

Forward, backward selection and variation analysis of growth traits in half-sib *Larix kaempferi* families

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Abstract

Tree height and diameter at breast height of 30 half-sib *Larix kaempferi* families were analyzed at different ages. Analysis of variance revealed a significant difference in growth among different families. Phenotypic variation coefficients of the traits tree height and diameter at breast height among families of different ages ranged from 11.04 % to 31.74 % and 19.01 % to 19.83 %, respectively. Average heritability of tree height and diameter at breast height ranged from 0.87 to 0.96 and 0.93 to 0.96, respectively. Significant positive correlations were observed among all traits at different ages. By the method of multiple-traits comprehensive, six families (L18, L12, L8, L3, L25 and L20) were selected as being elite using a 20 % selection ratio at 12 years of age. Average values of these elite families were 11.15 % and 16.83 % higher than the total average for height and diameter at breast height, and genetic gains were 10.53 % and 15.79 %, respectively. Forty five elite individual plants were selected using a 5 % selection ratio which were 23.47 % and 24.90 % higher than the overall average for height and diameter at breast height, respectively.

Keywords: : Half-sib; *Larix kaempferi*; Genetic; Variation; Comprehensive evaluation

Introduction

Larix kaempferi is one of the most successful exotic species in China, having been introduced from Japan approximately 100 years ago (Toda and Mikami 1976). It is an excellent species for conifer plantations because of its strong adaptability, wide distribution, strong resistance, and rapid growth (Kurino 2005). *L. kaempferi* has been extensively used as materials for building, furniture making, paper manufacture, and biofuel generation (Fukatsu et al. 2013). For centuries, there are many studies on *L. kaempferi*, including growth traits (Teruyoshi et al. 2014; Hou et al. 2012), wood properties (Cáceres et al. 2017), photosynthetic traits (Watanabe et al. 2011), genetic diversity (Achere 2004), and molecular markers (Moriguchi et al. 2008).

Because cutting and tissue culture was difficult to achieve in *L. kaempferi*, and grafting showed a severe effect on rootstock, seed orchards are one of the most important improvement methods for *L. kaempferi*. The earliest seed orchards were established in the 1960s (Wang et al. 2000), and many seed orchards were established after that. To date, most of the seed orchards had been flowering and fruiting, and the elite seeds produced were widely used in reforestation (Ding et al. 2002; Zhang, 2013; Zheng et al. 2014). To obtain greater genetic gains, improvement or advanced seed orchards should be established as the next step. Backward selection and forward selection is a necessary channel for improvement of seed orchard construction. Backward selection is a method to choose superior parents, based on the results of progeny testing

(Cornelius, 1994) with the parents chosen to construct an improved seed orchard. In forward selection, the elite offspring are selected to establish the next generation of seed orchards (Wright, 1976). In *L. kaempferi* seed orchards, most studies used on genetic variation and genetic gain in growth traits to evaluate offspring (Zhang et al. 2013; Du et al. 2015) with the backward selection and forward selection seldom reported. In this study, tree height (H) and diameter at breast height (DBH) were measured in 30 *L. kaempferi* families over several growth years, genetic variation parameters were calculated, and elite families in different growth years under different selection ratios were selected. Forward and backward selections were used to construct different improved seed orchards. This research could provide the basis for advanced *L. kaempferi* breeding.

Materials and Methods

Experimental sites

The experimental was conducted in Wudaogou forestry farm (N 41°54', E 125°17'), located in Liuhe County, in Jilin Province of northeast China. The area has a continental monsoon climate, the average annual temperature was 5.5°C, the precipitation was 736 mm, the frost-free season was 145 days, and the duration of sunshine was 2479 hours. *L. kaempferi* trees grew well at the experimental site with the local climate.

Experimental methods

A total of 30 *L. kaempferi* half-sib families (table 4) were used as sources for seed collection in the autumn of 2002. These seeds were sown the following year, and the experimental stand was established in the spring of 2005. The experimental design consisted with 5 blocks and 10 trees row plots was used. The test was established using 2-year old seedling at a spacing of 2×2m.

Data measurement

The tree height (H/m) of all living and unbroken trees was measured in 2006 (4 years old), 2008 (6 years old), 2010 (8 years old), 2012 (10 years old) and 2014 (12 years old). The diameter at breast height (DBH/cm) of each tree was measured in 2010 (8 years old), 2012 (10 years old) and 2014 (12 years old).

Statistical analyses

Statistical analysis was carried out using SPSS 19.0 (Statistical Package for the Social Science) software. The significance of fixed effects was tested by analysis of variance (ANOVA) *F*-tests. Variation among families of the same age was analyzed by ANOVA according to Hansen (1996) as following formula :

$$y_{ij} = \mu + \alpha_i + \beta_j + \alpha\beta_{ij} + \varepsilon_{ij}$$

where y_{ij} is the performance of an individual of family i within block j , μ is the overall mean, α_i is the random effect of family ($i = 1, \dots, 30$), β_j is the fixed effect of block ($j = 1, \dots, 5$), $\alpha\beta_{ij}$

is the random effect of family i within block j , and ε_{ij} is the random error.

Phenotypic coefficient of variation PCV (%) and genotypic coefficient of variance (GCV) were estimated by the formulas below as used by Jonah et al. (2011):

The coefficient of phenotypic variation (PCV) was calculated using the following formula (Zhao et al. 2013b):

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100\%$$

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100\%$$

Where σ_p^2 is variance components of phenotypic, σ_g^2 is variance components of genotypic, \bar{X} is the mean value of a growth character.

Heritability (h^2) was calculated according to Zhao (2013b) as:

$$h^2 = \frac{\sigma_F^2}{\sigma_F^2 + \sigma_{FB}^2/B + \sigma_e^2/NB}$$

Where h^2 is family heritability, σ_F^2 is variance components of family, σ_{FB}^2 is variance components of family by block interaction, σ_e^2 is variance components of residual error, F is the number of families, B is the number of blocks and N is the number of values per family.

The phenotypic correlation coefficient was calculated using the following formula (Fernando et al. 2016):

$$r_A(xy) = \frac{\sigma_{a(xy)}}{\sqrt{\sigma_{a(x)}^2 \cdot \sigma_{a(y)}^2}}$$

where $\sigma_{a(xy)}$ denotes the phenotypic covariance between the traits x and y , and $\sigma_{a(x)}^2$ and $\sigma_{a(y)}^2$ denote the phenotypic variance of traits x and y , respectively.

The phenotypic correlation, $r_{a(xy)}$ of traits x and y was calculated according to Liang et al. (2018 a) as follows:

$$r_A(xy) = \frac{\sigma_{a(xy)}}{\sqrt{\sigma_{a(x)}^2 \cdot \sigma_{a(y)}^2}}$$

where $\sigma_{a(x)}^2$ is the family variance component for trait x , $\sigma_{a(y)}^2$ is the family variance component for trait y , and $\sigma_{a(xy)}$ is the family covariance component.

The genetic correlation $r_g(xy)$ of traits x and y was calculated as Liang et al. (2018 b):

$$r_g(xy) = \frac{COV_{g(xy)}}{\sqrt{\sigma_{g_x}^2 \cdot \sigma_{g_y}^2}}$$

where $\sigma_{g(xy)}^2$ is the genetic variation between traits x and y, and $\sigma_{g_x}^2$ and $\sigma_{g_y}^2$ are the variance component for traits in x and y, respectively.

The estimation of parental breeding values of the traits for all families was calculated according to the phenotypic observed values, and the formula of the breeding value is as follows (Kung FH, 1979):

$$Z = \bar{Y} + h^2(Y - \bar{Y})$$

where Z is the breeding value of a trait of each family, \bar{Y} is the overall mean of a trait of all families, h^2 is the heritability of different traits, and Y is the average value of a trait of each family.

The comprehensive evaluation was conducted using the method of Qi value evaluation. Qi was calculated as follows (Liu et al. 2015):

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

where $a_i = X_{ij}/X_{jmax}$, Q_i is the comprehensive valuation value of i family, X_{ij} is the mean of a character, X_{jmax} is the maximum value of a character, and n is the number of evaluation index.

The estimated genetic gain was calculated using the formula (Silva et al. 2008):

$$\Delta G = (h^2 W / \bar{X}) \times 100 \%$$

where ΔG is the genetic gain of a trait for the families, h^2 is the heritability of the traits, W is the difference of the average values of the traits between selected families and all families, namely, the selection difference, and \bar{X} is the mean value of a growth character (H or DBH) among all families.

Results

Analyses of variance

ANOVA analysis of H and DBH for all families during different ages are shown in Table 1. All variance sources were non-significant except for families. At each age, a significant difference was observed between different families ($P < 0.01$).

Genetic and variation parameters

Genetic and variation parameters of H and DBH among different families are shown in Table 2. The average H and DBH of all families varied from 0.42 to 13.20 m and 3.50 to 19.00 cm, respectively, at different ages. *PCVs* of H and DBH at different ages ranged from 11.04 % to 31.74 % and 19.01 % to 19.83 %, respectively. *GCVs* of H and DBH at different ages ranged from 6.83 % to 17.93 % and 11.26 % to 15.12 %, respectively. *PCVs* and *GCVs* of H decreased with tree growth. *PCVs* and *GCVs* of DBH were higher than H from ages 8 to 12 years. The

Table 1
ANOVA analysis of H and DBH of *L. kaempferi* families in different growth years

Traits	Age	Variance source	SS	df	MS	F	Sig
H	12	Block	0.907	4	0.227	0.291	0.886
		Family	409.704	29	14.128	18.114	0.000
		Plant	4.882	5	0.976	1.236	0.290
		Block × Family	90.471	116	0.780	0.988	0.521
		Error	588.323	745	0.790		
		Block	0.829	4	0.207	0.218	0.919
	10	Family	655.956	29	22.619	23.745	0.000
		Plant	5.679	5	1.136	1.287	0.267
		Block × Family	110.498	116	0.953	1.079	0.281
		Error	657.478	745	0.883		
		Block	0.577	4	0.144	0.419	0.866
		Family	198.877	29	6.858	19.937	0.000
	8	Plant	1.765	5	0.353	0.779	0.565
		Block × Family	39.901	116	0.344	0.759	0.968
		Error	337.632	745	0.453		
		Block	0.220	4	0.055	0.551	0.751
		Family	39.098	29	1.348	13.514	0.000
		Plant	0.426	5	0.085	0.742	0.592
	6	Block × Family	11.572	116	0.100	0.869	0.826
		Error	85.479	745	0.115		
		Block	0.070	4	0.017	0.449	0.816
		Family	8.732	29	0.301	7.722	0.000
		Plant	0.261	5	0.052	1.161	0.327
		Block × Family	4.524	116	0.039	0.869	0.828
4	Error	33.442	745	0.045			
	Block	14.029	4	3.507	0.983	0.432	
	Family	1679.773	29	57.923	16.236	0.000	
	Plant	6.676	5	1.352	0.368	0.871	
	Block × Family	413.838	116	3.568	0.970	0.571	
	Error	2739.240	745	3.677			
DBH	10	Block	2.113	4	0.528	0.398	0.845
		Family	916.913	29	31.618	23.838	0.000
		Plant	4.656	5	0.931	0.615	0.689
		Block × Family	153.861	116	1.326	0.875	0.814
		Error	1128.736	745	1.515		
		Block	1.467	4	0.367	0.480	0.792
8	Family	320.677	29	11.058	14.466	0.000	
	Plant	6.523	5	1.305	1.506	0.186	
	Block × Family	88.669	116	0.764	0.882	0.800	
	Error	645.610	745	0.867			

Note: H Tree height, DBH diameter at breast height, df degree of freedom, MS mean square, F value in F test.

heritability of H increased with tree growth; all values were greater than 0.87, with a maximum of 0.96. All values of DBH were greater than 0.93, representing a high heritability. The variance components of H and DBH increased with tree growth and development with values of 0.0087 to 0.7222 and 0.3431 to 1.8119, respectively.

Table 2
Genetic and variation parameters of different families in different growth years

Traits	Age	Variation range	$\bar{X} \pm SD$	PCV	GCV	h^2	σ
H	4	0.42-1.46	0.81 ± 0.26	31.74	17.93	0.87	0.0087
	6	1.85-3.95	2.46 ± 0.42	17.06	10.05	0.93	0.0416
	8	3.00-7.80	5.44 ± 0.87	15.93	10.03	0.95	0.2171
	10	5.00-10.80	8.46 ± 1.28	15.10	10.23	0.96	0.7222
	12	7.00-13.20	10.25 ± 1.13	11.04	6.83	0.94	0.4449
DBH	8	3.50-8.50	6.08 ± 1.16	19.01	11.26	0.93	0.3431
	10	4.50-13.00	8.36 ± 1.66	19.83	15.12	0.96	1.0097
	12	6.00-19.00	12.07 ± 2.37	19.62	11.51	0.94	1.8119

Note: the unit of H was m, DBH was cm, the unit of PCV and GCV was %.

Correlation analysis

The results of phenotypic and genetic correlation analyses are shown in Table 3. All phenotypic correlation coefficients between growth traits were significantly and positively correlated. Correlation coefficients of H at different ages varied from 0.459 (4 and 10 years of age) to 0.785 (4 and 6 years of age). Correlation coefficients of DBH at different ages varied from 0.647 (8 and 10 years of age) to 0.853 (10 and 12 years of age). Correlation coefficients between growth traits at different ages ranged from 0.514 (between the H of the 10-year-old trees and the DBH of the 8-year-old trees) to 0.933 (between the H and the DBH of the 8-year-old trees). Genetic correlation is stable for inheritance and more important for breeding, but it is difficult to reach the level of statistical significance because of the large sampling error in the estimation of genetic correlation. Therefore, significance test was not conducted. The genetic correlation coefficients were closely to phenotypic correlation coefficients, which ranged from 0.252 (between 6-year-old H and 10-year-old) to 0.935 (between the H and the DBH of the 8-year-old).

Table 3
Correlation analysis of different traits in different growth years

Traits	H					DBH		
	4	6	8	10	12	8	10	12
4H	1	0.423	0.854	0.518	0.759	0.912	0.712	0.701
6H	0.785**	1	0.470	0.252	0.389	0.411	0.275	0.403
8H	0.754**	0.756**	1	0.627	0.673	0.935	0.756	0.716
10H	0.459*	0.677**	0.630**	1	0.743	0.513	0.785	0.774
12H	0.668**	0.744**	0.678**	0.742**	1	0.659	0.811	0.930
8DBH	0.771**	0.692**	0.933**	0.514**	0.659**	1	0.669	0.661
10DBH	0.602**	0.765**	0.729**	0.814**	0.824**	0.647**	1	0.845
12DBH	0.624**	0.771**	0.716**	0.775**	0.931**	0.659**	0.853**	1

Note: **correlation is significant at the 0.01 level (2-tailed). Left and lower triangle represent phenotypic correlation, right and upper represent genetic correlation.

Breeding value of Height in different growth year

Breeding values of H among all families were ranked. The top ranked family was scored at 30 points, the second at 29 points, and so on, with the last family scored at 1 point. Finally, H was also ranked according to the same 1 to 30 scoring method. The analysis for the breeding values of H for different families, and the ranking results, are shown in table 4. Values varied for different ages of trees. The overall average breeding values of H for all families ranged from 0.82 m to 10.32 m at different ages. In years 4, 6, 8, 10 and 12, families L18, L20, L18, L18 and L18 showed higher total scores than other families, respectively. Families L4, L23, L4, L23 and L23 showed lower total scores than other families at different ages.

Table 4
Breeding values of H among different families in different growth years

Families	The 4 th growth year			The 6 th growth year			The 8 th growth year			The 10 th growth year			The 12 th growth year		
	breeding value	Rank	Scores	breeding value	Rank	Scores	breeding value	Rank	Scores	breeding value	Rank	Scores	breeding value	Rank	Scores
L1	0.84	17	14	2.39	23	8	5.66	12	19	7.46	27	4	9.80	25	6
L2	0.86	10	21	2.50	13	18	5.86	5	26	9.21	6	25	10.49	10	21
L3	0.87	8	23	2.61	4	27	5.79	8	23	9.17	8	23	11.32	3	28
L4	0.69	30	1	2.30	29	2	4.69	30	1	7.37	29	2	9.66	29	2
L6	0.78	23	8	2.41	20	11	5.56	14	17	8.58	16	15	9.95	20	11
L7	0.80	21	10	2.32	26	5	5.17	24	7	7.44	28	3	9.98	19	12
L8	0.85	13	18	2.51	11	20	5.86	6	25	9.12	9	22	11.32	4	27
L9	0.84	16	15	2.47	17	14	5.24	21	10	7.50	26	5	9.86	22	9
L10	0.87	6	25	2.56	8	23	5.87	4	27	9.01	12	19	10.49	9	22
L11	0.75	26	5	2.37	25	6	5.42	16	15	7.69	23	8	9.68	28	3
L12	0.87	4	27	2.65	3	28	5.90	2	29	9.24	3	28	11.66	2	29
L13	0.81	20	11	2.41	19	12	5.23	22	9	7.79	22	9	9.78	26	5
L14	0.86	11	20	2.56	7	24	5.69	11	20	9.06	11	20	10.42	12	19
L15	0.86	12	19	2.55	10	21	5.26	19	12	9.06	10	21	10.53	8	23
L16	0.77	25	6	2.43	18	13	5.32	18	13	7.93	19	12	9.72	27	4
L17	0.87	7	24	2.56	9	22	5.90	15	16	8.44	17	14	10.32	13	18
L18	0.89	1	30	2.73	2	29	5.96	1	30	9.25	1	30	11.79	1	30
L19	0.78	22	9	2.31	27	4	4.92	29	2	7.89	20	11	10.28	15	16
L20	0.88	2	29	2.76	1	30	5.12	26	5	9.24	2	29	10.89	5	26
L21	0.83	18	13	2.50	14	17	5.16	25	6	8.62	15	16	10.34	14	17
L22	0.87	5	26	2.51	12	19	5.76	10	21	9.22	5	26	10.46	11	20
L23	0.72	29	2	2.27	30	1	5.79	7	24	7.27	30	1	9.56	30	1
L24	0.87	9	22	2.61	5	26	5.79	9	22	9.21	7	24	10.65	7	24
L25	0.88	3	28	2.61	6	25	5.89	3	28	9.22	4	27	10.85	6	25
L26	0.85	14	17	2.50	15	16	5.18	23	8	7.60	24	7	9.87	21	10
L27	0.81	19	12	2.31	28	3	5.06	28	3	7.82	21	10	10.10	17	14
L28	0.74	27	4	2.39	22	9	5.07	27	4	8.70	14	17	10.16	16	15
L29	0.77	24	7	2.40	21	10	5.35	17	14	8.30	18	13	9.82	24	7
L30	0.84	15	16	2.49	16	15	5.59	13	18	7.50	25	6	9.86	23	8
L31	0.74	28	3	2.37	24	7	5.25	20	11	8.96	13	18	10.02	18	13
Average values	0.82	—	—	2.48	—	—	5.46	—	—	8.43	—	—	10.32	—	—

Comprehensive evaluation

The results of Multi-traits comprehensive evaluation were shown in Table 5. Elite families were selected by H values (at ages 4 and 6 years) and Qi values (at ages 8, 10, and 12 years) with different selection ratios at different years. Different numbers of families (18 families at ages 4; 15 at age 6; 12 at age 8, 9 at age 10; and 6 at age 12) were selected as elite families (Table 5) using different selection ratios. Additionally, the rank of different families varied according to age, although families L18, L12, L8, L3, L25, and L20 were always selected as elite families at different ages under different selection ratios. Family L18 showed the highest values of H or Qi at different ages. Family L24 grew fast during the early stages, but its low Qi value indicated that its DBH was poor, so it was not selected as an elite family at age 12. Conversely, family L8 grew slowly in the early stages but showed a higher Qi value later on.

Using a comprehensive evaluation method, six families (L18, L12, L8, L3, L25 and L20) were selected as elite families using a 20 % selection ratio at 12 years of age. The average H and DBH of the elite families were higher than the total average by 11.15 % and 16.83 %, –the genetic gains of H and DBH were 10.53 % and 15.79 %, respectively. Under the 5 % selection ratio, 45 elite individual plants were selected at age 12 (Table 6). Average H and DBH of elite individual plants were 12.65 m and 15.07 cm, which were 23.47 % and 24.90 % higher than the overall average, respectively.

Table 5
Elite families selected under different selected ratio in different growth years

The 4 th growth year		The 6 th growth year		The 8 th growth year		The 10 th growth year		The 12 th growth year	
Family	H	Family	H	Family	Qi	Family	Qi	Family	Qi
L18	0.96	L18	1.68	L18	1.27	L18	1.29	L18	1.31
L24	0.95	L24	1.67	L8	1.25	L8	1.27	L12	1.28
L25	0.95	L12	1.64	L25	1.25	L10	1.26	L8	1.27
L12	0.95	L3	1.63	L20	1.25	L20	1.26	L3	1.26
L22	0.95	L20	1.63	L2	1.24	L25	1.26	L25	1.24
L10	0.94	L25	1.63	L12	1.24	L12	1.26	L20	1.24
L17	0.94	L14	1.61	L3	1.24	L24	1.26		
L3	0.94	L10	1.61	L22	1.24	L3	1.25		
L20	0.94	L17	1.61	L24	1.23	L2	1.25		
L2	0.94	L15	1.60	L10	1.22				
L14	0.94	L8	1.59	L14	1.22				
L15	0.94	L22	1.59	L6	1.21				
L8	0.93	L2	1.59						
L26	0.93	L21	1.58						
L30	0.92	L26	1.58						
L9	0.92								
L1	0.92								
L21	0.92								

Table 6
Elite individual plant selected under a 5% selected ratio in the 12th growth year

single plant	family	H	single plant	family	H	single plant	family	H
661	25	13.20	456	18	12.80	450	18	12.50
662	25	13.20	79	2	12.70	657	25	12.50
97	3	13.00	437	18	12.70	434	18	12.40
179	8	13.00	451	18	12.70	449	18	12.40
187	8	13.00	458	18	12.70	514	20	12.40
306	12	13.00	459	18	12.70	515	20	12.40
433	18	13.00	303	12	12.60	516	20	12.40
454	18	13.00	304	12	12.60	439	18	12.30
457	18	13.00	308	12	12.60	506	20	12.30
460	18	13.00	318	12	12.60	524	20	12.30
513	20	13.00	249	10	12.50	525	20	12.30
527	20	13.00	250	10	12.50	526	20	12.30
452	18	12.90	316	12	12.50	564	22	12.30
448	18	12.80	317	12	12.50	619	24	12.30
455	18	12.80	361	14	12.50	557	22	12.10

Discussion

ANOVA

ANOVA analysis is one of the most important methods for estimating the extent of variability, and plays an essential role in selecting breeding populations (Zhao et al. 2014). In this research, a significant difference was observed among different families at different ages ($P < 0.01$). This finding indicated the existence of plentiful variation in growth traits among different families. These results are similar to the previous studies (e.g., Nakada et al. 2005), showing that selection of elite families is effective.

Variation and genetic

It is critical to the efficient usage of genetic resources by understanding the relationship of genetic variation within individuals or populations in breeding research (Hortensia et al. 2011). Large genetic variation and high heritability are requirements to achieve selection progress (Kroon et al. 2011; Kaushik et al. 2015). In this research, we observed high levels of heritability, the values of H ranging from 0.87 to 0.96 and DBH values all

>0.93, indicating that tree growth is weakly influenced by environmental effects. The PCVs of H decreased with tree growth, especially at age 12, when the value was 11.04%, indicating that phenotypic variation among families was small. The PCVs of H were lower than those for DBH from ages 8 to 12, suggesting that DBH is more effective than H in selecting elite families. This result is in agreement with the previous studies by Zas et al. 2004 and Collet and Chenost 2006.

Different variation trends with age were found for growth traits. We took measurements at various ages, and we observed that h^2 for H and DBH increased with tree growth, which was similar to the pattern seen in *Pinus taeda* (Gwaze et al. 2001) and *Norway spruce* (Isik et al. 2010). The h^2 of H and DBH increased with tree growth, which represented a higher heritability and were controlled genetically at a higher level, indicating that a fairly large genetic gain could be obtained through the selection of elite families. Variance components and heritability reflected the degree of genetic control of trait variation (Sun 2003). The age trends of variance components for growth traits may present different rules in different environment conditions (Diao et al. 2016). The variance components for H showed an increasing trend, but DBH first increased and then decreased with age at the Hubei experiment site (Diao et al. 2016). However, the variance components for H and DBH increased with time on the whole at the Liaoning experiment site in China (Diao et al. 2016). In this research, the variance components for H and DBH generally increased as the trees grew. This finding is in agreement with the results for *Scots pine* (Haapanen 2001) and *Douglas fir* (Dean and Stonecypher 2006), which displayed variation of H or DBH mainly controlled by additive genetic variance in this research.

Correlation analysis

In breeding programs, correlation coefficients could reflect the relationships between different traits and, therefore, have major implications for breeding strategies (Goncalves et al. 2005; Lee et al. 2002). The relationship of parameters between growth traits is rather complex (Sumida et al. 2013). In previous work, age-age correlations of growth traits reached a very high level at early stages in *Pinus taeda* (Xiang et al. 2013) and *Masson pine* (Zeng et al. 2013). In our research, there existed a significant positive correlation between all growth traits, indicating the possibility of early elite family evaluation and selection, which agrees with previous findings in *L. olgensis* (Xia et al. 2016), *Radiata pine* (Kumar and Lee 2002), and *Populus deltoides* (Dhillon et al. 2010).

At present, early selection could shorten breeding process as much as possible, which is an important method. The optimal age of early selection can be predicted by correlation coefficient, heritability and age trends of genetic parameters for growth traits (Svensson et al. 1999). Because of the different selected breeding objectives, there were different optimum early selection ages for *L. kaempferi* (Fujimoto et al. 2006). For growth traits, tree height was most ideal index for early selection in tree breeding (Balocchi et al. 1993), and the optimum early selection ages were 2, 4, 8 and 10 years for H in *L. kaempferi*. In this research, H was selected as an early evaluation

index, with the same selection ratio (20 %), and the same elite families were selected at ages 6 and 12 years. Results indicated that the 6 year selection age was the optimum for early selection, which can shorten the breeding cycle for next generation breeding programs.

Comprehensive evaluation

Comprehensive evaluation and selection for the same characteristics in different growth years are important for tree genetics and breeding to obtain stable characteristics (Kang 1985). However, in previous studies, the selecting of too many characteristics together could lead to low genetic gains in individual characteristics (Guan et al. 2005), resulting in an imprecise selection target. H and DBH are vital characteristics for the evaluation of tree growth that could make comprehensive evaluation more effective and reliable (Gwaze and Bridgwater 2002). In this study, different families had different growth patterns (Jansson et al. 2003), especially families L18 and L24 that showed opposing H and DBH values. Though the family ranks varied according to year, families L18, L12, L8, L3, L25 and L20 were always selected as elite families under different selection ratios, indicating that appropriate selection ratio and age are vital for elite family selection (Leksono et al. 2006).

Genetic gain is a crucial parameter for selecting elite families (Huang et al. 2006) and is often used as a measure for selection (Hannrup et al. 2000). Most breeding programs purposes are to achieve higher genetic gain, which can be realized by selection (Montes et al. 2008), and relatively high genetic gains have been observed when selection is dependent on high heritability, extensive of genetic variation, and low selection rate (Zhou et al. 2014). In this research, the genetic gains of H and DBH were higher than that achieved in previous studies on Hybrid *L. gmelinii* (Cao 2016) and *L. gmelinii* (Liu and Wang 2016), which were 10.53 % and 15.79 %, respectively, although these data could reflect differences in species (Yin et al. 2016). Using a 5 % selection ratio in 12 year old trees, 45 elite individual plants were selected, average Hs and DBHs of selected elite individual plants were 12.65 m and 15.07 cm, which were 23.47 % and 24.90 % higher than overall average, respectively.

Backward selection and forward selection

Backward and forward selections are affected by heritability, intensity of selection and genetic gain, but the relationships between these parameters vary (Hodge and White, 1993). Low heritability is favour to backward selection, which is one of the main factors supporting progeny testing, because on this occasion forward selection is not effective (Falconer and Mackey, 1996). In this research, heritabilities of H and DBH were higher than 0.87, which indicates higher heritability, therefore the forward selection is more effective.

Genetic gain is the most direct index to reflect improvement of seed orchards (Bai et al. 2012). In this research, 6 elite families were selected using a 20 % selection rate, and the genetic gains of H and DBH were 10.53 % and 15.79 %, respectively. These results were greater than those found in previous research (Zhang et al. 2013), where genetic gains of H and DBH for the family of Japanese larch were 7.5 % and 10.3 %,

respectively, on progeny test forests with open pollination. High genetic gain elite families were more suitable for the establishment of improved seed orchards.

Breeding Values

Breeding values can be predicted for each family and offspring (Namkoong et al. 1966). In this research, the breeding value scores of different families also varied with different ages, but the elite families exhibited higher scores in the same stage, which were similar with the selected families using the method of a Qi value under the 20 % selection ratio in the 12 year old tree. e.g., family F18. Therefore, breeding value scores were more accurate and stable for selection while conducting Qi value with the breeding value concerned (Israel C et al., 2000; Pan XQ, 2014). Selected families could be utilized as excellent subjects for the establishment of improved seed orchards, and it could also provide the theoretical basis for excellent family selection and evaluation of *L. kaempferi*.

Conclusion

The early evaluation and selection of elite families is important for shortening the breeding cycle and improving breeding efficiencies of tree species. In this research, the genetic and variation parameters among different families were observed to vary based on age. 6 elite families and 45 12-year-old elite individual plants were selected using a 20 % and the 5 % selection ratio. Selected elite families and plants can provide characteristics for the establishment of improved or next generation seed orchards. These could be used for future afforestation, and the research can directly apply to other conifer breeding programs. Additionally, the technique could provide the theoretical basis for early selection of other tree species. Further research on *L. kaempferi* should focus on wood properties, flowering rules, stress resistance, and molecular breeding.

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