Scientific Reports

https://doi.org/10.1038/s41598-026-38477-9

Article in Press

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Received: 4 November 2025

Accepted: 29 January 2026

Published online: 08 February 2026

Cite this article as: Wang J., Xing X., Yan P. *et al.* Genetic variation analysis and comprehensive evaluation of multiple traits among *Larix olgensis* families. *Sci Rep* (2026). https://doi.org/10.1038/s41598-026-38477-9

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Genetic Variation Analysis and Comprehensive Evaluation of Multiple Traits among *Larix olgensis* Families

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Abstract In forest genetics research, precise evaluation of half-sib families provides essential insights for the selection and improvement of key species. This study systematically examined 40 half-sib families of *L. olgensis* from northeast China, analyzed 21 traits related to growth, form, wood, photosynthesis, and physiological traits. The research employed analysis of variance (ANOVA), genetic parameter estimation, and correlation analysis to assess family variation and trait relationships. The results indicated that 16 traits differed significant or highly significant ($P < 0.05$) among families. The coefficient of variation (CV) ranged from 7.78% to 65.16%, and family heritability ranged from 0.037 to 0.835. Wood traits showed negative correlations with growth and form traits. Based on average realized gains, we identified the estimation method of breeding value as optimal, leading to the selection of eight superior families at a 20% selection rate, with genetic gains ranged from 1.98% to 65.55%. The realized gains for tree height, diameter at breast height, volume, crown width, straightness, branching angle, lateral branch thickness, wood density, hemicellulose, holocellulose, and lignin were 5.97%, 8.11%, 20.44%, 10.32%, 3.06%, 3.22%, 10.74%, 1.99%, -1.26%, -1.36%, and 2.57%, respectively. These findings demonstrate that multi-trait, breeding-value-based selection effectively improves *L. olgensis*. This study provides both a theoretical basis and practical guidance for the genetic improvement of this economically important species.

Keywords *L. olgensis*, half-sib family, growth traits, wood traits, breeding value, comprehensive selection

L. olgensis, a species within the genus *Larix* (Pinaceae), is a major tree species used for afforestation and timber production in northeastern China. It possesses high economic and ecological value, characterized by a straight and robust trunk, timber that is resistant to decay and humidity, rapid growth, wide adaptability, and a broad distribution. This species serves as an important timber source for industries such as electric utilities, coal mining, shipbuilding, bridge construction, and railroads[1,2]. Since the 1960s, genetic improvement programs for Chinese larch have yielded valuable research outcomes, reliable information, and improved genetic material[3]. The species is of great significance to both the national economy and the ecological environment, aligning with the need to protect ecosystems while meeting the demand for timber essential for daily life and development.

Forest phenotypic performance is generally governed by multiple interacting traits. Consequently, breeding programs that target several traits simultaneously often achieve better outcomes than those focusing on a single trait[4]. Early breeding efforts have primarily focused on the genetic improvement of individual traits, such as growth[5,6], wood[7,8], and cone[9,10]. For example, initial studies on *Pinus taeda* growth selection and *Picea abies* wood improvement relied largely on single-trait heritability estimates and response predictions[11,12]. However, complex genetic correlations among traits indicate that improving one trait may lead to the decline of another (e.g., growth at the expense of stress tolerance). As breeding objectives have diversified, research has increasingly shifted from single-trait selection toward the integrated evaluation of multiple traits[13]. Ding et al.[14] reported a significant negative correlation between holocellulose and 1% NaOH extract content in *L. kaempferi* clones, while Jia et al.[15] used PCA to select hybrid larch family excelling in growth, wood quality, and carbon storage. Similarly, Jastrzębowski et al.[16] found that wood density in *L. decidua* is influenced by both genetics and environment. In response to evolving market demands and the development of directional forest cultivation, the focus of forest genetic improvement is increasingly moving toward the integrated enhancement of both growth and material properties. This strategy supports the development of diverse seed sources for producing timber tailored to specific end uses[17].

This study systematically analyzed the genetic variation of 21 traits—covering growth, form, wood, photosynthesis, and physiological traits—in 10-year-old *L. olgensis*. The objectives were to elucidate the patterns of multi-trait genetic variation in this species and to identify optimal selection strategies. The findings establish a theoretical foundation for the integrated genetic improvement of *L. olgensis* and provide practical guidance for multi-trait breeding programs.

Materials and Methods

Materials sources and experimental design

The experimental materials were obtained from four *L. olgensis* seed orchards located in Heilongjiang Province: Cuohai, Hegang, Linkou, and Bohai (Table 1, Fig. 1). A total of 40 families were collected from these orchards. These included 40 families evaluated for growth, form, and wood traits, and 28 families assessed for photosynthesis and physiological traits. The families originated from local seed orchards, were sown and grown as seedlings in 2013, and were subsequently planted in Hegang City, Heilongjiang Province, in 2015. The planting area had an average annual temperature of 3.8℃ and an average annual precipitation of 651.5 mm; one local check was also included. The experimental design employed a completely randomized block layout, which consisted of four blocks, each containing four rows of 8 plants. The spacing was 1.5 m × 2 m between rows, resulting in a total of 128 individual plants per family.

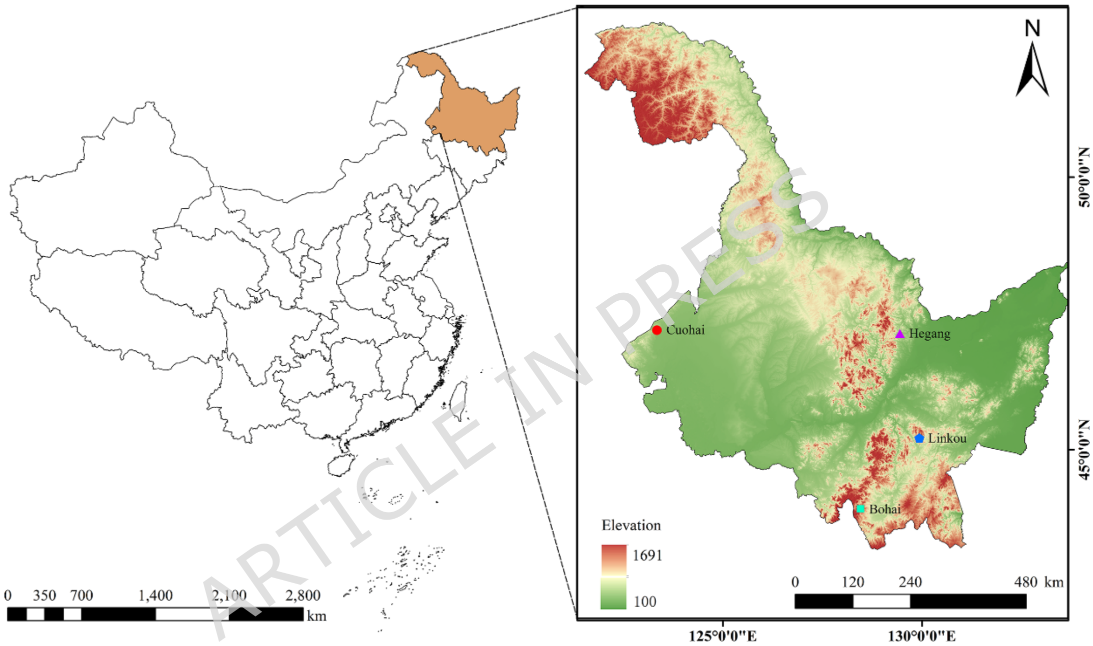

Fig. 1. Geographical locations of the four seed orchards. The figure was generated using ArcMap (version 10.7).

Seed orchards	**Abridge**	**Locations**	**Growth, form and wood traits investigation families**	**Photosynthesis, and physiological traits investigation families**
Cuohai	CH	122°51′ 51.37″E, 47° 27′ 26.75″N	CH303, CH9, CH161, CH252, CH264, CH29, CH27, CH171, CH23, CH211, CH278, CH349,	CH303, CH9, CH161, CH252, CH264, CH29, CH27, CH171, CH23, CH211

			CH309	
Hegang	HG	130°26′ 56.11″E, 47° 32′ 59.66″N	HG45, HG46, HG13, HG48, HG6, HG29, HG28, HG15	HG45, HG46, HG13, HG48, HG6
Linkou	LK	130°16′ 32.63″E, 45° 16′ 32.04″N	LK506, LK459, LK299, LK555, LK229, LK278, LK221, LK563, LK445	LK506, LK459, LK299, LK555, LK229, LK278
Bohai	BS, NB	128°42′ 14.31″E, 44° 10′ 10.39″N	NB124, NB129, NB186, BS18, BS54, BS544, BS309, BS349, BS542, BS209	NB124, NB186, BS18, BS54, BS544, BS309, BS349

Table 1. Information on seed orchards and family of *L. olgensis*

Data survey and analysis

In June 2022, a total of 369 specimens from blocks 1 to 3 were surveyed. Between 9:00 and 11:00 AM under clear weather conditions, three mature trees were randomly selected from each block to measure photosynthetic traits, including net photosynthetic rate (PHOTO, μmol CO_2 m^{-2} s^{-1}), stomatal conductance (COND, mol H_2O m^{-2} s^{-1}), intercellular CO_2 concentration (CI, μmol CO_2 mol^{-1}), and transpiration rate (TR, mmol H_2O m^{-2} s^{-1}). A portable photosynthesis system equipped with red and blue light sources was employed for the measurements. During the measurements, the leaf chamber temperature was maintained at 30°C, the gas flow rate at 500 μmol s^{-1}, and the CO_2 concentration in the leaf chamber at 400 μmol s^{-1}. Following photosynthetic measurements, leaves were collected and transported to the laboratory for analysis of physiological traits, including soluble protein (SP, mg/g), soluble sugar (SS, mg/g), chlorophyll a (CH a, mg/g), chlorophyll b (CH b, mg/g), and total chlorophyll (CH, mg/g). In October of the same year, after tree growth had ceased, all trees were assessed for growth traits, including tree height (H, /m) and diameter at breast height (DBH, /cm), form traits, including crown width (CW, /m), straightness (STR), branch angle (MA, /°), and lateral branch thickness (LBT, /cm). Lateral branches were also collected and sent to the laboratory for evaluation of wood traits, including wood density (WD, /g/cm^3), cellulose (CE, /%), hemicellulose (HC, /%), holocellulose (HO, /%), and lignin (LI, /%). Volume (V /m^3) was calculated based on H and DBH using a standard volume equation.

Photosynthetic traits were measured using a Li-6400XT portable photosynthesis system. Physiological traits were analyzed using assay kits from Suzhou Grise Biotechnology Co., Ltd. The colorimetric method was employed for physiological assays; this method was based on specific chemical reactions that produce colored compounds from target substances, with quantification achieved by measuring absorbance against a standard concentration-absorbance calibration curve. CW was measured along two horizontal directions using a measuring pole and averaged. MA and LBT were assessed on lateral branches located approximately 1.3 m above the base. Three branches per tree were measured in different directions, and the values were averaged. A protractor was used to determine the branching angle, and a digital caliper was employed to measure lateral branch diameter. STR was visually evaluated and classified into three categories: (1) completely straight stems with no bends, (2) stems with one bend, and (3) stems with two or more bends. Following data collection, a square root transformation was applied to normalize the STR data. WD was determined according to the Chinese national standard GB/T 1933-2009. The contents of CE, HC, HO, and LI were measured using an ANKOM 2000i automatic fiber analyzer (Beijing ANKOM Technology Co., Ltd.). H was measured using an ultrasonic hypsometer (Vertex IV, Haglöf Sweden AB), and DBH was determined with a diameter tape.

The formula for volume is[18]:

$$V = g_{1.3}(h + 3)f$$

Where $g_{1.3}$ is the cross-sectional area at the DBH; h is the tree height; f is the number of experimental forms, 0.41 for *larch*.

The ANOVA model is[19]:

$$y_{jk} = \mu + B_j + F_k + BF_{jk} + e_{jk}$$

Where μ is the overall mean; B_j is the effect of the block; F_k is the effect of family; BF_{jk} is the effect of the interaction between the block and the family; e_{jk} is the effect of random error.

The formula for CV is[20]:

$$CV = \frac{SD}{\overline{X}}$$

Where *SD* is the standard deviation of trait observations, $\overline{X}$ is the trait's mean.

The formula for family heritability is[21]:

$$h_F^2 = \frac{\sigma_F^2}{\sigma_F^2 + \frac{\sigma_{FB}^2}{b} + \frac{\sigma_E^2}{nb}}$$

Where σ_F^2 is the family's variance component, σ_{FB}^2 is the family and block interaction variance component, and σ_E^2 is the error variance component. n is the harmonic value of the number of plants per plot, b is the number of blocks.

The formula for genetic coefficient of variation (CV_G) and phenotypic coefficient of variation (CV_P) is[22]:

$$CV_G = \frac{\sigma_g}{\overline{X}} \times 100\%$$

$$CV_P = \frac{\sigma_p}{\overline{X}} \times 100\%$$

Where σ_g is the genetic standard deviation, σ_p is the phenotypic standard deviation, $\overline{X}$ is the family mean.

The genetic gain (ΔG) for each trait is[23]:

$$\Delta G = \frac{i \times \sigma_P \times h_F^2}{\overline{X}} \times 100\%$$

Where i is the intensity of selection (the magnitude is determined by the select rate and group size, which can be found from the normal distribution table), σ_P is the overall standard deviation, h_F^2 is the family heritability, $\overline{X}$ is the mean value of the trait.

The realized gain (G) for each trait is[24]:

$$G = \frac{X_i - \overline{X}}{\overline{X}} \times 100\%$$

Where X_i is the mean of the select family, $\overline{X}$ is the mean of the family.

The formula for comprehensive evaluation method of Brekhin's multiple traits (Q_i) is[25]:

$$Q_i = \sqrt{\sum_{j=1}^{n}(X_{ij}/X_{jmax})}$$

Where X_{ij} is the mean of a trait family, X_{jmax} is the maximum of a trait family, *n* is the number of evaluation indexes.

The best linear unbiased prediction (BLUP) method was employed to estimate breeding values. The formula for breeding value of the family is[26]:

$$y = X\beta + Z\mu + \varepsilon$$

Where β is the block effect, μ is the family effect, ε is the random error effect, X and Z are the incidence matrices of the block effect β and the family effect μ.

The formula for affiliation function formula is[27]:

$$U(X) = \frac{(X - X_{min})}{(X_{max} - X_{min})}$$

Where $U(X)$ is the value of the affiliation function, X is the trait mean, X_{min} and X_{max} are the minimum and maximum of the trait indexes of the participating family.

Data organization and parameter calculations were performed using Microsoft Excel 2021. Analysis of variance and breeding value estimations were conducted with R 4.2.2. Descriptive statistics, correlation analyses, and principal component analyses were executed using SPSS 22.0 and Origin 2024.

Results

Descriptive statistics and ANOVA of multiple traits

ANOVA indicated highly significant differences among families for traits including H, DBH, V, CW, LBT, WD, HC, PHOTO, COND, CI, and TR. Significant differences among families for traits including STR, MA, HO, LI, and SS. These results indicated that the variation in these traits was primarily under genetic control, highlighting their potential for genetic selection and improvement. The CV varied widely across traits, ranging from 7.78% to 65.16% (Table 2).

Trait	**Mean±SD**	**CV (%)**	□	**F-value**	□
			Family	**Block**	**Family×Block**
H	4.78 ± 0.83	17.37	10.275 **	5.545**	4.279**
DBH	4.73 ± 1.38	29.19	4.867**	3.894**	2.303**
V	0.0064 ± 0.0042	65.16	4.727**	2.588	2.266**
CW	2.42 ± 0.51	21.12	11.025 **	1.866	1.825**
STR	1.47 ± 0.67	45.56	1.395*	2.866	1.262
MA	76.83 ± 10.25	13.34	1.581*	1.25	1.164
LBT	1.29 ± 0.30	23.59	4.698**	4.755**	1.55**
WD	0.54 ± 0.05	8.94	1.797**	0.27	1.074
CE	45.04 ± 4.93	10.95	1.183	0.357	1.244
HC	14.79 ± 1.15	7.78	2.861**	1.239	1.03
HO	59.89 ± 5.12	8.55	1.331*	0.199	1.086
LI	28.56 ± 5.57	19.50	1.641*	1.199	1.054
PHOTO	7.40 ± 2.46	33.24	4.633**	5.378**	6.498**
COND	0.17 ± 0.07	41.99	7.633**	8.642**	7.732**
CI	385.00 ± 71.72	18.63	4.334**	9.034**	3.499**
TR	3.51 ± 1.17	33.33	12.195 **	37.361 **	4.606**
SP	11.07 ± 4.67	42.19	0.821	0.132	0.767
SS	0.0314 ± 0.0051	16.07	1.825*	1.579	1.967**
CH a	0.84 ± 0.25	29.76	1.182	0.92	0.832

CH b	0.51 ± 0.22	43.14	1.064	0.904	0.959
CH	1.35 ± 0.41	30.37	1.038	0.249	0.699

Table 2. Descriptive statistics and ANOVA of multiple traits. SD, Standard deviation.
* Significant at 5% level of significance, ** Significant at 1% level of significance

Estimation of genetic parameters

Genetic parameters for each trait were estimated. Family heritability ranged from 0.037 to 0.835 (Fig. 2A). CW exhibited the highest heritability (0.835), whereas CH b showed the lowest (0.037). All growth traits had heritability estimates exceeding 0.7, indicating strong genetic control. With the exception of STR, the heritability of other form traits exceeded 0.2, reflecting moderate or higher genetic control. Similarly, all wood traits except HO were governed by moderate to high genetic control. Photosynthesis traits, COND and TR, also demonstrated moderate genetic control. In contrast, physiological traits showed heritability values below 0.2, suggesting limited genetic control. These results imply that selecting superior families based on growth, form, and wood traits could yield higher genetic and realized gains.

The phenotypic coefficient of variation (CV_P) exceeded the genetic coefficient of variation (CV_G) for all traits. CV_P ranged from 7.87% (HC) to 65.70% (V), while CV_G varied from 1.59% (STR) to 15.98% (V) (Fig. 2B).

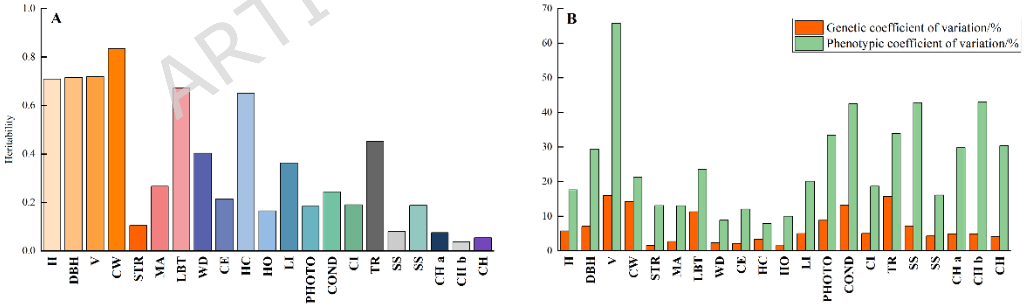

Fig. 2. Family heritability (A), CV_P and CV_G (B) of each trait.

Multiple comparisons among families with different traits

A series of comparative analyses was conducted for multiple traits among the *L. olgensis* families.

For growth traits (Fig. 3), the mean H was 4.78 m, the five highest-performing families exceeded the control group by 27.25% and the overall mean by 9.41% (Fig. 3A). The mean DBH was 4.73 cm, the five highest-performing families exceeded the control group by 39.39% and the overall mean by 11.91% (Fig. 3B). The V was

0.0064 m^3. the five highest-performing families exceeded the overall mean by 31.72% (Fig. 3C).

For form traits (Fig. 4), the mean CW was 2.42 m, the five highest-performing families exceeded the control group by 41.51% and the overall mean by 23.97% (Fig. 4A). The mean STR was 1.47, the five highest-performing families exceeded the control group by 76.58% and the overall mean by 33.33% (Fig. 4B). The mean MA was 76.83°, the five highest-performing families exceeded the control group by 13.89% and the overall mean by 8.03% (Fig. 4C). The mean LBT was 1.29 cm, the five highest-performing families exceeded the control group by 25.83% and the overall mean by 17.05% (Fig. 4D).

For wood traits (Fig. 5), the mean WD was 0.54 g/cm^3, the five highest-performing families exceeded the control group by 2.15% and the overall mean by 5.54% (Fig. 5A). The mean CE was 45.04%, the five highest-performing families exceeded the control group by 1.37% and the overall mean by 6.56% (Fig. 5B). The mean HC was 14.79%, the five highest-performing families exceeded the control group by 9.34% and the overall mean by 6.09% (Fig. 5C). The mean HO was 59.89%, the five highest-performing families exceeded the control group by 1.19% and the overall mean by 4.87% (Fig. 5D). The mean LI was 28.56%, the five highest-performing families exceeded the control group by 13.26% and the overall mean by 11.59% (Fig. 5E).

For photosynthetic traits (Fig. 6), the mean PHOTO was 7.40 μmol CO_2 m^{-2} s^{-1}, the five highest-performing families exceeded the control group by 26.72% and the overall mean by 15.04% (Fig. 6A). The mean COND was 0.17 mol H_2O m^{-2} s^{-1}, the five highest-performing families exceeded the control group by 20.48% and the overall mean by 17.65% (Fig. 6B). The mean CI was 385.00 μmol CO_2 mol^{-1}, the five highest-performing families exceeded the control group by 4.47% and the overall mean by 9.30% (Fig. 6C). The mean TR was 3.51 mmol H_2O m^{-2} s^{-1}, the five highest-performing families exceeded the control group by 64.36% and the overall mean by 22.54% (Fig. 6D).

For physiological traits (Fig. 7), the mean SP was 11.07 mg/g, the five highest-performing families exceeded the control group by 19.26% and the overall mean by 17.00% (Fig. 7A). The mean SS was 0.0314 mg/g, the five highest-performing families exceeded the control group by 8.88% and the overall mean by 10.51% (Fig. 7B). The mean CH a was 0.84 mg/g, the five highest-performing families exceeded the control group by 7.69% and the overall mean by 15.29% (Fig. 7C). The mean CH b was 0.51 mg/g, the five highest-performing families exceeded the control group by 11.86% and the overall mean by 26.92% (Fig. 7D). The mean total CH was 1.35 mg/g, the five highest-performing families exceeded the control group by 3.97% and the overall mean by 15.44% (Fig. 7E).

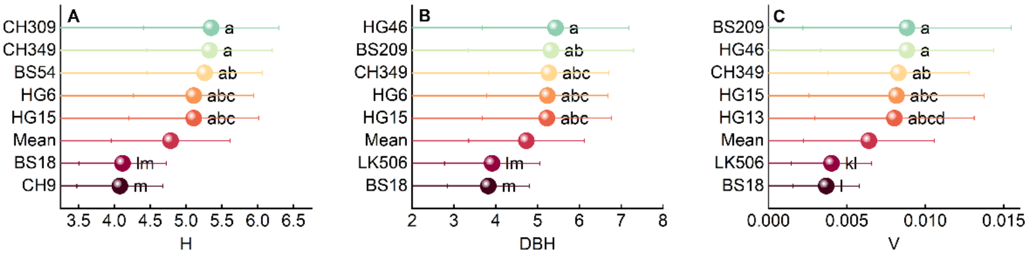

Fig. 3. Multiple comparisons of H (A), DBH (B) and V (C). Due to the large number of families, the chart only displays the top 5, the average, and the bottom 2. The letters in the figure indicate significant differences.

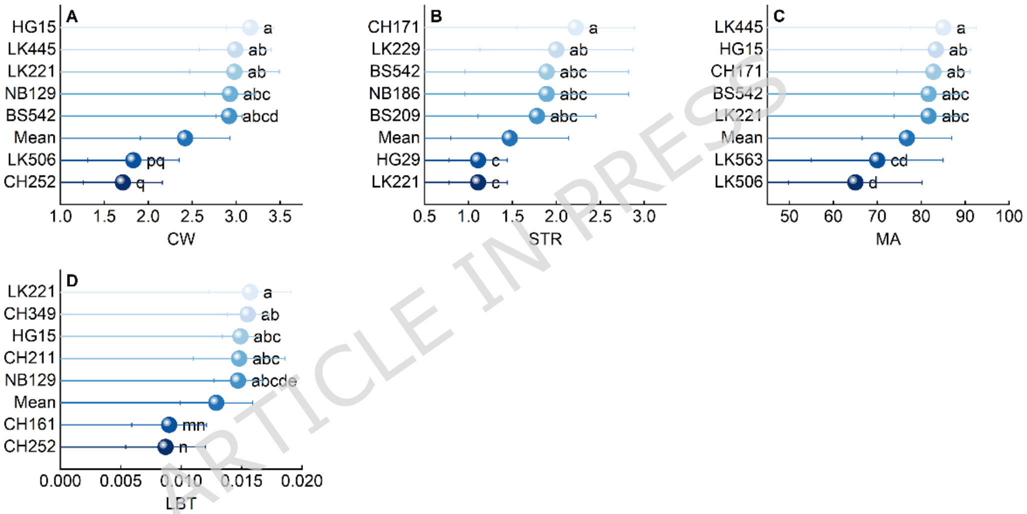

Fig. 4. Multiple comparisons of CW (A), STR (B), MA (C) and LBT (D). Due to the large number of families, the chart only displays the top 5, the average, and the bottom 2. The letters in the figure indicate significant differences.

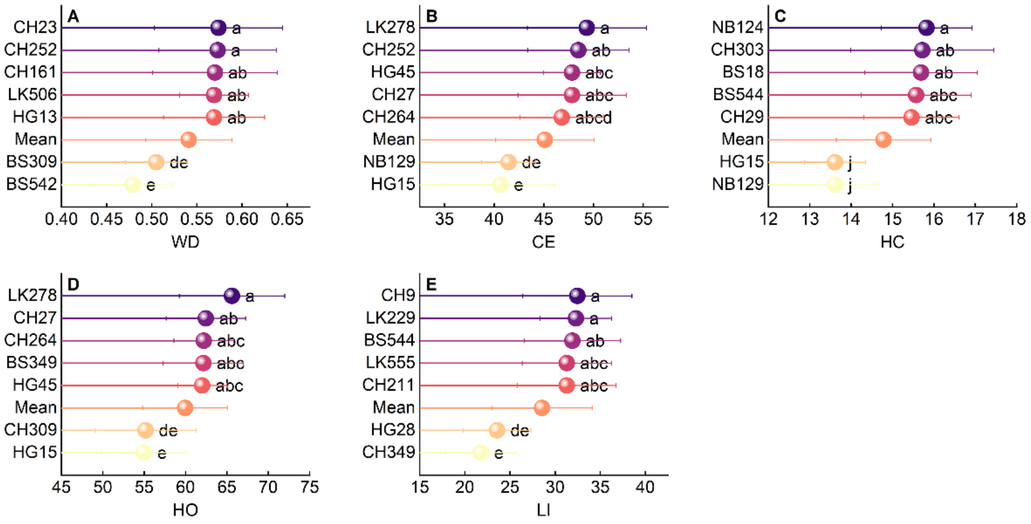

Fig. 5. Multiple comparisons of WD (A), CE (B), HC (C), HO (D) and LI (E). Due to the large number of families, the chart only displays the top 5, the average, and the bottom 2. The letters in the figure indicate significant differences.

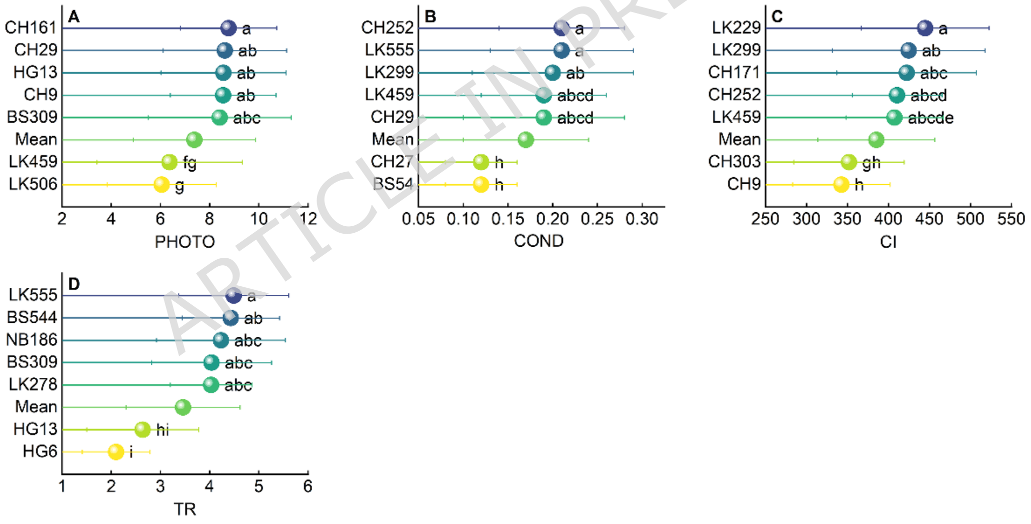

Fig. 6. Multiple comparisons of PHOTO (A), COND (B), CI (C) and TR (D). Due to the large number of families, the chart only displays the top 5, the average, and the bottom 2. The letters in the figure indicate significant differences.

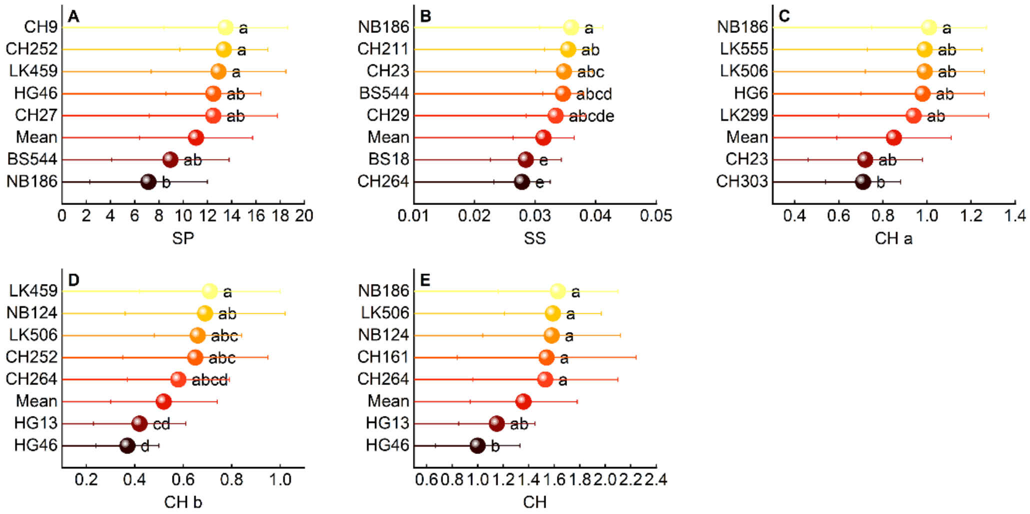

Fig. 7. Multiple comparisons of SP (A), SS (B), CH a (C), CH b (D) and CH (E). Due to the large number of families, the chart only displays the top 5, the average, and the bottom 2. The letters in the figure indicate significant differences.

Correlation analysis of traits

To examine the relationships among traits in *L. olgensis* families, correlation analysis was performed (Fig. 8). Growth traits showed highly significant positive correlations. Form traits, except for STR, also showed highly significant positive correlations. For wood traits, CE showed a highly significant positive correlation with HC, while both traits showed highly significant negative correlations with LI. For photosynthetic traits, stomatal conductance showed a significant or highly significant positive correlation with PHOTO, CI, and TR. CI also showed a significant positive correlation with TR. For physiological traits, SP showed a highly significant negative correlation with SS, whereas CH showed a highly significant positive correlation with both CH a and CH b.

Wood traits showed negative correlations with growth and form traits. Notably, significant or highly significant negative correlations were observed between HC and H, DBH, V, and CW. In addition, WD showed a significant negative correlation with CW. These results indicate independent selectivity between growth and wood traits, implying that superior families can be selected according to different breeding objectives. CI showed a highly significant or significant positive correlation with STR, MA, CH a and CH. SP showed a significant positive correlation with WD. Furthermore, SS showed a highly significant or significant positive correlation with H, CW, MA, LBT and TR. In contrast, CH b showed a highly significant negative correlation with growth and form traits.

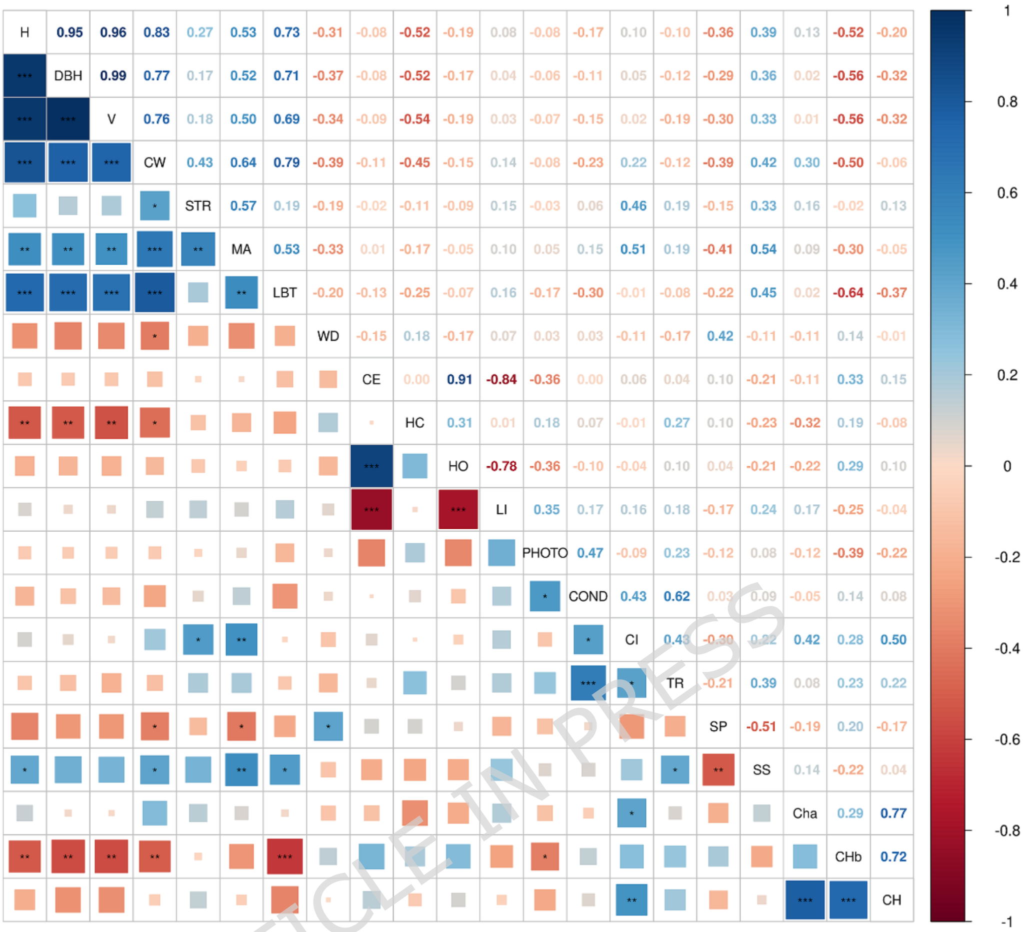

Fig. 8. The correlation matrix of traits is presented, with blue indicating positive correlations and red indicating negative correlations.

PCA and selection of superior families

To prevent one-sidedness in family selection, PCA, comprehensive evaluation method of Brekhin's multiple traits, estimation method of breeding value, and comprehensive evaluation method of affiliation function value were used. We performed PCA on a total of 11 traits with significant differences in growth, form and wood traits. To eliminate dimensional effects and prevent the PCA results from being dominated by traits with high variance, the range method was used to standardize the data for each trait. The 4 principal components together accounted for 82.693% of the cumulative contribution. The first principal component contributed 50.086%, with H, DBH, V, CW, MA, LBT and HC having high absolute loadings. The second principal component contributed 13.184%, with STR having high absolute loadings. The third principal component contributed 10.737%, with WD and LI having high absolute loadings. The fourth principal component contributed 8.686%, with HO having high absolute loadings (Table 3).

Trait	Ingredient			
	1	2	3	4
H	0.913	0.197	-0.148	-0.196
DBH	0.856	0.23	-0.257	-0.35
V	0.875	0.208	-0.227	-0.327
CW	0.905	-0.137	0.168	0.181
STR	0.063	0.791	0.162	0.274
MA	0.67	0.284	0.108	0.382
LBT	0.817	-0.111	0.025	-0.08
WD	0.513	0.222	0.529	0.212
HC	0.743	-0.441	-0.032	0.121
HO	0.531	-0.406	-0.415	0.548
LI	0.375	-0.411	0.723	-0.26
Eigenvalue	5.509	1.45	1.181	0.955
Variance contribution/%	50.086	13.184	10.737	8.686
Cumulative contribution/%	50.086	63.27	74.007	82.693

Table 3. PCA of multiple traits

The expression for the first four principal components was:

$$Y_1=0.166X_1+0.155X_2+0.159X_3+0.164X_4+0.011X_5+0.122X_6+0.148X_7+0.093X_8+0.135X_9+0.096X_{10}+0.068X_{11}$$

$$Y_2=0.136X_1+0.159X_2+0.144X_3-0.095X_4+0.545X_5+0.196X_6-0.077X_7+0.153X_8-0.304X_9-0.280X_{10}-0.284X_{11}$$

$$Y_3=-0.125X_1-0.218X_2-0.192X_3+0.142X_4+0.137X_5+0.092X_6+0.021X_7+0.448X_8-0.027X_9-0.352X_{10}+0.612X_{11}$$

$$Y_4=-0.205X_1-0.366X_2-0.343X_3+0.189X_4+0.287X_5+0.400X_6-0.083X_7+0.222X_8+0.126X_9+0.574X_{10}-0.22X_{11}$$

The principal component score formula was:

$$Y=0.50086Y_1+0.13184Y_2+0.10737Y_3+0.08686Y_4$$

The variables X_1, X_2, X_3, X_4, X_5, X_6, X_7, X_8, X_9, X_{10}, and X_{11} correspond to H, DBH, V, CW, STR, MA, LBT, WD, HC, HO, and LI. Based on the characteristic roots and eigenvectors of each index, the contribution of each trait to the composite index and the normalized weight coefficients were calculated. In the evaluation system, the weighting coefficients for H, DBH, V, CW, STR, MA, LBT, WD, HC, HO, and LI were 10.82%, 8.88%, 9.27%, 12.37%, 8.24%, 12.84%, 9.25%, 12.03%, 6.92%, 4.49%, and 4.89%, respectively.

The principal component score formula was utilized to calculate the index value for each family. At a selection rate of 20%, eight superior families were identified. The index value ranged from 0.477 to 1.047. The realized gain for each trait was 7.25%, 10.01%, 24.34%, 13.88%, 1.13%, 2.50%, 11.76%, 0.19%, -2.18%, -1.29%, and -1.24%, respectively (Table 4).

Family	**Realized gain/%**											**Index value**
	H	**DBH**	**V**	**CW**	**STR**	**MA**	**LBT**	**WD**	**HC**	**HO**	**LI**	
LK229	6.08	8.03	15.89	13.54	34.83	5.57	12.70	2.21	-1.56	-2.47	13.53	1.047
BS209	6.08	12.76	38.04	14.06	20.00	1.95	10.69	-2.74	-1.87	0.50	-7.88	0.772
HG15	7.16	10.75	27.56	30.23	-17.75	8.46	15.95	-0.70	-7.97	-8.22	1.34	0.686
BS54	10.37	7.44	19.98	3.45	5.17	1.23	6.10	0.50	1.18	0.91	4.61	0.681
HG6	7.17	10.98	25.51	10.60	-17.75	3.40	10.04	3.43	-1.58	-2.23	6.46	0.673
LK221	2.34	9.52	21.04	22.89	-25.17	6.29	21.56	1.67	-3.00	-1.58	-5.95	0.545
CH349	11.79	11.72	29.70	17.62	-2.92	-5.28	20.36	-0.65	-6.77	-1.05	-23.56	0.499
BS349	6.99	8.92	17.01	-1.32	12.59	-1.66	-3.30	-2.19	4.13	3.79	1.55	0.477
Mean	7.25	10.01	24.34	13.88	1.13	2.50	11.76	0.19	-2.18	-1.29	-1.24	0.499

Table 4. Index value and realized gain of superior families

Brekhin 's method for selection of superior families

The selection of superior families among the 40 *L. olgensis* families was conducted based on growth, form, and wood traits, using comprehensive evaluation method of Brekhin's multiple traits. At a selection rate of 20%, eight superior families were identified. The Qi values ranged from 3.110 to 3.185. The realized gain for each trait was 6.22%, 5.52%, 15.84%, 16.98%, 12.25%, 4.94%, 8.93%, -3.60%, -2.96%, -2.26%, and -5.23%, respectively (Table 5).

Family	**Realized gain/%**											**Qi value**
	H	**DBH**	**V**	**CW**	**STR**	**MA**	**LBT**	**WD**	**HC**	**HO**	**LI**	
BS542	6.52	0.66	4.21	20.48	27.42	6.29	6.83	-11.45	-0.71	-0.48	-9.67	3.185
CH309	12.27	7.50	21.88	15.55	-2.92	4.12	5.75	-6.18	-6.49	-7.89	-6.41	3.161
HG15	7.16	10.75	27.56	30.23	-17.75	8.46	15.95	-0.70	-7.97	-8.22	1.34	3.138
LK445	3.26	-2.01	-1.23	23.58	-10.34	10.63	9.10	-5.64	-0.66	-0.84	-12.45	3.131
BS209	6.08	12.76	38.04	14.06	20.00	1.95	10.69	-2.74	-1.87	0.50	-7.88	3.128
LK229	-3.44	-5.26	-9.32	0.79	49.67	7.74	-9.91	-3.60	2.31	2.37	3.28	3.119
CH171	11.79	11.72	29.70	17.62	-2.92	-5.28	20.36	-0.65	-6.77	-1.05	-23.56	3.112
CH349	6.08	8.03	15.89	13.54	34.83	5.57	12.70	2.21	-1.56	-2.47	13.53	3.110
Mean	6.22	5.52	15.84	16.98	12.25	4.94	8.93	-3.60	-2.96	-2.26	-5.23	3.14

Table 5. Qi value and the realized gain of superior families

Estimation method of breeding value for selection of superior families

The selection of superior families among the 40 *L. olgensis* families was conducted based on growth, form, and wood traits, using the estimation method of breeding value. The relative importance of each trait was assessed by calculating its weight coefficient through

PCA, and these values were subsequently used to assign weights to each trait. At a selection rate of 20%, eight superior families were identified. The breeding value ranged from 0.344 to 0.822. The realized gain for each trait was 5.97%, 8.11%, 20.44%, 10.32%, 3.06%, 3.22%, 10.74%, 1.99%, -1.26%, -1.36%, and 2.57%, respectively (Table 6).

Family	**Realized gain/%**											**Breeding value**
	H	**DBH**	**V**	**CW**	**STR**	**MA**	**LBT**	**WD**	**HC**	**HO**	**LI**	
LK229	6.08	8.03	15.89	13.54	34.83	5.57	12.70	2.21	-1.56	-2.47	13.53	0.822
HG6	7.17	10.98	25.51	10.60	-17.75	3.40	10.04	3.43	-1.58	-2.23	6.46	0.561
BS209	6.08	12.76	38.04	14.06	20.00	1.95	10.69	-2.74	-1.87	0.50	-7.88	0.546
HG15	7.16	10.75	27.56	30.23	-17.75	8.46	15.95	-0.70	-7.97	-8.22	1.34	0.540
LK221	2.34	9.52	21.04	22.89	-25.17	6.29	21.56	1.67	-3.00	-1.58	-5.95	0.525
BS54	10.37	7.44	19.98	3.45	5.17	1.23	6.10	0.50	1.18	0.91	4.61	0.508
CH23	3.46	2.73	5.30	-9.44	12.59	2.68	7.96	6.20	2.18	1.53	3.45	0.479
HG13	5.06	2.67	10.22	-2.77	12.59	-3.83	0.90	5.36	2.52	0.67	5.00	0.344
Mean	5.97	8.11	20.44	10.32	3.06	3.22	10.74	1.99	-1.26	-1.36	2.57	0.54

Table 6. Breeding value and realized gain of superior families

Comprehensive evaluation method of affiliation function value for selection of superior families

The selection of superior families among the 40 *L. olgensis* families was conducted based on growth, form, and wood traits, using the comprehensive evaluation method of affiliation function value. Weights were assigned to each trait according to the weight coefficients derived from PCA, and the affiliation function value for each trait was computed using the appropriate formula. The comprehensive judgment value for each family was determined by multiplying its weight by the corresponding affiliation function value. At a selection rate of 20%, eight superior families were identified. The comprehensive judgment value ranged from 0.630 to 0.742. The realized gain for each trait was 5.97%, 8.11%, 20.44%, 10.32%, 3.06%, 3.22%, 10.74%, 1.99%, -1.26%, -1.36%, and 2.57%, respectively (Table 7).

Family	**Realized gain/%**											**Comprehensive judgment value**
	H	**DBH**	**V**	**CW**	**STR**	**MA**	**LBT**	**WD**	**HC**	**HO**	**LI**	
LK229	6.08	8.03	15.89	13.54	34.83	5.57	12.70	2.21	-1.56	-2.47	13.53	0.742
BS209	6.08	12.76	38.04	14.06	20.00	1.95	10.69	-2.74	-1.87	0.50	-7.88	0.688
HG6	7.17	10.98	25.51	10.60	-17.75	3.40	10.04	3.43	-1.58	-2.23	6.46	0.686
HG15	7.16	10.75	27.56	30.23	-17.75	8.46	15.95	-0.70	-7.97	-8.22	1.34	0.684
LK221	2.34	9.52	21.04	22.89	-25.17	6.29	21.56	1.67	-3.00	-1.58	-5.95	0.676
BS54	10.37	7.44	19.98	3.45	5.17	1.23	6.10	0.50	1.18	0.91	4.61	0.675
CH23	3.46	2.73	5.30	-9.44	12.59	2.68	7.96	6.20	2.18	1.53	3.45	0.653
HG13	5.06	2.67	10.22	-2.77	12.59	-3.83	0.90	5.36	2.52	0.67	5.00	0.630
Mean	5.97	8.11	20.44	10.32	3.06	3.22	10.74	1.99	-1.26	-1.36	2.57	0.68

Table 7. Comprehensive judgment value and realized gain of superior families

Comparative evaluation of four methods

The selection results indicated that the LK229, BS209, and HG15 families were identified by all four methods concurrently. Further analysis showed that the realized gain for growth traits in the superior families selected by PCA was 13.87%. The realized gain for form traits in the superior families selected by comprehensive evaluation method of Brekhin's multiple traits was 10.77%. The realized gain for wood traits in the superior families selected by estimation method of breeding value was 0.48%. Notably, the overall realized gain achieved through PCA was the highest at 6.03%. However, the negative value for wood traits derived from PCA suggested that the families identified by this method were less favorable for wood traits and may have even regressed. Conversely, although the overall realized gain from the estimation method of breeding value was slightly lower than that from PCA, it exhibited positive average realized gain across growth, form, and wood traits. Furthermore, the estimation method of breeding value effectively mitigated environmental errors, enhancing the reliability of the data. Given that the comprehensive evaluation method of affiliation function value and the estimation method of breeding value produced identical results, the estimation method of breeding value was adopted as the primary approach. The genetic gain based on 20% selection rate ranged from 1.98% to 65.55%.

Discussion

Genetic assessment plays a vital role in the enhancement of forest trees, as it effectively evaluates the genetic performance of breeding materials through testing[28]. In this study, we examined genetic variation across 21 traits in 10-year-old families of *L. olgensis*, encompassing growth, form, wood, photosynthesis, and physiological traits. Our analysis indicated significant or highly significant differences in 16 traits among families, indicated substantial genetic variation. Therefore, the selection of high-quality families is critical for enhancing breeding efficiency. This finding aligns with results from studies on *Quercus acutissima*[29] and *hybrid larch*[30].

Accurate estimation of genetic parameters is crucial for predicting genetic gains, facilitating early selection, and formulating effective breeding strategies[31-33]. Among these parameters, heritability is particularly significant as it indicates the reliability of genotype selection within a population. Estimating family heritability and individual heritability allows for the determination of selection methods and selection intensity. High heritability is advantageous for genetic improvement[21]. Furthermore, heritability is influenced not only by the specific trait but also by factors such as stand age, environmental exposure, and experimental design[34,35]. Su et al.[36] reported that the heritability of various growth traits, wood traits, and chemical compositions of *Pinus massoniana* ranged from 0.31 to 0.95, indicating substantial potential for selective breeding. Our findings indicated that the heritability of most traits exceeded 0.2, suggesting that these traits are predominantly under moderate genetic control and that selecting superior families could yield stable and significant genetic gain. Notably, the average heritability of growth, form, and wood traits surpasses that of photosynthesis and physiological traits. Given that *L. olgensis* is an important material species, the selection of superior families based on these three indices can lead to substantial genetic improvements. Additionally, the CV serves as an indicator of population dispersion and is instrumental in assessing the potential for selection. In *L. olgensis*, the CV_P for each trait exceeds the CV_G. Notably, the CV_P and CV_G for growth and form traits are higher than those for other traits, suggesting that *L. olgensis* possesses greater genetic potential for growth and form traits.

Correlation studies among forest tree traits reveal the degree of correlation between traits, thus providing an important reference for the genetic improvement of forest trees[37]. By analyzing the correlation between traits, we can make trade-offs on traits in the selection process and enhance the selection efficiency of trees. As an important wood species, *L. olgensis* stands out for its growth and wood traits. In the present study, we found highly significant positive correlations between growth traits and form traits, except for STR. This result is in agreement with the results of the M. pauhoi study[38]. This finding means that in most cases, selecting individuals with faster growth naturally yields better shape and quality synchronously. This greatly simplifies early selection. We can take growth traits as the dominant index for early selection, which can indirectly improve the morphological structure of trees while increasing yield, which is highly beneficial for the cultivation of timber forests and landscape forests. However, these two traits showed no significant negative correlations with wood traits other than LI. This result is consistent with the findings for *Pinus kesiya*[39]. Although the correlation is negative, it reveals a potential and subtle trade-off: excessive pursuit of growth speed may lead to a slight decline in wood traits. Therefore, we should establish a multi-trait selection index and assign different economic weights to growth, form, and wood traits according to different breeding objectives.

PCA is a statistical technique that uses fewer and independent indicators to replace multiple related indicators while retaining the original information, and it can provide an objective evaluation of the performance of different traits[40]. In this study, PCA was conduct on 11 traits of growth, form, and wood traits of *L. olgensis*. The results indicated that the 11 traits were divided into four principal components, and each principal component represents different characteristics of trees. The first principal component represents the growth potential and biomass accumulation capacity. The second principal component represents the quality of the trunk. The third principal component represents the substantial density and strength of wood. The fourth principal component represents the total amount of cell wall polysaccharides in wood. The four principal components provide a clear breeding selection axis: if we aim to cultivate high-yield industrial timber forest, we should focus on materials with high scores in the first and second principal components. If we intend to cultivate high-quality structural materials, we should balance the selection of the first and third principal components while ensuring a high score in the second principal component. If the goal is to cultivate special pulpwood, we should prioritize materials with high scores in the first and fourth principal components.

In the early stages of forest tree genetic improvement research, most selection studies on breeding materials concentrate on single-trait variation and selection. However, single-trait selection methods do not yield optimal results. With the diversification of breeding objectives, especially for high-generation breeding materials, selection needs to consider multiple aspects such as growth, adaptability, wood quality, resistance, and nutrient use efficiency. Breeders shift their focus from single-trait selection to a more comprehensive evaluation of multiple traits. This shift can significantly accelerate breeding progress and enhance trait improvement efficiency, and the rationality of the selection method directly impacts selection results[26,41,42]. Moreover, selecting too many traits during evaluation might affect selection gain and reduce individual trait efficiency. Therefore, this study selects the main *L. olgensis* traits for comprehensive evaluation. Four methods are used to select superior families in this study: PCA, comprehensive evaluation method of Brekhin's multiple traits, estimation method of breeding value, and multiple factor comprehensive evaluation method of affiliation function value. Each has its advantages and disadvantages. Brekhin’s method can systematize and standardize weights for indicators[43], but it does not emphasize objective trait weights in multiple-trait evaluation, possibly overlooking families with excellent objective indexes. PCA combines multiple variables into a few indicators that still largely reflect the original variables[44].

The estimation method of breeding value, as an additive effect of phenotypic genetics, can effectively remove the influence of non-genetic factors from environmental variations in complex mountainous areas and improve selection accuracy[45]. The affiliation function value method based on affiliation function values calculates each family's affiliation function value for each trait index via a formula and sums them to obtain a comprehensive evaluation value for selection[26]. The results of the study indicate that the estimation method of breeding value shows positive gain effects in growth, form, and wood traits, although the overall realized gain is slightly lower than that of the PCA. However, considering the impact of non-genetic factors such as environment on the selection of superior families, the estimation method of breeding value is ultimately chosen as the final evaluation method for family selection in this study.

From the current situation of forest genetic improvement, traditional breeding has great limitations. First, many important traits are susceptible to environmental interference, and the accuracy of relying only on phenotypic observation is limited. Moreover, the generation cycle of trees is long, and most tree species need several years or even decades to blossom and bear fruit, leading to the slow breeding process. However, molecular marker technology can predict the target traits through DNA analysis at seedling stage and even seed stage, which can significantly shorten the breeding cycle. And the markers closely linked to the traits can directly select the ideal genotype without environmental interference. In the future, we will also study the genetic diversity of tree species through molecular marker technology, and combine it with the phenotypic traits of trees to study the construction technology of tree population, so as to provide a theoretical basis for the construction of higher generation breeding population of trees.

Conclusion

In this study, there were significant or highly significant differences in most traits among families. This indicates that selecting superior families can lead to higher genetic gain. Growth, form, and wood traits exhibited relatively high heritability, indicating that these traits were subject to strong genetic control. Selecting superior families based on these traits can achieve higher realized gain. Correlation analysis indicated that growth and form traits showed significant negative correlations with wood traits, suggesting that the genetic control among them is independent. Superior families were screened according to four methods. After comparison, it was found that if the estimation method of breeding value was used for screening, favorable realized gain values can be obtained for growth, form, and wood traits. Therefore, based on the estimation method of breeding value, eight superior families were screened out with a 20% selection rate as the standard. These families can be promoted in the Hegang area of China and other regions with similar site conditions, thereby providing technical support and superior materials for the genetic improvement of *L. olgensis*.

Data availability

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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Acknowledgements

Thank the forest farm where the experimental forest is located for its support to this experiment.

Author contributions

Jiaxing Wang analyzed the data and wrote the manuscript. Xuemei Xing and Pingyu Yan helped to analyze the data. Haohao Wang and Zixiong Xie measured the traits. Hanguo Zhang proposed the idea, provided financial support and scientifically contributed to the writing of the manuscript draft.

Funding

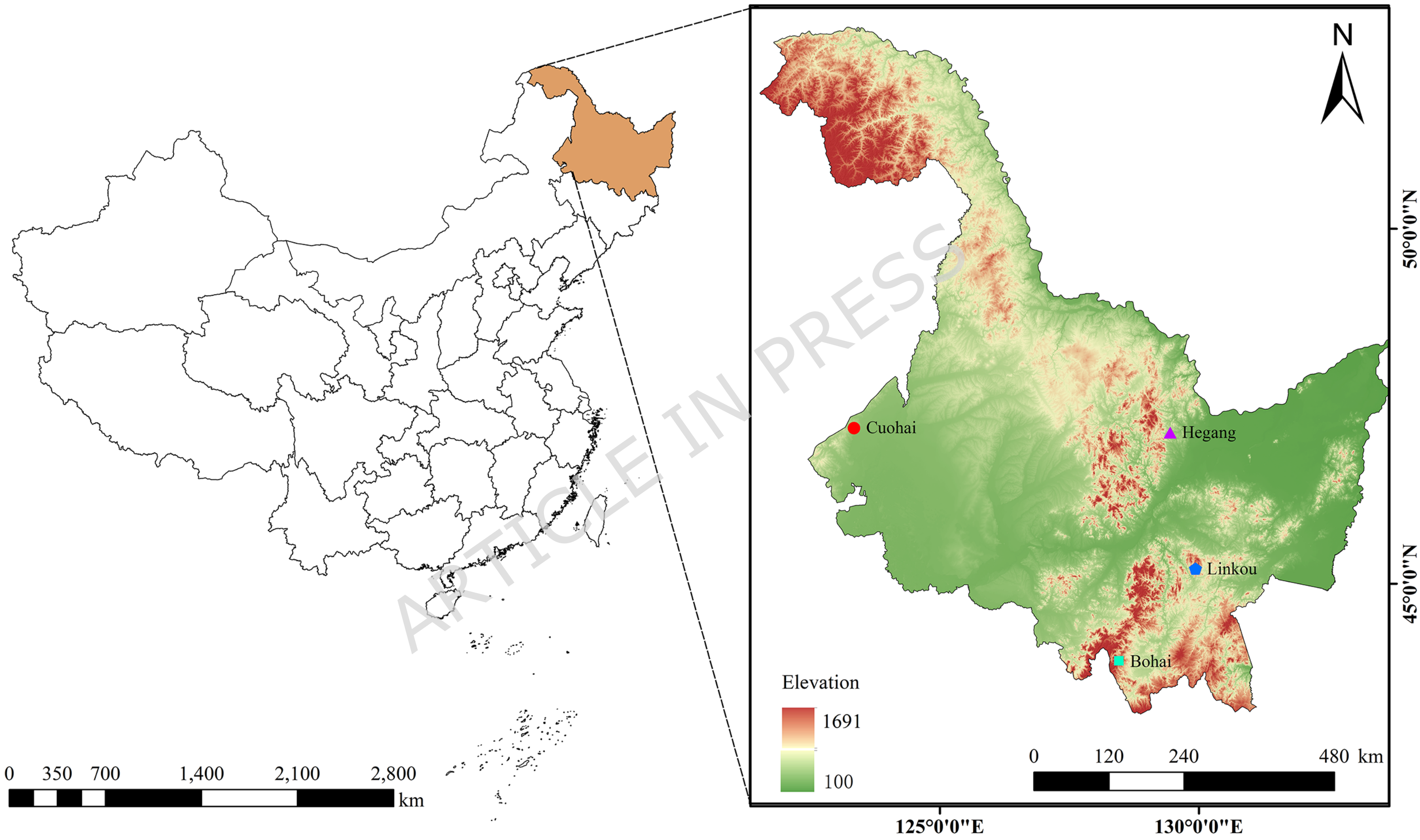
This research was funded by the grants from the Science and T echnology Innovation 2030-Agricultural Biological Breeding Majo r Project (Grant no. 2023ZD040590303).

Competing interests

The authors declare no competing interests.

Ethics approval

This study focused exclusively on tree research and did not involve any human or animal subjects. As a result, it did not require approval from an ethics committee. The research adhered to all applicable guidelines and regulations for plant studies to ensure ethical and responsible conduct of the research.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km
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50°0'0"N
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Cuohai
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Linkou
Bohai
Elevation
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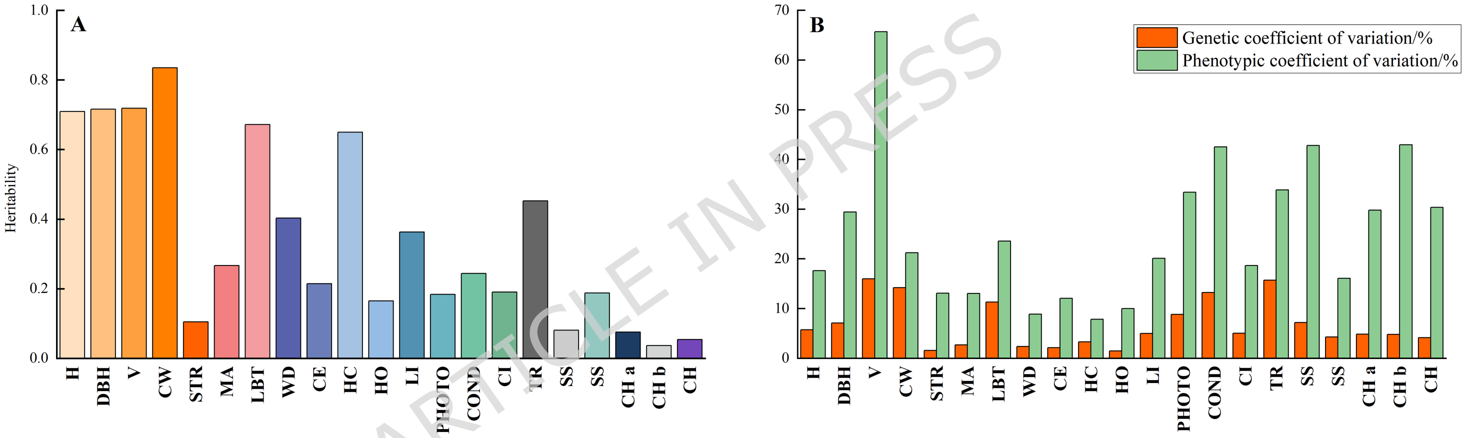
km
125°0'0"E
130°0'0"E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CE
HC
HO
LI
PHOTO
COND
CI
TR
SS
SS
CH a
CH b
CH
B
0
10
20
30
40
50
60
70
Genetic coefficient of variation/%
Phenotypic coefficient of variation/%
H
DBH
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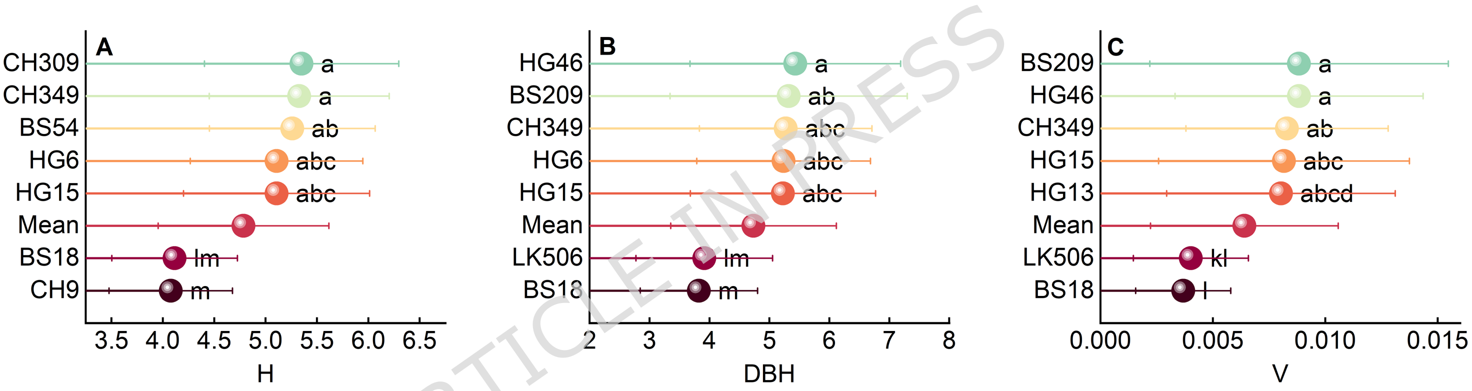
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7
8
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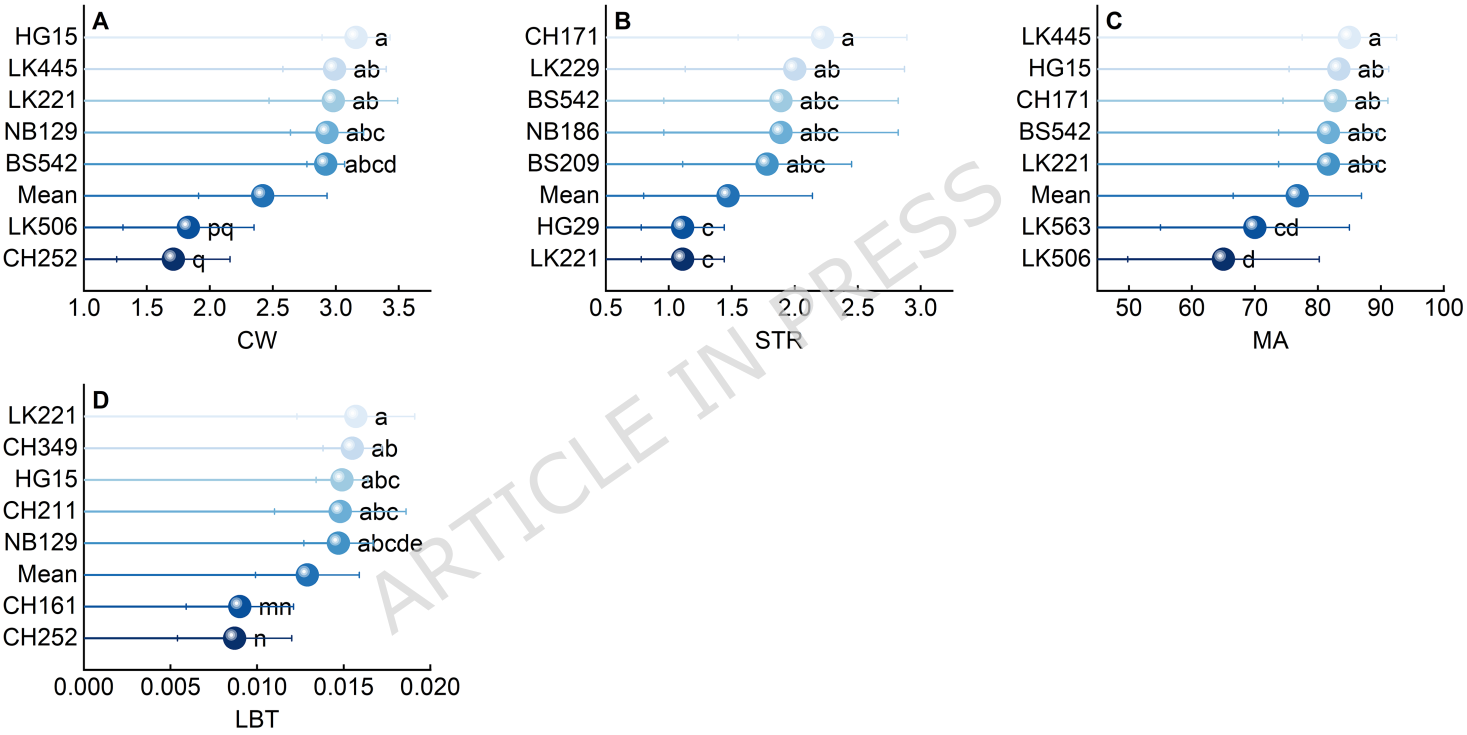
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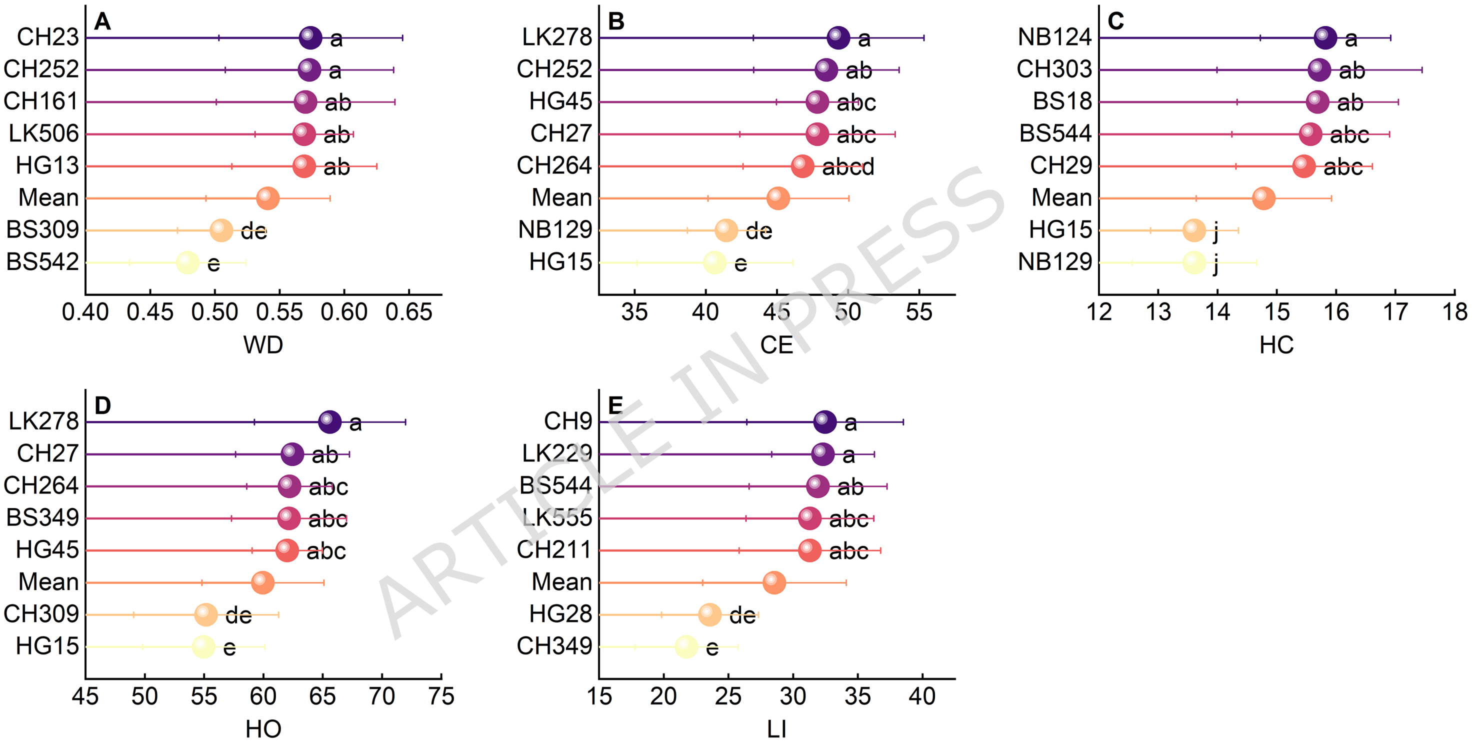
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abc
abcd
de
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40
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CE
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NB124
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Mean
HG15
NB129
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ab
ab
abc
abc
j
j
12
13
14
15
16
17
18
HC
D
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CH27
CH264
BS349
HG45
Mean
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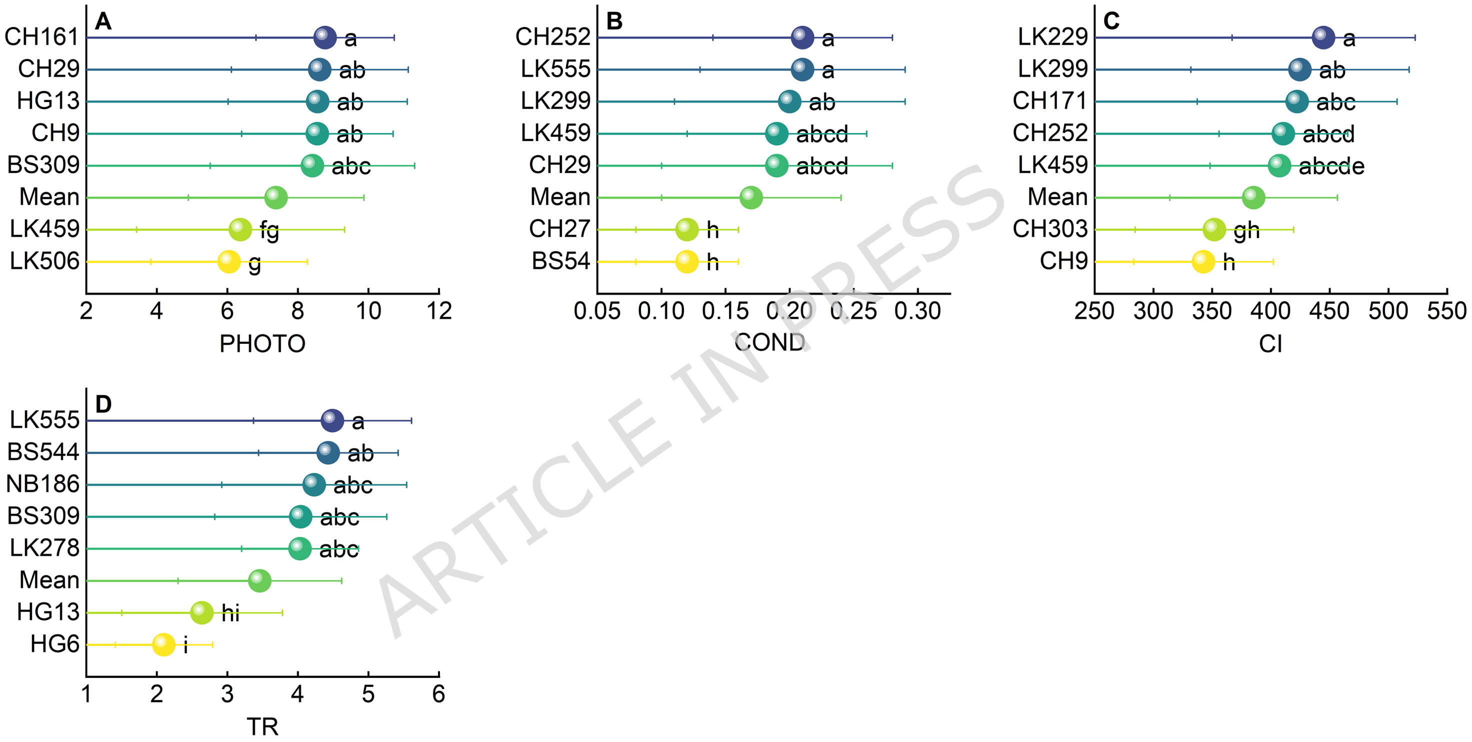
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abcd
Mean
CH27
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BS54
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0.15
0.20
0.25
0.30
COND
C
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LK299
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CH171
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CH252
abcd
LK459
abcde
Mean
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gh
CH9
h
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300
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400
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500
550
CI
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2
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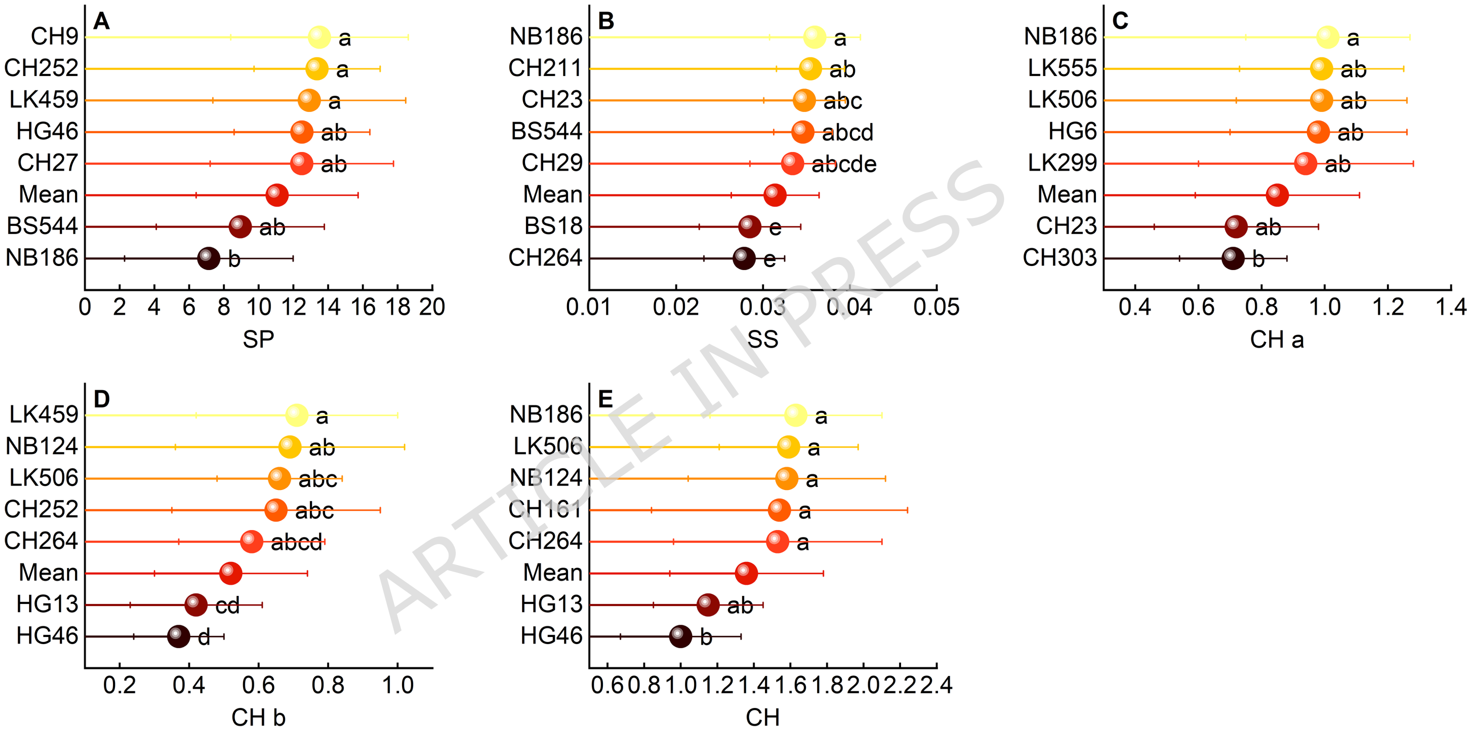
4
5
6
TR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CH27 ab
Mean
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NB186 b
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SP
B
NB186 a
CH211 ab
CH23 abc
BS544 abcd
CH29 abcde
Mean
BS18 e
CH264 e
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SS
C
NB186 a
LK555 ab
LK506 ab
HG6 ab
LK299 ab
Mean
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CH303 b
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CH a
D
LK459 a
NB124 ab
LK506 abc
CH252 abc
CH264 abcd
Mean
HG13 cd
HG46 d
0.2 0.4 0.6 0.8 1.0
CH b
E
NB186 a
LK506 a
NB124 a
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CH264 a
Mean
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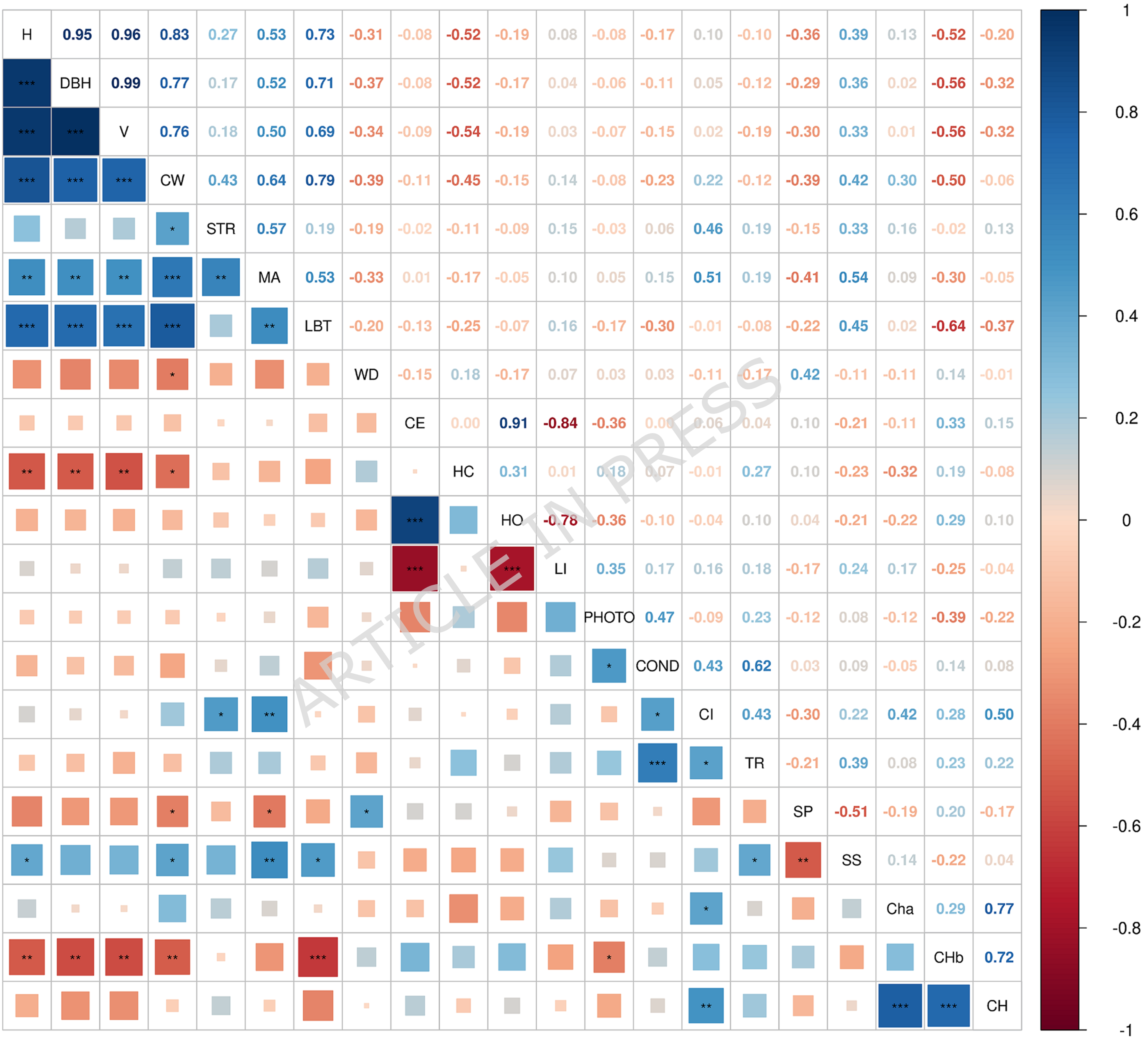
CH



H	0.95	0.96	0.83	0.27	0.53	0.73	-0.31	-0.08	-0.52	-0.19	0.08	-0.08	-0.17	0.10	-0.10	-0.36	0.39	0.13	-0.52	-0.20
***	DBH	0.99	0.77	0.17	0.52	0.71	-0.37	-0.08	-0.52	-0.17	0.04	-0.06	-0.11	0.05	-0.12	-0.29	0.36	0.02	-0.56	-0.32
***	***	V	0.76	0.18	0.50	0.69	-0.34	-0.09	-0.54	-0.19	0.03	-0.07	-0.15	0.02	-0.19	-0.30	0.33	0.01	-0.56	-0.32
***	***	***	CW	0.43	0.64	0.79	-0.39	-0.11	-0.45	-0.15	0.14	-0.08	-0.23	0.22	-0.12	-0.39	0.42	0.30	-0.50	-0.06
			*	STR	0.57	0.19	-0.19	-0.02	-0.11	-0.09	0.15	-0.03	0.06	0.46	0.19	-0.15	0.33	0.16	-0.02	0.13
**	**	**	***	**	MA	0.53	-0.33	0.01	-0.17	-0.05	0.10	0.05	0.15	0.51	0.19	-0.41	0.54	0.09	-0.30	-0.05
***	***	***	***		**	LBT	-0.20	-0.13	-0.25	-0.07	0.16	-0.17	-0.30	-0.01	-0.08	-0.22	0.45	0.02	-0.64	-0.37
			*				WD	-0.15	0.18	-0.17	0.07	0.03	0.03	-0.11	-0.17	0.42	-0.11	-0.11	0.14	-0.01
								CE	0.00	0.91	-0.84	-0.36	0.00	0.06	0.04	0.10	-0.21	-0.11	0.33	0.15
**	**	**	*						HC	0.31	0.01	0.18	0.07	-0.01	0.27	0.10	-0.23	-0.32	0.19	-0.08
								***		HO	-0.78	-0.36	-0.10	-0.04	0.10	0.04	-0.21	-0.22	0.29	0.10
								***		***	LI	0.35	0.17	0.16	0.18	-0.17	0.24	0.17	-0.25	-0.04
												PHOTO	0.47	-0.09	0.23	-0.12	0.08	-0.12	-0.39	-0.22
												*	COND	0.43	0.62	0.03	0.09	-0.05	0.14	0.08
				*	**								*	CI	0.43	-0.30	0.22	0.42	0.28	0.50
													***	*	TR	-0.21	0.39	0.08	0.23	0.22
			*		*		*									SP	-0.51	-0.19	0.20	-0.17
*			*		**	*									*	**	SS	0.14	-0.22	0.04
														*				Cha	0.29	0.77
**	**	**	**			***						*							CHb	0.72
														**				***	***	CH

Seed orchards	**Abridge**	**Locations**	**Growth, form and wood-property traits investigation families**	**Photosynthesis, and physiological traits investigation families**
Cuohai	CH	122°51′ 51.37″E, 47° 27′ 26.75″N	CH303, CH9, CH161, CH252, CH264, CH29, CH27, CH171, CH23, CH211, CH278, CH349, CH309	CH303, CH9, CH161, CH252, CH264, CH29, CH27, CH171, CH23, CH211
Hegang	HG	130°26′ 56.11″E, 47° 32′ 59.66″N	HG45, HG46, HG13, HG48, HG6, HG29, HG28, HG15	HG45, HG46, HG13, HG48, HG6
Linkou	LK	130°16′ 32.63″E, 45° 16′ 32.04″N	LK506, LK459, LK299, LK555, LK229, LK278, LK221, LK563, LK445	LK506, LK459, LK299, LK555, LK229, LK278
Bohai	BS, NB	128°42′ 14.31″E, 44° 10′ 10.39″N	NB124, NB129, NB186, BS18, BS54, BS544, BS309, BS349, BS542, BS209	NB124, NB186, BS18, BS54, BS544, BS309, BS349

Table 1. Information on seed orchards and family of *L. olgensis*

Trait	Mean±SD	CV (%)		F-value	
			Family	Block	Family×Block
H	4.78 ± 0.83	17.37	10.275**	5.545**	4.279**
DBH	4.73 ± 1.38	29.19	4.867**	3.894**	2.303**
V	0.0064 ± 0.0042	65.16	4.727**	2.588	2.266**
CW	2.42 ± 0.51	21.12	11.025**	1.866	1.825**
STR	1.47 ± 0.67	45.56	1.395*	2.866	1.262
MA	76.83 ± 10.25	13.34	1.581*	1.25	1.164
LBT	1.29 ± 0.30	23.59	4.698**	4.755**	1.55**
WD	0.54 ± 0.05	8.94	1.797**	0.27	1.074
CE	45.04 ± 4.93	10.95	1.183	0.357	1.244
HC	14.79 ± 1.15	7.78	2.861**	1.239	1.03
HO	59.89 ± 5.12	8.55	1.331*	0.199	1.086
LI	28.56 ± 5.57	19.50	1.641*	1.199	1.054
PHOTO	7.40 ± 2.46	33.24	4.633**	5.378**	6.498**
COND	0.17 ± 0.07	41.99	7.633**	8.642**	7.732**
CI	385.00 ± 71.72	18.63	4.334**	9.034**	3.499**
TR	3.51 ± 1.17	33.33	12.195**	37.361**	4.606**
SP	11.07 ± 4.67	42.19	0.821	0.132	0.767
SS	0.0314 ± 0.0051	16.07	1.825*	1.579	1.967**
CH a	0.84 ± 0.25	29.76	1.182	0.92	0.832
CH b	0.51 ± 0.22	43.14	1.064	0.904	0.959
CH	1.35 ± 0.41	30.37	1.038	0.249	0.699

Table 2. Descriptive statistics and ANOVA of multiple traits. SD, Standard deviation.
* Significant at 5% level of significance, ** Significant at 1% level of significance

Trait	Ingredient			
	1	2	3	4
H	0.913	0.197	-0.148	-0.196
DBH	0.856	0.23	-0.257	-0.35
V	0.875	0.208	-0.227	-0.327
CW	0.905	-0.137	0.168	0.181
STR	0.063	0.791	0.162	0.274
MA	0.67	0.284	0.108	0.382
LBT	0.817	-0.111	0.025	-0.08
WD	0.513	0.222	0.529	0.212
HC	0.743	-0.441	-0.032	0.121
HO	0.531	-0.406	-0.415	0.548
LI	0.375	-0.411	0.723	-0.26
Eigenvalue	5.509	1.45	1.181	0.955
Variance contribution/%	50.086	13.184	10.737	8.686
Cumulative contribution/%	50.086	63.27	74.007	82.693

Table 3. PCA of multiple traits

Family	Realized gain/%											Index value
	H	DBH	V	CW	STR	MA	LBT	WD	HC	HO	LI	
LK229	6.08	8.03	15.89	13.54	34.83	5.57	12.70	2.21	-1.56	-2.47	13.53	1.047
BS209	6.08	12.76	38.04	14.06	20.00	1.95	10.69	-2.74	-1.87	0.50	-7.88	0.772
HG15	7.16	10.75	27.56	30.23	-17.75	8.46	15.95	-0.70	-7.97	-8.22	1.34	0.686
BS54	10.37	7.44	19.98	3.45	5.17	1.23	6.10	0.50	1.18	0.91	4.61	0.681
HG6	7.17	10.98	25.51	10.60	-17.75	3.40	10.04	3.43	-1.58	-2.23	6.46	0.673
LK221	2.34	9.52	21.04	22.89	-25.17	6.29	21.56	1.67	-3.00	-1.58	-5.95	0.545
CH349	11.79	11.72	29.70	17.62	-2.92	-5.28	20.36	-0.65	-6.77	-1.05	-23.56	0.499
BS349	6.99	8.92	17.01	-1.32	12.59	-1.66	-3.30	-2.19	4.13	3.79	1.55	0.477
Mean	7.25	10.01	24.34	13.88	1.13	2.50	11.76	0.19	-2.18	-1.29	-1.24	0.499

Table 4. Index value and realized gain of superior families

Family	Realized gain/%											Qi value
	H	DBH	V	CW	STR	MA	LBT	WD	HC	HO	LI	
BS542	6.52	0.66	4.21	20.48	27.42	6.29	6.83	-11.45	-0.71	-0.48	-9.67	3.185
CH309	12.27	7.50	21.88	15.55	-2.92	4.12	5.75	-6.18	-6.49	-7.89	-6.41	3.161
HG15	7.16	10.75	27.56	30.23	-17.75	8.46	15.95	-0.70	-7.97	-8.22	1.34	3.138
LK445	3.26	-2.01	-1.23	23.58	-10.34	10.63	9.10	-5.64	-0.66	-0.84	-12.45	3.131
BS209	6.08	12.76	38.04	14.06	20.00	1.95	10.69	-2.74	-1.87	0.50	-7.88	3.128
LK229	-3.44	-5.26	-9.32	0.79	49.67	7.74	-9.91	-3.60	2.31	2.37	3.28	3.119
CH171	11.79	11.72	29.70	17.62	-2.92	-5.28	20.36	-0.65	-6.77	-1.05	-23.56	3.112
CH349	6.08	8.03	15.89	13.54	34.83	5.57	12.70	2.21	-1.56	-2.47	13.53	3.110
Mean	6.22	5.52	15.84	16.98	12.25	4.94	8.93	-3.60	-2.96	-2.26	-5.23	3.14

Table 5. Qi value and the realized gain of superior families

Family	**Realized gain/%**											**Breeding value**
	H	**DBH**	**V**	**CW**	**STR**	**MA**	**LBT**	**WD**	**HC**	**HO**	**LI**	
LK229	6.08	8.03	15.89	13.54	34.83	5.57	12.70	2.21	-1.56	-2.47	13.53	0.822
HG6	7.17	10.98	25.51	10.60	-17.75	3.40	10.04	3.43	-1.58	-2.23	6.46	0.561
BS209	6.08	12.76	38.04	14.06	20.00	1.95	10.69	-2.74	-1.87	0.50	-7.88	0.546
HG15	7.16	10.75	27.56	30.23	-17.75	8.46	15.95	-0.70	-7.97	-8.22	1.34	0.540
LK221	2.34	9.52	21.04	22.89	-25.17	6.29	21.56	1.67	-3.00	-1.58	-5.95	0.525
BS54	10.37	7.44	19.98	3.45	5.17	1.23	6.10	0.50	1.18	0.91	4.61	0.508
CH23	3.46	2.73	5.30	-9.44	12.59	2.68	7.96	6.20	2.18	1.53	3.45	0.479
HG13	5.06	2.67	10.22	-2.77	12.59	-3.83	0.90	5.36	2.52	0.67	5.00	0.344
Mean	5.97	8.11	20.44	10.32	3.06	3.22	10.74	1.99	-1.26	-1.36	2.57	0.54

Table 6. Breeding value and realized gain of superior families

Family	Realized gain/%											Comprehensive judgment value
	H	DBH	V	CW	STR	MA	LBT	WD	HC	HO	LI	
LK229	6.08	8.03	15.89	13.54	34.83	5.57	12.70	2.21	-1.56	-2.47	13.53	0.742
BS209	6.08	12.76	38.04	14.06	20.00	1.95	10.69	-2.74	-1.87	0.50	-7.88	0.688
HG6	7.17	10.98	25.51	10.60	-17.75	3.40	10.04	3.43	-1.58	-2.23	6.46	0.686
HG15	7.16	10.75	27.56	30.23	-17.75	8.46	15.95	-0.70	-7.97	-8.22	1.34	0.684
LK221	2.34	9.52	21.04	22.89	-25.17	6.29	21.56	1.67	-3.00	-1.58	-5.95	0.676
BS54	10.37	7.44	19.98	3.45	5.17	1.23	6.10	0.50	1.18	0.91	4.61	0.675
CH23	3.46	2.73	5.30	-9.44	12.59	2.68	7.96	6.20	2.18	1.53	3.45	0.653
HG13	5.06	2.67	10.22	-2.77	12.59	-3.83	0.90	5.36	2.52	0.67	5.00	0.630
Mean	5.97	8.11	20.44	10.32	3.06	3.22	10.74	1.99	-1.26	-1.36	2.57	0.68

Table 7. Comprehensive judgment value and realized gain of superior families