB, SF, and BRA showed higher levels than that of other traits. Growth traits were under moderate and relatively higher

genetic control rather than quality traits based on family heritabilities. The DBH, height, HCB, and CW were under relatively higher genetic control, had a stronger discriminating ability on genotype differences, and were also strongly correlated with other traits, they should be paid more attention to in the multi-trait selection. The superior and stable provenances and families selected by GGE biplot analysis should be applied in the practice of *B. alnoides* plantation forestry.

**Author Contributions:** J.Z., J.G., C.W., and Z.Z. designed the experiment; M.Y., J.G., C.W., Z.Z. and J.Z. performed the experiments and collected the data; M.Y. and J.G. analyzed the data; M.Y. and J.G. contributed to writing the manuscript.

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**Conflicts of Interest:** We declare that we have no conflict of interest.

## Appendix A

**Table A1.** Location of 25 provenances of *Betula alnoides* investigated in the trials.

Provenances	Location	Latitude N	Longitude E	Altitude (m)	Number of Family Tested
A	Mengla, Yunnan	21°33′	101°29′	950–1100	3
B	Yuanyang, Yunnan	23°07′	103°01′	1000–1130	3
C	Mojiang, Yunnan	23°30′	101°46′	1500–1600	12
D	Jinghong, Yunnan	22°24′	100°59′	1300	7
E	Xichou, Yunnan	23°15′	104°33′	1400–1600	8
F	Zhenyuan, Yunnan	23°59′	101°09′	1570–1900	4
G	Tengchong, Yunnan	24°56′	98°36′	1820–2100	2
H	Jingguo, Yunnan	23°29′	100°34′	1650–1800	9
I	Ruili, Yunnan	23°56′	98°03′	1120–1250	8
J	Fengqing, Yunnan	24°54′	99°55′	1380–1850	12
K	Pingbian, Yunnan	23°03′	103°38′	1230–1320	10
L	Jiangcheng, Yunnan	22°35′	101°47′	1190–1280	10
M	Shuangjiang, Yunnan	23°26′	99°39′	1560–1670	7
N	Lancang, Yunnan	22°36′	99°59′	1280–1500	9
O	Lingyun, Gaungxi	24°00′	106°35′	700–900	6
P	Longzhou, Gaungxi	22°25′	106°40′	600–800	8
Q	Donglan, Gaungxi	24°29′	107°34′	500–680	3
R	Tianlin, Gaungxi	24°25′	105°43′	740–920	11
S	Debao, Gaungxi	23°20′	106°38′	800–900	4
T	Tian'e, Gaungxi	25°11′	107°13′	650–750	7
U	Pingguo, Gaungxi	23°42′	107°23′	650–800	12
V	Baise, Gaungxi	23°47′	106°30′	500–900	5
W	Tianyang, Gaungxi	23°52′	107°08′	550–700	15
X	Jingxi, Gaungxi	23°01′	106°20′	800–1000	10
Y	Napo, Gaungxi	23°11′	105°51′	600–850	14

**Table A2.** Growth and quality traits for 25 provenances of *Betula alnoids* at Mengla site.

Provenances	MADBDH (cm·Year <sup>-1</sup> )	MAH (m·Year <sup>-1</sup> )	HCB-Height <sup>-1</sup>	CW (m)	MAVOL (m <sup>3</sup> ·Year <sup>-1</sup> )	SF	CS	BRA
A	1.19 (0.07) e	1.26 (0.07) abcd	0.59 (0.03) abcd	3.67 (0.50) abc	0.0155 (0.0022) e	0.77 (0.05) ab	0.75 (0.09) ab	0.96 (0.04) a
B	1.49 (0.08) a	1.24 (0.06) abcd	0.53 (0.03) de	3.16 (0.32) abc	0.0242 (0.0036) ab	0.65 (0.08) abcde	0.68 (0.08) ab	0.68 (0.08) bcd
C	1.38 (0.04) abcde	1.31 (0.03) ab	0.63 (0.02) a	3.73 (0.23) ab	0.0222 (0.0016) abcde	0.67 (0.04) abcde	0.69 (0.04) ab	0.87 (0.03) ab
D	1.36 (0.05) abcde	1.25 (0.04) abcd	0.58 (0.02) abcde	3.47 (0.26) abc	0.0207 (0.0021) abcde	0.66 (0.05) abcde	0.76 (0.05) ab	0.76 (0.05) bcd
E	1.38 (0.04) abcde	1.25 (0.03) abcd	0.54 (0.02) cde	3.95 (0.25) ab	0.0205 (0.0015) abcde	0.68 (0.04) abcde	0.76 (0.04) ab	0.68 (0.04) cd
F	1.38 (0.10) abcde	1.29 (0.06) abc	0.61 (0.03) abc	3.52 (0.35) abc	0.0217 (0.0035) abcde	0.75 (0.07) abcd	0.69 (0.07) ab	0.88 (0.05) ab
G	1.42 (0.08) abcd	1.35 (0.08) a	0.61 (0.02) abcd	2.51 (0.24) c	0.0231 (0.003) abc	0.78 (0.11) a	0.78 (0.08) ab	0.86 (0.09) abc
H	1.42 (0.05) abcd	1.29 (0.03) abc	0.57 (0.02) abcde	3.99 (0.26) ab	0.0225 (0.0017) abcde	0.68 (0.04) abcde	0.77 (0.04) ab	0.80 (0.04) abcd
I	1.34 (0.05) abcde	1.26 (0.04) abcd	0.57 (0.02) abcde	3.76 (0.24) ab	0.0209 (0.002) abcde	0.65 (0.05) abcde	0.72 (0.05) ab	0.82 (0.04) abc
J	1.35 (0.04) abcde	1.27 (0.03) abc	0.60 (0.02) abcd	3.52 (0.25) abc	0.0209 (0.0016) abcde	0.61 (0.04) abcde	0.61 (0.04) abc	0.85 (0.04) abc
K	1.45 (0.04) abc	1.27 (0.03) abcd	0.58 (0.02) abcde	4.15 (0.21) a	0.0231 (0.0015) abcd	0.70 (0.04) abcd	0.70 (0.04) ab	0.77 (0.04) bcd
L	1.46 (0.05) ab	1.31 (0.03) ab	0.56 (0.02) abcde	3.86 (0.23) ab	0.0250 (0.0018) a	0.72 (0.04) abcd	0.71 (0.04) ab	0.85 (0.04) abc
M	1.28 (0.06) bcde	1.27 (0.04) abcd	0.63 (0.02) ab	3.81 (0.31) ab	0.0192 (0.0023) abcde	0.75 (0.05) abc	0.70 (0.05) ab	0.86 (0.04) abc
N	1.28 (0.05) bcde	1.16 (0.04) cd	0.57 (0.02) abcde	3.00 (0.21) bc	0.0180 (0.0019) abcde	0.56 (0.05) cde	0.65 (0.05) abc	0.76 (0.05) bcd
O	1.27 (0.04) cde	1.15 (0.04) d	0.57 (0.02) abcde	3.59 (0.25) abc	0.0162 (0.0015) cde	0.52 (0.05) e	0.48 (0.05) c	0.64 (0.06) d
P	1.41 (0.05) abcd	1.28 (0.03) abc	0.51 (0.02) e	4.11 (0.28) a	0.0216 (0.0017) abcde	0.57 (0.05) cde	0.62 (0.05) abc	0.71 (0.05) bcd
Q	1.28 (0.08) bcde	1.18 (0.04) bcd	0.58 (0.04) abcde	3.57 (0.52) abc	0.0163 (0.0026) cde	0.56 (0.09) cde	0.84 (0.06) a	0.72 (0.10) bcd
R	1.28 (0.03) bcde	1.18 (0.03) bcd	0.56 (0.02) abcde	4.05 (0.25) ab	0.0169 (0.0012) bcde	0.57 (0.04) bcde	0.59 (0.04) bc	0.75 (0.04) bcd
S	1.25 (0.07) cde	1.12 (0.08) d	0.55 (0.03) bcde	3.37 (0.47) abc	0.0161 (0.0023) de	0.53 (0.08) de	0.58 (0.08) bc	0.73 (0.08) bcd
T	1.35 (0.06) abcde	1.20 (0.04) abcd	0.55 (0.02) abcde	3.49 (0.33) abc	0.0197 (0.0018) abcde	0.58 (0.05) abcde	0.58 (0.06) bc	0.75 (0.05) bcd
U	1.21 (0.04) de	1.15 (0.03) cd	0.59 (0.02) abcd	4.24 (0.2) a	0.0156 (0.0012) e	0.56 (0.04) cde	0.60 (0.04) bc	0.73 (0.04) bcd
V	1.30 (0.06) abcde	1.17 (0.05) bcd	0.57 (0.03) abcde	3.59 (0.31) abc	0.0180 (0.002) abcde	0.71 (0.05) abcd	0.64 (0.06) abc	0.82 (0.05) abcd
W	1.32 (0.03) abcde	1.19 (0.02) bcd	0.59 (0.01) abcd	4.05 (0.21) ab	0.0187 (0.0012) abcde	0.56 (0.03) cde	0.61 (0.03) abc	0.77 (0.03) abcd
X	1.28 (0.04) bcde	1.17 (0.03) bcd	0.54 (0.02) cde	3.90 (0.23) ab	0.0177 (0.0015) bcde	0.65 (0.04) abcde	0.59 (0.04) bc	0.71 (0.04) bcd
Y	1.36 (0.03) abcde	1.23 (0.03) abcd	0.57 (0.02) abcde	3.72 (0.17) ab	0.0203 (0.0013) abcde	0.60 (0.03) abcde	0.64 (0.03) abc	0.76 (0.03) bcd

**Notes:** A, Mengla; B, Yuanyang; C, Mojiang; D, Jinghong; E, Xichou; F, Zhenyuan; G, Tengchong; H, Jinggu; I, Ruili; J, Fengqing; K, Pingbian; L, Jiangcheng; M, Shuangjiang; N, Lancang; O, Lingyun; P, Longzhou; Q, Donglan; R, Tianlin; S, Debao; T, Tiane; U, Pingguo; V, Baise; W, Tianyang; X, Jingxi; Y, Napo; MADBDH, mean annual increment of diameter at breast height; MAH, mean annual increment of tree height; HCB-Height<sup>-1</sup>, rate of height to live crown base to tree height; CW, crown width; MAVOL, mean annual increment of stem volume; SF, stem form; CS, crown shape; BRA, branchiness. Means with standard error in parenthesis were of significant difference at 0.05 level according to Duncan's multiple range tests if followed by wholly different small letters in the same row.

**Table A3.** Growth and quality traits for 25 provenances of *Betula alnoids* at Pingxiang site.

Provenances	MADBH (cm·Year <sup>-1</sup> )	MAH (m·Year <sup>-1</sup> )	HCB·Height <sup>-1</sup>	CW (m)	MAVOL (m <sup>3</sup> ·Year <sup>-1</sup> )	SF	CS	BRA
A	0.89 (0.05) fghi	0.85 (0.06) bcdef	0.67 (0.05) abcde	5.59 (0.76) ab	0.0058 (0.0009) def	0.74 (0.07)	0.59 (0.14) abcd	0.74 (0.13)
B	0.94 (0.09) defghi	0.85 (0.06) bcdef	0.64 (0.02) abcdef	4.36 (0.39) bc	0.0075 (0.0021) bcdef	0.79 (0.08)	0.68 (0.06) abcd	0.77 (0.09)
C	0.84 (0.04) fghi	0.83 (0.03) cdef	0.66 (0.02) abcd	3.90 (0.34) cd	0.0058 (0.0008) cdef	0.58 (0.06)	0.55 (0.06) bcd	0.69 (0.06)
D	0.91 (0.06) efghi	0.87 (0.04) bcdef	0.70 (0.02) a	3.05 (0.31) d	0.0067 (0.0012) cdef	0.73 (0.06)	0.66 (0.05) bcd	0.88 (0.05)
E	1.11 (0.04) abcdef	0.97 (0.05) abcde	0.59 (0.02) cdef	4.37 (0.31) bcd	0.0105 (0.0011) abcdef	0.69 (0.06)	0.67 (0.05) abcd	0.75 (0.05)
F	0.79 (0.09) hi	0.81 (0.08) def	0.59 (0.04) def	3.59 (0.35) cd	0.0055 (0.0018) ef	0.70 (0.07)	0.57 (0.12) bcd	0.77 (0.07)
G	0.87 (0.07) ghi	0.87 (0.07) bcdef	0.69 (0.04) ab	3.36 (0.52) cd	0.0059 (0.0014) cdef	0.66 (0.13)	0.51 (0.15) cd	0.85 (0.08)
H	0.95 (0.08) cdefghi	0.80 (0.05) ef	0.69 (0.02) ab	3.63 (0.46) cd	0.0080 (0.0020) bcdef	0.75 (0.06)	0.48 (0.06) d	0.71 (0.07)
I	0.90 (0.07) bcdefghi	0.96 (0.06) abcde	0.62 (0.03) abcdef	3.73 (0.59) cd	0.0088 (0.0018) bcdef	0.63 (0.07)	0.52 (0.07) bcd	0.62 (0.09)
J	0.83 (0.04) hi	0.86 (0.04) bcdef	0.69 (0.02) a	3.49 (0.34) cd	0.0054 (0.0007) ef	0.64 (0.07)	0.46 (0.07) d	0.78 (0.06)
K	1.06 (0.04) abcdefg	1.00 (0.04) abc	0.60 (0.01) cdef	3.11 (0.27) cd	0.0106 (0.0012) abcde	0.63 (0.05)	0.64 (0.05) abcd	0.83 (0.05)
L	0.81 (0.05) i	0.74 (0.03) f	0.65 (0.03) abcde	3.35 (0.35) cd	0.0047 (0.0009) f	0.74 (0.05)	0.47 (0.07) d	0.71 (0.07)
M	1.01 (0.05) bcdefghi	0.91 (0.05) abcde	0.68 (0.02) abc	4.00 (0.54) bcd	0.0084 (0.0012) bcdef	0.75 (0.07)	0.42 (0.07) d	0.80 (0.09)
N	0.89 (0.04) fghi	0.89 (0.04) bcdef	0.61 (0.03) abcdef	2.91 (0.33) d	0.0062 (0.0008) cdef	0.69 (0.07)	0.51 (0.06) bcd	0.75 (0.06)
O	1.07 (0.04) abcdefg	0.89 (0.04) bcdef	0.64 (0.02) abcde	3.43 (0.36) cd	0.0086 (0.0010) bcdef	0.77 (0.07)	0.60 (0.08) bcd	0.78 (0.06)
P	1.12 (0.07) abcd	0.99 (0.05) abcd	0.59 (0.02) def	3.36 (0.32) cd	0.0130 (0.0018) ab	0.76 (0.04)	0.71 (0.06) abcd	0.81 (0.05)
Q	1.05 (0.05) abcdefghi	0.89 (0.03) bcdef	0.57 (0.03) def	3.47 (0.37) cd	0.0084 (0.0011) bcdef	0.66 (0.06)	0.75 (0.08) abc	0.64 (0.10)
R	1.21 (0.05) ab	1.00 (0.04) abc	0.60 (0.02) cdef	3.57 (0.26) cd	0.0133 (0.0012) ab	0.69 (0.05)	0.64 (0.06) bcd	0.74 (0.04)
S	1.06 (0.07) abcdefg	0.94 (0.05) abcde	0.56 (0.05) f	6.18 (0.53) a	0.0092 (0.0015) bcdef	0.70 (0.08)	0.89 (0.06) a	0.65 (0.13)
T	1.08 (0.05) abcdefg	0.98 (0.04) abcde	0.57 (0.02) def	4.22 (0.31) bcd	0.0103 (0.0015) abcdef	0.71 (0.06)	0.76 (0.06) abc	0.81 (0.05)
U	1.14 (0.04) abcde	0.95 (0.03) abcde	0.56 (0.01) ef	3.93 (0.23) cd	0.0115 (0.0011) abcd	0.70 (0.04)	0.71 (0.04) abcd	0.64 (0.04)
V	1.27 (0.06) a	1.12 (0.05) a	0.56 (0.02) ef	4.00 (0.33) cd	0.0152 (0.0020) a	0.71 (0.07)	0.77 (0.06) abc	0.82 (0.05)
W	1.14 (0.04) abcde	1.00 (0.03) abc	0.60 (0.01) bcdef	3.15 (0.22) cd	0.0117 (0.0011) abc	0.70 (0.04)	0.62 (0.04) bcd	0.75 (0.04)
X	1.05 (0.05) abcdefgh	0.92 (0.04) bcde	0.59 (0.02) def	4.32 (0.28) bcd	0.0098 (0.0011) abcdef	0.70 (0.05)	0.77 (0.04) ab	0.71 (0.05)
Y	1.17 (0.04) abc	1.03 (0.03) ab	0.58 (0.01) def	3.83 (0.23) cd	0.0129 (0.0011) ab	0.63 (0.04)	0.77 (0.04) ab	0.79 (0.04)

**Notes:** A, Mengla; B, Yuanyang; C, Mojiang; D, Jinghong; E, Xichou; F, Zhenyuan; G, Tengchong; H, Jinggu; I, Ruili; J, Fengqing; K, Pingbian; L, Jiangcheng; M, Shuangjiang; N, Lancang; O, Lingyun; P, Longzhou; Q, Donglan; R, Tianlin; S, Debao; T, Tiane; U, Pingguo; V, Baise; W, Tianyang; X, Jingxi; Y, Napo; MADBH, mean annual increment of diameter at breast height; MAH, mean annual increment of tree height; HCB·Height<sup>-1</sup>, rate of height to live crown base to tree height; CW, crown width; MAVOL, mean annual increment of stem volume; SF, stem form; CS, crown shape; BRA, branchiness. Means with standard error in parenthesis were of significant difference at 0.05 level according to Duncan's multiple range tests if followed by wholly different small letters in the same row.

**Table A4.** Growth and quality traits for 25 provenances of *Betula alnoids* at Hua'an site.

Provenances	MADBH (cm·Year <sup>-1</sup> )	MAH (m·Year <sup>-1</sup> )	HCW-Height <sup>-1</sup>	CW (m)	MAVOL (m <sup>3</sup> ·Year <sup>-1</sup> )	SF	CS	BRA
A	1.31 (0.09) e	1.14 (0.09) cd	0.62 (0.05) ab	4.03 (0.47) abcd	0.0135 (0.0023) e	0.70 (0.15) ab	0.36 (0.11) h	0.74 (0.14) abcde
B	1.49 (0.07) abcde	1.17 (0.05) abcd	0.60 (0.02) abc	3.17 (0.36) de	0.0190 (0.0022) bcde	0.57 (0.08) abc	0.65 (0.07) bcdef	0.73 (0.07) abcde
C	1.38 (0.06) bcde	1.15 (0.04) bcd	0.60 (0.02) abcd	3.61 (0.27) bcd	0.0172 (0.0021) bcde	0.49 (0.07) cd	0.56 (0.06) cdefgh	0.70 (0.05) abcde
D	1.37 (0.07) cde	1.14 (0.04) cd	0.60 (0.02) abcd	4.50 (0.28) ab	0.0161 (0.0019) de	0.64 (0.09) abc	0.46 (0.07) fgh	0.73 (0.06) abcde
E	1.47 (0.04) abcde	1.15 (0.03) cd	0.56 (0.02) abcde	4.14 (0.23) abc	0.0190 (0.0012) bcde	0.45 (0.04) cd	0.72 (0.04) abcd	0.58 (0.04) cde
F	1.46 (0.10) abcde	1.12 (0.03) cd	0.66 (0.02) a	3.54 (0.51) bcd	0.0179 (0.0027) bcde	0.64 (0.07) abc	0.40 (0.08) gh	0.89 (0.05) a
G	1.58 (0.09) ab	1.36 (0.07) a	0.59 (0.04) abcde	4.83 (0.42) a	0.0242 (0.0036) abcd	0.57 (0.09) abc	0.77 (0.1) abc	0.73 (0.09) abcde
H	1.41 (0.05) bcde	1.17 (0.03) abcd	0.55 (0.03) bcdef	3.50 (0.28) bcd	0.0172 (0.0015) bcde	0.58 (0.07) abc	0.61 (0.07) bcdefg	0.75 (0.05) abcd
I	1.56 (0.07) abc	1.25 (0.04) abc	0.58 (0.03) abcde	4.36 (0.41) abc	0.0225 (0.0026) abcd	0.65 (0.08) abc	0.54 (0.09) cdefgh	0.70 (0.07) abcde
J	1.52 (0.04) abcde	1.18 (0.03) abcd	0.59 (0.02) abcde	3.93 (0.27) abcd	0.0201 (0.0015) bcde	0.58 (0.05) abc	0.55 (0.06) cdefgh	0.67 (0.05) abcde
K	1.41 (0.04) bcde	1.16 (0.03) abcd	0.59 (0.02) abcde	3.90 (0.27) abcd	0.0174 (0.0013) bcde	0.56 (0.06) abc	0.58 (0.06) cdefgh	0.77 (0.04) abc
L	1.34 (0.07) de	1.17 (0.05) abcd	0.60 (0.03) abcde	3.48 (0.33) bcd	0.0168 (0.0023) cde	0.74 (0.06) a	0.47 (0.07) efgh	0.78 (0.07) ab
M	1.49 (0.06) abcde	1.19 (0.04) abcd	0.59 (0.03) abcde	2.41 (0.23) e	0.0193 (0.0018) bcde	0.58 (0.07) abc	0.47 (0.07) fgh	0.74 (0.07) abcde
N	1.54 (0.10) abcd	1.20 (0.05) abcd	0.57 (0.03) abcde	3.42 (0.3) cde	0.0244 (0.0041) abc	0.44 (0.08) cd	0.51 (0.08) defgh	0.57 (0.07) cde
O	1.41 (0.04) bcde	1.22 (0.04) abc	0.54 (0.02) cdef	3.31 (0.23) cde	0.0176 (0.0013) bcde	0.54 (0.05) bcd	0.73 (0.05) abcd	0.64 (0.05) bcde
P	1.64 (0.06) a	1.31 (0.04) ab	0.54 (0.02) cdef	3.85 (0.23) abcd	0.0278 (0.0025) a	0.62 (0.05) abc	0.81 (0.05) ab	0.62 (0.05) bcde
Q	1.59 (0.05) ab	1.22 (0.04) abc	0.48 (0.03) f	3.38 (0.33) cde	0.0216 (0.0016) abcd	0.52 (0.07) bcd	0.92 (0.04) a	0.60 (0.07) cde
R	1.61 (0.04) ab	1.21 (0.03) abcd	0.50 (0.01) ef	3.64 (0.16) bcd	0.0256 (0.0017) ab	0.46 (0.03) cd	0.71 (0.03) abcd	0.53 (0.03) e
S	1.30 (0.06) e	1.06 (0.04) d	0.56 (0.03) abcdef	3.95 (0.33) abcd	0.0132 (0.0015) e	0.33 (0.07) d	0.60 (0.07) cdefg	0.71 (0.07) abcde
T	1.42 (0.04) abcde	1.13 (0.03) cd	0.56 (0.02) bcdef	3.77 (0.19) abcd	0.0166 (0.0012) cde	0.42 (0.05) cd	0.66 (0.05) bcdef	0.60 (0.05) bcde
U	1.61 (0.05) ab	1.22 (0.04) abc	0.52 (0.02) def	3.84 (0.22) abcd	0.0246 (0.0018) ab	0.43 (0.04) cd	0.69 (0.04) abcde	0.54 (0.04) de
V	1.56 (0.05) abcd	1.09 (0.04) cd	0.54 (0.02) bcdef	3.59 (0.38) bcd	0.0197 (0.0017) bcde	0.42 (0.05) cd	0.73 (0.05) abcd	0.56 (0.06) cde
W	1.62 (0.03) ab	1.18 (0.02) abcd	0.53 (0.01) cdef	4.01 (0.14) abcd	0.0230 (0.001) abcd	0.43 (0.03) cd	0.72 (0.03) abcd	0.56 (0.03) cde
X	1.44 (0.04) abcde	1.12 (0.03) cd	0.54 (0.01) cdef	3.73 (0.16) abcd	0.0184 (0.0013) bcde	0.52 (0.04) bcd	0.64 (0.04) bcdef	0.59 (0.04) cde
Y	1.49 (0.03) abcde	1.18 (0.02) abcd	0.56 (0.01) abcdef	3.86 (0.14) abcd	0.0198 (0.001) bcde	0.52 (0.03) bcd	0.75 (0.03) abc	0.70 (0.03) abcde

**Notes:** A, Mengla; B, Yuanyang; C, Mojiang; D, Jinghong; E, Xichou; F, Zhenyuan; G, Tengchong; H, Jinggu; I, Ruili; J, Fengqing; K, Pingbian; L, Jiangcheng; M, Shuangjiang; N, Lancang; O, Lingyun; P, Longzhou; Q, Donglan; R, Tianlin; S, Debao; T, Tiane; U, Pingguo; V, Baise; W, Tianyang; X, Jingxi; Y, Napo; MADBH, mean annual increment of diameter at breast height; MAH, mean annual increment of tree height; HCB-Height<sup>-1</sup>, rate of height to live crown base to tree height; CW, crown width; MAVOL, mean annual increment of stem volume; SF, stem form; CS, crown shape; BRA, branchiness. Means with standard error in parenthesis were of significant difference at 0.05 level according to Duncan's multiple range tests if followed by wholly different small letters in the same row.

**Table A5.** Growth and quality traits for 25 provenances of *Betula alnoids* at Changning site.

Provenances	MADBH (cm·year <sup>-1</sup> )	MAH (m·year <sup>-1</sup> )	HCW·Height <sup>-1</sup>	CW (m)	MAVOL (m <sup>3</sup> ·year <sup>-1</sup> )	SF	CS	BRA
A	0.76 (0.04) abcd	0.74 (0.06) cde	0.56 (0.05) bcd	3.39 (0.37) bc	0.0017 (0.0002) abcd	0.85 (0.05) a	0.78 (0.07)	0.78 (0.08)
B	0.86 (0.05) a	0.91 (0.07) a	0.47 (0.03) d	4.08 (0.42) abc	0.0026 (0.0005) ab	0.80 (0.07) ab	0.63 (0.14)	0.77 (0.08)
C	0.82 (0.04) ab	0.87 (0.04) abcd	0.51 (0.02) bcd	4.79 (0.28) ab	0.0024 (0.0003) abc	0.76 (0.06) ab	0.65 (0.07)	0.69 (0.06)
D	0.74 (0.03) abcd	0.82 (0.04) abcde	0.52 (0.02) bcd	3.13 (0.29) c	0.0018 (0.0002) abcd	0.70 (0.06) ab	0.67 (0.06)	0.71 (0.06)
E	0.81 (0.03) abc	0.90 (0.04) ab	0.50 (0.02) cd	3.54 (0.33) abc	0.0023 (0.0002) abc	0.81 (0.05) ab	0.67 (0.05)	0.78 (0.05)
F	0.80 (0.05) abc	0.81 (0.03) abcde	0.47 (0.02) d	3.79 (0.46) abc	0.0020 (0.0003) abcd	0.87 (0.05) a	0.81 (0.07)	0.70 (0.08)
G	0.77 (0) abcd	0.83 (0) abcde	0.51 (0) bcd	2.99 (0.72) c	0.0020 (0) abcd	0.77 (0) ab	0.65 (0)	0.73 (0)
H	0.79 (0.04) abc	0.85 (0.05) abcde	0.50 (0.03) cd	3.60 (0.40) abc	0.0020 (0.0003) abcd	0.83 (0.07) a	0.68 (0.09)	0.83 (0.07)
I	0.60 (0.05) e	0.73 (0.05) de	0.54 (0.03) bcd	3.95 (0.49) abc	0.0011 (0.0002) d	0.79 (0.06) ab	0.66 (0.09)	0.66 (0.09)
J	0.75 (0.04) abcd	0.84 (0.04) abcde	0.56 (0.03) bcd	4.08 (0.35) abc	0.0019 (0.0002) abcd	0.81 (0.05) ab	0.71 (0.08)	0.81 (0.06)
K	0.77 (0.05) abc	0.83 (0.07) abcde	0.59 (0.05) b	4.99 (0.72) a	0.0019 (0.0003) abcd	0.84 (0.05) a	0.59 (0.12)	0.75 (0.09)
L	0.79 (0.02) abc	0.83 (0.03) abcde	0.52 (0.02) bcd	4.08 (0.27) abc	0.0020 (0.0002) abcd	0.80 (0.04) ab	0.64 (0.05)	0.73 (0.05)
M	0.71 (0.04) bcde	0.78 (0.04) abcde	0.51 (0.02) bcd	3.87 (0.37) abc	0.0016 (0.0002) bcd	0.67 (0.06) ab	0.72 (0.07)	0.66 (0.07)
N	0.77 (0.03) abc	0.83 (0.03) abcde	0.50 (0.02) cd	3.16 (0.27) c	0.0020 (0.0002) abcd	0.73 (0.05) ab	0.69 (0.05)	0.71 (0.06)
O	0.71 (0.03) bcde	0.74 (0.03) cde	0.58 (0.03) bc	4.11 (0.34) abc	0.0015 (0.0002) cd	0.70 (0.06) ab	0.61 (0.08)	0.71 (0.07)
P	0.87 (0.04) a	0.90 (0.03) abc	0.48 (0.02) d	4.85 (0.36) ab	0.0027 (0.0003) a	0.72 (0.05) ab	0.64 (0.06)	0.67 (0.06)
Q	0.72 (0.04) abcd	0.83 (0.07) abcde	0.52 (0.05) bcd	3.50 (0.48) abc	0.0016 (0.0003) abcd	0.70 (0.13) ab	0.90 (0.06)	0.81 (0.13)
R	0.82 (0.03) abc	0.87 (0.03) abcd	0.51 (0.02) bcd	3.47 (0.24) bc	0.0023 (0.0002) abc	0.77 (0.04) ab	0.69 (0.05)	0.76 (0.04)
S	0.63 (0.06) de	0.69 (0.06) e	0.69 (0.10) a	3.12 (0.42) c	0.0011 (0.0003) d	0.59 (0.08) b	0.55 (0.11)	0.66 (0.11)
T	0.78 (0.04) abc	0.84 (0.05) abcde	0.49 (0.03) cd	4.83 (0.44) ab	0.0020 (0.0003) abcd	0.70 (0.10) ab	0.55 (0.12)	0.55 (0.11)
U	0.71 (0.03) bcde	0.81 (0.04) abcde	0.52 (0.02) bcd	4.27 (0.32) abc	0.0017 (0.0002) abcd	0.78 (0.05) ab	0.58 (0.06)	0.77 (0.06)
V	0.77 (0.05) abcd	0.84 (0.04) abcde	0.47 (0.02) d	3.95 (0.44) abc	0.0020 (0.0003) abcd	0.82 (0.06) ab	0.69 (0.09)	0.81 (0.07)
W	0.84 (0.03) ab	0.86 (0.03) abcd	0.49 (0.02) cd	3.93 (0.32) abc	0.0023 (0.0002) abc	0.76 (0.06) ab	0.56 (0.07)	0.68 (0.07)
X	0.68 (0.03) cde	0.75 (0.03) bcde	0.48 (0.01) d	4.04 (0.30) abc	0.0014 (0.0002) cd	0.71 (0.05) ab	0.49 (0.06)	0.74 (0.05)
Y	0.84 (0.03) ab	0.87 (0.03) abcd	0.50 (0.02) cd	3.47 (0.29) bc	0.0024 (0.0003) abc	0.85 (0.03) a	0.69 (0.06)	0.76 (0.05)

**Notes:** A, Mengla; B, Yuanyang; C, Mojiang; D, Jinghong; E, Xichou; F, Zhenyuan; G, Tengchong; H, Jinggu; I, Ruili; J, Fengqing; K, Pingbian; L, Jiangcheng; M, Shuangjiang; N, Lancang; O, Lingyun; P, Longzhou; Q, Donglan; R, Tianlin; S, Debao; T, Tiane; U, Pingguo; V, Baise; W, Tianyang; X, Jingxi; Y, Napo; MADBH, mean annual increment of diameter at breast height; MAH, mean annual increment of tree height; HCB-Height<sup>-1</sup>, rate of height to live crown base to tree height; CW, crown width; MAVOL, mean annual increment of stem volume; SF, stem form; CS, crown shape; BRA, branchiness. Means with standard error in parenthesis were of significant difference at 0.05 level according to Duncan's multiple range tests if followed by wholly different small letters in the same row.

## References

1. Zeng, J.; Wang, Z.; Zhou, S.; Bai, J.; Zheng, H. Allozyme variation and population genetic structure of *Betula alnoides* from Guangxi, China. *Biochem. Genet.* **2003**, *41*, 61–75. [[CrossRef](#)] [[PubMed](#)]
2. Wang, C.S.; Zhao, Z.G.; Hein, S.; Zeng, J.; Schuler, J.; Guo, J.J. Effect of planting density on knot attributes and branch occlusion of *Betula alnoides* under natural pruning in southern China. *Forests* **2015**, *6*, 1343–1361. [[CrossRef](#)]
3. Sur, T.K.; Pandit, S.; Battacharyya, D.; Kumar, C.K.A.; Lakshmi, S.M.; Chattopadhyay, D.; Mandal, S.C. Studies on the anti-inflammatory activity of *Betula alnoides* bark. *Phytother. Res.* **2002**, *16*, 669–671. [[CrossRef](#)] [[PubMed](#)]
4. Raj, A.D.A.; Malarvili, T.; Velavan, S. Restorative effect of *Betula alnoides* bark on hepatic metabolism in high fat diet fed Wistar rats. *Int. J. Pharma Biol. Sci.* **2015**, *6*, 1281–1288.
5. Zeng, J.; Guo, W.F.; Zhao, Z.G.; Weng, Q.J.; Yin, G.T.; Zhen, H.S. Domestication of *Betula alnoides* in China: Current Status and Perspectives. *For. Res.* **2006**, *19*, 379–384. (In Chinese with English Abstract)
6. Zeng, J.; Zheng, H.; Weng, Q. Geographic distributions and ecological conditions of *Betula alnoides* in China. *For. Res.* **1999**, *12*, 479–484. (In Chinese with English Abstract)
7. Wang, C.S.; Hein, S.; Zhao, Z.G.; Guo, J.J.; Zeng, J. Branch occlusion and discoloration of *Betula alnoides*, under artificial and natural pruning. *For. Ecol. Manag.* **2016**, *375*, 200–210. [[CrossRef](#)]
8. Chen, G.B. Preliminary experimental report on *Betula alnoides* provenance and family in Zhangzhou, Fujian. *J. Fujian For. Sci. Technol.* **2005**, *32*, 78–81. (In Chinese with English Abstract)
9. Guo, W.F.; Zeng, J.; Li, M. Provenance and family trials for *Betula alnoides* in Pingxiang Guangxi province I. early variation of growth traits. *For. Res.* **2008**, *21*, 652–656. (In Chinese with English Abstract)
10. Lin, W.F. The growth difference for different family of *Betula alnoides* in Wutaishan. *Guangdong For. Sci. Technol.* **2008**, *24*, 16–21. (In Chinese with English Abstract)
11. Yang, Y.P.; Guo, J.J.; Huang, J.C.; Zhao, Z.G.; Zhou, Z.M.; Zeng, J. Early choose of *Betula alnoides* provenance and family in western part of Yunnan province. *Seed* **2012**, *31*, 67–70. (In Chinese with English Abstract)
12. Li, Y.J.; Suontama, M.; Burdon, R.D.; Dungey, H.S. Genotype by Environment Interactions in Forest Tree Breeding: Review of Methodology and Perspectives on Research and Application. *Tree Genet. Genomes* **2017**, *13*, 60. [[CrossRef](#)]
13. Costa, S.J.; Potts, B.; Dutkowski, G. Genotype by environment interaction for growth of *Eucalyptus globulus* in Australia. *Tree Genet. Genomes* **2006**, *2*, 61–75. [[CrossRef](#)]
14. Li, B.; McKeand, S.E. Stability of loblolly pine families in the southeastern US. *Silvae Genet.* **1989**, *38*, 96–101.
15. Kim, I.S.; Kwon, H.Y.; Ryu, K.O.; Choi, W.Y. Provenance by site interaction of *Pinus densiflora* in Korea. *Silvae Genet.* **2008**, *57*, 131–139. [[CrossRef](#)]
16. Zhao, X.Y.; Bian, X.Y.; Li, Z.X.; Wang, X.W.; Yang, C.J.; Liu, G.F.; Jiang, J.; Kentbayev, Y.; Kentbayeva, B.; Yang, C.P. Genetic stability analysis of introduced *Betula pendula*, *Betula kirghisorum*, and *Betula pubescens* families in saline-alkali soil of northeastern China. *Scand. J. For. Res.* **2014**, *29*, 639–649. [[CrossRef](#)]
17. Falkenhagen, E. A comparison of the AMMI method with some classical statistical methods in provenance research: The case of the south African *Pinus radiata* trial. *For. Genet.* **1996**, *3*, 81–87.
18. Osorio, L.F.; White, T.L.; Huber, D.A. Age trends of heritabilities and genotype-by-environment interactions for growth traits and wood density from clonal trials of *Eucalyptus grandis* Hill ex Maiden. *Silvae Genet.* **2001**, *50*, 30–37.
19. Suontama, M.; Low, C.B.; Stovold, G.T.; Miller, M.A.; Fleet, K.R.; Li, Y.; Dungey, H.S. Genetic parameters and genetic gains across three breeding cycles for growth and form traits of *Eucalyptus regnans* in New Zealand. *Tree Genet. Genomes* **2015**, *11*, 1–14. [[CrossRef](#)]
20. Wang, C.S.; Zhan, Z.G.; Zeng, J.; Guo, J.J.; Sha, E.; Guo, W.F.; Zeng, J.; Zheng, H.S. Relationship between planting density and tree growth process of *Betula alnoides* mid-young plantations in Pingxiang, Guangxi. *For. Res.* **2013**, *26*, 257–262. (In Chinese with English Abstract)
21. Wang, H.; Guo, J.J.; Zhang, D.; Li, Y.F.; Wang, C.S.; Zhao, Z.G.; Zeng, J. Growth, form variation and early selection of hybrid clones of birch in *Betula* section betulaster. *Mol. Plant Breed.* **2018**, *16*, 1638–1646. (In Chinese with English Abstract)



22. Merk, H.L.; Yarnes, S.C.; Van Deynze, A.; Tong, N.K.; Menda, N.; Mueller, L.A.; Mutschler, M.A.; Loewen, S.A.; Myers, J.R.; Francis, D.M. Trait diversity and potential for selection indices based on variation among regionally adapted processing tomato germplasm. *J. Am. Soc. Hortic. Sci.* **2012**, *137*, 427–437. [[CrossRef](#)]
23. Lai, M.; Dong, L.M.; Yi, M.; Sun, S.W.; Zhang, Y.Y.; Fu, L.; Xu, Z.H.; Lei, L.; Leng, C.H.; Zhang, L. Genetic variation, heritability and genotype  $\times$  environment interactions of resin yield, growth traits and morphologic traits for *Pinus Elliottii* at three progeny trials. *Forests* **2017**, *8*, 409. [[CrossRef](#)]
24. Liu, Q.H.; Zhou, Z.C.; Fan, H.H.; Liu, Y.R. Genetic variation and correlation among resin yield, growth, and morphologic traits of *Pinus massoniana*. *Silv. Genet.* **2013**, *62*, 38–44. [[CrossRef](#)]
25. Diao, S.; Hou, Y.; Xie, Y.; Sun, X. Age trends of genetic parameters, early selection and family by site interactions for growth traits in *Larix Kaempferi* open-pollinated families. *BMC Genet.* **2016**, *17*, 104. [[CrossRef](#)]
26. Yan, W.; Hunt, L.A.; Sheng, Q.; Szlavniks, Z. Cultivar evaluation and mega-environment investigation based on the GGE Biplot. *Crop. Sci.* **2000**, *40*, 597–605. [[CrossRef](#)]
27. Yan, W. GGEbiplot—A windows application for graphical analysis of multi-environment trial data and other types of two-way data. *Agron. J.* **2001**, *93*, 1111–1118. [[CrossRef](#)]
28. Baltunis, B.S.; Brawner, J.T. Clonal stability in *Pinus Radiata* across New Zealand and Australia. I. Growth and form traits. *New For.* **2010**, *40*, 305–322. [[CrossRef](#)]
29. Pliura, A.; Zhang, S.Y.; MacKay, J.; Bousquet, J. Genotypic variation in wood density and growth traits of poplar hybrids at four clonal trials. *For. Ecol. Manag.* **2007**, *238*, 92–106. [[CrossRef](#)]
30. Ivković, M.; Gapare, W.J.; Yang, H.X.; Dutkowski, G.; Buxton, P.; Wu, H. Pattern of genotype by environment interaction for radiata pine in southern Australia. *Ann. For. Sci.* **2015**, *72*, 391–401. [[CrossRef](#)]
31. Dungey, H.S.; Low, C.B.; Lee, J.; Miller, M.A.; Fleet, K.; Yanchuk, A.D. Developing breeding and deployment options for Douglas-fir in New Zealand: Breeding for future forest conditions. *Silvae Genet.* **2012**, *61–63*, 104–115. [[CrossRef](#)]
32. Gapare, W.J.; Ivković, M.; Dutkowski, G.W.; Spencer, D.J.; Buxton, P.; Wu, H.X. Genetic parameters and provenance variation of *Pinus radiata* D. Don. ‘Eldridge collection’ in Australia 1: Growth and form traits. *Tree Genet. Genomes* **2012**, *8*, 391–407. [[CrossRef](#)]
33. Ramesh, K.J. A Study of Variability, Associations, and path analysis in poplar (*Populus deltoides* Bartr. ex Marsh). *J. Sustain. For.* **2012**, *31*, 185–204.
34. Stener, L.G.; Hedenberg, O. Genetic Parameters of wood, fibre, stem quality and growth traits in a clone test with *Betula Pendula*. *Scand. J. For. Res.* **2010**, *18*, 103–110. [[CrossRef](#)]
35. Wang, H.; Zeng, J.X.; Luo, B.G.; Guo, J.J.; Wang, C.S.; Zhao, Z.G.; Zeng, J. Multiple-trait combined selection of superior *Betula alnoides* clones in eastern Guangdong. *J. Cent. South Univ. For. Technol.* **2017**, *37*, 72–75. (In Chinese with English Abstract)
36. Flores, F.; Moreno, M.T.; Cubero, J.I. A comparison of univariate and multivariate methods to analyze G $\times$ E interaction. *Field Crop. Res.* **1998**, *56*, 271–286. [[CrossRef](#)]
37. Liziniewicz, M.; Berlin, M. Differences in growth and areal production between Norway spruce (*Picea abies* L. Karst) regeneration material representing different levels of genetic improvement. *For. Ecol. Manag.* **2019**, *435*, 158–169. [[CrossRef](#)]
38. Grattapaglia, D.; Ribeiro, V.J.; Rezende, G.D.S.P. Retrospective selection of elite parent trees using paternity testing with microsatellite markers: An alternative short term breeding tactic for *Eucalyptus*. *Theor. Appl. Genet.* **2004**, *109*, 192–199. [[CrossRef](#)]

