



Genetic variation and selection of half-sib families of *Pinus sibirica* in the Xinlin district of the Greater Khingan Range

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Abstract To investigate the genetic variation patterns of multiple traits in *Pinus sibirica* half_sib families introduced to the Greater Khingan Range, this study aims to establish a comprehensive trait evaluation system based on genetic parameters and identify fast-growing, high-quality genetic materials. The findings provide scientific support for advanced-generation seed orchard development and multi-objective genetic improvement. A total of 66 half-sib families from a 26-year-old trial plantation of the Tomsk seed source were evaluated. Eleven traits were measured, including growth traits (tree height, diameter at breast height, volume, and crown width), morphological traits (lateral branch diameter), wood quality traits (Pilodyn value), and needle traits (fresh weight, dry weight, moisture content, needle length, and needle width). Genetic parameters were estimated using variance component decomposition.

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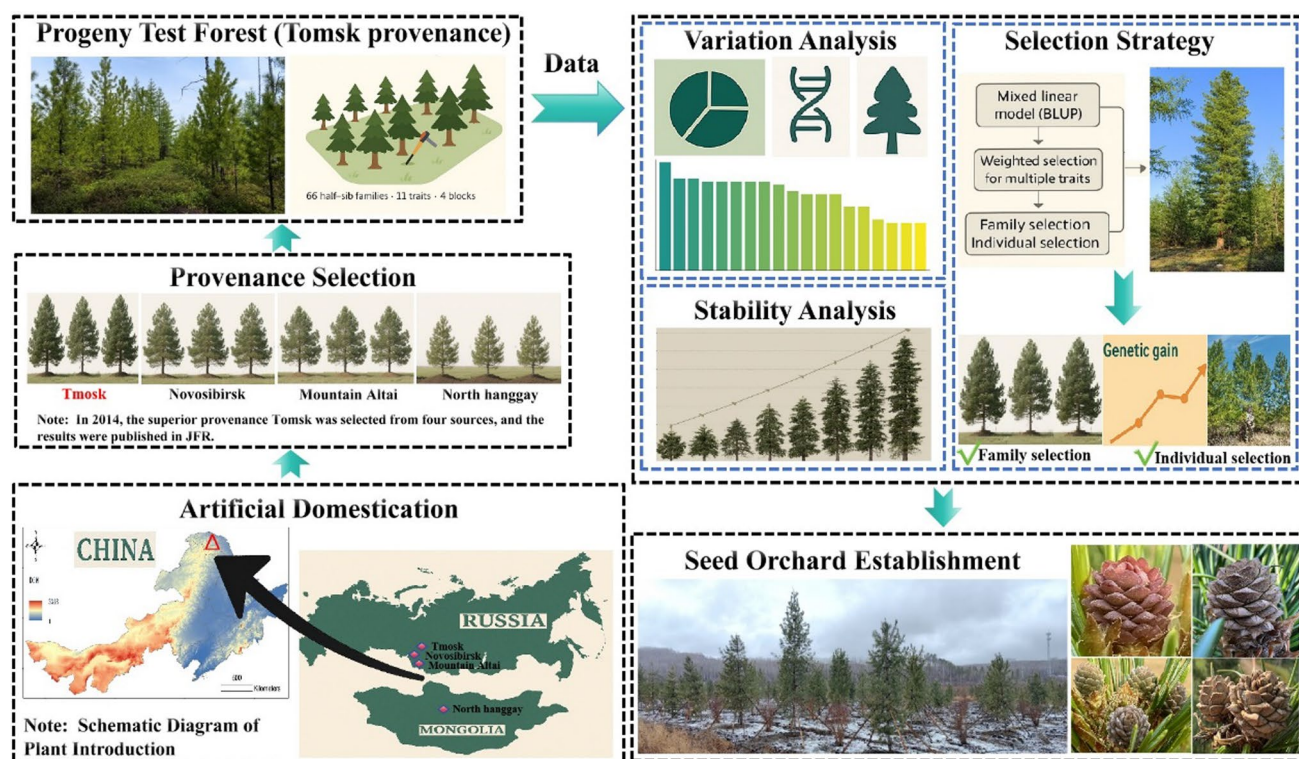
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Superior families with favorable performance in both growth and wood density traits were identified using Best Linear Unbiased Prediction (BLUP) weighted by genetic correlation coefficients. Additionally, individual tree selection was conducted based on growth traits using the index selection method. Significant genetic differences among families (Z ratio > 1.50) were observed for 10 traits, including growth, wood density, and needle traits. The phenotypic coefficient of variation (PCV: 5.05–62.50%) and genetic coefficient of variation (GCV: 2.19–13.81%) exhibited substantial heterogeneity. Volume displayed the highest variation (PCV = 62.50%, GCV = 13.81%), while the highest family heritability was observed for the needle length-to-width ratio ($h^2 = 78.30\%$), and the highest individual heritability was recorded for needle moisture content ($H^2 = 95.22\%$). Genetic correlations analysis revealed strong positive associations between volume and tree height ($r = 0.880$), diameter at breast height ($r = 0.968$), and Pilodyn value ($r = 0.508$). Using the BLUP method, 13 superior families (e.g., Families 59, 11, and 51) were identified, with an average genetic gain in volume of 13.377% and a family retention rate of 70%, significantly exceeding the population mean (65.10%). Through index selection, 94 elite individual trees were selected, 52.14% of which originated from superior families. The genetic gain in individual tree volume reached 26.80%, with the within-family gain for elite individuals increasing to 28.47%. This study establishes the first multi-trait genetic evaluation model for *P. sibirica* and proposes a “family-individual” collaborative selection strategy. The selected superior families achieved a volume genetic gain of 3.864–32.307% and an overall genetic gain of 2.729–20.069%, while elite individual trees exhibited a volume genetic gain of 16.328–52.716%. These findings would provide critical technical support for multi-objective breeding and seed orchard development in cold-temperate coniferous species.

Graphic abstract



Keywords *Pinus sibirica* · Half-sib family · Genetic parameter estimation · Selection of families and single plants

Introduction

The Greater Khingan Range of China, with a forest area of approximately 150,000 km², accounts for 25% of the total forest area in Northeast China. This region serves as a critical ecological barrier, supporting the industrial, agricultural, pastoral, and fishing industries in Northeast China and Inner Mongolia. However, challenges persist, including a simplified forest structure dominated by single-species, even-aged stands, fragile ecosystems, and low economic value of forest products. These issues severely hinder the region's sustainable development. To enhance ecosystem stability and improve economic benefits, the introduction of valuable shade-tolerant tree species for establishing multi-layer, uneven-aged mixed forests has become an important area of focus.

Pinus sibirica, known as the “King of the Taiga” in the temperate coniferous forests of Eurasia, is a key species for forest formation in cold-temperate regions (Zhao et al. 1991a). This species shares morphological characteristics

and economic value with *Pinus koraiensis*, which is also found in Northeast China. Both species are economically valuable for both timber production and nut yield and are naturally distributed in the northwestern Altai Mountains and the Greater Khingan Range of China (Zhao 1981). To optimize the forest structure of the Greater Khingan Range, Professor Zhao Guangyi's team at Northeast Forestry University has conducted systematic feasibility studies on the introduction of *P. sibirica* since the 1980s. These studies have compared the species' morphological and anatomical features (Zhao et al. 1989, 1998), ecological adaptability (Zhao et al. 1991b; Liu et al. 2002), seed biological characteristics (Mao et al. 2003), and genetic diversity (Yang et al. 2005). As a result, seeds from various seed sources, such as Tmsk and Ulan-Ude in Russia, have been introduced for regional trials (Wei et al. 2011). After more than 30 years of observation, *P. sibirica* has been confirmed to be well-adapted to the Greater Khingan Range, with Tmsk and Ulan-Ude identified as superior seed sources (Zhao et al. 2014; Ji et al. 2023). However, most existing studies have focused on seed source selection, while genetic improvement at the family and individual tree levels remains largely unexplored.

This study focuses on the half-sibling family trial forest of the Tmsk seed source. By combining the Best Linear Unbiased Prediction (BLUP) method with the index selection

Table 1 Environmental factors of Tomsk province and the experimental site in Xinlin

Site	Longitude	Latitude	Annual mean temperature (°C)	Annual mean precipitation (mm)	Average temperature in June (°C)	Average temperature in July (°C)	Average temperature in August (°C)	Average temperature in September (°C)
Tomsk	84°57' E	56°29' N	−0.6	435	16.2	19.1	15.9	10.0
Xinlin	124°31' E	51°46' N	−1.7	500	15.8	18.8	16.1	9.4

method, a multi-trait comprehensive evaluation model is constructed. The research systematically addresses the following objectives: (1) Selection of superior, fast-growing, high-yield families based on BLUP values for growth traits; (2) Evaluation of family stability through retention rate analysis; (3) Selection of superior individual trees by calculating the individual tree selection index and its standard deviation. The findings of this research will provide a theoretical foundation for the genetic improvement of *P. sibirica* and contribute to the development of a multi-objective forest management system in cold-temperate forest regions.

Materials and methods

Plant materials and experimental site

In 1991, Professor Vorobyov from the Institute of Monitoring of Climatic and Ecological Systems, Siberian Branch of the Russian Academy of Sciences, kindly donated 66 trees and more than 80 kg of high-quality *P. sibirica* seeds to Professor Zhao Guangyi at Northeast Forestry University. The seeds were collected from Tomsk Province, located in the southeastern part of the West Siberian Plain, Russia. This region falls under the cold-temperate continental climate zone, with specific environmental parameters detailed in Table 1. In the spring of 1992, the seeds were transported to the Xinlin District Bianzhou Forest Farm nursery in the Greater Khingan Range of China for standardized seedling cultivation.

After a four-year nursery cultivation period, a *P. sibirica* introduction trial was established in 1996 at Bizhou Forest Farm (Compartment 200) on a northwest-facing slope with a 7° inclination and an elevation of 506 m. The trial site is situated in a cold temperate continental climate zone, with environmental factors analyzed and compared to those of the seed source regions (Table 1). Due to differences in seed availability, germination rates, and seedling survival among families, the initial number of seedlings per family varied before planting. To ensure balanced family representation across all blocks, seedlings were evenly distributed among four blocks based on survival rates at the time of planting, with each family initially assigned approximately 3 to 28 seedlings per block. As of the latest assessment, the

number of surviving individuals per family ranges from 1 to 17 per block, with a total of 1424 surviving trees across the entire trial. The trial was established with a planting density of 2 m × 2 m. The climate data utilized in this study were retrieved and organized through the Climate Analysis Platform (<http://climateap.net>).

Trait surveys and measurement methods

A systematic survey of growth traits, conifer traits, wood density, and retention in the test stand was conducted in 2022. The specific methods are as follows:

1. Growth traits the whole-forest per-tree survey method was used to determine the tree height (H), diameter at breast height (D), crown width and lateral branch thickness of all sample trees. Tree height was measured vertically with a tower ruler (accuracy 0.1 m), diameter at breast height was measured at 1.3 m with a diameter at breast height ruler (accuracy 0.1 cm), crown width was measured with a tape measure (accuracy 1 cm) to determine the diameter of the east–west and north–south crowns, and lateral branch roughness was measured with a numerical vernier caliper (accuracy 0.01 mm) to measure the diameter of the middle section of the first round of lateral branches at the base.

The volume of timber per plant (V) was obtained by the following formula (Chen 2010):

$$V = 0.000059502551D^{1.9430646}H^{0.91842984} \quad (1)$$

2. Needle leaf traits Three standard trees were randomly selected from each family line in three blocks, and one cluster of biennial needles was collected from each of the four directions: east, south, west and north. The length and maximum width of needles were measured using digital vernier calipers (precision 0.01 mm), and the fresh weight was determined using a one ten-thousandth electronic balance (precision of 0.0001 g), then the samples were placed in an oven at 80 °C to dry to a constant weight and the dry weight was recorded.
3. Wood density Based on the negative correlation between wood density and Pilodyn value, a portable wood tester

(Pilodyn 6 J Forest model) was used for indirect determination (Zhu et al. 2008). Three sample trees were selected from each family line in each of the three zone groups, and after stripping the surface bark at a breast height of 1.3 m in a north direction, the probe was driven vertically and the penetration depth value (unit: mm) was recorded, and the average value was repeated three times.

4. Calculation of preservation rate Based on the ratio of the number of existing plants of each family line to the number of plants initially planted in the 1996 experimental forest, the preservation rate was calculated according to the formula:

$$\text{Preservation rate (\%)} = \left(\frac{\text{number of existing plants}}{\text{number of plants in the original afforestation}} \right) \times 100 \quad (2)$$

Statistical analysis

Field survey data were compiled and processed using Microsoft Excel, and percentage traits were subjected to arcsine transformation. A heterogeneous variance mixed linear model was fitted using the ASReml-R 4.0 package in R to estimate variance components for fixed and random effects, significance levels, and other genetic parameters, accounting for the unequal number of families within blocks (Lin 2017). Breeding values (BLUPs) for each trait were predicted from the mixed linear model using the coef() function. The tidyverse package was employed for data visualization, selection of superior families, and identification of elite individual trees.:

Mixed linear model:

$$x_{ijk} = \mu + F_i + B_j + (FB)_{ij} + \epsilon_{ijk} \quad (3)$$

where, x_{ijk} is the observed value of the k th individual in the j th family within the i th block; μ is the overall mean; B_i is the fixed effect of the block effect; F_i is the random effect of the family; FB_{ij} represents the interaction effect between the family and the block, treated as a random effect; ϵ_{ijk} is the random error.

Due to the imbalanced family data across blocks and the unequal variances of the family means, the average values are used as a substitute when defining family heritability. The family heritability for growth traits is calculated using the following method (Becker 1985; Tong and Shi 2014):

$$h^2 = \frac{\sigma_F^2}{\sigma_F^2 + k_1 \sigma_{FB}^2 + k_2 \sigma_\epsilon^2} \quad (4)$$

where, h^2 is the family heritability; σ_F^2 is the variance component of the family; σ_B^2 is the variance component of the

block; σ_{FB}^2 is the variance component of the interaction between the family and the block; σ_ϵ^2 is the variance component of the error; k_1 is the weighting coefficient for σ_{FB}^2 , used to adjust the weight of the family-block interaction variance in the formula, considering the information on the number of families and blocks; and k_2 is the weighting coefficient for σ_ϵ^2 , used to adjust the weight of the error variance in the formula, which is related to the number of individuals within each family.

$$k_1 = \frac{1}{F} \sum_{j=1}^F \frac{1}{n_j^2} \sum_{i=1}^B n_{ij}^2 \quad (5)$$

$$k_2 = \frac{1}{F} \sum_{j=1}^F \frac{1}{n_j} \quad (6)$$

where, F is the number of families involved in the study; B is the number of blocks in the experiment; j represents the family, used to distinguish between different family individuals; n_{ij} represents the number of individuals in the i th block for the j th family; n_j represents the total number of individuals in the j th family across all blocks, which is overall sample size for that family.

The wood density and needle traits data come from each block, and the data are balanced. The heritability formula is simplified as follows:

$$h^2 = \frac{\sigma_F^2}{\sigma_F^2 + \sigma_{FB}^2/B + \sigma_\epsilon^2/Bm} \quad (7)$$

where m represents the number of individuals in each block.

The genetic variance between half-sibling families accounts for only one-quarter of the additive genetic variance. Therefore, when calculating the heritability of a single plant, σ_F^2 is multiplied by 4, and the denominator is substituted with the variance of the single plant, $\text{var } y_{ijk}$ (Wright 1976). Additionally, the formula for calculating single plant heritability is applicable to both balanced and unbalanced data. Accordingly, the heritability formula for each trait is as follows:

$$H^2 = \frac{4\sigma_F^2}{\sigma_F^2 + \sigma_{FB}^2 + \sigma_\epsilon^2} \quad (8)$$

where H^2 is the heritability of the single plant.

Coefficient of phenotypic variation (PCV) and Coefficient of genetic Variation (GCV) are calculated using the following formulas (Hai et al. 2015):

$$PCV = \frac{\sqrt{\sigma_P^2}}{\bar{X}} \times 100\% \quad GCV = \frac{\sqrt{\sigma_F^2}}{\bar{X}} \times 100\% \quad (9)$$

where σ_P^2 is the phenotypic variance; σ_F^2 is the family variance components; $\bar{X}$ is the trait mean value.

The formula for calculating the correlation between traits x and y is as follows (Zhang et al. 2022):

$$r = \frac{Cov(x, y)}{\sqrt{\sigma_x^2 \cdot \sigma_y^2}} \quad (10)$$

where, $Cov(x, y)$ is the covariance between traits x and y , σ_x^2 and σ_y^2 are the variance component for trait x and y , respectively.

The Z-score standardization is calculated using the following formula (Wang et al. 2025):

$$z_i = \frac{x_i - \bar{x}}{s} \quad (11)$$

where z_i is the standardized score, x_i is the i th sample value in the original dataset, $\bar{x}$ is the mean of the dataset, and s is the standard deviation of the dataset.

Due to the differing units of measurement for each trait, the calculated breeding values lack comparability. In this study, the breeding values of each trait were standardized by using the normalized genetic correlation coefficients between volume and other traits as weight coefficients, with the following formula (Liu et al. 2017):

$$\omega_{(xi)} = \frac{r_{1j}^2}{\sum_{i=1}^n r_{1j}^2} \quad (12)$$

where $\omega_{(xi)}$ is the weight of the i th indicator, and r_{1j}^2 is the correlation coefficient between the i th indicator and volume.

The calculation of the composite score:

$$Y = \sum_{i=1}^4 z_i w_{(xi)} \quad (13)$$

The genetic gain (ΔG) is estimated by equation (Liu et al. 2023):

$$\Delta G_F = \frac{Sh^2}{\bar{X}} \times 100\% \quad \Delta G_D = \frac{SH^2}{\bar{X}} \times 100\% \quad (14)$$

$$\Delta G_Z = \sum_{i=1}^2 \frac{Sh^2}{\bar{X}} \omega_{(xi)} \times 100\% \quad (15)$$

where ΔG_F , ΔG_Z , ΔG_D , $\omega_{(xi)}$, S , $\bar{X}$, H^2 and H^2 represent family, comprehensive, individual genetic gain, weight coefficient, selection differential, mean value, family heritability, and individual heritability, respectively.

Selection formula for superior individual trees in forestry (Zhang et al. 2024):

$$y = aH + bDBH + cV \quad (16)$$

where y represents the individual tree trait index value; a , b , and c are the weight values for each trait (the product of the reciprocal of individual tree heritability and standard deviation); H , DBH , and V represent the individual tree height, diameter at breast height, and volume, respectively.

Results

Analysis of genetic variation and genetic parameters

In this study, a mixed linear model with heterogeneous variance was fitted, where blocks were treated as fixed effects and family and family $\times$ block interactions as *random* effects. The results of the fixed effects analysis (Table 2) show that volume, crown width, and Pilodyn value exhibited highly significant differences ($P < 0.01$), while tree height and diameter at breast height showed significant differences ($P < 0.05$). No significant differences ($P > 0.05$) were found for side branch diameter and needle traits (fresh weight, dry weight, moisture content, leaf length, leaf width, and leaf length-to-width ratio) between blocks.

Random effects analysis (Table 3) revealed significant differences (Z ratio > 1.50) among families for 10 traits, including tree height, diameter at breast height, volume, crown width, Pilodyn value, and various needle traits (length, width, length-to-width ratio, fresh weight, dry weight, and moisture content). Among these, only tree height, diameter at breast height, crown width, and Pilodyn value showed significant interactions between family and block, indicating that the traits of *P. sibirica* half-sibling families are significantly influenced by genotype, with the genetic variation primarily stemming from family effects.

The analysis of the genetic coefficient of variation indicates that the phenotypic coefficient of variation for volume (62.50%) and the genetic coefficient of variation (13.81%) are the highest among all traits, reflecting strong environmental plasticity and substantial potential for genetic gain. Genetic parameter estimates indicate that family heritability for volume and Pilodyn value exceeds 40%, suggesting strong genetic control over these traits. In contrast, the

Table 2 Fixed effects analysis in the linear mixed model for traits of *P. sibirica* half-sibling families

	Trait	Effect variable	df	Sum of squared difference	Wald	P
Growth traits	Hight of tree (m)	Block	3	11.3	10.2	0.01678*
		Residual		1.1		
	Diameter at breast height (cm)	Block	3	34.0	10.3	0.0159*
		Residual		3.3		
	Volume (m ³)	Block	3	0.000913	15.38	0.001518**
		Residual		0.000059		
Morphological traits	Crown width (m)	Block	3	1.79	14.3	0.002561**
		Residual		0.13		
	Lateral branch thickness (mm)	Block	3	46	3.9	0.2771
		Residual		12		
Timber density	Pilodyn (mm)	Block	2	123	18	0.0001272**
		Residual		7		
Needle-leaf traits	Length (mm)	Block	2	2	0	0.9916
		Residual		147		
	Width (mm)	Block	2	0.016	2.9	0.2379
		Residual		0.006		
	Aspect ratio	Block	2	686	1.8	0.404
		Residual		378		
	Fresh weight (g)	Block	2	0.000010	0.2	0.9236
		Residual		0.000063		
	Dry weight (g)	Block	2	0.000004	0.3	0.8822
		Residual		0.000014		
	Moisture content (%)	Block	2	2	0	0.8503
		Residual		5		

*Significant at $p < 0.05$, **significant at $p < 0.01$

heritability for side branch diameter is only 7.70%, making it a typical low heritability trait, highly influenced by environmental factors. The family heritability for needle traits ranges from 64.81% to 78.30%, indicating a high level of heritability, and the trend for single plant heritability is consistent with that of family heritability, both showing high genetic conservatism. This provides an important theoretical basis for subsequent selection breeding.

Multi-trait combined selection of superior families

According to the genetic correlation analysis results between traits (Table 4), this study used the normalized genetic correlation coefficients between each trait and volume as the weight coefficients for the BLUP method. The weight coefficients for tree height, DBH, volume, and Pilodyn value were 26.22%, 28.84%, 29.80%, and 15.14%, respectively. Considering the genetic correlation characteristics between volume and Pilodyn value, their combined genetic gain weight coefficients were normalized to 63.29% and 36.71%, respectively. It is important to note that, because Pilodyn value has a significant negative correlation with wood density

($r = -0.41$, $P < 0.01$), it was transformed into a positive indicator by reversing the value in the calculation process.

Based on the estimation of breeding values for each trait in 66 families using the BLUP method, the Z-Score standardization was applied to all trait breeding values. The Pilodyn value breeding values were reversed to meet the positive selection requirements, and the final family comprehensive scores (ranging from -2.019 to 2.190) were obtained. The results, sorted in descending order, showed that 34 families (51.52%) had scores greater than 0. Figure 1 illustrates the distribution characteristics of the top 20 families based on comprehensive scores, with a selection threshold set at a comprehensive score ≥ 1.00 , identifying 13 outstanding families, including families 59, 11, and 51. The average genetic gain for volume in the selected families was 13.377%, while the average genetic gain for Pilodyn value was -1.211%. The overall average genetic gain was 8.022%, indicating significant potential for genetic improvement.

Table 3 Random effects analysis and key parameter estimates in the linear mixed model for traits of *P. sibirica* half-sibling families

Trait	Effect variable	Mean	Variance component	Stand error	Z ratio	PCV (%)	GCV (%)	Family heritability (h^2) (%)	Heritability plan (H^2) (%)
Growth traits	Height of Tree (m)	5.23	4.80×10^{-2}	2.23×10^{-2}	2.15*	20.84	4.19	35.61	16.05
	Family × Block		4.00×10^{-2}	2.55×10^{-2}	1.56*				
	Residual		1.11×10^0	4.54×10^{-1}	24.40*				
	Diameter at breast height (cm)	6.74	1.44×10^{-1}	6.66×10^{-2}	2.16*	28.04	5.62	35.43	16.11
	Family × Block		1.34×10^{-1}	7.94×10^{-2}	1.69*				
	Residual		3.29×10^0	1.35×10^{-1}	24.35*				
Morphological traits	Volume (m ³)	0.0128	3.00×10^{-6}	1.00×10^{-6}	2.48*	62.50	13.81	40.93	19.49
	Family × Block		2.00×10^{-6}	1.00×10^{-6}	1.23				
	Residual		5.90×10^{-5}	2.00×10^{-6}	24.40*				
	Crown width (m)	1.77	5.41×10^{-3}	2.60×10^{-3}	2.08*	20.92	4.15	34.31	15.73
	Family × Block		6.39×10^{-3}	3.15×10^{-3}	2.02*				
	Residual		1.26×10^{-1}	5.17×10^{-3}	24.35*				
Timber density	Lateral branch thickness (mm)	13.10	8.21×10^{-2}	1.61×10^{-1}	0.51	27.25	2.19	7.70	2.59
	Family × Block		5.90×10^{-1}	2.92×10^{-1}	2.02*				
	Residual		1.20×10^1	4.89×10^{-1}	24.54*				
	Pilodyn (mm)	38.15	1.16×10^0	4.44×10^{-1}	2.61*	8.10	2.82	49.47	50.23
	Family × Block		1.19×10^0	4.86×10^{-1}	2.44*				
	Residual		6.88×10^0	5.13×10^{-1}	13.42*				

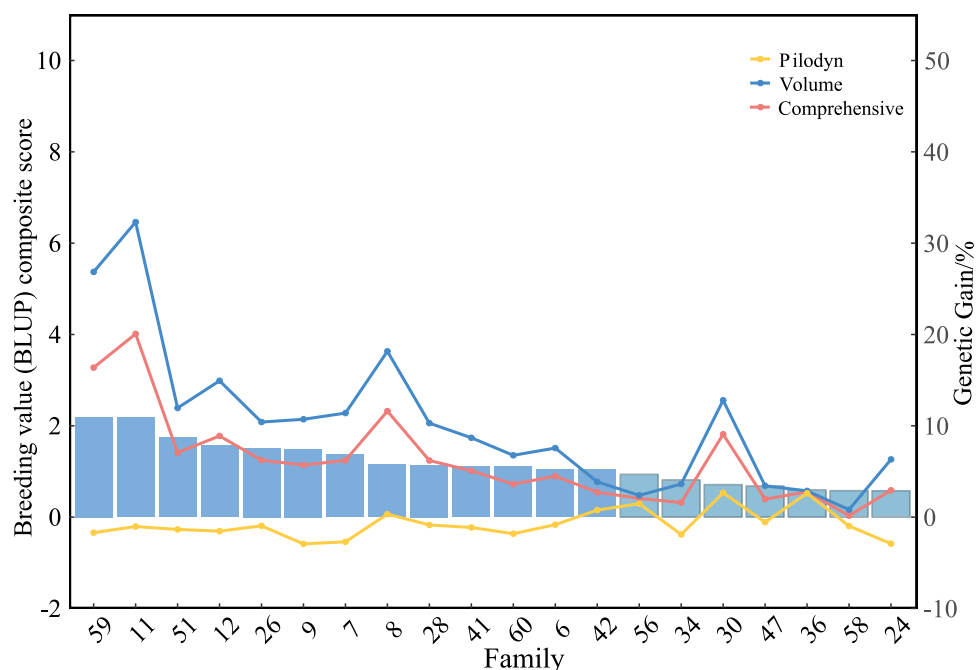
Table 3 (continued)

Trait	Effect variable	Mean	Variance component	Stand error	Z ratio	PCV (%)	GCV (%)	Family heritability (h^2) (%)	Heritability plan (H^2) (%)
Needle-leaf traits	Length (mm)	97.29	4.33×10^1	1.06×10^1	4.07*	14.55	6.76	72.79	85.79
	Family × Block		1.19×10^1	6.40×10^0	1.86*				
	Residual		1.47×10^2	8.52×10^0	17.20*				
Width (mm)	Family	0.71	1.03×10^{-3}	2.88×10^{-4}	3.58*	11.27	4.52	64.81	59.32
	Family × Block		2.66×10^{-4}	2.24×10^{-4}	1.18				
	Residual		5.65×10^{-3}	3.28×10^{-4}	17.21*				
Aspect ratio	Family	138.58	1.14×10^2	2.56×10^1	4.45*	15.98	7.70	78.30	92.48
	Family × Block		2.39×10^{-4}	NA	NA				
	Residual		3.78×10^2	1.99×10^1	19.00*				
Fresh weight (g)	Family	0.0367	1.30×10^{-5}	4.00×10^{-6}	3.76*	24.25	10.00	67.69	67.41
	Family × Block		4.00×10^{-6}	3.00×10^{-6}	1.38				
	Residual		6.30×10^{-5}	4.00×10^{-6}	17.20*				
Dry weight (g)	Family	0.0171	3.00×10^{-6}	1.00×10^{-6}	3.72*	24.56	10.13	67.08	66.29
	Family × Block		1.00×10^{-6}	1.00×10^{-6}	1.45				
	Residual		1.40×10^{-5}	1.00×10^{-6}	17.20*				
Moisture content (%)	Family	53.57	1.57×10^0	4.04×10^{-1}	4.34*	5.05	2.47	77.14	95.22
	Family × Block		2.08×10^{-1}	2.09×10^{-1}	1.00				
	Residual		5.40×10^0	3.13×10^{-1}	17.22*				

*Significant at Z ratio > 1.50

Table 4 Genetic correlation analysis and weighting factors

Traits	V	H	DBH	Pilodyn	Weighting factor	
V		0.880**	0.968**	0.508**	29.80%	63.29%
H	0.880**		0.904**	0.453**	26.22%	
DBH	0.968**	0.904**		0.557**	28.84%	
Pilodyn	0.508**	0.453**	0.557**		15.14%	36.71%

Fig. 1 Comprehensive ranking of breeding values of families and the trend chart of genetic gain

Analysis of family preservation rates

The statistics for the initial number of planted seedlings, surviving seedlings, and survival rate of 66 families are presented in Fig. 2. The results show:

Initial Seedling Distribution: The range of initial seedlings across families was 7–112, with a significant dispersion (mean $\pm$ standard deviation: 38.80 ± 20.01). Family 62 had the highest number of initial seedlings (112), while Family 30 had the lowest (7). Only 9.1% (6 families) had more than 80 initial seedlings.

Surviving Seedlings: The range of surviving seedlings was 3 to 65 (mean $\pm$ standard deviation: 25.30 ± 13.36). Family 62 had the highest number of surviving seedlings (65), while Family 29 had the lowest (3). The number of surviving seedlings was significantly positively correlated with the initial number of seedlings ($r = 0.96$, $P < 0.01$).

Survival Rate Classification: The survival rate for families ranged from 36.36% to 88.89% (mean $\pm$ standard deviation: $65.10\% \pm 11.05\%$). The survival rate was classified into the following intervals:

- $\geq 75\%$: 12 families (18.20%), including Family 8 (88.89%), showing strong adaptability;
- 60–75%: 35 families (53.00%), forming the main group;
- 50–60%: 13 families (19.70%), requiring attention to environmental interaction effects;
- $< 50\%$: 6 families (9.09%), such as Family 1 (36.36%), with low adaptability and recommended for elimination.

Selection of exceptional individual trees

The family and individual tree variation of *P. sibirica* is rich, providing a foundation for the selection of exceptional individual trees. In this study, exceptional individual trees were selected based on tree height, DBH, and volume, both across the entire forest and within exceptional families. A simple selection index method was used to construct the equation, as follows:

$$y = 0.147248 \times H + 0.085238 \times DBH + 24.30175 \times V \quad (17)$$

where, y represents the selection index; H represents tree height; DBH represents diameter at breast height; V represents volume.

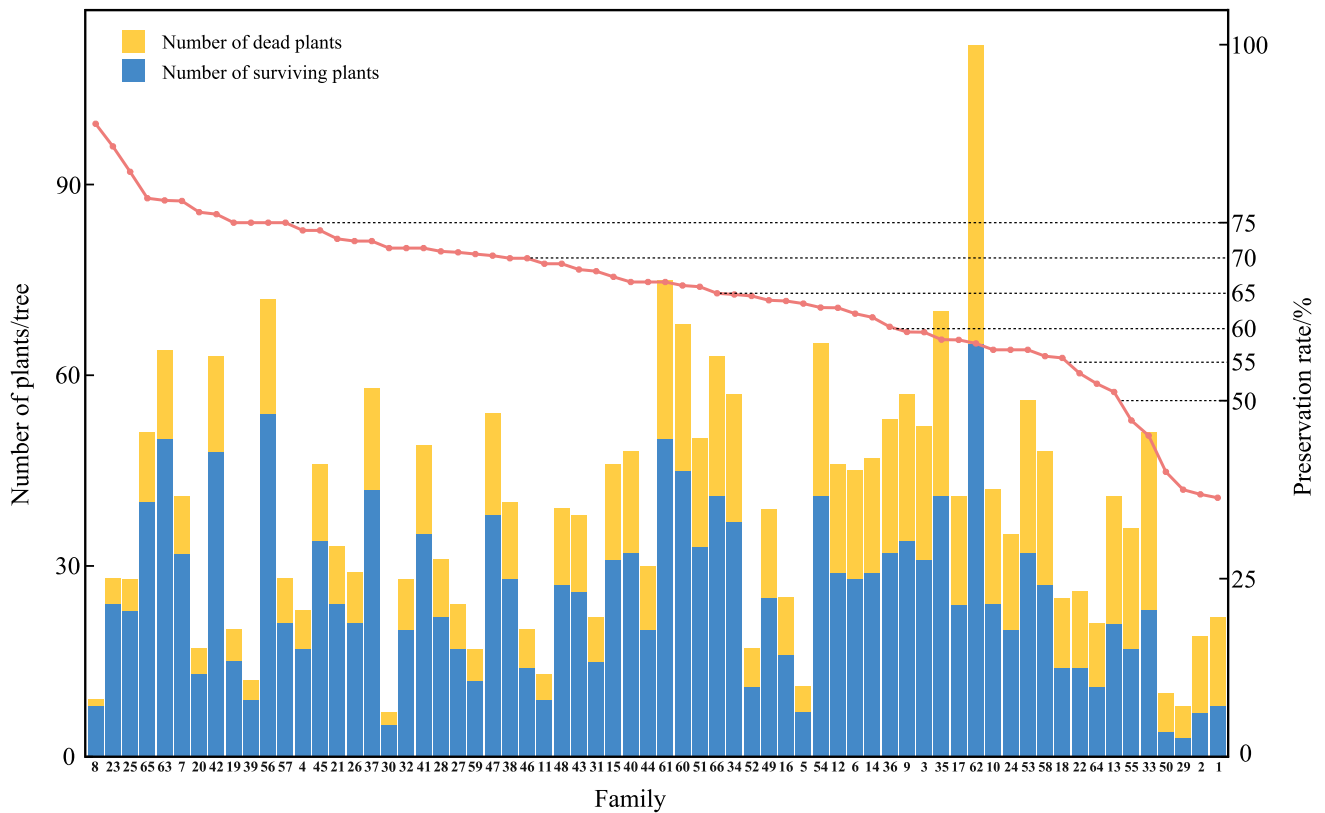


Fig. 2 Comparison of the number of surviving and dead plants in families and the change in preservation rate

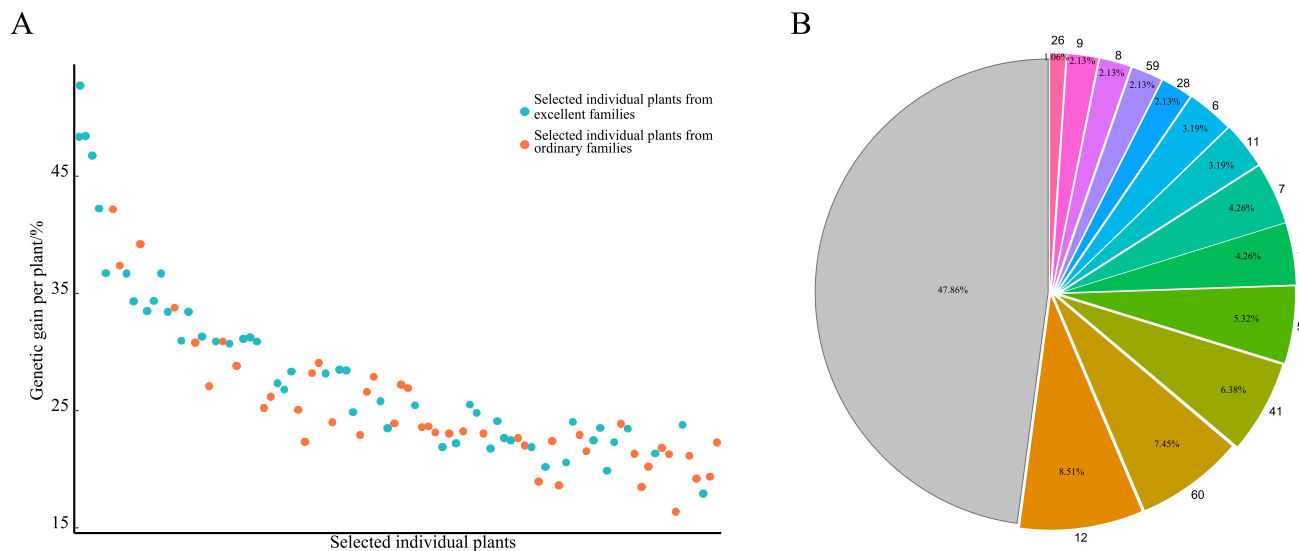


Fig. 3 Analysis of genetic gain in volume of selected superior trees and family contribution rate

The mean stand value was substituted into the single-plant selection index equation, yielding an average index value of 1.655673. The standard deviation of the single-plant index values, calculated based on the phenotypic values of each plant, was 0.504. Among the plants, 1267 individuals

had an index value greater than 1.00, and 366 individuals had an index value greater than 2.00. Using the threshold of “average single-plant index value + 1.5 times the standard deviation” (2.411673) for selection, a total of 94 superior single plants (selection rate of 6.60%) were selected. The

Table 5 Mean values of growth traits and genetic gain of selected good single plants

	Phenotypic value			Genetic gain (%)		
	H (m)	DBH (cm)	V (m ³)	H	DBH	V
Mean value	5.23	6.74	0.0128	0	0	0
Mean value of selected single plants	6.91	9.92	0.0304	5.16	7.60	26.80
Mean value of selected single plants of good family lines	6.88	10.13	0.0315	5.06	8.10	28.47

genetic gain in volume for the selected plants ranged from 16.328 to 52.716% (Fig. 3A). The growth traits and average genetic gain for these selected plants are detailed in Table 5.

The selected superior single plants had mean phenotypic values for tree height, diameter at breast height (DBH), and volume of 6.91 m, 9.92 cm, and 0.0304 m³, respectively, which represent increases of 32.12%, 47.18%, and 137.50% compared to the stand mean. The corresponding average genetic gains were 5.16%, 7.60%, and 26.80%. Among these, 49 selected single plants (52.14% of the total, Fig. 3B) originated from superior families. Their mean phenotypic values for tree height, DBH, and volume were 6.88 m, 10.13 cm, and 0.0315 m³, respectively, reflecting increases of 31.55%, 50.30%, and 146.09% compared to the stand mean. The genetic gains for these plants were 5.06%, 8.10%, and 28.47%, respectively.

Comparative analysis showed that the mean phenotypic values for tree height, diameter at breast height (DBH), and volume of the selected single plants from superior families changed by −0.43%, +2.12%, and +3.62%, respectively, compared to the overall selected single plants. The genetic gains exhibited differences of −1.94%, +6.58%, and +6.23%, respectively.

Discussion

Genetic variation and heritability are fundamental to forest tree genetic improvement, as demonstrated in this study. The results demonstrate significant differences among the *P. sibirica* families in terms of growth traits and wood density (Z ratio > 1.50). Except for side branch diameter, the heritability of all traits exceeded 34% ($h^2 > 0.34$), indicating moderate to high genetic control and showcasing considerable potential for genetic improvement. Analysis of the phenotypic coefficient of variation shows that the coefficient for individual tree volume reaches 62.50%, surpassing the reported value of 58.3% for individual tree volume in *P. koraiensis* (Shang et al. 2024). This result not only underscores the greater genetic diversity of *P. sibirica* but also suggests its potential evolutionary advantage in terms of environmental adaptability and stress resilience.

The genetic parameters of needle traits show that the family variance component is significantly higher than

the family-block interaction variance component, indicating that genetic factors mainly drive the phenotypic variation of these traits. The research findings for *Pinus yunnanensis* corroborate each other (Huang 2015), both exhibiting typical characteristics of low genetic variation coefficients (< 15%) and high heritability (> 0.60). It is noteworthy that the wood quality-related traits exhibit differentiated genetic control patterns. The family heritability of Pilodyn value reaches 49.47%, with the individual heritability exceeding 50%, confirming its strong genetic determinism. In contrast, the family heritability of side branch diameter is only 7.70%, and the individual heritability is as low as 2.95%, indicating that this trait is more susceptible to environmental factors such as site conditions and planting density. This provides a theoretical basis for optimizing wood mechanical properties through silvicultural practices, such as density control. The construction of a multi-trait integrated evaluation system is a significant breakthrough in this study. In response to the limitations of traditional methods such as the Best Linear Unbiased Prediction (BLUP), which treat traits equally, an innovative approach was developed by using a normalized weighting method based on the genetic correlation coefficients between volume traits (e.g., volume) and wood traits (e.g., wood density). This effectively integrates multiple indicators. Thirteen superior families (with a composite score ≥ 1.00) were selected, demonstrating significant genetic gain: the mean volume gain reached 13.377%. Although the Pilodyn value gain was −1.211% (with a moderate reduction in density potentially improving processing performance), the comprehensive genetic gain still reached 8.022%. This result confirms that the weight assignment strategy based on genetic parameters can effectively balance the antagonistic relationships between traits and is more biologically meaningful than methods such as principal component analysis or subjective weighting methods used in species like birch and cypress (Yang et al. 2023; Zhang et al. 2024).

The survival rate, as a core indicator of ecological adaptability, is thoroughly validated in this study. The average survival rate of superior families reaches 70% (ranging from 36.4 to 88.9%), which corresponds with historical observational data: the 18-year-old Tomsk provenance achieved a survival rate of 92.67% at the Bizhou Experimental Site

(Zhao et al. 2014), while the 16-year-old Tomsk provenance had a survival rate of 83% at the Mao'er Mountain Experimental Forest Station (Wu et al. 2024). These data collectively contribute to the creation of an ecological adaptability map for *P. sibirica* across latitudes (45° N to 53° N) and elevations (500–1200 m). Whether its stress resistance mechanisms are closely related to genetic traits such as needle cuticle thickness (Zhang et al. 2025) and secondary metabolites composition (Dong and Lin 2021; Raza et al. 2021) requires further research.

The innovation of the individual tree selection system lies in the multi-level selection coupling approach: using the index selection method, 94 superior trees were selected from the entire forest (with a volume gain of 26.80%), of which 49 trees (52.14%) came from superior families, with a volume gain as high as 26.80%. This “family-individual tree” dual-track selection strategy not only ensures the breadth of the genetic base (utilizing inter-family variation) but also taps into the variation potential within families, providing gradient materials for seed orchard construction. Notably, the superior individual trees also exhibited synergistic gains in growth traits such as tree height (5.16%) and DBH (7.60%), confirming the feasibility of multi-trait integrated selection.

Conclusion

This study systematically analyzed the genetic variation patterns of 66 half-sibling families of *P. sibirica* and established three key findings:

1. The genetic regulation patterns of core economic traits were revealed, confirming that traits such as volume, Pilodyn value, and needle moisture content are under strong genetic control ($h^2 > 0.40$);
2. A multi-trait BLUP selection model based on weighted genetic parameters was constructed, leading to the identification of 13 superior families (e.g., 59, 11, 51), achieving a genetic gain of 13.38% in volume;
3. An innovative “family-individual” collaborative selection strategy was developed, resulting in the identification of 94 superior trees (with an average volume gain of 26.80%), among which the volume gain for superior trees within the family reached 28.47%.

The integrated evaluation system and selection methods established in this study provide a paradigm reference for multi-objective breeding of coniferous species. The results can be directly applied to the construction of high-generation seed orchards for *P. sibirica* and offer theoretical guidance for the genetic improvement of species in the same genus.

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