Variations in growth traits and wood physicochemical properties among *Pinus koraiensis* families in Northeast China

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Abstract This study aimed to explore and improve the different economic values of *Pinus koraiensis* (Siebold and Zucc.) by examining the variations in 6 growth traits and 9 physicochemical wood properties among 53 *P. koraiensis* half-sib families. Growth traits assessed included height, diameter at breast height, volume, degree of stem straightness, stem form, and branch number per node, while wood properties assessed included density, fiber length and width, fiber length to width ratio, and cellulose, hemicellulose, holocellulose, lignin, and ash contents. Except for degree of stem straightness and branch number per node, all other traits exhibited highly significant variations ($P < 0.01$) among families. The coefficients of variation ranged from 5.3 (stem form) to 66.7% (ash content), whereas, the heritability ranged from 0.136 (degree of stem straightness) to 0.962 (ash content). Significant correlations were observed among growth traits and wood physicochemical properties. Principal component analysis identified four distinct groups representing growth traits, wood chemical and physical properties, and stem form traits. Multi-trait comprehensive evaluation identified three groups of elite families based on breeding objectives, including rapid growth, improved timber production for building and furniture materials, and pulpwood production. These specific families should be used to establish new plantations.

Keywords Growth and wood traits · *Pinus koraiensis* · Principal component analysis · Family selection · Economic benefits

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Introduction

Pinus koraiensis (Sieb. and Zucc.) is an economically valuable species in Northeast China (Wang et al. 2015), and an important protected plant in the country (Zhang et al. 2015a, b). It is generally distributed in the mountains of Xiaoxing'an, Wanda, Zhangguangcai, Laoye, and Changbai (Xia et al. 1991). *P. koraiensis* wood is of high quality (Son et al. 2001) with strong corrosion resistance; the seeds have

high nutritional value and are marketed as pine nuts (Imbs and Pham 1996). To improve these economic benefits, *P. koraiensis* should be established in seed orchards as sources of quality regeneration material for future plantations (Xue et al. 2009).

A seed orchard is important to improve forest productivity (Kjaer and Foster 1996). Numerous coniferous plantations world-wide have originated from seed orchards (Lindgren and Prescher 2005). In some areas, the establishment of third-generation seed orchards has been achieved (Chen and Shen 2005). China began to establish the clonal seed orchard of *Cedrus atlantica* (Endl.) Manetti ex Carriere in 1964 (Wang 2013). Today, over 20 tree species have established in seed orchards (Chen 2001). Similarly, large-scale breeding of *P. koraiensis* in China began in the 1980s, and researchers mainly selected materials from natural *P. koraiensis* forests (Liu 2017). However, most of these seed orchards are in the primary stages because *P. koraiensis* is characterized by slow growth (Liu et al. 2015).

Currently, several *P. koraiensis* research programs are primarily concerned with the study of chemical components of pine nuts (Kim et al. 2012; Shpatov et al. 2017; Lee et al. 2018), the identification of molecular markers (Kim et al. 2005; Chen et al. 2011), asexual reproduction techniques (Liu 2004; Song et al. 2007), the establishment of seed orchards (Oh et al. 2008; Feng et al. 2010) and eco-physiological attributes (Makoto and Koike 2007; Sun et al. 2016). There has been limited conventional breeding research on *P. koraiensis* although the evaluation of progenies from seed orchards can serve as materials for the selection of elite families and single plants.

In this study, variations in growth traits and wood physicochemical properties among *P. koraiensis* families were evaluated. Growth and wood traits are crucial reference standards in tree breeding, particularly as a reference for selecting high performance families and clones for the establishment of seed orchards (Zhang et al. 2017). The economic value of wood is determined by its material properties, and this directly affects wood processing and utilization (Li et al. 2018). Earlier studies focused on selection and application of growth trait variation (Zhen et al. 2007), but the genetic gain of a single pursuit of growth traits may lower wood quality (Li et al. 2014). In addition, reports indicate that growth traits are weakly or negatively correlated with wood density (Ru et al. 2001; Su 2001). Therefore, simultaneous selection of growth and wood traits is of considerable significance towards achieving greater economic benefits. *P. koraiensis* wood is used in building and furniture construction; however, reports on *P. koraiensis* pulpwood are scarce. This paper investigates the economic value of *P. koraiensis* to improve them.

A targeted evaluation method can be applied to select families and clones with superior genetic stability according to different breeding objectives (Matziris 1997; Wu et al. 2018). Several evaluation methods are available (Luo et al. 2010). In this study, the multi-character comprehensive evaluation method was used. Half-sib progenies of *P. koraiensis* of the Jilin Provincial Forestry Bureau were used as research materials to: (1) evaluate the variations in growth traits and wood physicochemical properties among 53 *P. koraiensis* half-sib families, and search for links between growth and wood traits; (2) select high performance families based on different breeding goals; and, (3) provide a new approach for the improvement of *P. koraiensis* to increase productivity and improve economic benefits.

Materials and methods

Experimental site

The experimental site was the Sanchazi seed orchard, 126°56′ E, 41°95′ N in Baishan City, Jilin Province at an altitude of 520 m. The area is characterized by a temperate continental monsoon climate with an average annual temperature of 2.5 °C, annual precipitation of 725.5 mm, and annual sunshine of 2,300 h, with a frost-free period of 110 d.

Progeny plantation

For this study, seeds of 53 half-sib families [(family 1, 10, 49, 65, 77, 82, 83, 84, 85, 87, 88, 90, 91, 92, 93, 94, 96, 97, 98, 100, 101, 102, 103, 105, 106, 108, 109, 110, 111, 112, 113, 114, 115, 117, 118, 120, 122, 125, 129, 130, 132, 133, 134, 135, 136, 137, 138, 140, 143, 144, 145, 148, 163),] each with 6 individuals, were acquired from the Sanchazi seed orchard, planted in the spring of 1990 in the nursery and cultivated for 4 years. The progeny plantation was established in 1995 in the spring as a completely randomized block design with 5 blocks and 6 replicates in each plot in rows at 2.0 m × 3.0 m spacing.

Growth traits measurements

Growth traits included height (H), diameter at breast height (DBH), volume (V), degree of stem straightness (SSD), stem fullness (SF), and branch number per node (BNN), which were measured at 24 years. SSD was estimated according to Zhao et al. (2014) in a scale of 1−5. A tree with more than two obvious bends in the stem received a score of 1, those with more than two slight bends or with one obviously bend scored 2, those with two slight bends scored 3, those with one slight bend received a score of 4,

and finally, those with a completely straight stem scored 5. The SSD values were squared before ANOVA. SF was estimated as the ratio of DBH to basal diameter. Volume was calculated following Zhang et al. (2014) as follows:

$$V = \pi(D_{1.3}/2)^2(H+3)f \tag{1}$$

where, f denotes the form factor of *P. koraiensis* as 0.33; and $D_{1.3}$ denotes the DBH.

Wood traits measurements

Fifteen wood cores per family (one per tree and three trees per block) were taken from the north to south sides of the stem at 1.3 m (Luo et al. 2004), wrapped in straw and transported to the laboratory for analysis (Sun et al. 2018). Wood density (WD), fiber length (FL), fiber width (FW), fiber length to width ratio (LWR), cellulose (CC), hemicellulose (HEC), holocellulose (HOC), lignin (LC), and ash (AC) contents were determined. WD was determined as described by Li et al.(2018) using five wood cores for each family. Thirty FLs and FWs were measured on five cores per each family that were mixed (Tang et al. 2018), and LWR was calculated. Dry matter production (DMP), as the product of WD and V, and cellulose production (CP), as the product of DMP and CC, were calculated for each family.

The remaining wood cores were ground in a ball mill and mixed to determine chemical properties using an ANKOM A2000i automatic fiber analyzer following Liu (2017). Neutral detergent fiber (NDF) was determined following the digestion of neutral washing solution, and the residues include hemicellulose, cellulose, and lignin. Acid detergent fiber (ADF) was determined following the digestion of the acid washing solution, and the residues include cellulose and lignin. Acid detergent lignin (ADL) treated with 72% sulfuric acid resulted in a lignin residue. Cellulose (CC), HEC, HOC, and LC were determined using the following relationships:

$$P_{HEC} = P_{NDF} - P_{ADF} \tag{2}$$

$$P_{CC} = P_{ADF} - P_{ADL} \tag{3}$$

$$P_{HOC} = P_{NDF} - P_{ADL} \tag{4}$$

$$P_{LC} = P_{ADL} - P_{AC} \tag{5}$$

where P_{HEC}, P_{CC}, P_{HOC} and P_{LC} denote percentage hemicellulose (HEC), cellulose (CC), holocellulose (HOC), lignin (LC) contents; and P_{NDF}, P_{ADF}, P_{ADL} and P_{AC} denote percentage neutral detergent fiber (NDF), acid detergent fiber (ADF), acid detergent lignin (ADL) and ash contents (AC).

Statistical analysis

The significant variations in growth traits among families and blocks were tested by ANOVA using the following linear model (Xia et al. 2016):

$$X_{ijk} = \mu + \alpha_i + b_j + \alpha b_{ij} + e_{ijk} \tag{6}$$

where X_{ijk} denotes the observation value of the kth individual tree in the ith family growing in jth block, μ the family mean, α_i the family effects, b_j the block effect, αb_{ij} the effect of the interaction between family i and block j, e_{ijk} represent the random error.

Family variations in wood traits were analyzed using the following linear model:

$$Y_{ij} = \overline{X} + E_{ij} \tag{7}$$

where Y_{ij} denotes the observation value of jth individual tree in ith family, $\overline{X}$ the family mean, E_{ij} the random error.

Phenotypic coefficient of variation (PCV) was calculated using the following formula (Metougui et al. 2017):

$$PCV = \frac{\sqrt{\sigma_p^2}}{\overline{X}} \times 100\% \tag{8}$$

where σ_p^2 denotes the phenotypic variance component of a given trait.

Heritability of growth (h^2) and heritability of wood traits (h_f^2) were calculated according to Eqs. 9 and 10 (Li 2018):

$$h^2 = \frac{\sigma_f^2}{\sigma_f^2 + \sigma_b^2/b + \sigma_e^2/nb} \tag{9}$$

$$h_f^2 = \frac{\sigma_f^2}{\sigma_f^2 + \sigma_e^2/r} \tag{10}$$

where σ_f^2 denotes variance component for the family effect, σ_b^2 the variance component for family by block interaction effects, and σ_e^2 the residual error, b represents the number of blocks, n the number of plots, and r the number of values per family.

The phenotypic correlation between traits was computed according to Han et al. (2017):

$$r_P(x, y) = \frac{Cov_P(x, y)}{\sqrt{\sigma_{P_x}^2 \cdot \sigma_{P_y}^2}} \tag{11}$$

where $Cov_P(x, y)$ denotes phenotypic covariance between trait x and y, and $\sigma^2_{P_x}$ and $\sigma^2_{P_y}$ represent the phenotypic variance component for trait x and y, respectively.

The comprehensive evaluation values (Q_i) for different families were computed following Zhao et al. (2016):

$$Q_i = \sqrt{\sum_{j=1}^{n} a_i} \tag{12}$$

where ai is Xij/Xjmax; and Xij, Xjmax and n denote the average value of a trait, the maximum value of the trait and the number of traits, respectively.

The genetic gain (ΔG) was estimated following Silva et al. (2008), and the real gain (ΔG_r) following Ye (2011) as follows:

$$\Delta G = h^2 \Delta S / \overline{X} \times 100\% \tag{13}$$

$$\Delta G_r = S / \overline{X} \times 100\% \tag{14}$$

where h^2 is heritability; ΔS and S are the differential of selection; $\overline{X}$ is the family mean. All statistical analysis were performed using Statistical Product and Service Solution (SPSS) software, version 26.0 (IBM Corp., Armonk, NY, USA).

Results

Variations in growth and wood traits

Highly significant differences ($P < 0.01$) in growth traits among families and blocks were detected; except for SSD (degree of stem straightness) and BNN (branch number per node) but the interactions were significant for all growth traits (Table 1). Similarly, there were significant differences in wood traits among families (Table 2). There were moderate variations in growth traits, particularly in volume and high variation in ash content (Table 3). The PCV of traits ranged from 5.33% for stem form of 66.67% for ash content (Table 3). The PCV of volume, fiber length, fiber length to width ratio, and hemicellulose content were larger than 25%, whereas the PCV of stem fullness and wood density were less than 10%. The h^2 of growth traits was > 0.7 except for height and degree of stem straightness, in which the h^2 of SSD (0.136) was minimal (Table 3). The h^2 of each wood trait was > 0.8. The highest h^2 was for lignin content (0.960) and ash content (0.962).

Correlation analysis

There were highly significant ($p < 0.01$) positive correlations between H, DBH and V, with strong correlation ($r = 0.98$) between DBH and V (Fig. 1). SF (stem fullness) showed a significant ($p < 0.01$) correlation with H (0.49), DBH (0.67),

Table 1 ANOVA results for examining variations in growth traits among families and blocks

Traits	Variance source	df	MS	F
Height	Family	52	3.514	1.783**
	Block	4	35.345	17.932**
	Family × Block	208	1.971	7.739**
DBH	Family	52	60.532	3.939**
	Block	4	93.515	6.085**
	Family × Block	208	15.368	4.415**
Volume	Family	52	0.007	3.928**
	Block	4	0.017	9.542**
	Family × Block	208	0.002	4.284**
Stem straightness degree	Family	52	0.096	1.157
	Block	4	0.365	4.525**
	Family × Block	208	0.083	2.568**
Stem form	Family	52	0.007	5.622**
	Block	4	0.025	21.137**
	Family × Block	208	0.004	3.502**
Branch number per node	Family	52	5.355	3.834**
	Block	4	3.079	2.205
	Family × Block	208	1.397	1.253*

**Represents extremely significant differences at $p < 0.01$, and *Represents significant differences at $p < 0.05$, respectively

and V (0.65). SSD (degree of stem straightness) and BNN (branch number per node) were significantly ($p = 0.04$) correlated (0.30). For wood traits, fiber length was significantly ($p < 0.01$) correlated with fiber width (0.42) and fiber length to width ratio ($p < 0.01$; $r = 0.45$), but fiber width was significantly ($p < 0.05$) negatively correlated (-0.61) with fiber length to width ratio. In addition, holocellulose content was highly ($p < 0.01$) correlated with cellulose content (0.70) and hemicellulose content (0.69). Lignin content was significantly ($p < 0.01$) correlated with DBH ($r = 0.43$) and volume ($r = 0.42$).

Principal components analysis

Principal Component Analysis (PCA) summarizes the information in five significant components (Table 4). The eigenvalue for component I was 3.584 with a contribution of 23.9%; and the eigenvalues of H, DBH, V, and SF were higher, and therefore component 1 mainly represented the growth traits. The eigenvalue for component II was 2.263, with a contribution of 15.1%; and the eigenvalue of CC, HEC, and HOC were higher, and therefore this component represented the wood chemical properties. The eigenvalue for component III was 1.935, with a contribution of 12.9%; and the absolute eigenvalues of WD, FW, and LWR were higher, thus this component represented the physical properties of wood. The eigenvalue for component IV was 1.556,

Table 2 ANOVA results for examining variations in wood traits among families

Traits	Variance source	SS	df	MS	F
Wood density	Family	141,067.393	52	2712.834	9.344**
Fiber length	Family	76,120,014.064	52	1,463,846	6.038**
Fiber width	Family	32,844.393	52	631.623	17.782**
Length to width ratio	Family	124,093.515	52	2386.414	15.515**
Cellulose content	Family	2775.195	52	53.369	21.342**
Hemicellulose content	Family	2729.210	52	52.485	21.048**
Holocellulose content	Family	5339.773	52	102.688	19.178**
Lignin content	Family	3957.510	52	76.106	25.221**
Ash content	Family	33.326	52	0.641	26.577**

**Represents extremely significant differences at $p < 0.01$, and *Represents significant differences at $p < 0.05$, respectively

Table 3 Descriptive statistics for different growth and wood traits together with phenotypic coefficient of variation (PCV) and heritability (h^2)

Traits	Mean	Max	Min	SD	PCV	h2
Height	7.60	8.57	7.00	0.82	10.79	0.439
DBH	16.38	20.79	12.91	2.67	16.30	0.746
Volume	0.0770	0.1317	0.0464	0.0288	37.40	0.745
Stem straightness degree	3.94	4.43	3.33	0.78	19.80	0.136
Stem form	0.75	0.78	0.71	0.04	5.33	0.822
Branch number per node	5.56	6.58	4.47	1.14	20.50	0.739
Wood density	469.59	563.17	405.39	32.38	6.90	0.889
Fiber length	1772.06	2178.98	1431.91	531.41	29.99	0.834
Fiber width	31.58	41.66	23.31	7.42	23.49	0.944
Length to width ratio	56.93	78.63	45.25	15.06	26.45	0.936
Cellulose content	30.80	39.38	22.82	4.39	14.25	0.952
Hemicellulose content	16.03	29.32	9.25	4.35	27.14	0.953
Holocellulose content	46.83	58.31	36.05	6.12	13.07	0.948
Lignin content	23.67	34.94	15.70	5.20	21.97	0.960
Ash content	0.72	2.19	0.10	0.48	66.67	0.962

with a contribution of 10.4%; the eigenvalues of SSD and BNN were 0.643 and 0.659, respectively. Therefore, this component represented the stem form traits. The cumulative contribution of the five principal components was 71.1%, which provided most of the information on the growth and wood traits of the families.

Family selection

To improve the growth of *P. koraiensis*, H, DBH, V, and SF were applied as evaluation indices of growth traits through principal components analysis. The results of multiple-trait comprehensive evaluation analysis are shown in Table 5. At a 10% selection intensity, five families (115, 117, 120, 133 and 138) were identified as families with rapid growth. The selected families had Q_i values of 1.997, 1.915, 1.863, 1.870, and 1.917, and with average H, DBH, V, and SF of 0.48 m, 2.66 cm, 0.0304 m³, and 0.02, respectively whereas

their genetic gains were 2.8%, 12.1%, 29.4%, and 1.9%, respectively.

High-quality materials for building and furniture construction could be obtained through the selection of families based on H, DBH, V, SF of growth traits and WD, FW, and LWR of physical properties of wood as evaluation indices. The results of the multiple-trait comprehensive evaluation analysis are shown in Table 6. At a 10% selection intensity, five families (112, 115, 117, 135, and 138) were identified as elite families for production of high-quality timber. The selected families had Q_i values 2.160, 2.145, 2.219, 2.140, and 2.126. Average H, DBH, V, SF, WD, FW and LWR were 8.0 m, 18.9 cm, 0.105 m³, 0.8, 488.4 kg m⁻³, 28.4 μm and 66.6, whereas their genetic gains were 2.4%, 11.4%, 26.9%, 1.8%, 3.6%, − 9.5% and 15.9%, respectively.

Families with superior pulp properties were selected via the multi-trait comprehensive evaluation of fiber length (FL), length/width ratio (LWR) and cellulose production per plant (CP) as evaluation indices. The Q_i values are presented

Fig. 1 Correlations between different growth and traits of *P. koraiensis* families (numbers are the correlation coefficients between different traits). Where H, DBH, V, SSD, SF, BNN, WD, FL, FW, LWR, CC, HEC, HOC. LC, and AC stand for height, diameter at breast height, volume, stem straightness degree, stem fullness, branch number per node, wood density, fiber length, fiber width, fiber length to width ratio, cellulose content, hemicellulose content, holocellulose content, lignin content and ash content, respectively. * Correlation is significant at 5% level; and ** Correlation is significant at 1% level

Table 4 Principal component analysis of different traits resulting in four distinct groupings that represented growth traits (Component I), chemical properties of wood (Component II), physical properties of wood (Component III) and stem form traits (Component IV)

Principal component factor	Component I	Component II	Component III	Component IV	Component V
Eigenvalue	3.584	2.263	1.935	1.556	1.322
Contribution (%)	23.89	15.09	12.9	10.37	8.82
Cumulative contribution (%)	23.89	38.98	51.88	62.25	71.06
Height	0.776	0.023	−0.203	0.334	−0.031
Diameter at breast height	0.923	0.067	−0.078	−0.082	−0.109
Volume	0.942	0.036	−0.116	-0.001	−0.102
Stem straightness degree	0.007	−0.135	0.174	0.643	−0.367
Stem form	0.74	0.057	−0.231	0.034	−0.105
Branch number per node	0.164	0.171	0.385	0.659	−0.037
Wood density	−0.042	−0.145	0.586	0.095	0.212
Fiber length	0.155	−0.431	−0.017	0.302	0.624
Fiber width	−0.144	−0.124	−0.785	0.366	0.375
Length to width ratio	0.272	−0.394	0.75	−0.101	0.144
Cellulose content	0.257	0.602	0.284	0.179	0.165
Hemicellulose content	−0.211	0.67	−0.072	−0.059	0.274
Holocellulose content	0.034	0.914	0.153	0.086	0.315
Lignin content	0.534	0.017	0.089	−0.321	0.016
Ash content	−0.387	0.166	−0.038	0.165	−0.595

Table 5 Q_i value of different families that are suitable for improving growth

Family	Qi	Family	Qi	Family	Qi	Family	Qi	Family	Qi
115	1.997	90	1.839	101	1.808	114	1.764	132	1.740
138	1.917	135	1.839	92	1.806	85	1.762	105	1.740
117	1.915	144	1.838	65	1.804	84	1.762	145	1.738
133	1.870	93	1.831	113	1.793	77	1.760	111	1.735
120	1.863	1	1.825	49	1.784	109	1.751	97	1.735
137	1.861	96	1.814	143	1.782	88	1.748	10	1.728
134	1.853	140	1.813	100	1.778	102	1.747	87	1.693
136	1.851	130	1.812	148	1.778	94	1.747	106	1.663
129	1.851	122	1.812	125	1.777	83	1.744	91	1.652
118	1.847	82	1.811	110	1.776	98	1.743		
112	1.845	108	1.809	163	1.768	103	1.742		

Note that the first five families are selected to be candidates for fast growth of *P. koraiensis*

Table 6 Q_i value of different families for improving timber for building material and furniture

Family	Qi	Family	Qi	Family	Qi	Family	Qi	Family	Qi
117	2.219	134	2.057	82	2.013	113	1.972	105	1.931
112	2.160	85	2.054	65	2.013	163	1.972	114	1.922
115	2.145	118	2.051	10	2.013	97	1.969	102	1.912
135	2.140	120	2.041	137	2.006	98	1.958	83	1.900
138	2.126	129	2.040	136	2.004	122	1.953	87	1.897
130	2.116	77	2.038	143	2.002	111	1.949	106	1.878
1	2.113	101	2.036	90	1.991	132	1.942	109	1.870
100	2.092	145	2.036	125	1.985	92	1.941	91	1.856
84	2.091	93	2.031	94	1.981	110	1.940	103	1.851
133	2.073	140	2.030	108	1.980	88	1.937		
144	2.064	96	2.028	148	1.978	49	1.933		

Note that the first five families are elite families suitable for improved production of timber for building materials and furniture

Table 7 Q_i value of different families for improving pulpwood materials

Family	Qi	Family	Qi	Family	Qi	Family	Qi	Family	Qi
115	1.637	84	1.521	136	1.447	97	1.403	83	1.362
117	1.619	113	1.507	138	1.444	114	1.401	110	1.356
1	1.603	108	1.506	140	1.441	65	1.395	111	1.346
112	1.593	145	1.500	10	1.436	132	1.393	93	1.343
130	1.582	120	1.488	88	1.435	143	1.385	105	1.340
129	1.572	125	1.485	49	1.427	102	1.381	109	1.334
135	1.559	96	1.477	77	1.425	92	1.380	137	1.334
100	1.543	144	1.466	106	1.410	98	1.376	87	1.320
82	1.543	133	1.461	101	1.409	91	1.369	163	1.294
134	1.530	90	1.456	118	1.407	103	1.368		
85	1.528	122	1.454	94	1.404	148	1.366		

Note that the first five families are selected to be the best suited families for improved production of pulpwood materials

in Table 7. At 10% selection intensity, five elite families (1, 112, 115, 117, and 130) were chosen for the production of high- quality pulp. The selected families had Q_i values 1.603, 1.593, 1.637, 1.619, and 1.582. Average FL, LWR, and CP were 1934.02 μm, 70.52 and 16.01 kg, and their real gains were 9.1%, 23.9%, and 43.2%, respectively.

Discussion

Variability in growth traits and wood physico-chemical properties

Genetic variation drives evolution, which in turn enables the adaptation and survival of organisms under different environmental conditions (Cardoso et al. 2015). Therefore, to understand the genetic variation of forest growth, the growth and wood properties of 28-year-old half-sib families of *P. koraiensis* were evaluated. All wood traits and most of the growth traits were significantly different among families, which concurs with the findings of Yin (2017). Thus, there is room for improvement through the selection of elite families.

Assessment of inter- and intra-population variation is a prerequisite for developing effective forest genetic resource conservation strategies (Papi et al. 2012). In this research, a lower average of growth and wood traits was reported than those reported by Wang et al. (2018a), which may be ascribed to different tree ages. In addition, the HOC and LC of wood characteristics were lower, 46.8% and 23.7%, respectively, which may be explained by the fact that the wood samples were too finely ground. Consequently, the exudation of the sample from the filter bag led to low experimental results.

The phenotypic coefficient of variation (PCV) is a widely adopted scaleless measure of variability (Wang et al. 2018b). It reflects the potential genetic variation among various traits in each population. Our study revealed that the PCV of H, DBH, and V was 10.8%, 16.3%, and 37.4%, respectively, lower than that of *Eucalyptus urophylla* S.T. Blake (Lu et al. 2010). The PCV of FL, FW, and LWR were 30.0%, 23.5%, and 26.4%, respectively, higher than that of *Eucalyptus camaldulensis* Dehnh. (Shang et al. 2017. The PCV of CC, HEC and LC was 17.1%, 11.1%, and 13.9%, respectively and higher than those of *Trachycarpus fortunei* (Hook.) H. Wendl. reported by Hu and Zhao (2018). Results of the present study demonstrated abundant variations in growth and wood traits, which necessitates genetic improvement in different directions according to different breeding objectives.

Similarly, heritability is the measure of the degree to which parents pass on genetic characteristics to offspring (Abengmeneng et al. 2015). The heritability of each wood trait in this study was over 0.8, significantly higher than that for *Pinus massoniana* Lamb. reported by Chen et al. (2015). These findings lay a foundation for the selection of families for pulpwood and building materials. Moreover, the heritability of H, DBH, and V in our study was 0.439, 0.746, and 0.745, respectively. These values are higher than the results of Chen et al. (2016); higher heritability is beneficial for parents to pass on good characteristics to their offspring, making the selection of families more meaningful.

Association between growth traits and wood properties

There were highly significant positive correlations between height, diameter at breast height, and volume, which concur with the results of Liang et al. (2018) for different clones of *P. koraiensis*. In most cases, height, diameter, and volume production are used to evaluate genetic variation in tree growth. Because these traits are relatively easy to assess, they have become a common indicator for the evaluation of forestry production (Rweyongeza et al. 2005). In our study, there were strong correlations between height, diameter at breast height, and volume, which are beneficial to the evaluation and selection of fast-growing *P. koraiensis* families. Among wood physical properties, fiber length was significantly positively correlated with fiber width (0.422) and fiber length/width ratio (0.452). Similar results were reported by Wang (2009) who studied *P. massoniana*. The findings suggest the possibility of synchronized improvement of fiber length and width through selection of one of these traits. There was a highly significant correlation between holocellulose and cellulose (0.700) and hemicellulose contents (0.693), but lignin content was not strongly correlated with cellulose and hemicellulose contents, which is different from the results of Yin et al. (2017). This may be attributed to the fine grinding of the sample, whereby the sample leaks out of the filter bag and affects the calculation of cellulose, hemicellulose, and lignin contents. On the other hand, lignin was strongly correlated with diameter at breast height (0.432) and volume (0.420); this is different and contrary to findings from previous studies. For instance, Zhang et al. (2015a, b) reported the lack of a significant correlation between lignin content and growth traits of *Populus tomentosa* Carriére, whereas Yu (2015) reported a significant negative correlation between lignin content and growth traits of *Larix gmelinii* Ledebe ex Gordon. Therefore, the correlation of growth traits with wood properties is possibly related to different species and growing environments. The correlation analysis aimed to find the best linear combination between two sets of multivariate data that maximizes the correlation coefficient between them (Malacarne 2014). As a common statistical tool, correlation analysis can intuitively reflect the correlation between the datasets (Jendoubi and Strimmer 2019).

Principal components analysis (PCA) is a classic multivariate technique that reduces the dimensional complexity of a set of variables to a new set of unrelated variables, known as the principal component, which retains all the variable information (Fernández et al. 2015). It is applicable in the exploration of the relationship between different tree characters (Hoeber et al. 2014). In this study, all traits were divided into five principal components with a cumulative contribution rate of 71.1%, lower than the results of a study by López de Heredia et al. (2009) on oaks. Following the analysis,

principal component factors described growth traits, wood chemical properties, wood physical properties, and stem form. Each principal component objectively reflected the relationship among the analyzed traits and provided a basis for the evaluation and selection of elite families.

Selection of elite families

To select elite *P. koraiensis* families with different attributes, the families were screened according to three breeding objectives: fast-growth, production of high-quality construction timber, and production of pulpwood.

Fast growing families

Regarding best growth in height, diameter, volume, and stem fullness, five elite families were selected that had better growth for timber production and urban planting. These elite families showed 2.8%, 12.1%, 29.4%, and 1.9% genetic gain in height, diameter, volume, and stem fullness, respectively. The results were higher than that reported for *P. koraiensis* by Wang et al. (2018a), and similar to a study on Douglas-fir (Clair et al. 2004). The growth performance of these selected elite families was good; thus they can be used as source of planting material for the establishment of fast-growing *P. koraiensis* plantations. Elite families with higher genetic gains are beneficial to promote and apply in forestry production.

Families suitable for production of high quality building materials

To obtain high-quality materials for building and furniture, height, diameter, volume, stem fullness, density, fiber width, and fiber length/width ratio were used as indicators for comprehensive evaluation based on the results of principal component analysis. Principal component analysis found wood density and fiber length to width ratio as representing the physical properties of wood. Wood density is an important feature of trees that is central to many functional processes, and is considered a trait that powerfully integrates various wood characteristics (Woodall et al. 2015). It directly affects wood quality. Fiber width and the ratio between fiber length and width are common wood fiber characteristics. Some studies have shown that fiber width is related to the wood structure, which is applied to judge the thickness of the wood (Huang and Chen 2014). A fine wood structure implies that the material is more compact, the surface is smoother, and is easier to cut and machine. Following the screening of 53 *P. koraiensis* families, 5 elite families with these characteristics were identified. The genetic gains of each trait were 2.4%, 11.4%, 26.9%, 1.8%, 3.6%, −9.5%, and 15.9% for height, diameter, volume, stem fullness, density, fiber width,

and fiber length/width ratio, respectively, higher than those reported by Wang et al. (2018a). The wood density of elite families was relatively high at 488.4 kg m^{-3}. The selected elite families can be utilized for structural and decorative materials, including floor platforms and garden furniture.

Families suitable for pulpwood production

There are limited studies on the pulpwood production of *P. koraiensis*. However, given its long fiber length (0.90 − 3.00 mm), *P. koraiensis* is highly suitable to produce high-strength paper (Wang 2000). Therefore, the utilization value of *P. koraiensis* for pulpwood was evaluated. Fiber length, length/width ratio, and cellulose production were evaluation indices for pulpwood. Notably, the nature of wood determines its economic value and directly affects wood processing and utilization. Fiber length is the most important morphological parameter in papermaking. Wang et al. (2016) showed that longer fibers could achieve higher tear strength, tensile strength, and flexural strength. The length/width ratio of fiber is an important morphological index second only to fiber length. A larger length/width ratio is related to a larger bonding area of the fiber, a higher paper index, and higher paper strength (Chang et al. 2007). In this study, 5 elite families were identified using fiber length, length/width ratio, and cellulose production as evaluation indexes. The real gains were 9.1%, 23.9%, and 43.2%, respectively. The genetic improvement is remarkable and can provide valuable material with fine quality fiber.

Conclusion

We examined variations in growth and wood properties of 53 half-sib families of *P. koraiensis*. Substantial genetic variations in growth traits and wood physicochemical properties were found among families with good heritability, which in turn enabled selection of elite families. Consequently, five elite families that had better growth for timber production and urban planting; five families suitable for production of high-quality building materials; and five elite families suitable for pulpwood production were selected, with good genetic gain. Thus, these families should be used in future plantation establishment to achieve economic objectives.

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