

Age trends of genetic variation and early selection for growth traits in *Cunninghamia lanceolata* open-pollinated families

Sirui Li¹, Jiayi Li¹, Hanbo Yang¹, Changdong Yang², Yunjie Gu³, Zhi Chen³, Hongying Guo⁴, Zhen Huang³, Peng Zhu^{1*}

¹Forestry Ecological Engineering in the Upper Reaches of the Yangtze River Key Laboratory of Sichuan Province, National Forestry and Grassland Administration Key Laboratory of Forest Resource Conservation and Ecological Safety on the Upper Reaches of the Yangtze River, Rainy Area of West China Plantation Ecosystem Permanent Scientific Research Base, College of Forestry, Sichuan Agricultural University, Chengdu 611130, China

²Hongya State-Owned Forest Farm, Rainy Area of West China Plantation Ecosystem Permanent Scientific Research Base, Meishan 620364, China

³Sichuan Academy of Forestry, Sichuan Key Laboratory of Ecological Restoration and Conservation for Forest and Wetland, Chengdu 610081, China

⁴Sichuan Academy of Grassland Sciences, Chengdu 610041

Corresponding author: Peng Zhu, E-mail: 14034@sicau.edu.cn

Abstract

The present study measured the growth traits of 98 open-pollinated half-sibling families from the second-generation clonal seed orchard of Chinese fir for 6 consecutive years from age 2 to 7, the change patterns of genetic variation in growth traits and genetic parameters were analyzed, and best linear unbiased prediction (BLUP) was used for early selection to determine the excellent families. The growth traits of Chinese fir revealed highly significant differences between families, indicating that there was significant genetic variation at the family level, which serves as the foundation for exceptional family selection. The heritabilities of family and individual for H (height) ranged from 0.61 to 0.65 and 0.41 to 0.46, respectively; for DGH (the diameter at ground height)/DBH (the diameter at breast height), they were 0.55 to 0.66 and 0.35 to 0.46, respectively; and for V (tree volume), they were 0.66 to 0.70 and 0.48 to 0.49, respectively. The growth traits of genetic control were at a greater level at age 5. The findings of the coefficient of variation analysis demonstrated that the phenotypic variation coefficient were larger than the genetic variation coefficient for three growth traits at various ages. The juvenile-mature genetic and phenotypic correlations revealed an increasing tendency with age, and mainly controlled by genetic factors. Compared to other age groups for growth traits, age 5 had greater phenotypic and genetic association coefficients, as well as greater efficiency of early selection. Based on the selection method of breeding value, nine families were selected with a 9.2 % selection rate.

Keywords: Chinese fir; Half-sibling family; Genetic variation; Early selection; Juvenile-mature correlation

Introduction

Within the genetic improvement of trees, selective breeding is a common method employed in tree genetic enhancement for forest trees (MacLachlan et al. 2017). Currently, the selection of families is mainly focused on seedling growth and growth traits as indicators of superiority (Dong et al. 2018). For instance, Li et al. (2021) investigated the genetic variation of growth traits of 34 full-sib families in different growth years, using the multiple-traits comprehensive evaluation method, seven families of *Pinus koraiensis* were selected at different ages. In three *Eucalyptus pellita* seedling orchards, Leksono and Kurinobu (2005) discovered a tendency within family-plot selection, which was analyzed with the retrospective selection index using data on height (H), diameter at breast height (DBH) and stem form measured before each selection in South Sumatra. After conducting a multipoint conjoint analysis on 53 half-sibling families from the main seed orchard of *Betula platyphylla*, Liu et al. (2017) identified eleven superior families based on their survey results for the H, DBH, and tree volume (V). Bai et al. (2018) analyzed the phenotypic correlations between seed qualities and early growth traits to determine which female parents would be best for controlled cross-breeding of *Populus tomentosa*. When choosing exceptional families, growth traits including H, V and the diameter at ground height DGH/DBH

are crucial factors to be considered, along with their potential for genetic diversity. Moreover, they also serve as a crucial tool for classifying timber resources and evaluating the value of a forest stand in ecological and commercial domains (Tao et al. 2021). Enhanced genetic gains can be achieved by utilizing genetically improved material derived from plus trees with superior growth and stability (Lee et al. 2020). In this context, one of the main indicators of the effectiveness of selection in forest tree breeding is the genetic gain of growth traits, which can estimate the potential increase of the progeny relative to the parents under a particular selection intensity (Perek et al. 2022). To determine the effects of genetic and environmental factors on *Pinus koraiensis* growth, Lee et al. (2020) analyzed H, DBH and V of the offspring. Mihai et al. (2019) estimated the strategy based on recurrent selection from the first-generation progeny at the juvenile age, which will yield the greatest genetic gain in the next breeding generation. To select the superior second-generation families and obtain a better breeding strategy, Li et al. (2017) evaluated the genetic gain and the genetic variation of growth traits of an open-pollinated family in *Pinus kesiya* var. *langbianensis* progenies plantation.

Grasping the juvenile-mature correlation coefficients of growth traits is essential for determining the appropriate time and the viability of early selection, and for estimating the effects of early selection (Lai et al. 2014). Several investigations involving various tree species have demonstrated the validity of early selection based on juvenile-mature correlation coefficients. For example, an early evaluation study by Pan et al. (2017) examined the juvenile-mature correlation of growth traits of *Larix kaempferi* clones, suggesting that the optimum early selection age is the 6th–8th growth year. Zhang et al. (2022) evaluated the age trends of genetic variation of *Larix olgensis* in radial growth from various provenances and juvenile-mature correlations, which showed that the early selection for DBH could be made at the age of 10–13 years old at different places. Que et al. (2021) investigated the efficiency of early selection in *Neolamarckia cadamba* by monitoring the growth traits in 39 half-sib families from 11 provenances, and revealed the feasibility of early selection for growth is best performed at age 5. These studies had tiny study samples and focused less on juvenile-mature correlations in young trees. Therefore, research on the early selection and juvenile-mature correlations of young Chinese fir forests with large sample sizes are required.

Chinese fir (*Cunninghamia lanceolata* (Lamb.) Hook) is one of the timber species with the largest afforestation area in Southern China (Ma et al. 2007). At the present time, the species is cultivated commercially in 17 provinces or provincial cities south of the Qinling Mountains and the Huaihe River in China, with production centers in Hunan, Guangxi, Jiangxi, and Fujian Provinces (Zhou et al. 2020). Chinese fir timber is used in a wide range of architectural and decorative applications, due to its fast-growing capacity, excellent disease resistance and durable wood, with a short rotation time of approximately 25 years (Zhang et al. 2004). On the other hand, a tremendous role in maintaining ecological functions also played by Chinese fir (Zhou et al. 2020). The research hitherto on the early selection of Chinese fir families has mainly focused on middle-age,

mature age and intermittent (Zheng et al. 2016, Wu et al. 2019), and current-year growth trait measurements (Chu et al. 2021, Jing et al. 2023). Nevertheless, there are still a few intriguing and pertinent issues with early selection and cultivation efforts for Chinese fir that need to be addressed. Also, the breeding procedures must be enhanced (Zhou et al. 2020). Given this, the present study measured the growth traits of 98 half-sibling families of free-pollinated plants over the course of six consecutive years in a two-generation asexual seed orchard of Chinese fir, analyzed the change patterns of genetic variation in growth traits of the family lines with the increase of age, and estimated the genetic parameters, in order to select excellent families. And the juvenile-mature correlation of growth traits and the efficiency of early selection were evaluated to finalize the selection age for Chinese fir. This research provides a theoretical basis for breeding improvement of Chinese fir.

Materials and methods

Test materials and design

Chinese fir half-sibling families used in this experiment were originally collected from the progeny of open-pollinated plants in the two-generation clonal seed orchard of Hongya Forest Farm in Hongya County, Sichuan Province (102°49'–103°32'E, 29°24'–30°00'N). The source information for these 98 clones is shown in Table 1. We gathered seeds in 2012 and proceeded to plant seedlings at the progeny test at the end of 2013 by using one-year-old seedlings with a trial altitude of about 1000 m. This region experiences subtropical monsoon humidity, with an annual mean temperature of 16.6°C and annual rainfall of 1435.5 mm. The average January temperature was 8°C, while its average July temperature was 28.6°C in this region. The length of the frost-free period is about 307 days. The field design for each family was the randomized complete blocks with five replications and a 10-tree plot in a spacing of 2 × 2 m.

Data collection

The tree height (H/m, 0.1 m) was measured for all trees in experimental plantations from the 2nd to the 7th growth year in the winter. The diameter at ground height (DGH/cm, 0.1 cm) was measured from the 2nd to the 4th growth year, and the diameter at breast height (DBH/cm, 0.1 cm) was measured from the 5th to the 7th growth year thereafter. Tree crown width (CW/m, 0.1 m) was measured from the 2nd to the 5th growth year, and the number of branches whorl (NBW) and the number of lateral branches (NLB) were measured from the 2nd to the 4th growth year. Individual tree volume (V/ m³) was calculated using the following tree volume formula (Chen 2013):

$$V = 0.000872DBH^{1.785388607}H^{0.9313923697}$$

Table 1
The essential information of 98 clones in tests trials.

Origin	Order of clones	Number of clones	Origin	Order of clonal	Number of clones
YuejiangSeed orchard	T2-T3,T5-T17	15	Fushun Seed orchard	EQ58-EQ62, EQ47-EQ48, T406	8
Xuyongda'an forestry farm	T358-T361,T363, T376,T378-T380, EQ21-EQ25, EQ27- EQ30, T320R, T312R, T334R	26	Junlian Seed orchard	T101,T103- T107,T109, T112- T115, T119-T122,EQ81	16
Nanchuan forest Fine variety base	T301, T305-T321, T328, T334-T335, T204R-T205R, T170R	25	Hongya forestry farm	T204-T207, T209, T217-T218	7
Gongxianminsheng Seed orchard	T50	1	total		98

Statistical analysis

Descriptive statistics and multi-factor analysis of variance were performed using the statistical software SPSS16.0. Genetic parameters, phenotypic and genetic correlation coefficients were calculated separately using a mixed linear model from ASReml-R to calculates the variance components.

The method of Best linear unbiased prediction (BLUP) was used to estimate the breeding values of individuals (Xiang et al. 2002).

$$Y_{ijk} = \mu + b_i + f_i + fb_{ij} + e_{ijk} \quad (\text{Eq. 1})$$

Where Y_{ijk} is the observation on the k th tree in the j th family in i th replicate, and μ is the overall mean. The b_i , f_i and fb_{ij} are the fixed effect of i th replicate, the random effect of j th family which follows the normally and independently distribution, and the random interaction effect of the i th replicate by the k th family, respectively. e_{ijk} is random error within plot.

The family heritability (h_f^2) and individual heritability (h_i^2) were calculated using the following equations:

$$h_f^2 = \sigma_f^2 / (\sigma_e^2 / rn_h + \sigma_{fb}^2 / r + \sigma_f^2) \quad (\text{Eq. 2})$$

$$h_i^2 = 4\sigma_f^2 / (\sigma_e^2 + \sigma_{fb}^2 + \sigma_f^2) \quad (\text{Eq. 3})$$

where σ_f^2 is among-family variance, σ_e^2 is the residual variance, and σ_{fb}^2 is the family by block variance.

The phenotypic variation coefficient and genetic variation coefficient was calculated using the following formulas:

$$CVG(\%) = \sqrt{\sigma_f^2} / \bar{X} \times 100 \quad (\text{Eq.4})$$

$$CVP(\%) = \sqrt{\sigma_p^2} / \bar{X} \times 100 \quad (\text{Eq.5})$$

Where $\bar{X}$ is the phenotypic mean of the trait average. σ_f^2 and σ_p^2 are phenotypic variance and family variance, respectively. The equation expresses a standardized measure of the genetic variance relative to the mean of trait.

The phenotypic (rp) and genetic (rg) correlation between traits at early year with the corresponding trait at late stage were calculated as:

$$rp = \sigma p(xy) / \sqrt{\sigma_{p(x)}^2 \times \sigma_{p(y)}^2} \quad (\text{Eq.6})$$

$$rg = \sigma g(xy) / \sqrt{\sigma_{g(x)}^2 \times \sigma_{g(y)}^2} \quad (\text{Eq.7})$$

Where $\sigma p(xy)$ is the phenotype covariance component between traits x and y , $\sigma_{p(x)}^2$ is the phenotype variance component for trait x and $\sigma_{p(y)}^2$ is the phenotype variance component for trait y . The $\sigma g(xy)$ refers to the genotypic covariance between traits x and y , $\sigma_{g(x)}^2$ denotes the genotypic variance component for trait x and $\sigma_{g(y)}^2$ is the genotypic variance component for trait y .

The Genetic gain (ΔG , %) was estimated using the correlated genetic gain equation (Peng 2020):

$$\Delta G(\%) = S h^2 / \bar{X} \times 100\% \quad (\text{Eq.8})$$

Where S is the selection difference and h^2 is the heritability and $\bar{X}$ is the overall mean of growth traits.

Early selection efficiency E_{gen} can be calculated using the following (Wen et al. 2023):

$$E_{gen} = r_g \times \frac{h_E \times i_E}{h_R \times i_R} \quad (\text{Eq.9})$$

Where i_E and i_R are the selection intensity at the early and reference age, respectively, h_E and h_R are the square root of the heritability at the early and reference ages, respectively. And the reference age, which was 6 years in this work. The same selection intensity for the early and reference ages was used in this calculation.

Results

The growth traits of Chinese fir families

There were significant differences in growth traits among families each year (Table 2). Over the period studied, the average H of the 98 half-sibling families ranged from 0.83 to 9.51 m (from the 2nd to the 7th growth year). The average DGH of all families was 1.39 cm in the 2nd growth year and the average of DBH was 6.88 cm in the 7th growth year. Meanwhile, the annual H increment was a mean of 1.74 m, the annual average DGH and DBH increment were 0.893 cm and 1.289 cm, respectively. The annual V increment was 0.00684 m³. The mean values of the CW increased from 0.612 m² at age 2 to 1.96 m² at age 5, the NLB increased from 24 at age 2 to 33 at age 4, and the NLB increased from 12 at age 2 to 49 at age 4. Annual growth rates of the three traits of H, DGH/DBH and V were 33.53 %, 30.18 %, and 135.11 %, respectively. It is also interesting to see that the differences in various growth traits were not only significant among blocks, but also between the interactive effect of families and blocks. The findings revealed that growth traits in Chinese fir were rich in familial genetic variation. All these implicated that variations of different growth traits may result from distinct patterns of genetic regulation within families as well as environmental influences. Traits such as H, DGH/DBH and V showed highly apparent differences in growth in all the years of measurement (Fig.1).

Genetic parameters of growth traits in families with different tree ages

Maximum values of the individual heritability estimate (h_i^2) and family heritability estimate (h_f^2) for the three major growth traits in the Chinese half-sibling family were appeared at age 5 (Fig. 2). For H, the greatest h_i^2 and h_f^2 was 0.46 and 0.65, respectively. For DGH/DBH, the greatest h_i^2 and h_f^2 was 0.46 and 0.66, respectively. For V, the greatest h_i^2 and h_f^2 was 0.49 and 0.70, respectively. Both h_i^2 and h_f^2 for DGH/DBH and V had the minimum at age 2, while h_i^2 and h_f^2 for H was at its lowest in the fourth year. The h_f^2 for H, DGH/DBH and V ranged from 0.61 to 0.65, 0.55 to 0.66 and 0.66 to 0.71, respectively. The h_i^2 for H, DGH/DBH and V were ranged from 0.41 to 0.46, 0.35 to 0.46 and 0.48 to 0.49, respectively. The phenotypic variation

coefficient (CVP) and genetic variation coefficient (CVG) for H ranged from 0.43 to 0.80 and 0.29 to 0.53 respectively, and those for DGH/DBH ranged from 0.37 to 0.91 and 0.30 to 0.59 respectively, and the low value could be attributed to the possibility of the stronger affinities among the seedlings, given that the seedlings were all native superior trees in Sichuan and that the relatives of the seedlings might not be too far apart. The CVP and CVG for V were always higher than those for H and DGH/DBH each year, ranging from 2.40 to 3.78 and 1.74 to 2.75. Age trends of CVP and CVG in these three growth trials are shown in Fig. 3. The CVG of traits was relatively smaller than the CVP of traits. Wherein, it is evident that the CVP and CVG of V were higher than those of H and DGH/DBH for all ages. The CVP and CVG of H remained in the narrow range, there was no obvious change in all measured years. And then both the CVP and CVG for DGH/DBH and V showed a declining trend over time. Analyses of the variance coefficient indicated that H growth traits are relatively stable from year to year.

The Juvenile-mature genetic and phenotypic correlations

There were high and significant juvenile-mature genetic and phenotypic correlations between growth traits (H, DGH/DBH) at early ages in Chinese fir families (Fig. 4). The genetic correlation coefficients and phenotypic correlation coefficients for H traits among ages varied from 0.77 to 0.99 and 0.54 to 0.94, respectively. The genetic correlation coefficients and phenotypic correlation coefficients for DGH/DBH among ages varied from 0.65 to 1.00 and 0.50 to 0.97, respectively. The genetic correlation coefficients and phenotypic correlation coefficients for V among ages varied from 0.56 to 1.00 and 0.52 to 0.97, respectively. Which, at age 5, the genetic correlation of H, DGH/DBH, and V between age 5 and all tree ages were significant and more than 0.7, and the corresponding phenotypic correlations were also significant (more than 0.6). For the three traits of other ages, age 5 had the highest juvenile-mature genetic and phenotypic correlations among the three traits in the other age groups, followed by age 6 and age 7.

Efficiencies of Early Selection

Fig. 5 shows the efficiencies achieved through early selection for H, DGH/DBH, and V at a reference age of 6. For H and DGH/DBH, selection efficiency increased overall with age between age 2 and 5, and was highest at age 5 (1.014 and 1.024 for H and DGH/DBH), while V showed the highest efficiency at age 6 (1.010). The data in the figure show that comparing the efficiency of selection at different ages of fir, we noticed that the efficiency was overall higher by performing direct selections of growth traits on Chinese fir of age 5. The growth potential of Chinese fir is not fully expressed during the period of early growth. Accordingly, early selection of Chinese fir less than the age of 4 may have detrimental effects.

Genetic gain and early selection

Based on the age-age correlation analyses of growth traits in Chinese fir families, H, DGH/DBH and V as selection indicators were employed for the rank correlations of calculated

Table 2
Statistics and variance analysis of growth traits for families in different ages.

Age/a	Source of variation	Degree of freedom	H/m		DBH(DGH)/cm		V/m ³		CW/m ²		NBW/piece		NLB/piece	
			Mean	F	Mean	F	Mean	F	Mean	F	Mean	F	Mean	F
2	Block	4		37.65*		66.59*		39.02*		16.46*		14.02*		14.97*
	Family	97	0.83	3.37*	1.39	2.63*	0.0001	2.50*	0.61	1.50*	12.48	1.74*	24.09	1.71*
	Block × Family	381		1.92*		2.21*		2.24*		1.51*		1.40*		1.48*
3	Block	4		12.68*		32.04*		31.74*		65.83*		33.68*		49.30*
	Family	97	1.67	2.90*	2.96	2.69*	0.0009	2.46*	1.07	1.77*	26.83	2.05*	27.76	2.16*
	Block × Family	381		1.75*		1.71*		1.80*		1.41*		1.41*		1.45*
4	Block	4		12.89*		24.05*		24.30*		43.13*		4.62*		7.72*
	Family	97	5.54	3.04*	3.17	2.43*	0.0037	2.69*	1.51	1.57*	49.17	1.89*	32.53	1.91*
	Block × Family	381		1.87*		1.74*		2.21*		1.51*		1.52*		1.44*
5	Block	4		21.97*		29.60*		24.81*		23.40*				
	Family	97	6.10	3.08*	4.30	3.21*	0.0059	2.98*	1.96	1.70*				
	Block × Family	381		1.92*		1.85*		2.15*		1.55*				
6	Block	4		32.25*		27.62*		21.45*						
	Family	97	7.91	2.93*	5.54	2.62*	0.011	3.11*						
	Block × Family	381		2.02*		1.72*		2.27*						
7	Block	4		39.92*		24.52*		21.45*						
	Family	97	9.52	2.83*	6.88	2.46*	0.020	3.11*						
	Block × Family	381		1.93*		1.69*		2.27*						

Note: * = significant at 0.05 level.

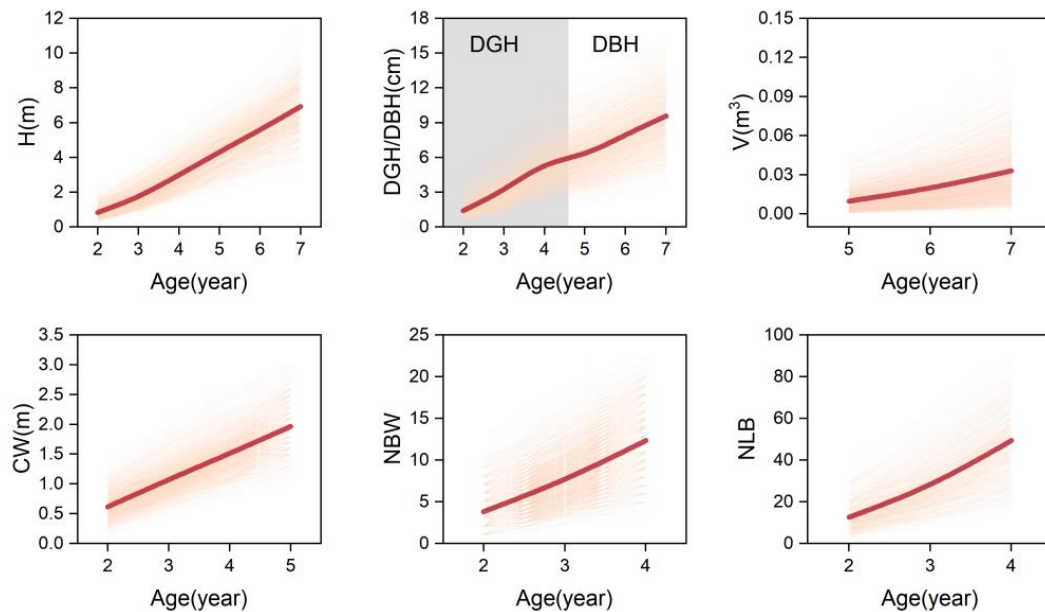


Fig. 1

Growth trajectories of growth traits with age. The thin lines with orange color represent the growth performance of different families and the thick lines with red color represent the growth performance on the whole. The second graph shows the trend in DGH with age from second to fourth year, and the trend in DBH with age from fifth to seventh years.

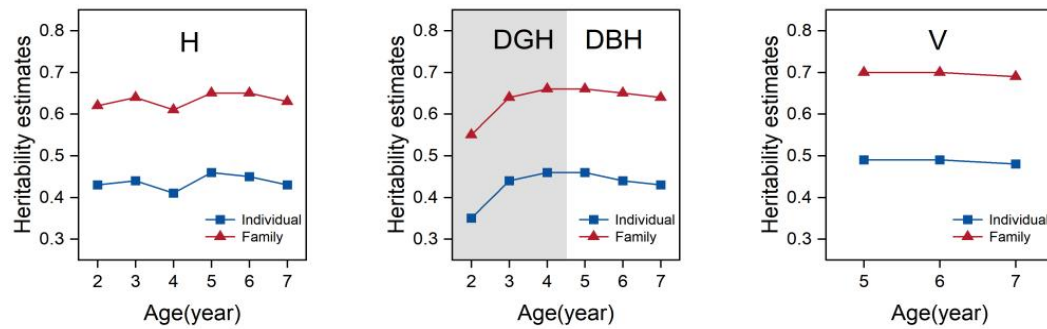


Fig. 2

The age trends of heritability estimates for growth traits. The figures represent the age trends of individual-tree and family heritability estimates for H, DGH/DBH and V respectively. For DGH, these were years 2 through 4, and for DBH, they were years 5 through 7, in second graph. The lines with red triangles represent the family heritability estimates and the lines with blue squares represent the individual heritability estimates.

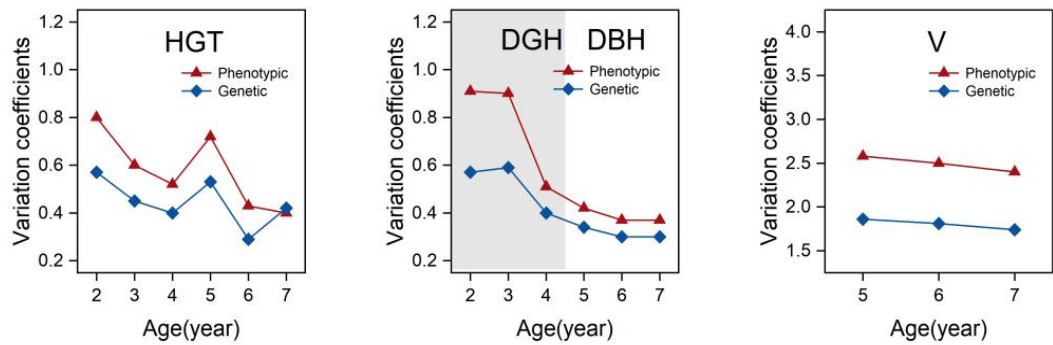


Fig. 3

Age trend of coefficient of variation for different traits. For DGH, these were years 2 through 4, and for DBH, they were years 5 through 7, in second graph. The lines with red triangles represent the phenotypic correlations and the lines with blue squares represent the genetic correlations.

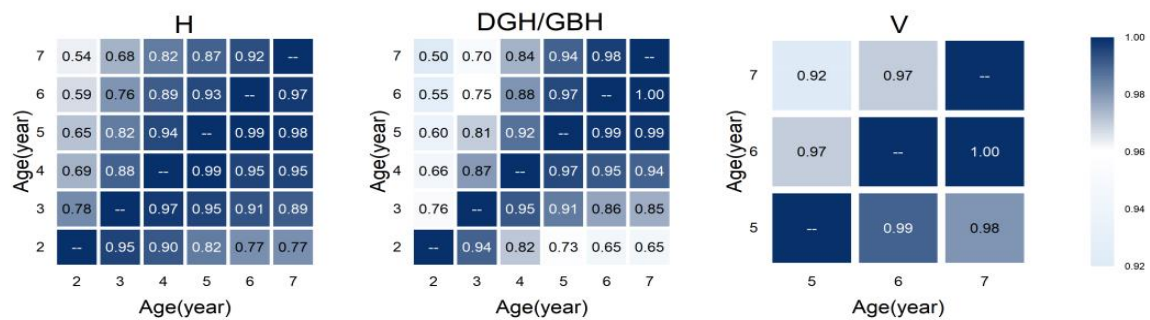


Fig. 4

Juvenile-mature correlation coefficients for H, DGH(DBH) and V between different ages. The phenotypic correlation coefficients are represented by the upper left triangular data, and the genetic correlation coefficients are represented by the lower right triangle data. In the second graph, these were years 2 through 4 for DGH and years 5 through 7 for DBH. Significant differences were exhibited significant ($P < 0.05$).

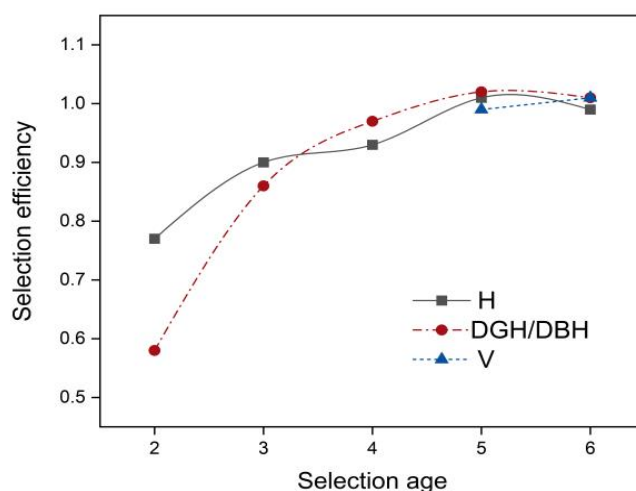


Fig. 5
Selection efficiency for the three growth traits at different selection ages. Growth traits at age 7 were used as a reference.

Table 3
Mean and Genetic gain of selected families under different selection rates

Inclusion rate	Selected families	H/m		DBH/cm		V/m3	
		Mean	Genetic gain/%	Mean	Genetic gain/%	Mean	Genetic gain/%
9.2 %	9	3.44	14	5.17	20.0	0.010	45.3
14.3 %	14	3.26	9.9	4.46	14.3	0.009	34.7
19.4 %	19	3.32	11.2	4.68	15.1	0.009	33.3

Table 4
Breeding Value of selected families under different selection rates

Inclusion rate	Number of families	H/m	DGH/DBH/cm	V/m3	Mean breeding value
9.2 %	T317	0.362	0.661	0.002	0.342
	T310	0.251	0.587	0.002	0.280
	T114	0.243	0.578	0.002	0.274
	T2	0.216	0.508	0.001	0.242
	T205	0.229	0.473	0.001	0.234
	T312R	0.138	0.440	0.001	0.193
	EQ25	0.133	0.417	0.001	0.184
	EQ24	0.143	0.415	0.001	0.186
	T3	0.179	0.378	0.001	0.186
14.3 %	EQ59	0.154	0.313	0.000	0.156
	EQ58	0.168	0.311	0.001	0.160
	T306	0.062	0.298	0.001	0.120
	T105	0.144	0.290	0.001	0.145
	T8	0.163	0.263	0.000	0.142
19.4 %	T359	0.101	0.260	0.001	0.120
	T209	0.096	0.252	0.001	0.116
	T217	0.141	0.251	0.000	0.131
	T301	0.091	0.248	0.001	0.113
	EQ21	0.117	0.227	0.000	0.115

Table 5
Distribution of excellent family groups

Number of families	Breeding value	H/m		DGH/DBH/cm		V/m ³	
		Mean	Genetic gain/%	Mean	Genetic gain/%	Mean	Genetic gain/%
T317	0.66	3.39	12.7	4.88	15.1	0.01	49.3
T310	0.59	4.09	28.9	6.09	35.4	0.012	71.5
T114	0.58	3.01	3.9	4.5	8.9	0.008	29.7
T2	0.51	3.38	12.6	5.08	18.6	0.011	56.9
T205	0.47	3.92	25	5.68	28.5	0.01	46.2
T312R	0.44	3.05	4.9	4.7	12.1	0.009	35.1
EQ25	0.42	3.58	17.1	5.42	24.2	0.009	40.5
EQ24	0.41	3.17	7.6	4.73	12.7	0.008	28.6
T3	0.38	3.74	20.8	5.45	24.7	0.01	49.9

combined family breeding values, which were obtained from the superior trees of age 5 (Table 3). 9, 14 and 19 families were selected, when the selection ratios were 9.2, 14.3 and 19.4 %. The breeding values for H, DGH/DBH and V for these selected families ranged from 0.062 to 0.362, from 0.227 to 0.661, and from 0.000 to 0.002, with an average of 0.168, 0.377 and 0.001, respectively (Table 4, Additional file 1).

The growth traits such as H, DGH/DBH and V in the families within the 9.2 % selection rate had significant average and genetic gain, with averages of 3.44 m, 5.17 cm, and 0.010 m³, respectively, and average genetic gain of 14.0 %, 20.0 %, and 45.3 %, respectively. Accordingly, 9 excellent families were selected, namely T310, T114, T2, T205, T312R, EQ25, EQ24 and T3, based on the 9.2% selection rate (Table 5). In particular, their mean values for H, DGH/DBH and V ranged from 3.01 to 4.09 m, 4.50 to 6.09 cm, and 0.008 to 0.012 m³, respectively, and their genetic gain ranged from 3.9 % to 28.9 %, 8.9 % to 35.4 % and 28.6 % to 56.9 %, respectively.

Discussion

Genetic variation is the basis of selection, therefore a sufficient comprehension of the variance in the forest is required to accurately assess the reliability of a genetic improvement (Peixoto et al. 2016). Besides, tree improvement involves both genetic evaluation and selection, and through the determination and selection of excellent progenies and families, seed orchards can be built to serve the production of seedlings for use in commercial reforestation (Lan 2016, Yang et al. 2018). Our research found that there were significant differences in growth traits (H, DGH/DBH, V, CW, NBW and NLB) between the 98 families of Chinese fir each age by performing statistical and variance analyses of the six traits. These findings, which was in accordance with previous studies on other tree species, including *Larix principis-rupprechtii* (Dong et al. 2018), *Betula platyphylla* (Xu et al. 2015), and *Pinus massoniana* Lamb. (Tan et al. 2017), showed that there was a great potential for early genetic

improvement at the family line level. In the meantime, our results also revealed that there were extremely significant interactions between the Chinese fir families and the blocks in terms of the growth traits, indicating that genetic and forested environmental interactions have an effect on traits like H, DGH/DBH and V in Chinese fir. Numerous investigations have also confirmed genotype-environment interactions in several species of forest trees (Alía et al. 1997, McKeand et al. 1997, Zas et al. 2004). Furthermore, according to Wu et al. (2019), the average yearly growth of Chinese fir at age 31 for H, DBH, and V was 0.39-0.58 m, 0.56-0.98 cm, and 0.0047-0.0171 m³, respectively. This is in contrast to 1.74 m, 0.893 cm (DGH)/1.289 cm (DBH) and 0.00684 m³ (V), which is generally less than the findings of our study regarding the average yearly growth of young trees aged 2 to 7 years. This could be explained by the fact that certain some species of trees are known to have fast and slow growing periods, with early juvenile trees growing more quickly than mature trees overall, mostly because of the genetic traits unique to the species. The process of photosynthesis in trees affects the size of CW (Yang and Huang 2017). As trees grow, CW and NBW grow, and the lower branches of single trees are subjected to progressively more shade as well as competition to promote taller growth in the stand, which also exacerbates shading, resulting in higher NLB (Crecente-Campo et al. 2013). In this study, different families had different growth rates of CW, NBW, and NLB, indicating that photosynthetic impacts and shade tolerance vary among families of Chinese fir. Thereby, this may serve as a foundation for future decisions about the photosynthetic characteristics of various families of Chinese fir.

The heritability, or the magnitude of the parent's ability to pass on a trait to their offspring, is considered to be an important parameter in determining genetic gain (Diao et al. 2016). The results of this study also demonstrated that the family heritability outweighed the individual heritability, which is consistent with many prior findings on other tree species as *Picea crassifolia* (Ouyang et al. 2018) and *Pinus elliottii* (Lai et al. 2017). However, there were some differences in the magnitude of heritability, compared to other experiments. The genetic

parameters of the *Schima superba* plus tree were analyzed by Wang et al. (2020), who revealed that the family heritability was 0.23 to 0.76, and their individual plant heritability was 0.09 to 0.70, while the interval span of their research results was wider than the results of the present study, which the family heritability was 0.55 to 0.71, and the individual plant heritability was 0.35 to 0.49. In Wu et al.'s (2018) study on the growth traits of half-sib families of *P. elliotii*, the heritability of H, DBH and V were found to be 0.799, 0.779 and 0.770 for the family, and 0.683, 0.829 and 0.742 for the individual plants. The study's findings had a higher heritability within both families and among individuals than that of results in the present study. The different species, genotypes and sites may be the cause of these disparate conclusions. The coefficient of variation is one of the most important criteria for evaluating whether a material may be chosen for evaluation or not (Lai et al. 2014). Likewise, the larger the phenotypic coefficient of variation, the more favorable it is for evaluating the selection (Bogdan et al. 2004, Liu et al. 2022), whatever the H, DGH/DBH or V, the phenotypic coefficient of variation was relatively significant based on the results of the coefficients of variation for each growth trait of Chinese fir half-sibling family of different ages. In the present study, the CVG and the CVP for DGH/DBH and V decreased with aging, which was in accordance with a previous study (Lai et al. 2014). While H exhibits a pattern of small fluctuation, as evidenced by a reduction followed by an increase and a decrease. The above may have been inflated by the trend of variation induced by genetic factors, which differed for each of the growth traits at different tree ages.

Due to the long growth rotation of forest trees and the time required for genetic determination of progeny, which suggests that selection at an early age is highly desirable for tree breeding and it may well be in the range where meaningful improvements can be achieved by reducing the length of the breeding cycle and accelerating high-generation breeding (Gaspar et al. 2008, Li et al. 2021, Hao et al. 2022). Of these, one of the appropriate routes to choose an early selection of forest trees is juvenile-mature correlation analyses of traits (Hao et al. 2022). When assessing the sawn and dried boards for structural traits of *Picea abies*, Hallingbäck et al. (2018) indicated that the optimal age of early selection at the tree age 10-16 years would result in more genetic gain annually than selection at later ages for wood density and grain angle. Resende et al. (2021) investigated the genetic variation for growth traits of *Araucaria angustifolia*, and measurements at ages 7, 24, 32, 33 and 35 were used to provide annual estimates for unmeasured ages, and growth data indicate potential for early selection for growth at age 7-10. In addition, the magnitude of early selection efficiency for growth traits is an influential basis for determining the age of early selection (Hallingbäck et al. 2018). Whilst the efficiency of early selection, is mainly seen as an artifact of the juvenile-mature correlation and the temporal advantage of updating breeding generations more quickly through early selection (Lambeth 1980), which has been examined in some research to establish the ideal age for selection. Bin et al. (2003) determined the optimal selection age for various selection methods by analyzing the efficiency of early

selection in loblolly pine. Hong et al. (2015) studied the efficiency of early selection for wood quality traits in the Scots pine breeding program and concluded that selection at 8 years of age was most beneficial.

In this paper, we investigated the juvenile-mature correlation between growth traits such as H, DGH/DBH and V, by measuring the growth traits of 98 half-sibling families of Chinese fir over a period of 6 years. The study demonstrated that considerable genetic and phenotypic correlations of the three major growth traits between age 5 and those of other ages, as well as higher early selection efficiency. The early selection of Chinese fir has also been reported in the associated literature. According to Wu et al. (2019), the early selection of Chinese fir provenances can be carried out after a forest age of five years. Ma et al. (2000) showed that the appropriate selection age for Chinese fir early selection should be about the period of 4-6 years. Nevertheless, the feasibility of screening for excellent family based on the altering pattern of genetic variation in growth traits with age is further supported by these results. In subsequent studies, we are required to take more account of the actual selection effect and additional validation of early selection. Environmental factors invariably affected phenotypic data, thus reducing the accuracy of breeding selections, whereas breeding values contributed to eliminating this effect, reflecting authentic genetic effects and selecting accurately for superior material (Jansson et al. 2020, Rockwood et al. 2022). Zheng et al. (2023) decided the appropriate breeding strategies for *Larix gmelinii* var. *principis-rupprechtii* families based on the breeding values estimated using the method of best linear unbiased prediction (BLUP). Wang et al. (2022) studied the growth and cone production traits of parent clones at 3-year-olds in the third-generation breeding gardens of Chinese fir, and estimated the breeding values of each parent clone regarding different growth traits, ultimately elite parents were identified. By evaluating the accuracy of the predicted breeding values, Ukrainetz and Mansfield (2020) compared the three methods (HBLUP, ABLUP and GBLUP), and the results demonstrated that HBLUP as an effective method resulted in more precise estimates of genetic parameters and breeding values. In this study, nine excellent families (T317, T310, T114, T2, T205, T312R, EQ25, EQ24 and T3) were selected on incorporation of the combined breeding values at 9.2 % entry rate as well as the basis of genetic and phenotypic correlation coefficients for each trait. Selected excellent families in this instance have value for the development of breeding strategies for Chinese fir and the efficiency of variety improvement. Therefore, to maintain long-term genetic gains in Chinese fir breeding programs, it will also be necessary to verify differences in previously selected genetic variants, progeny trials with larger sample sizes, and at additional sites involving different generations are desirable, in subsequent studies.

Funding

This work received partial funding from the Key Research and Development Project of Sichuan Province (2021YFYZ0032) and the Natural Science Foundation of Sichuan Province (2022NSF-SC1062).

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