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Progeny performance and selection of superior trees within families in *Larix olgensis*

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Abstract *Larix olgensis* is one of the most important timber species in Northeast China. Although *L. olgensis* seed orchards have been established for many years and some progeny tests have been conducted, studies of progeny performance and the selection of superior families are still lacking. These tests are important for upgrading and improvement of seed orchards. Here, we estimate the genetic variation for major economic traits between families to provide selection materials for the establishment of a second-generation seed orchard. This study examined 71 half-sib families and 2 control families of *L. olgensis* in the Xiyang forest seed orchard in Yongji County, Northeast China. We measured tree height, diameter at breast height, volume, branch angle, stem straightness degree and crown width of 4-year-old progeny. Genetic parameters for the studied traits were determined, and comprehensive analyses of multiple traits and breeding values were used for selection of superior families and individual trees within families. The results show that all these traits are significantly different ($P < 0.01$) among families where family variance was greater than environmental variance. The phenotypic and genotypic coefficients of variation ranged from 9.01% to 78.22% and from 1.81% to 39.20%, respectively. The heritability values of families and individual trees ranged from 0.663 to 0.959 and 0.034 to 0.983, respectively. There was a significant positive correlation between investigated traits. Using the multiple-traits comprehensive evaluation method, seven families and 56 superior individual trees were selected. Selection of superior parents using breeding values for timber yield, stem quality and crown width as a proxy for planting density again resulted in the selection of seven superior families. We determined that the comprehensive multiple-traits evaluation approach is effective for selecting superior families and individual trees for the establishment of advanced second generation seed orchards. Families selected based on breeding value may be used as preferred parents for future hybridization breeding.

Keywords Seed orchard · Genetic variation · Family heritability · Genetic gain

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Introduction

Larix olgensis is an economically valuable species in the family Pinaceae that is mainly distributed in the Changbai Mountain area of China and in North Korea and Russia (Peng et al. 2014; Hu et al. 2015). It grows rapidly and exhibits several valuable features including short rotation age, strong adaptability, superior wood quality, strong decay-resistance and high economic value; therefore, it is one of the main fast-growing tree species in Northeast China (Cui et al. 2012; Liu and Guo 2017; Peng et al. 2018). The wood can be used not only as raw materials for the wood fiber industry and for papermaking and biofuels, but also for construction and in the shipbuilding and railway industries (Xia et al. 2016a).

Genetic improvement of *L. olgensis* was carried out in the 1960s and 1970s, with the establishment of several clonal seed orchards in Heilongjiang, Jilin and Liaoning Provinces, China (Qi 1994; Zheng et al. 1993; Li et al. 2010). Seed orchards are special artificial forests established for the purpose of producing good seeds, playing an important and necessary role in tree breeding (Xia et al. 2016b). For conifer species, seed orchards are the most important source of reproductive materials (Dušan et al. 2003). Although *L. olgensis* seed orchards have been established for many years and some progeny tests have been performed (Han et al. 2009; Li et al. 2008), evaluation of progeny performance and the selection of superior families and parents are still needed. Progeny tests are a core technology for updating and upgrading seed orchards (Hu and Mao 2007).

Volume of trunk production together with improving adaptation to current conditions has been the focus for Chinese *L. olgensis* breeding (Xia et al. 2016a; Han et al. 2009). However, in recent years there has been a growing interest in stem quality traits and crown architecture. Stem quality traits such as stem straightness have a great impact on lumber recovery in sawmills. In addition, aspects of crown architecture such as crown width have an impact on planting density; i.e. the larger the crown width, the greater the spacing when planting. Thus, selection of families for multiple traits is paramount to simultaneously improve growth traits, stem quality and crown architecture. With advances in breeding technology, the emphasis in tree breeding has gradually changed from growth characters to multiple-trait genetic improvement (Zhao 2010). This can be achieved by applying a comprehensive evaluation of multiple traits, which can avoid the one-sidedness and instability resulting from selection on a single trait (Jia et al. 2016a).

The main purpose of this study was to estimate the genetic variation of some important economic traits of families to provide materials for the establishment of improved second generation seed orchards (He et al. 2011). For this purpose, 71 half-sib families and 2 control families of *L. olgensis* were studied. Growth traits were measured and analyzed to quantify genetic variations among different families, and the selection of superior families and individual trees within families was performed to provide materials for the improvement of advanced second generation seed orchards.

Materials and methods

Experimental materials

The experimental materials were obtained from the Xiyang forest tree seed orchard in Yongji County (E126°17′40″, N43°35′30″), Jilin Province. The Xiyang forest seed orchard, with an average altitude of 360 m, is subject to a temperate continental monsoon climate. The annual average temperature, precipitation, effective accumulated temperature, and frost-free season were 4.8 °C, 690 mm, 2700 degrees centigrade and 125 days, respectively. The dark brown soil is suitable for growing *L. olgensis*. Experimental plantations were established in 2013, using a randomized complete block design with 5 blocks and 8 trees per block, with a 3.0 × 3.0 m spacing.

Measurements of traits

Tree height (TH), diameter at breast height (DBH), branch angle (BA), and crown width (CW) were measured in 2017 using a tower ruler, Vernier caliper and protractor, respectively. Single crown width was the average value of the crown width from east to west and from north to south. The single branch angle was the average value of the lowest branch in the north–south direction. Stem straightness degree (SSD) was estimated by quantification based on the method of

Zhao et al. (2012). Trees were divided into 5 classes according to the following SSD criteria. If there were more than two obvious bend points in the stem, it was scored as 1; more than two slight bend points or one obvious bend point in the stem was scored as 2; two slight bend points in the stem was scored as 3; one slight bend point in the stem was scored as 4; and completely straight stem was scored as 5. The values were squared when calculated for each parameter.

Statistical analyses

Tree volume (V) was calculated using the average experimental shape method (Deng et al. 2010)

$$V = (H + 3) \times g_{1.3}f \tag{1}$$

The average experimental number f of larch was 0.41, so

$$V = 0.32 \times (H + 3) \times d^2 \times 10^{-4} \tag{2}$$

where H was tree height, d was diameter at breast height, and $g_{1.3}$ was the cross-sectional area at breast height.

Statistical analyses were carried out using SPSS version 19.0 (Shi 2012). The significance of fixed effects was tested using analysis of variance (ANOVA) F tests.

The following linear model was used for joint analysis of families and blocks (Xu 2006):

$$X_{ijk} = \mu + F_i + B_j + FB_{ij} + e_{ijk} \tag{3}$$

where X_{ijk} was the performance of an individual tree k in family i within block j, μ was the overall mean, F_i was the effect of family i, B_j was the effect of block j, FB_{ij} was the interactive effect of family i and block j, and e_{ijk} was the random error.

The coefficient of variation was calculated by adopted the formula of Mohamed et al. (2017):phenotypic coefficient of variation (PCV):

$$PCV = \frac{\sqrt{\sigma_p^2}}{X} \times 100 \tag{4}$$

genotypic coefficient of variation (GCV):

$$GCV = \frac{\sqrt{\sigma_g^2}}{X} \times 100 \tag{5}$$

where σ_p^2 was the phenotype variance component of the trait, σ_g^2 was the genetic variance component of the trait, and X was the average value of the trait.

Family heritability (FH) and single tree heritability (SH) were estimated following the formula of Xu (2006):

$$H^2 = \frac{\sigma_F^2}{\sigma_F^2 + \sigma_{FB}^2/B + \sigma_e^2/NB} \tag{6}$$

$$h_N^2 = \frac{4\sigma_F^2}{\sigma_F^2 + \sigma_{FB}^2 + \sigma_e^2} \tag{7}$$

where σ_F^2 was the variance component of the family, σ_{FB}^2 was the variance component of the interaction between the family and the block, σ_e^2 was the variance component of error, B was the number of blocks, N was the total number of every family.

Calculation of general combining ability (GCA) of families adopted the formula of Sun et al. (2011):

$$g_i = x_i - \mu \tag{8}$$

where x_i was the mean value of the offspring of a family for a certain trait, μ was the total average value of all the offspring for the trait. The breeding value is twice the general combining ability.

The comprehensive analysis of multiple characters was computed using the comprehensive evaluation method of Xie et al. (2008):

$$Q_i = \sqrt{\sum_{i=1}^{n} a_i} \tag{9}$$

$$a_i = x_{ij}/x_{jmax} \tag{10}$$

where Qi was the value of colligation assessment, x_{ij} was an average value of one trait, x_{jmax} was the maximum of the trait, and n was the trait number.

Genetic gain was estimated using the formula of Zhu (1989):

$$\Delta G = H^2 S/X \text{ (genetic gain of family)} \tag{11}$$

$$\Delta G = h_N^2 S/X \text{ (genetic gain of a single tree)} \tag{12}$$

where S was the selection difference, X, H^2 and h_N^2 were the mean value, family heritability and single tree heritability of a given trait, respectively.

Results

Estimates of variance components and heritability

Significant differences in all traits were observed among families, blocks and their interactions (Table 1). The magnitude of family variation was greater for total height, diameter at breast height, volume and crown width than for stem straightness degree and branch angle. The variance components of family were between 4.00 and 54.89%; among which TH, DBH, V and CW were all above 50%. The variance components of environment were all low, ranging from 0.90 to 6.68%. Because of the higher variance component of blocks, BA and SSD were the lowest variance components of family.

The descriptive statistics together with phenotypic and genotypic coefficients of variation are presented in Table 2. The average value of TH for all families was 3.07 m, the amplitude of variation was 1.40 to 5.20 m, and the maximum value was 3.71 times the minimum value. The mean value of DBH was 2.91 cm, the amplitude of variation was 0.46 to 7.56 cm, and the maximum was 16.43 times the minimum value. The average value of V was 0.00196 m^3, the amplitude of variation was 0.00003 to 0.01489 m^3, and the maximum was 496.33 times the minimum value. The average value of BA was 68.77°, the amplitude of variation was 30.00° to 85.00°, and the maximum was equal to 2.83 times the minimum value. The mean value of SSD was 4.91, the amplitude of variation was 1 to 5, and the maximum was 5 times the minimum value. The mean value of CW was 2.08 m, the amplitude of variation was 0.44 to 3.55 m, and the maximum was 8.07 times the minimum value.

The phenotypic and genotypic coefficient of variation for each trait was 9.01% to 78.22% and 1.81% to 39.20%, respectively (Table 2). The range of family heritability was 0.663 to 0.959 among which, the heritabilities for TH, DBH, V and CW were all greater than 0.940. The range of single tree heritability was 0.034 to 0.983, among which TH, DBH and CW were all greater than 0.900.

Table 1 Variance components of different traits

Traits	σ_B^2 (%)	σ_F^2 (%)	σ_{BF}^2 (%)	σ_E^2 (%)
TH	34.59**	53.34**	9.43**	2.64
DBH	32.45**	54.89**	10.19**	2.46
V	36.44**	50.98**	9.70**	2.88
BA	92.98**	4.00**	2.13**	0.90
SSD	56.47**	19.79**	17.06**	6.68
CW	32.40**	53.35**	12.07**	2.18

TH tree height, *DBH* diameter at breast height, *V* volume, *BA* branch angle, *SSD* stem straightness degree, *CW* crown width, σ_B^2 variance components of block, σ_F^2 variance components of family, σ_{BF}^2 variance components of interaction of block and family, σ_E^2 variance components of environment

**F value < 0.01

Inter-trait correlation analysis

Significant positive correlations were observed among traits (Table 3). There was an extremely high significant positive correlation between TH, DBH and V, and the correlation coefficient between DBH and V was as high as 0.958. Crown width had a strong positive correlation with TH, DBH and V. Though significant, the correlations between BA and SSD and other traits were weak.

Selection of families and individual trees

All traits of 73 families were comprehensively evaluated. The *Q*i value is presented in Table 4. The maximum *Q*i value (1.721) is for family 235 and the minimum (1.057) is for family c67. Using *Q*i value to select families using a 10% selection intensity, seven families (families 235, 143, 218, 182, 220, 188, and 229) were selected. The average TH, DBH and V of the selected families were 3.58 m, 3.79 cm, and 0.00336 m^3, all greater than the control average by 41.39%, 87.79% and 300.20%, higher than the total average by 16.69%, 30.14% and 71.42%, and genetic gains were 15.87%, 28.79% and 67.38%, respectively.

With regard to selection of individual trees from superior families using a 20% selection intensity, 56 superior individuals were identified (Table 5). The average TH, DBH and V of the selected families were greater than the control average by 65.71%, 156.86% and 652.58% and greater than the total average by 36.76%, 78.01% and 222.35%, with genetic gains of 34.94%, 74.51% and 209.78%, respectively.

Table 2 Mean, PCV and heritability of different traits

Traits	Mean	Range	SD	PCV	GCV	FH	SH
TH	3.07	1.40–5.20	0.6234	20.32	10.67	0.951	0.958
DBH	2.91	0.46–7.56	1.0310	35.39	18.98	0.955	0.983
V	0.00196	0.00003–0.01489	0.0015	78.22	39.20	0.943	0.866
BA	68.77	30.00–85.00	9.2432	13.44	3.39	0.776	0.171
SSD	4.91	1–5	0.4422	9.01	1.81	0.663	0.034
CW	2.08	0.44–3.55	0.4743	22.77	12.20	0.959	0.929

The units of each trait: TH (m), DBH (cm), V (m^3), CW (m), coefficient of variation (%), are the same for tables below

SD standard deviation, *PCV* phenotypic coefficient of variation, *GCV* genotypic coefficient of variation, *FH* family heritability, *SH* single tree heritability

Table 3 Correlation coefficients among different traits

	TH	DBH	V	BA	SSD
DBH	0.868**				
V	0.830**	0.958**			
BA	0.080**	0.093**	0.098**		
SSD	0.132**	0.117**	0.108**	0.067**	
CW	0.728**	0.763**	0.702**	0.059**	0.112**

**Significant correlation at the 0.01 level (2-tailed)

Analysis of breeding value for selecting superior parents

The analysis of breeding values of different traits revealed 38 families with positive and 35 families with negative breeding values for TH. Family 218 had the highest value (1.385), while c67 had the lowest (− 1.556) (Table 6). For DBH, there were 40 families with positive values and 33 families with negative values. Family 235 had the highest (2.557) and family c67 had the lowest (− 2.609) value. With regard to V, there were 38 families with positive values and 35 families with negative values. Family 235 had the highest breeding value (0.004), and family c67 he lowest (− 0.003). For BA, 39 families showed positive values while 34 families showed negative values. Family 220 had the maximum (14.528) and family 191 had the minimum (− 12.553) values. With respect to SSD, there were 42 families with positive values and 31 families with negative values. Family 142 had the highest breeding value and family 252 the lowest. For

Table 4 *Q*i values of different families

Family	*Q*i	Family	*Q*i	Family	*Q*i	Family	*Q*i	Family	*Q*i	Family	*Q*i
235	1.721	Za	1.544	c89	1.459	233	1.410	c78	1.288	ck5	1.210
143	1.655	206	1.529	74	1.454	155	1.403	c94	1.284	c45	1.198
218	1.654	149	1.526	199	1.453	191	1.398	252	1.284	c60	1.183
182	1.611	165	1.524	201	1.451	222	1.392	c8	1.281	c36	1.174
220	1.607	240	1.520	254	1.443	c44	1.387	246	1.275	c64	1.154
188	1.606	225	1.514	186	1.438	142	1.371	c5	1.270	ck3	1.121
229	1.604	154	1.512	Hun	1.428	146	1.366	c80	1.261	c65	1.120
173	1.592	184	1.512	195	1.422	167	1.364	c46	1.253	c67	1.057
196	1.587	208	1.511	250	1.420	243	1.362	c7	1.250		
224	1.582	231	1.492	209	1.420	185	1.331	c72	1.247		
213	1.573	170	1.492	187	1.416	c83	1.306	c81	1.243		
217	1.570	226	1.485	251	1.416	153	1.296	c30	1.220		
190	1.569	210	1.459	248	1.416	c58	1.295	c76	1.218		

Table 5 *Q*i values of different single plants

Block	Family	Number	*Q*i	Block	Family	Number	*Q*i
4	218	3	2.382	1	220	5	2.191
1	235	2	2.308	2	218	2	2.19
2	188	4	2.294	1	143	3	2.184
2	182	8	2.234	2	235	1	2.179
2	235	7	2.231	2	143	6	2.173
5	220	6	2.22	5	143	5	2.171
1	235	5	2.216	5	188	3	2.17
3	229	8	2.205	1	188	5	2.167
1	182	2	2.2	1	229	7	2.162
1	235	4	2.193	3	235	3	2.16
.	.	.	.	.	.	.	.
.	.	.	.	.	.	.	.
.	.	.	.	.	.	.	.
3	188	5	1.796	4	220	4	1.687
1	182	5	1.789	3	218	5	1.682
5	229	5	1.774	3	229	1	1.681
4	220	8	1.769	2	229	1	1.67
5	188	7	1.764	5	229	7	1.666
5	188	5	1.737	3	235	7	1.658
4	143	8	1.735	4	188	2	1.636
4	182	2	1.731	4	188	1	1.621
4	235	5	1.723	4	182	8	1.609
3	235	6	1.717	5	229	1	1.507

CW, there were 38 families with positive values and 35 families with negative values. Family 235 had the highest value (0.900), and family ck3 the lowest (− 1.281).

Based on breeding values of a family to select superior parents using a 10% selection intensity for timber and using total height as indicator, seven families (218, 143, 235, 190, 229, 182, and 188) were selected. The average total height of the selected families was 41.70% higher than the control average and 16.94% higher than the total average. Using DBH as an index, families 235, 143, 218, 173, 220, 182, and 196 were selected. The average DBH of the selected families was 88.36% greater than the control average and 30.54% greater than the total average.

Taking V as an index, families 235, 218, 143, 182, 188, 229, and 220 were selected. The average V of the selected families was 300.20% greater than the control average and 71.42% greater than the total average. Taking BA and SSD as indicators of stem quality, families 170, 143, 208, 167, and c94 were selected. The average BA and SSD were greater than the control average by − 8.40% and 5.34% and greater than the total average by − 5.58% and 1.83%, respectively. From the perspective of planting density, with CW used as an index, families 235, 143, 149, 154, 213, 206, and 196 were selected. Their average was 59.46% greater than the control average and 19.05% greater than the total average. Giving all traits, family 143 was selected, with TH, DBH, V, BA, SSD, and CW greater than the control average by 44.33%, 93.19%, 306.34%, − 8.84%, 5.34%, and 62.71% and greater than the total average by 19.12%, 33.89%, 74.05%, − 6.03%, 1.83% and 21.47%, respectively.

Discussion

Evaluation of the genetic performance of trees is essential for improved efficiency of forest tree breeding (Yin et al. 2017). Analysis of variance is the most important method for estimating the degree of

Table 6 Breeding values of different traits for each family

Family	TH breeding value	Family	DBH breeding value	Family	V breeding value	Family	BA breeding value	Family	SSD breeding value	Family	CW breeding value
218	1.385	235	2.557	235	0.004	220	14.528	142	0.181	235	0.900
143	1.173	143	1.975	218	0.003	186	14.248	143	0.181	143	0.894
235	1.092	218	1.666	143	0.003	ck3	13.582	153	0.181	149	0.867
190	0.976	173	1.603	182	0.002	c5	8.175	167	0.181	154	0.740
229	0.892	220	1.601	188	0.002	c44	7.765	170	0.181	213	0.736
182	0.883	182	1.555	229	0.002	c81	6.207	184	0.181	206	0.715
188	0.876	196	1.501	220	0.002	213	5.948	186	0.181	196	0.702
.	.	.	.	.	.	.	.	.	.	.	.
.	.	.	.	.	.	.	.	.	.	.	.
.	.	.	.	.	.	.	.	.	.	.	.
c45	− 0.942	c45	− 1.500	c45	− 0.002	c94	− 6.668	c30	− 0.276	c76	− 0.799
ck5	− 0.979	c36	− 1.676	c36	− 0.002	167	− 6.743	c44	− 0.335	ck5	− 0.830
c36	− 1.100	c60	− 1.700	c60	− 0.002	208	− 6.930	Hun	− 0.419	c36	− 0.838
c64	− 1.138	c64	− 1.915	c64	− 0.002	165	− 8.127	ck3	− 0.469	c65	− 0.926
ck3	− 1.165	c65	− 1.927	c65	− 0.002	143	− 8.293	185	− 0.664	c60	− 0.959
c65	− 1.535	ck3	− 2.238	ck3	− 0.003	170	− 9.740	c64	− 0.669	c67	− 1.196
c67	− 1.556	c67	− 2.609	c67	− 0.003	191	− 12.553	252	− 0.809	ck3	− 1.281

variation in breeding populations (Zhao et al. 2014), an approach with great significance in the genetic improvement and selection of forest trees (Weston et al. 2008). The ANOVA results of this study demonstrated that there are significant differences for all traits among families, similar to those in Meng and Zhang (2014), indicating that growth, stem quality and crown architecture traits hold great potential for genetic improvement at the family level. In addition, the variance components of family accounted for more than half of the total phenotypic variation for some traits, indicating adequate genetic variability for these traits (Loha et al. 2009). The coefficient of variation provides an important basis for selection (Yu et al. 2017): the greater the coefficient of variation the greater the variation and the more favorable for selection (Zhao et al. 2015). In this study, the phenotypic coefficient of variation for V was the greatest, 78.22%, and for TH and DBH, 20.32% and 35.39%, respectively, similar to values reported by Yin et al. (2016), and greater than those reported by Li (2012), indicating that the superior traits evaluated and identified using these methods represent a significant improvement in tree characteristics.

Heritability is an important parameter for estimating genetic gain. Higher heritability ensures stable inheritance of traits from parents to offspring. The range of family heritability observed in the present study ranged between 0.663 and 0.959. In particular, the heritabilities of TH, DBH, V and CW were all greater than 0.940, which are higher than those reported by Wang et al. (2018). The results showed that all traits of the selected families could be inherited stably, which was beneficial to the selection and utilization of superior families. The range of single tree heritability was between 0.034 and 0.983, where TH, DBH and CW were all greater than 0.900, all higher than the values for *Larix laempferi* (Lamb.) Carr. at the age of 4 years (Wang and Xiang 2009), which suggested the superior individuals selected were significance.

For forest tree genetic improvement, multi-trait improvement is usually the goal, so the correlation between traits is crucial (Lin 2010), reflecting the relationship between specific traits and providing information necessary for multi-trait association breeding (Jia et al. 2016b). The results of the correlation analysis in this study show that there is a highly significant positive correlation between tree height, diameter at breast height and volume, similar to those reported in Zhang et al. (2017), indicating that these three traits are strongly associated with each other and can be used together to evaluate and select superior materials. Using multiple-traits comprehensive evaluation to identify families using a 10% selection intensity, families 235, 143, 218, 182, 220, 188, and 229 were selected, with averages for TH, DBH and V greater than the total average by 16.69%, 30.14% and 71.42%, respectively. When compared to the total average, the genetic gains for the three traits were greater by 15.87%, 28.79% and 67.38%, respectively. These genetic gain values are greater than those reported by Yin et al. (2016). Using *Q*i value to select superior individual trees using a 20% selection intensity, 56 superior individuals were selected with average TH, DBH and V values greater than the total average by 36.76%, 78.01% and 222.35%, and with genetic gains greater by 34.94%, 74.51% and 209.78%, respectively, greater than the values reported by Xia (2017). The genetic gains observed in this study indicate that the selected families or individuals can provide a high degree of economic benefit.

Breeding value is the additive genetic effect on phenotypic values, eliminating the influence of environmental factors (Sun et al. 2011; Sun and Yang 2012). It can be used to measure the practical value and potential for parental breeding. As an important indicator for evaluating parents, breeding value indicates parental influence. The higher the breeding value the more advantageous selection of the parents will be (Li et al. 2006). In this study, the breeding values for each trait are positive and negative. Parents with higher breeding values are more likely to pass on beneficial traits to their offspring. Using timber yield, taking TH, DBH and V as proxy, four superior families (families 218, 143, 235, and 182) were selected. Using stem quality, taking BA and SSD as proxy, five superior families (families 170, 143, 208, 167 and c94) were selected. Using planting density, with CW employed as a proxy, seven superior families (families 235, 143, 149, 154, 213, 206 and 196) were selected. Considering all traits, family 143 was selected, with values for TH, DBH, V, BA, SSD and CW greater than the total average value by 19.12%, 33.89%, 74.05%, − 6.03%, 1.83% and 21.470%, respectively. The parents of selected families potentially can be used as preferred parents for future hybridization breeding programs with different breeding objectives.

Conclusions

In this study, the growth, stem quality and crown architecture traits of 73 half-sibs of *L. olgensis* were measured and analyzed. Wide ranges in variation coefficients and strong heritabilities indicated that the superior materials selected were feasible and meaningful. Seven superior families and 56 superior individuals were selected using the multi-traits comprehensive evaluation approach. Several parents were selected with higher breeding values for various investigated traits. The selected superior families, individuals and parents can provide foundation materials for the establishment of improved second generation seed orchards.

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