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Genetic Variation in Growth and Cone Traits of *Pinus Koraiensis* Half-Sib Families in Northeast China

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Abstract: Genetic parameters were evaluated for growth and cone characteristics (tree height, diameter at breast height, volume, cone number, thousand seeds weight and single cone seeds weight) on 86 half-sib families of *Pinus koraiensis* aged 31 years. Analyses of variance revealed significant differences ($p < 0.001$) in all growth and cone traits among families while no significant differences were detected among blocks and the interaction between blocks and families. The average family values for growth traits were 17.22 m, 8.67 cm and 0.43 m^3 for tree height, diameter at breast height and volume, respectively. The average cone number, thousand seeds weight and single cone seeds weight were 17.57, 748.91 g and 77.25 g, respectively. Genotypic additive variance and phenotypic variances ranged from 0.00009 to 3.820 and from 0.0005 to 23.066, while genotypic and phenotypic coefficients of variation ranged from 2.693% to 37.196% and 4.963% to 60.595%, respectively. Heritability at the individual and family level ranged from 0.152 to 0.215 and 0.611 to 0.862, respectively. Growth traits were significantly positively correlated with each other, but cone traits showed a weak correlation with growth traits. Based on 10% selection rate, nine families each were selected as elite materials in terms of high performance in volume and cone numbers, with 22.16% and 43.82% genetic gain in volume and cone number, respectively. These results provide beneficial information to select excellent families and establish orchards of *P. koraiensis* from improved seeds.

Keywords: *Pinus koraiensis*; half-sib families; genetic; variation; selection

1 Introduction

Pinus koraiensis Siebold & Zucc is a dominant tree species in mixed-climate broadleaf-conifer forests at the Xiaoxing'anling mountain, Zhangguangcai ridge, Laoye ridge, and Changbai Mountains in northeastern China [1,2]. The distribution area extends to the northern regions of North Korea, the central region of Japan and the southern part of Far East Russia [3,4]. Because of natural *P. koraiensis* forests' edible nuts and excellent timber quality, these forests have been overexploited [5], particularly during the years 1975-1988, which was characterized by large-scale timber harvesting and wood production by the clear-cut method practiced in China [6]. The devastated natural areas have been offset by artificial forests [7].

Due to poor quality production in certain artificial forest stands [8], slow growth and late sexual maturity of this species [9], there have been efforts to improve *P. koraiensis* for decades in China. Thus, a series of studies were conducted at different stages of improvement program of this species. As an example, the selection of plus trees and different provenances in natural forests [10,11], the implementation of seed orchards [12] and selection of superior families and parents [13-15]. Because of high demand for timber in past several years, the improved genotypes of *P. koraiensis* have been selected based on growth traits and wood properties [16]. But according to the economic value of seeds and the protection project of natural forest, the cone yield turned into the main objective in *P. koraiensis* breeding in recent years.

Quantifying genetic variation between generations is a fundamental element in the tree improvement process [17]. For *P. koraiensis*, though several seed orchards were established and a large number of progeny test plantation have been established, rigorous statistical analyses of genetic variation of these seedlings were rare [18,19]. Breeding objectives determine breeding methods, and growth traits and wood properties are the most important traits for breeder's consideration when elite families or clones are to be selected [20]. For evaluation of genetic differences, most research focus on several growth traits or together with wood properties by comprehensive evaluation methods [21-22]. Though the seed yield has more importance than wood properties due to higher economic values, the cone trait had rarely been investigated by breeders in recent years. In this study, growth and cone traits of 86 half-sib *P. koraiensis* families at the age of 31 years were investigated, and the main objectives were (1) to investigate the genetic variation of each traits among different families; (2) explore the relationship between growth traits and cone traits; (3) evaluate and select elite families according to their growth and cone traits, which can provide a theoretical basis for improved variety breeding and upgraded seed orchard.

2 Materials and Methods

2.1 Site Description

The experiment was conducted in Naozhi Forestry Seed Orchard (41°05'N, 126°06'E), located on the western hillside of Changbai Mountain, Linjiang City, Northeast China. The climate type is temperate monsoon, and the average frost-free season, average elevation, mean annual precipitation and mean annual temperature were 128 days, 510 m, 744 mm and 8.2°C respectively. The soil type in this region is dark brown soil of silty texture with varying proportion of sand (15.13%), Silt (63.31%) and Clay (21.56%) [23]. Pure *P. koraiensis* monoculture plantations and broadleaf mixed forest are typical at this region at the foot of the Changbai Mountain [24].

2.2 Materials

We used 86 *P. koraiensis* half-sib families as experimental materials including two controls (Tab. 1). CK1 was derived from mixed seed in the forest at Ice Lake town and CK2 was mixed seed which were collected from superior trees in Linjiang city, other families were cultivated with free pollination family seeds which parents were selected in natural distribution of Linjiang forestry bureau. The experimental design consisted of 3 blocks with four-year-old seedlings of each family planted using a completely randomized block design in row plots containing 10 trees with 3 × 4 m spacing in 1989.

Table 1: Half-sib families represented in this study together with control families

Material source	Families
83 half-sib families	F2, F3, F11, F12, F16, F20, F25, F32, F35, F36, F37, F38, F39, F40, F41, F42, F44, F45, F46, F47, F48, F49, F50, F51, F54, F55, F56, F57, F59, F60, F62, F63, F64, F65, F66, F67, F68, F71, F72, F73, F76, F79, F80, F81, F82, F84, F85, F86, F87, F88, F89, F90, F92, F94, F95, F96, F97, F98, F99, F102, F104, F106, F107, F108, F110, F111, F112, F113, F119, F121, F123, F124, F126, F127, F128, F130, FA046, FA050, FA064, FA079, FA085, FA093, FA125
Two controls	CK1 CK2

2.3 Trait Measurement

Different traits were measured on living plants of each family on September 2015 at the age of 31 years. The traits measured included: Tree height (Ht), Diameter at breast height (DBH), Cone numbers per plant (CN), thousand seeds weight (TSW) and single cone seeds weight (SCSW). Tree height was directly measured by the Vertex Laser instrument (Haglof, Sweden), and diameter was measured with a circumference ruler. Cone number per tree was directly counted, while the single cone seedS weight and one thousand seeds weight were measured with a high precision balance. The volume (V) of trees was estimated using the formula proposed by Huber for conifers with a form factor of 0.41 [25].

2.4 Statistical Analyses

The IBM SPSS statistics software version 20 [26] was used to perform the statistical analyses. The significance of fixed effects (Eq. (1)) was tested by analysis of variance (ANOVA) F test [27-28]. The linear model used to calculate the performance of individual trees in different families is shown below [29]:

$$X_{ijk} = \mu + \alpha_i + \beta_j + \alpha\beta_{ij} + \varepsilon_{ijk} \tag{1}$$

where X_{ijk} is the performance of **k** individual trees from **i** family growing in block **j**; μ is the overall mean; α_i is the effect of family i; β_j is the effect of block j, $\alpha\beta_{ij}$ is the effect of interaction of family i and block j and ε_{ijk} is the random error.

The family variance component (σ_F^2), the phenotypic variance (σ_P^2) and phenotypic variance of family mean ($\sigma_{P\_HS}^2$) were calculated following formula proposed by Isik [30]

$$\sigma_F^2 = \frac{\sigma_A^2}{4} \tag{2}$$

$$\sigma_P^2 = \sigma_F^2 + \sigma_{bF}^2 + \sigma_\varepsilon^2 \tag{3}$$

$$\sigma_{P\_HS}^2 = \sigma_F^2 + \frac{\sigma_{bF}^2}{b} + \frac{\sigma_\varepsilon^2}{bn} \tag{4}$$

where σ_A^2, σ_{bF}^2 and σ_ε^2 were additive genetic variance, the phenotypic variance of the interaction of family and block and residual variance, respectively. b and n were block number and number of tree per family per block.

The heritability at the individual tree (h_i^2) and at the average (family) level (h_{HS}^2) with their associated standard errors SE were calculated by formula below [30]:

$$h_i^2 = \frac{\sigma_A^2}{\sigma_P^2} = 4\frac{\sigma_F^2}{\sigma_F^2 + \sigma_{bF}^2 + \sigma_\varepsilon^2} \text{ and } SE(h_i^2) = \sqrt{Var(h_i^2)} \tag{5}$$

$$h_{HS}^2 = \frac{\sigma_F^2}{\sigma_{P\_HS}^2} \text{ and } SE(h_{HS}^2) = \sqrt{Var(h_{HS}^2)} \tag{6}$$

h_{bF}^2, was the phenotypic variance for the interaction between family and block.

The phenotypic coefficient of variation PCV (%) and genotypic coefficient of variance (GCV) were estimated by the formula below [31].

$$PCV = \frac{\sqrt{\sigma_P^2}}{\overline{X}} \times 100 \tag{7}$$

$$GCV = \frac{\sqrt{\sigma^2_{F\_HS}}}{\overline{X}} \times 100 \qquad (8)$$

where $\overline{x}$ was mean value of the trait.

The trait relationships were estimated by Pearson's correlation coefficient, $r_A(xy)$, which was derived from the covariance of related traits $COV_{P(x,y)}$ divided by the product of multiplying their respective variances $\sigma_p(x) \times \sigma_p(y)$ [32].

$$r_A(xy) = \frac{\text{cov}_{P(xy)}}{\sigma_P(x)\sigma_P(y)} \qquad (9)$$

The best linear unbiased predictors (BLUP) of families were calculated according to Eq. (10) [33], which was used to obtain the general combining ability (GCA) of parent trees in order to deduce the family's breeding values according to Eq. (11) [29].

$$P_{0,HS} = \mu_\circ + GCA_F \qquad (10)$$
$$BV_{HS} = 2GCA_F \qquad (11)$$

where $P_{0,HS}$ and μ_O were the family phenotypic value and the average of offspring population from the same family, respectively.

The genetic gain was estimated by the following formula (Eq. (12)) [34].

$$\Delta G = h^2_{HS} \times S \qquad (12)$$

where S was the selection difference between the selected families performance and h^2_{HS} was the heritability at the family level as defined above.

3 Results

3.1 Average Values for Growth and Cone Traits

Significant differences in growth and cone traits were detected among *P. koraiensis* families ($P < 0.001$). The other source of variance (block and the interaction of block and family) had shown no significant differences for all traits analyzed. The average values of different traits of all families are shown in Tab. 2. The overall average values for growth traits were 17.43 cm, 8.73 m and 0.044 m³ in Ht, DBH and V, respectively. The overall means for cone traits were 17.71, 750.32 g and 77.28 g for cone number per plant, thousand seeds weight and single cone seeds weight, respectively. The highest average values differed from the lowest average values by 17.78 cm, 3.49 m and 0.66 m³ for DBH, Ht and V, respectively. Three families (F84, F65 and F56) had higher average in DBH, two families (F56 and FA079) had higher average in Ht and family F56 had higher value in V. Eight families (F66, F55, F35, F128, FA093, F106, F25 and F81) showed particularly low average values in DBH, Ht and V. The highest cone number per plant was observed in two families (F38 and F107), and two families (F38 and F48) also showed higher thousand seeds weight than others. The differences between the highest and the lowest average value in cone number, thousand seed weight and single cone seeds weight were 33.67, 130.90 g and 23.30 g, respectively.

Table 2: Average values and standards errors of traits of all families, tree height (Ht, m), diameter at breast height (DBH, cm), stem volume (V, m³), cone numbers per plant (CN), thousand seed weight (TSW, g) and single cone seed weight (SCSW, g)

Families	Ht	DBH	V	CN	TSW	SCSW
F2	16.21 ± 0.036	7.92 ± 0.035	0.327 ± 0.004	33.00 ± 1.000	789.73 ± 5.823	77.13 ± 0.981
F3	12.20 ± 0.017	8.44 ± 0.035	0.280 ± 0.002	3.00 ± 1.000	703.27 ± 5.020	69.37 ± 2.183
F11	10.78 ± 0.029	9.55 ± 0.011	0.317 ± 0.001	34.33 ± 1.155	778.93 ± 2.871	88.07 ± 2.013
F12	18.27 ± 0.050	10.22 ± 0.015	0.615 ± 0.002	16.67 ± 2.082	800.73 ± 1.531	80.47 ± 1.721

F16	23.91 ± 0.025	7.62 ± 0.006	0.447 ± 0.004	5.67 ± 0.577	762.00 ± 4.321	85.17 ± 1.617
F20	22.84 ± 0.025	8.54 ± 0.006	0.536 ± 0.001	21.67 ± 0.577	770.37 ± 2.902	76.33 ± 0.702
F25	8.18 ± 0.021	8.61 ± 0.025	0.195 ± 0.001	19.00 ± 1.000	723.10 ± 4.279	73.97 ± 0.751
F32	11.71 ± 0.023	8.85 ± 0.025	0.295 ± 0.001	8.67 ± 1.155	740.63 ± 6.721	69.57 ± 1.457
F35	10.11 ± 0.020	7.27 ± 0.040	0.172 ± 0.002	19.67 ± 1.528	715.73 ± 6.178	74.20 ± 0.693
F36	22.04 ± 0.010	8.54 ± 0.036	0.517 ± 0.004	7.67 ± 1.155	777.30 ± 4.937	72.73 ± 1.193
F37	18.87 ± 0.010	8.78 ± 0.015	0.469 ± 0.002	30.33 ± 1.155	738.40 ± 4.763	73.47 ± 0.462
F38	23.20 ± 0.026	8.01 ± 0.026	0.479 ± 0.004	35.00 ± 1.000	812.97 ± 5.431	67.97 ± 1.457
F39	25.28 ± 0.040	8.41 ± 0.040	0.576 ± 0.006	25.33 ± 1.528	752.03 ± 4.065	85.97 ± 1.531
F40	13.27 ± 0.045	7.34 ± 0.006	0.230 ± 0.001	10.00 ± 0.300	781.27 ± 3.828	85.57 ± 1.097
F41	24.63 ± 0.031	8.30 ± 0.017	0.546 ± 0.002	13.67 ± 2.082	755.37 ± 3.946	70.20 ± 0.721
F42	17.07 ± 0.021	8.62 ± 0.025	0.408 ± 0.002	31.33 ± 0.577	764.40 ± 2.722	81.70 ± 1.411
F44	11.61 ± 0.020	9.63 ± 0.021	0.346 ± 0.002	9.00 ± 1.732	797.13 ± 1.106	85.77 ± 1.115
F45	13.43 ± 0.020	7.24 ± 0.026	0.227 ± 0.001	16.33 ± 1.528	708.33 ± 4.329	87.57 ± 1.721
F46	10.37 ± 0.010	9.77 ± 0.012	0.318 ± 0.001	13.67 ± 0.577	766.10 ± 4.371	72.60 ± 0.866
F47	9.93 ± 0.012	8.12 ± 0.012	0.211 ± 0.001	14.67 ± 1.155	763.43 ± 4.140	86.77 ± 2.850
F48	12.48 ± 0.017	9.55 ± 0.012	0.367 ± 0.001	26.00 ± 1.732	814.87 ± 3.493	80.40 ± 0.794
F49	20.84 ± 0.023	7.25 ± 0.026	0.353 ± 0.003	8.67 ± 0.577	728.43 ± 5.093	79.83 ± 0.551
F50	14.07 ± 0.006	7.63 ± 0.021	0.264 ± 0.001	31.33 ± 0.577	732.10 ± 2.621	77.87 ± 1.290
F51	22.76 ± 0.030	10.38 ± 0.010	0.789 ± 0.001	5.00 ± 0.900	718.60 ± 1.400	66.83 ± 1.358
F54	20.62 ± 0.023	10.04 ± 0.025	0.669 ± 0.004	4.67 ± 4.726	747.67 ± 6.096	82.87 ± 1.656
F55	9.99 ± 0.025	7.14 ± 0.021	0.164 ± 0.001	33.67 ± 1.155	807.30 ± 2.456	73.73 ± 0.611
F56	23.08 ± 2.790	9.02 ± 1.305	0.632 ± 0.249	21.33 ± 13.530	766.88 ± 7.308	77.07 ± 7.308
F57	21.73 ± 0.021	7.50 ± 0.045	0.393 ± 0.004	32.67 ± 1.528	699.73 ± 7.406	86.00 ± 0.794
F59	21.83 ± 0.023	8.94 ± 0.036	0.561 ± 0.004	33.67 ± 1.155	803.67 ± 2.237	78.27 ± 1.570
F60	12.77 ± 0.021	7.56 ± 0.015	0.235 ± 0.001	17.33 ± 1.528	727.40 ± 1.808	80.83 ± 1.422
F62	11.98 ± 0.020	10.12 ± 0.025	0.395 ± 0.002	13.33 ± 0.577	734.40 ± 4.204	74.57 ± 0.862
F63	10.45 ± 0.029	9.82 ± 0.006	0.324 ± 0.001	19.33 ± 0.577	774.07 ± 5.910	83.37 ± 2.122
F64	21.47 ± 0.010	7.87 ± 0.015	0.428 ± 0.002	22.33 ± 0.577	788.60 ± 6.155	81.87 ± 2.205
F65	25.82 ± 0.021	9.45 ± 0.035	0.742 ± 0.005	22.67 ± 1.528	683.97 ± 2.250	75.43 ± 1.050
F66	8.51 ± 0.015	6.94 ± 0.023	0.132 ± 0.001	2.00 ± 1.732	700.30 ± 4.085	74.60 ± 0.854
F67	18.40 ± 0.020	7.29 ± 0.036	0.315 ± 0.003	6.33 ± 0.577	741.43 ± 1.858	69.20 ± 2.307
F68	22.34 ± 0.023	10.40 ± 0.023	0.778 ± 0.003	22.00 ± 0.800	710.03 ± 3.308	87.10 ± 0.819
F71	15.82 ± 0.006	9.34 ± 0.045	0.444 ± 0.004	26.33 ± 1.155	704.77 ± 6.562	74.03 ± 1.097
F72	25.41 ± 0.032	9.34 ± 0.023	0.714 ± 0.004	7.33 ± 1.155	807.47 ± 6.391	85.83 ± 0.961
F73	23.13 ± 0.015	8.90 ± 0.029	0.589 ± 0.004	17.67 ± 1.528	716.87 ± 4.858	67.13 ± 0.603
F76	12.47 ± 3.412	7.69 ± 0.968	0.254 ± 0.126	30.00 ± 4.517	736.63 ± 59.100	84.18 ± 3.743
F79	18.09 ± 0.010	9.91 ± 0.010	0.572 ± 0.001	13.00 ± 0.900	808.40 ± 6.102	77.20 ± 1.249
F80	15.32 ± 0.015	7.47 ± 0.032	0.275 ± 0.003	15.67 ± 0.577	747.70 ± 6.210	81.87 ± 2.458
F81	8.46 ± 0.045	8.91 ± 0.029	0.216 ± 0.001	10.33 ± 0.577	726.43 ± 5.123	78.17 ± 0.862
F82	22.61 ± 0.029	7.83 ± 0.015	0.447 ± 0.002	4.00 ± 1.000	760.43 ± 9.577	76.63 ± 1.531
F84	25.96 ± 0.010	7.53 ± 0.017	0.474 ± 0.002	19.00 ± 1.000	762.00 ± 1.825	74.87 ± 1.168
F85	13.63 ± 0.026	7.26 ± 0.020	0.231 ± 0.002	17.67 ± 1.155	717.93 ± 6.526	68.90 ± 1.277

F86	23.09 ± 0.025	9.72 ± 0.045	0.702 ± 0.006	26.67 ± 0.577	684.53 ± 3.669	79.30 ± 2.042
F87	19.32 ± 0.031	8.49 ± 0.025	0.448 ± 0.002	2.00 ± 1.000	805.10 ± 1.709	70.90 ± 2.900
F88	15.68 ± 0.020	9.17 ± 0.025	0.424 ± 0.002	3.67 ± 1.528	803.00 ± 6.509	66.53 ± 1.457
F89	20.05 ± 0.040	7.95 ± 0.012	0.408 ± 0.002	9.33 ± 0.577	689.60 ± 5.667	66.47 ± 1.060
F90	13.66 ± 2.045	8.64 ± 0.298	0.325 ± 0.027	15.33 ± 11.708	742.50 ± 11.342	70.43 ± 1.297
F92	16.34 ± 0.012	9.92 ± 0.040	0.517 ± 0.005	28.33 ± 0.577	706.03 ± 6.466	65.77 ± 2.074
F94	12.94 ± 0.031	9.53 ± 0.017	0.378 ± 0.001	7.33 ± 0.577	716.67 ± 2.558	82.93 ± 0.764
F95	14.63 ± 0.031	9.51 ± 0.025	0.425 ± 0.003	16.33 ± 1.155	795.73 ± 5.613	69.17 ± 1.498
F96	8.95 ± 0.015	8.95 ± 0.040	0.231 ± 0.002	7.00 ± 1.732	789.50 ± 7.063	70.20 ± 0.964
F97	23.24 ± 0.017	9.63 ± 0.026	0.694 ± 0.004	2.67 ± 1.155	786.40 ± 4.776	78.37 ± 0.808
F98	16.38 ± 0.030	10.14 ± 0.040	0.542 ± 0.003	7.00 ± 1.000	770.80 ± 2.066	85.53 ± 0.351
F99	16.09 ± 0.020	9.69 ± 0.021	0.487 ± 0.002	26.33 ± 1.528	739.57 ± 5.237	75.70 ± 0.300
F102	23.43 ± 0.025	10.17 ± 0.017	0.780 ± 0.002	8.67 ± 1.528	767.80 ± 1.179	87.50 ± 1.308
F104	18.40 ± 0.032	9.41 ± 0.017	0.524 ± 0.002	15.00 ± 1.000	807.03 ± 4.528	74.23 ± 0.833
F106	9.73 ± 0.035	7.90 ± 0.023	0.195 ± 0.001	23.33 ± 1.155	745.67 ± 3.002	88.87 ± 0.737
F107	24.59 ± 0.050	9.46 ± 0.010	0.708 ± 0.001	35.00 ± 1.000	718.37 ± 4.908	72.70 ± 1.868
F108	16.40 ± 0.006	9.49 ± 0.020	0.475 ± 0.002	34.33 ± 1.528	713.60 ± 2.352	70.87 ± 0.709
F110	16.48 ± 0.012	9.07 ± 0.040	0.436 ± 0.004	27.67 ± 2.082	745.23 ± 6.301	68.50 ± 1.803
F111	19.01 ± 0.012	7.33 ± 0.030	0.329 ± 0.003	16.67 ± 1.155	744.97 ± 4.028	77.03 ± 1.422
F112	15.09 ± 0.040	8.89 ± 0.046	0.384 ± 0.003	24.00 ± 1.732	780.97 ± 7.193	86.33 ± 1.193
F113	20.85 ± 3.120	7.39 ± 0.070	0.367 ± 0.061	21.17 ± 8.280	704.35 ± 18.139	80.57 ± 1.896
F119	20.87 ± 0.017	8.31 ± 0.021	0.464 ± 0.002	22.33 ± 1.528	737.70 ± 6.090	88.27 ± 0.513
F121	18.06 ± 0.021	8.47 ± 0.021	0.417 ± 0.002	12.33 ± 0.577	755.07 ± 3.850	65.57 ± 1.365
F123	23.22 ± 0.035	9.44 ± 0.017	0.666 ± 0.003	2.00 ± 1.000	751.93 ± 7.095	80.23 ± 1.914
F124	21.84 ± 0.010	8.88 ± 0.015	0.555 ± 0.002	1.33 ± 0.577	709.37 ± 3.750	85.87 ± 1.498
F126	21.48 ± 0.010	10.20 ± 0.021	0.719 ± 0.003	4.67 ± 1.528	685.60 ± 2.762	80.27 ± 0.907
F127	22.30 ± 0.032	10.16 ± 0.021	0.741 ± 0.004	28.67 ± 1.528	694.83 ± 3.612	82.77 ± 1.721
F128	8.78 ± 0.029	7.28 ± 0.017	0.150 ± 0.001	3.67 ± 0.577	731.17 ± 5.908	74.40 ± 1.562
F130	24.66 ± 0.036	9.56 ± 0.021	0.726 ± 0.002	32.67 ± 0.577	773.13 ± 3.137	74.80 ± 0.781
FA046	25.51 ± 0.025	8.45 ± 0.017	0.586 ± 0.003	29.67 ± 0.577	801.77 ± 3.855	67.37 ± 1.686
FA050	13.49 ± 0.010	8.51 ± 0.017	0.314 ± 0.001	27.00 ± 0.070	801.80 ± 4.583	81.27 ± 2.550
FA059	18.02 ± 0.035	8.01 ± 0.021	0.372 ± 0.003	24.33 ± 0.577	759.40 ± 0.600	84.07 ± 1.106
FA064	23.13 ± 0.006	8.09 ± 0.021	0.487 ± 0.003	3.33 ± 1.155	739.77 ± 8.113	72.87 ± 1.531
FA079	9.86 ± 0.045	10.44 ± 0.021	0.346 ± 0.003	17.00 ± 1.732	727.93 ± 6.144	65.87 ± 2.318
FA085	24.09 ± 0.035	9.73 ± 0.025	0.734 ± 0.003	10.67 ± 2.082	695.20 ± 5.587	88.27 ± 0.462
FA093	11.24 ± 0.010	9.30 ± 0.031	0.313 ± 0.002	26.00 ± 1.000	758.57 ± 0.929	68.23 ± 2.237
FA125	8.93 ± 0.031	7.49 ± 0.006	0.161 ± 0.001	32.33 ± 1.528	777.10 ± 5.828	80.67 ± 1.050
CK1	8.09 ± 0.026	6.87 ± 0.040	0.123 ± 0.001	2.33 ± 0.577	735.97 ± 2.542	74.70 ± 1.375
CK2	8.21 ± 0.031	6.84 ± 0.006	0.124 ± 0.001	3.33 ± 1.528	688.63 ± 2.859	73.40 ± 1.493

The DBH was expressed by (cm), the H by (m), the V by (m³), TSW and SCSW by (g).

3.2 Genetic Parameters

The genetic parameters for all traits in all families are given in Tab. 3. For growth traits, the higher and lower phenotypic and genotypic variances were observed in DBH and V, which ranged from 4.601% to 42.511%. The higher and lower genotypic and phenotypic coefficient of variation in cone traits was observed for TSW and CN, which ranged from 2.693% to 60.595%. Cone number showed higher genotypic and phenotypic variances. The highest and lowest heritability at the individual and average/family level were observed for CN and Ht, respectively. Heritability ranged from 0.15 to 0.21 and 0.61 to 0.84 at the individual and average/family levels, respectively.

Table 3: Genetic parameters for growth and cone traits

Traits	σ_F^2	σ_A^2	σ_P^2	$\sigma_{P\_HS}^2$	PCV (%)	GCV (%)	h_i^2	h_{HS}^2
Ht	0.351	0.088	0.417	0.352	31.962	28.519	0.21 ± 0.355	0.84 ± 0.355
DBH	0.012	0.003	0.017	0.012	11.898	4.601	0.17 ± 1.578	0.69 ± 1.578
V	0.0004	0.00009	0.0005	0.0003	42.511	27.997	0.17 ± 9.018	0.70 ± 9.018
CN	1.234	0.309	2.032	1.242	60.595	37.196	0.15 ± 0.137	0.61 ± 0.137
TSW	15.281	3.820	23.066	15.360	4.963	2.693	0.17 ± 0.042	0.67 ± 0.042
SCSW	0.520	0.130	0.653	0.521	8.884	7.687	0.20 ± 0.276	0.80 ± 0.276

Note: σ_F^2 family variance component; σ_A^2 additive variance, σ_P^2, total phenotypic variance $\sigma_{P\_HS}^2$; phenotypic variance on family mean GCV and PCV instead of the genotypic and phenotypic coefficients of variation; h_i^2 and h_{HS}^2 , instead of individual and family heritability and $SE(h_i^2)$, $SE(h_{HS}^2)$ are heritability's standard error.

3.3 Correlation Analysis Between Traits

The correlation coefficients between different traits were determined. All cone traits (CN, TSW and SCSW) showed weak positive or negative correlation with growth traits (Ht, DBH and V) and among each other (r = -0.026-0.101). TSW and SCSW were negatively correlated to Ht and DBH, respectively whereas CN was negatively correlated with DBH and V. Correlation coefficient was also significantly positive between DBH and V (r = 0.840), while a weak significant positive correlation was noted between DBH and Ht (r = 0.226).

3.4 Breeding Values and Genetic Gains of Elite Families

With 10% selection rate, 9 elite families (Tab. 4) were selected for stem volume (F51, F102, F68, F65, F127, FA085, F130, F126 and F72) and cone number (F38, F107, F11, F108, F55, F59, F2, F130, F57) each. The range of the breeding values for the selected families was from 0.285 m³ to 0.360 m³ and from 15.10 to 17.43 in volume and cone numbers per plant, respectively. Family F130 stood out as the best family in terms of high-performance value in both volume and cone numbers per plant (Tab. 4). The genetic gains from selection of families are shown in Tab. 5, which ranged from 5.20% to 22.16% and 10.12% to 43.82% in growth and cone traits, respectively. The V and CN had the highest genetic gain among growth and cone traits. Among all traits, Ht had the lowest genetic gain, with 5.20% genetic gain.

Table 4: Breeding values for volume and cone number of selected families

Families	BV_{HS}_V	Families	BV_{HS}_CN
F51	0.360	F38	17.43
F102	0.351	F107	17.43
F68	0.349	F11	16.76
F65	0.313	F108	16.76
F127	0.312	F55	16.10
FA085	0.304	F59	16.10
F130	0.297	F2	15.43
F126	0.290	F130	15.10
F72	0.285	F57	15.10

Note: BV_{HS}_V and BV_{HS}_CN represent breeding value for volume and cone number, respectively. The selection rate was 10%.

Table 5: Family genetic gain

Growth traits	Genetic gain (%)	Cone traits	Genetic gain (%)
DBH	11.36	CN	43.82
H	5.20	TSW	11.86
V	22.16	SCSW	36.25

4 Discussion

Each offspring in a half-sib family has unique phenotypic characteristics because of different genotype and different microenvironment, which may lead to a certain amount of variation among trees within the same family [35]. The analysis of variance helps to characterize this variation and enables selection of genetic resources in tree improvement research [17]. In the present study, significant differences ($P < 0.001$) were observed in all growth and cone traits among families whereas blocks and the interaction of block and family showed no significant differences. The lack of block effect may be due to the fact that all blocks closely resembled with the environmental and soil conditions of the region. Similar results have been reported for *Larix olgensisand* [36] and *Cornus wilsoniana* [37], which indicated that the selection of elite families was feasible.

Average family performance values of different traits were used to establish successive order in tree selection according to their ranks [38]. In the present study, the analysis on growth and cone traits of 86 *P. koraiensis* families showed great variation in average trait values among families but weak variation within families in different blocks, which was more favorable for family selection than individual selection. Although families had different mean values for various traits, with a default rounding, the growth measures presented approximate means for all growth and cone traits. In fact, the weak variation observed within trees in families led to the uniform pace in growth at the individual level. This finding could be due to the slow growing speed of trees at the maturity age [39-40], which also explains the slight decreasing trend of the difference between the maximum and minimum value observed in DBH.

Genetic variation is the basic element for evaluation and selection of excellent materials in forest tree improvement programs [41]. Genotypic variation reflects the difference between trees within families, while phenotypic variation indicates the difference between families. The higher value of these two coupled variations can enable a selection of the best descendant [42]. The phenotypic coefficients of variance were slightly higher for all traits compared to the genotypic coefficient of variance, generally because deviations from the averages in traits was greater among families than between trees of the same family sharing a half genotype although with different microsites [43] which showed similarity trend emerged in *Quercus robur* [44] and *Larix olgensis* families [45]. The narrow-sense heritability (h_i^2) as a measure of the relative amount of genetic control for a given trait in population [46] expresses the fraction of the phenotypic variance that is accounted for by the variance among the breeding values of trees [47]. In this study, all growth traits showed moderate to higher genotypic heritability at the individual and family level that ranged from 0.152 to 0.210 and from 0.611 to 0.862, respectively. This finding shows that the phenotypic measurement completely reflected the underlying breeding value of trees and the selected families might be less influenced by environmental effects [48].

Correlation coefficients between growth traits allow the understanding of relationships among measured traits. The correlation between different growth traits guides the selection of trees based on multiple traits in research on tree improvement [49]. In this research, traits related to cone and seed were weakly negatively correlated to growth traits which indicated that the improvement objectives for wood and seeds would be equally manageable. Thus, the selection of elite families would be evaluated for growth and cone traits independently. Similar weak correlation between cone and growth traits was observed for *Jatropha curcas* L [42] but significant positive correlation was reported for *Argania spinosa* [28] *and Pinus palustris* [50]. The reason may be related to tree spacing used in these studies, which impacts growth in diameter and height of trees as well as the widening of the branch and consequently on the family's number of cones. There exist higher correlation coefficients between V and Ht, which were

higher than correlation between DBH and V, DBH and H which also attributed to wider spacing, leading to better growth in height than diameter [51]. The correlation results corroborate those of Liang [52], who found strong correlation (0.899) between V and DBH on *P. koraiensis* clones.

Multiple-trait comprehensive evaluations had been developed for breeding cultivation materials with strong integrated ability, which are always used to select excellent families or clones [53]. An appropriate comprehensive evaluation method and suitable traits need to be selected for research because taking so many traits into consideration may decrease genetic gain [54]. In this study, two most important traits of *P. koraiensis* were volume and cone numbers, but due to weak correlation between these two traits, the selection of elite families were conducted for these two traits independently. With 10% selected rate, nine families each were selected as elite families based on volume or cone numbers. The genetic gain in volume in our study was higher than those reported for *P. koraiensis* clone by Liang et al. [52], as also for other tree species, such as *Coastal Douglas* [55], poplar clones [46] and *Larix olgensis* families [45], which showed an effective selection process. The genetic gain in cone traits in our study was also higher than the research by Jiang [55] and lower than the research of Jiang [56] on *P. koraiensis* under the same selection rate, which may be related to differences in age, environment and stand density. In all, the level of genetic gain depends on the repeatability, amplitude of genetic variation and selection rate, and most breeding programs aim to increase genetic gain via selection [57]. The families that were selected in our research could be used for forestation and female parents could be used in improved seed orchard establishment.

5 Conclusions

The study revealed significant differences in growth and cone traits among half-sib families of *P. koraiensis*, which enabled selection of elite families. Positive significant correlations were observed among growth traits, but cone traits were weakly correlated with growth traits, suggesting independent selection of elite families for these two traits. Phenotypic and genotypic variances were slightly lower for growth traits than for characters related to reproduction. Moderate to higher heritability was observed for growth and cone traits at the individual and average/family level. This study identified volume and cone numbers per tree as indices in the selection and evaluation of families. Thus, 18 elite families were selected based on 10% selection rate, with 22.16% and 43.82% genetic gain in volume and cone number, respectively. These results provide beneficial information to select excellent families and establish orchards of *P. koraiensis* from improved seeds. The families that were selected could be used for reforestation, and female parents would be useful for establishing improved seed orchard.

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Supplementary Materials

S1. ANOVA analysis of different traits

Traits	Source	SS	df	MS	F	Sig.
Ht	Block	0.006	2	0.003	0.010	0.991
	Family	7984.699	85	95.056	145594.001	0.000
	Block × family	0.110	170	0.001	0.000	0.989
DBH	Block	0.003	2	0.002	0.062	0.940
	Family	272.295	84	3.242	5057.212	0.000
	Block × family	0.108	170	0.001	0.001	0.980
V	Block	4E-05	2	2.019E-05	0.028	0.973
	Family	2322.293	85	27.646	514.40	0.000
	Block × family	0.0011	170	6.751E-06	0.000246	0.978
CN	Block	73.081	2	36.540	8.067	0.002
	Family	28338.867	85	337.367	346.629	0.000
	Block × family	163.511	170	0.973	0.007	0.995
TSW	Block	55.043	2	27.522	0.439	0.648
	Family	344545.004	85	4101.726	183.416	0.000
	Block × family	3756.982	170	22.363	0.014	0.997
SCSW	Block	0.109	2	0.055	0.148	0.863
	Family	2322.293	85	27.646	514.401	0.000
	Block × family	9.029	170	0.054	0.004	0.972

Note: *SS*, Sum of square; *df*, degree of freedom; *MS*, Mean Square; *F*, *F* value in F test; *Sig*, *P* value<0.001.

S2. Correlation coefficients of different traits

Traits	Ht	DBH	V	CN	TSW	SCSW
Ht	1	0.226**	0.840**	0.032	-0.017	0.055
DBH		1	0.685**	-0.013	0.061	-0.026
V			1	-0.014	-0.016	0.042
CN				1	0.052	0.101
TSW					1	0.003
SCSW						1

*Correlation is significant at the 0.01 level (2-tailed).