

JI Kongshu, FAN Minliang, XU Li'an

Variation analysis and fine family selection on half-sib progenies from clonal seed orchard of *Pinus massoniana*

© Higher Education Press and Springer-Verlag 2007

Abstract Variation of traits that include height, diameter at breast height (DBH), stem volume, crown width, straightness, wood basic density, tracheid length and width of open-pollinated progenies from clonal seed orchard of *Pinus massoniana* was analyzed. Differences in traits such as growth, tree form and wood quality among families was significant, which indicated that the improvement potential was notable. Heritability of height and wood basic density reached 0.691 and 0.640, respectively. According to a correlation analysis between traits, stem straightness could be improved indirectly when growth traits are improved; growth traits were significantly correlated with wood basic density; and wood basic density was not significantly correlated with length and width of the tracheid. Under the selection ratio of 10%, genetic gains were 19.74% and 19.32% respectively, and selected families from the progeny test stands at the age of five years and eight years were the same. Genetic correlation of height, DBH and stem volume was also significant at the level of 0.01. These show that selection of the short rotation of *P. massoniana* for pulp and paper use would be efficient for five-year-old trees. According to the comparison of the heritability of all the traits and taking into account the result of canonical correlation analysis, height could be considered as the most important index for selection. Given wood quality of all the families, and flowering and fruit settings of the clones in a seed orchard, twelve fine families were selected at 10% selection ratio of height growth and stem volume.

Keywords *Pinus massoniana*, clonal seed orchard, progeny test, trait variation, family selection

Translated from *Scientia Silvae Sinicae*, 2005, 41(6): 43–49 [译自: 林业科学]

JI Kongshu (✉), XU Li'an
The Key Laboratory of Forest Genetics and Gene Engineering of the State Administration of Forestry, Nanjing Forestry University, Nanjing 210037, China
E-mail: ksji32@163.com

FAN Minliang
Zhejiang Forest Seed and Seedling Administration, Hangzhou 310020, China

1 Introduction

Progeny test is an effective way to evaluate a tree's parental material and genetic parameters. Because the genetic improvement of main timber trees was listed in the National Key Project during "the Sixth Five-Year Plan", the selection of fine trees and the establishment of large-scale seed orchards were extensively carried out. The progeny test was made in time and played a very active part in evaluating genetic quality for fine trees. However, the progeny test of parental trees in seed orchards lags behind because of limitation by the flowering and fruit setting. For example, a progeny test of fine trees was carried out on growth and wood quality in Masson pine (*Pinus massoniana*), the most widespread conifer in China (The National Subject Cooperation Group of *P. massoniana* Seed Orchard, 1990; Zhou et al., 1994; Zheng et al., 1998; Long et al., 2002), which played an effective role in removing "fine trees" that did not have a good genotype through the phenotype selection. The seed orchard of Masson pine has grown more than 1,000 hm² since the 1970s (Ji, 2001). Because fine trees selected through phenotype without genetic testing were planted densely at the beginning, the problem of thinning and removing inferior trees became a restriction to seed orchard yields. The Masson pine would flower in the fifth or sixth year after planted, so early preliminary thinning should be according to the results of progeny test in fine trees, but not directly apply progeny as a guide. It is known that the fathers of the fine trees' progeny and orchard trees' progeny were different, making some errors possible if the progeny test of fine trees was taken as a guide. To increase seed orchard yields and maximize genetic potential, it is an urgent task to carry out a progeny test for re-selection in the seed orchard.

This research is based on the hereditary analysis of growth, stem form and wood property of the open-pollinated progenies of Masson pine clonal seed orchard for the selection of half-sib families and thinning at the Wuyi Forest Centre in Zhangping, Fujian Province. This study would support the development of an advanced generation seed orchard and raise genetic gains for the pulp and paper improvement of Masson pine.

2 Materials and methods

2.1 Seed orchard and progeny test

A clonal seed orchard of Masson pine was located in Guidong District, Wuyi Forest Centre in Zhangping, Fujian Province, 117°35' E, 25°15' N. The area's annual average temperature was above 20°C, the average temperature in January was above 10°C, the annual rainfall was 1,481–1,438 mm, frost-free period was 310–320 days, elevation was 400–500 m, main slopes were southeast-facing sunny slopes and half-sunny slopes, and soil fertility was medium. The buffer zone was made of natural hardwood forest, Chinese fir seed orchard and hardwood plantation.

There were 218 clones in the orchard, 15–25 clones every district, and the total area is 20 hm², with all clones from fine trees selected in 1980. Stocks were planted in 1985, grafting completed in 1987, original planting density was 625 individuals per hm², and saving rate was 82%. The orchard began to flower and bear fruit in 1991. The highest yield of seeds was in 1994–1995, after which yield decreased by 15%–35% annually. The first thinning with the strength 0.4 was done in 1997 on the ground of clones' phenotype in the seed orchard under no progeny test data, and canopy density decreased from 0.7–0.8 to 0.4–0.5. After thinning the yield of cones increased 1.3 times previous levels (Chen, 2000), but needed to be thinned again for the current canopy density was close to 0.8.

Open-pollinated seeds were collected in 1994, seedlings were raised in the spring of 1995, and a progeny test stand was constructed in the autumn. One hundred and twenty families were taken in the experiment, including a control (CK) from the local general stand. The test was designed randomly, at eight replications with four trees per plot in a block.

2.2 Methods

2.2.1 Surveys and methods

We used conventional methods to survey height, diameter at breast height (DBH), crown width and straightness—this last factor in terms of four levels: excellent, good, medium and bad, at 1 level for the best and 4 for the worst (take SQRT ($x + 1$) transformation in straightness treatment). The individual stem volume uses the standard formula of forestry issued (Xu et al., 1999).

$$V = 0.000,062,341,803D^{1.856,149,7}H^{0.956,849,2}$$

We surveyed the height, DBH, and crown width for five-year-old trees in January 2000, and then in April 2003 we measured eight-year-old trees' height, DBH, crown width and straightness, and sampled wood pith at breast height.

Wood density measurement adopts the largest water content method (Li et al., 1993); Tracheid length measurement uses nitrate segregation method. We randomly surveyed 50

tracheids after dyeing by safranin under projection microscope ($\times 40$), then took the average value; 30 tracheids were surveyed for width under ordinary microscope ($\times 45$), after which the average was also taken.

2.2.2 Statistical analysis

All the statistical variance was analyzed by SAS 6.12 (Hui and Jiang, 1996).

The analysis of variance model $Y_{ij} = \mu + b_i + f_j + bf_{ij} + \varepsilon$

where Y_{ij} is the observed values of the i th families and j th block, μ is the average effect of half-sib families, b_i is the effect of the i th block, f_j is the effect of the j th sib-half families; bf_{ij} is the effect between the i th sib-half families and the j th block; ε_{ij} is the random error of the i th families and the j th block.

The formula for phenotypic coefficient of variation (CV) and genetic coefficient variation (GCV)

$$CV(\%) = \bar{\sigma}_p/X; GCV(\%) = \bar{\sigma}_g/X.$$

In the formula, $\bar{\sigma}_p$, $\bar{\sigma}_g$ and X are the phenotypic standard deviation, genetic standard deviation and mean value, respectively.

The estimation of heritability

$$h_f^2 = \bar{\sigma}_f^2/(\bar{\sigma}_f^2 + \bar{\sigma}_{nb}^2/b + \bar{\sigma}_e^2/bn); h_i^2 = 4\bar{\sigma}_f^2/(\bar{\sigma}_f^2 + \bar{\sigma}_{nb}^2 + \bar{\sigma}_e^2)$$

where h_f^2 is the family heritability, h_i^2 is the single tree heritability, b is the blot number, and n is the harmonic block number; $\bar{\sigma}_f^2 = \text{var}(f_j)$, $\bar{\sigma}_{nb}^2 = \text{var}(bf_{ij})$, $\bar{\sigma}_e^2 = \text{var}(\varepsilon_{ij})$.

The genetic gain evaluation

$$\Delta G = Sh^2/X = i\bar{\sigma}_p h_f^2/X$$

where ΔG is the genetic gain, S is the selection difference, h_f^2 is the family heritability, i is the selection intensity and $\bar{\sigma}_p$ is the phenotypic standard deviation.

3 Results and analysis

3.1 Variation analysis of half-sib families' traits

3.1.1 Variation of growth traits

Growth, DBH, stem form and wood quality among families were significantly different, which indicated that the improvement potential was notable (Table 1). The CV and GCV of the stem volume were the largest, reaching 45.27% and 13.11% respectively; the minimum was that of the height, which was 11.77% and 4.57% respectively. The CV and GCV of the main characters followed a descending order: volume > DBH > height—a trend also observed in the analysis of the five-year-old trees except the heritability. The heritabilities of family and single trees followed the order of height > DBH > volume. The family heritability of height was 0.691, indicating a strong genetic level.

Table 1 Analysis of variation for growth traits of half-sib progenies of *P. massoniana* at age of eight years

Character	Mean	Variation range	F value	CV /%	GCV /%	h_f^2	h_i^2
Height /m	7.87	8.55–7.22	4.18**	11.77	4.57	0.691	0.338
DBH /cm	10.13	11.54–9.11	1.70**	22.15	6.63	0.264	0.059
Volume /m ³	0.035,14	0.047,32–0.027,34	1.65**	45.27	13.11	0.236	0.050

Note: ** Significance at 0.01 level. The same below.

3.1.2 Variation of tree form

Key traits of the timber species should include large volume; straight trunks; flat, thin branches; and high basic wood density of juvenile wood. Considering all the indexes of tree form traits, we used only four: crown width, straightness, height-diameter ratio (cm/cm), and crown-diameter ratio (cm/cm).

The crown width, straightness, height-diameter ratio and crown-diameter ratio among families were significantly different (Table 2), which indicated that the selection potential of the four traits was notable. The CV of the four traits reached 10%; the GCV of crown width was the maximum (9.82%), while straightness was the minimum (2.1%). The heritability of straightness was only 0.020, which is a weak genetic level and only a level of the previous reports on single tree heritability (Xu et al., 1999). Between the height-diameter ratio and crown-diameter ratio, the family heritability of the former is much higher than the latter, i.e. tree height had a higher heritability. Because the ultimate goal of forest management is timber production, planting density should be considered carefully to pursue the largest volume of the individual and that of the unit area, with the form traits as the main factors. Therefore, family selection requires large volume growth, narrow crown width, bigger height/diameter, smaller crown/diameter, and fine straightness.

3.1.3 Variation of wood traits

Tracheid character and wood basic density, which serve as crucial indices for wood quality of conifers, affect both the output of paper pulp and the quality of paper, giving both factors an important position in the conifer's improvement

(Shi, 1992). Tracheid length (mm) and width (μm) in the half-sib families had extremely significant differences, while the ratio of tracheid length to width was significantly different (Table 3). However, these traits were insignificantly different within families, which indicated that the selection of tracheid traits in half-sib families had certain benefits but lower heritability. Wood basic density between half-sib families has extremely significant differences, with an extensive range of variation from 0.347,5 to 0.424,9 and CV at 8.68%. The average phenotypic variation coefficient within half-sib families was 7.5% from 0.031 to 0.176, while wood density had insignificant difference (F value was 0.82, probability was 0.575,3). Family heritability was 0.640, reflecting a strong genetic level and consistency with previous research on natural forest fine trees of *P. massoniana* (Qiu, 1991) and close to results of *P. taeda* (Loo et al., 1984). All of these showed that the heritability of wood basic density was higher and had greater potential for improvement; selection between families would be effective.

3.2 Analysis of correlated traits

3.2.1 Correlation analysis

As an important trait index for conventional breeding, correlation among growth, stem form and wood quality could provide the basis for indirect selection. Correlation among the height, DBH, crown width, and volume are extremely different in the eight-year-old half-sib family (Table 4). The genetic correlation among straightness, wood basic density, tracheid length and width were significantly different, which indicated that the selection by tree form (straightness) could

Table 2 Analysis of variation for form traits of half-sib progenies of *P. massoniana* at age of eight years

Traits	Mean	Variation range	F value	CV /%	GCV /%	h_f^2
Crown width /m	3.24	3.47–2.93	1.65**	16.74	9.82	0.218
Straightness	1.37	1.71–1.10	1.55**	11.20	2.10	0.020
Height-diameter ratio	81.13	102.06–71.82	2.20**	23.21	7.79	0.461
Crown-diameter ratio	33.06	44.01–29.81	3.49**	26.23	7.44	0.177

Table 3 Analysis of variation for wood traits of half-sib progenies of *P. massoniana* at age of eight years

Character	Average	Variation range	F value	CV /%	GCV /%	h_f^2
Length of tracheid	2.41	1.06–3.12	2.05**	1.27	0.20	0.143
Width of tracheid	43.67	33.85–52.89	2.75**	39.8	10.10	0.227
Length width ratio of tracheid	0.056	0.041–0.073	1.65*	0.06	5.3×10^{-5}	0.104
Wood basic density	0.376,7	0.347,5–0.424,9	2.23**	8.68	4.2×10^{-4}	0.640

Table 4 Correlation coefficient of main traits of *P. massoniana* for pulp and paper use at age of eight years

Traits		Height	DBH	Crown width	Volume	Stem form	Wood basic density	Tracheid length
DBH	P	0.999,0						
	G	0.999,5						
	E	0.945,7						
Crown width	P	0.996,0	0.992,9					
	G	0.996,5	0.993,5					
	E	0.948,0	0.933,4					
Volume	P	0.997,4	0.994,0	0.997,1				
	G	0.998,1	0.996,0	0.998,1				
	E	0.915,5	0.783,6	0.881,5				
Stem form	P	0.990,1	0.984,7	0.997,5	0.996,2			
	G	0.991,3	0.986,8	0.998,2	0.996,6			
	E	0.839,4	0.738,9	0.898,6	0.954,5			
Wood basic density	P	0.036,8	0.996,4	0.994,3	0.998,6	0.991,2		
	G	0.999,0	0.997,4	0.995,3	0.538,1	0.993,0		
	E	0.926,8	0.889,1	0.890,7	0.864,1	0.800,4		
Tracheid length	P	0.789,8	0.791,9	0.752,5	0.796,8	0.757,6	0.105,1	
	G	0.793,7	0.795,8	0.755,4	0.800,9	0.760,8	0.147,6	
	E	-0.006,1	0.040,5	0.019,1	0.012,8	0.036,8	0.027,4	
Tracheid width	P	0.789,1	0.793,2	0.749,4	0.793,2	0.751,6	0.148,6	0.864,3
	G	0.792,6	0.798,8	0.751,7	0.797,0	0.754,3	0.236,6	0.913,0
	E	0.139,0	0.177,0	0.231,4	0.136,0	0.225,6	-0.023,3	0.749,2

Notes: P means phynotype correlation, G means genetic correlation, and E means environment correlation.

improve the wood quality, i.e. selecting trees with good straightness could indirectly improve the wood quality. Phenotypic correlation between height and wood basic density was insignificant, while the genetic correlation among height, DBH, crown width, volume and wood basic density, tracheid length and width was extremely significant. Correlation between wood basic density and tracheid length and width was not significant.

3.2.2 Canonical variable analysis

In extending analysis of the correlation among growth, tree form and wood properties, five traits (height, DBH, crown width, volume and straightness) were classified as one variable named Group 1, while the three wood traits (wood basic density, tracheid length, tracheid width) were as Group 2 for canonical variable analysis (Table 5). It was obvious that the

first canonical correlation coefficient was 0.926,136, reaching a significant level, and the contribution was 96.94%. The analysis of the contribution of growth and form traits to variation of wood traits (Table 6) and of wood traits to variation of growth and form traits (Table 7) showed that the contribution of the first canonical variable of growth and form traits to wood traits was 57.84%, while that of wood traits to growth and form traits was only 28.43%. The analysis of multiple determinative coefficient (Table 8) indicated that only wood basic density of the first canonical variable of wood traits had a preferable forecast for growth and form traits (the coefficient was 0.840,3), while all could be forecast except the volume in the first canonical variable of growth and tree form. Adding the close correlation between the growth traits and wood traits index analyzed above, the genetic correlation between wood basic density and height, DBH, crown width and volume was significant. Considering the importance of

Table 5 Canonical variable analysis on traits of *P. massoniana* at age of eight years

Canonical variable	Canonical correlation coefficient	Corrected canonical correlation coefficient	Standard error	Vector	Contribution	Cumulative
1	0.926,136**	0.926,096	0.001,42	6.028,8	0.969,4	0.969,4
2	0.392,843**	0.392,426	0.008,46	0.182,5	0.029,3	0.998,8
3	0.087,748**	0.086,673	0.009,92	0.007,8	0.001,3	1.000,0

Table 6 Contribution of growth and form traits to variation of wood traits of *P. massoniana* at age of eight years

Canonical variable	Independent canonical variable		Corresponding canonical variable		
	Contribution	Cumulative	R ²	Contribution	Cumulative
1	0.674,4	0.674,4	0.857,7	0.578,4	0.578,4
2	0.039,7	0.714,2	0.154,3	0.006,1	0.584,6
3	0.127,1	0.841,3	0.007,7	0.001,0	0.585,6

Table 7 Contribution of wood traits to variation of growth and shape traits of *P. massoniana* at age of eight years

Canonical variable	Independent canonical variable		Corresponding canonical variable		
	Contribution	Cumulative	R ²	Contribution	Cumulative
1	0.331,5	0.331,5	0.857,7	0.284,3	0.284,3
2	0.630,1	0.961,6	0.154,3	0.097,3	0.381,6
3	0.038,4	1.000,0	0.007,7	0.000,3	0.381,9

Table 8 Analysis on multiple determinative coefficient

Growth rate and stem form	First canonical variable of wood traits	Wood properties	First canonical variable of growth rate and stem form
Height	0.834,5	Wood basic density	0.840,3
DBH	0.747,2	Length of tracheid	0.005,8
Crown width	0.801,4	Width of tracheid	0.007,0
Volume	0.024,4		
Straightness	0.484,7		

wood basic density in the pulp paper industry, we should focus on the improvement of growth and wood basic density to enhance pulp wood from Masson pine. The analysis also showed that height was particularly important, making that factor also critical to pulpwood improvement.

3.3 Evaluation of growth index and selection of preferable families

Comparison in stem volume and height of families with CK (Table 9) showed that for a five-year-old tree and taking height as an evaluation index, there were 55.5% families higher than CK, while only 1.7% families are 10% higher than CK. Taking volume as an evaluation index, there were 64.7% families higher than CK, about 26.1% families 10% higher than CK, 6.7% families were 20% higher than CK, and only 0.8% families were 30% higher than CK. For the eight-year-old group and again using the height-based index, 37.8% families were higher than CK and no family 10% higher than CK. Using volume for the index, 55.5% families were higher than CK, 22.7% families were 10% higher than CK, 4.2% families were 20% higher and only 0.8% families were 30% higher than CK. Results clearly had some differences using the traits of volume and height growth for selection, which would change as the age of the stand rises. Therefore, we should consider both of them during selection.

Based on short rotation, genetic gains in height under different selection ratios are listed in Table 10. It could be seen that a gain under the same selection ratio of five-year-old

families was similar to eight-year-old families. There were six families different under the selection ratio of 30%, one family was different under 20% and all families the same under the selection ratio of 10%. A primary conclusion could be made that selection of the short rotation of Masson pine for pulp and paper use would be efficient for trees that are five years old. To verify the accuracy of this conclusion, further analysis about correlation between five- and eight-year-old provenances was made in height, DBH, and stem volume. The genetic correlation coefficient of the three traits was 0.923,4, 0.637,2 and 0.793,5, respectively, and the correlation was significant. Taking clonal flowering and fruit setting in the seed orchard (Chen, 2000) into account, 12 families were considered under a 10% selection ratio. Comparing with the selection result of height and volume, it was found that height and volume of seven families (No. 659, 8006, 1, 662, 168, 265, 225) ranked in the first 12 families. The height of No.15, 509, 14, 658 and 11 ranked in the first 12 families, but volume was not better than family No. 246, 12, 2, 341 and 773 the height growth of which ranked in the first 25 families. Integrating all results, there were 12 families (No. 659, 8006, 1, 662, 168, 265, 335, 246, 12, 2, 341 and 773) excellent in height and volume growth, and their wood traits (including density, tracheid length and width) ranked in the first 43 families, making them preferable families for pulpwood short rotation.

4 Conclusions and discussion

Traits of growth, tree form and wood quality among families of half-sib progenies from a clonal seed orchard of Masson pine were significantly different, which indicated that further selection should be made for fast-growing and high-yield plantations in these families. Quite a number of families' growth was not as good as CK from the 119 families covered by the experiment (Table 9). Thus, the selection of an excellent genotype requires, genetic testing. This conclusion is consistent with results of the fine-tree progeny test of *P.*

Table 9 Comparison in means of stem volume and height of families with CK

Age /year	Trait	Mean of families	Mean of CK	Number of families higher than CK	Number of families 10% higher than CK	Number of families 20% higher than CK	Number of families 30% higher than CK
5	Height /m	4.15	4.12	66	2	0	0
5	Volume /m ³	0.007,112	0.006,858	77	31	8	1
8	Height /m	7.87	7.93	45	0	0	0
8	Volume /m ³	0.035,14	0.034,586	66	27	5	1

Table 10 Genetic gain of stem volume and height under different selection ratios

Selection ratio	Height genetic gain		Volume genetic gain	
	Eight years	Five years	Eight years	Five years
0.1	6.10%	6.61%	19.23%	19.74%
0.2	4.61%	5.19%	14.95%	15.05%
0.3	3.68%	4.35%	12.33%	12.07%

massoniana (The National Subject Cooperation Group of *P. massoniana* Seed Orchard, 1990; Zhou et al., 1994; Zheng et al., 1998; Long et al., 2002). It could also be seen from Table 9 that as the age of the progenies increased, the number of families involved in the tests higher than the CK was descending. This might be related with the excellent provenance of CK in west Fujian Province (Xu et al., 1999). However, because the seed orchard materials were selected from the whole Fujian Province, the interaction between genotype and environment may be one of the reasons.

Considering that seeds from the orchard would be sold to the whole province, it was necessary to conduct more provenance tests to reveal the interaction between genotype and the environment, consequently to make a more comprehensive evaluation of genetic quality of the clones in the orchard, eventually achieve suitable land species, and establish the efficient genetic potential of female trees. Moreover, considering that seed orchards in our country started late, accelerating the process of having an advanced generation orchard would have involved their adoption of the principles of using while testing. Given this background, the seed orchard was instrumental in production and breeding. Thus, further studies should be taken on mating system, gene flow, and genetic diversity in the orchard, which would provide guidance for constructing an advanced generation seed orchard. Using the genetic parameters from the progeny test in seed orchards could not only help solve the academic problems of the orchard, but also evaluate the genetic background of the female trees efficiently. Therefore, trees of high general combining ability should be selected for further manual mating design to make a full-sib test and for advanced generation breeding. In sum, a progeny test for the clonal seed orchard was extremely important, and the current and long-term significance would be self-evident.

Evaluation of the respective estimates for family and single tree heritability of the height, DBH and volume of the eight-year-old half-sib progenies, straightness, and the ratio of height to diameter and crown to diameter of the family heritability showed that the height of single tree heritability was highest (0.338). Family heritability was arranged in a descending order: height (0.691) > height-diameter ratio (0.461) > DBH (0.264) > volume (0.236) > crown width (0.218) > crown-diameter ratio (0.177) > straightness (0.020), which meant that height had strong heritability while DBH and volume had weak heritability. This conclusion is slightly different from the result of a 13-year-old progeny test of fine-trees of *P. massoniana* (Zhou et al., 2000) which showed that height and DBH had medium or strong heritability.

Correlation among growth, stem form and wood traits of the eight-year-old half-sib families of Masson pine was significant, and also that of straightness and height. This indicated that straightness would be improved indirectly as traits of height, DBH, and volume improve. The correlation between wood basic density and tracheid traits was not significant, while that of tracheid length and width was very significant. The genetic correlation of volume and wood quality was positively significant and consistent with research on poplar (Guan et al., 2005); correlation of wood basic density and volume was extremely positive significant, which was different from research on a seedling seed orchard of *P. massoniana* (Fan et al., 2004) and progenies of *P. massoniana* provenance (Xu et al., 1997).

The correlation of growth and form traits to wood traits was significant, which meant that the improvement of growth trait benefited wood quality. Taking account of the large variation of the wood and growth traits enables a direct selection of families or individuals with high wood basic density, good tracheid width and length, and rapid growth, slightly different from previous provenance studies of *P. massoniana* (Wang, 1998). Zobel and van Buijtenen (1989) pointed out the correlation between the growth rate and wood basic density, with fiber length changed by the species, age and geography. Changes were either significant or not—an indication that the correlation analysis of growth traits and the wood quality index is related to the test material. Thus, attention should be given to indirect selection up to this point.

Canonical variable analysis indicated that only the wood basic density of the first canonical variable of wood traits had preferable forecasts for growth and form traits, with coefficient at 0.840,3, and all forecasts possible except for volume in the first canonical variable of growth and tree form. It could be seen further that correlation between growth traits and wood basic density was significant, reflecting a benefit for pulpwood breeding. It is well-known that the aim of pulpwood breeding is to pursue a high pulp ratio; growth and wood density can directly affect the total pulp ratio of a unit forest area. If the correlation of growth traits and wood basic density was significant, then in the pulpwood selection process we could just directly consider growth traits while the wood density index can be indirectly obtained.

According to analysis of heritability and correlation of traits, and taking into account the intuition of investigation and analysis, the fine family selection of Masson pine for pulpwood would focus on high-growth trees.

Under the selection ratio of 10 percent, the selected families from the progeny test stands at five and eight years were the same, with significant genetic correlation of height, DBH and stem volume. These all showed that selection of the short rotation of Masson pine for pulp and paper use would be efficient for trees that are five years old, which is consistent with previous selection of short rotation of excellent provenance (Wang et al., 1999). Seeing overall growth of the progeny test site, we found that some families have been middlebrow or inferior and needed to be eliminated early. If

the family test aims to guide seed orchard thinning and tries to eliminate middlebrow, we should consider the flowering and fruit setting of the clonal seed orchard, as the ultimate goal is to produce seeds through genetic improvement. Thus, in the seed orchard thinning process, both quantity of male and female flowers and genetic quality of female trees should be considered to promote a seed orchard with high-yield and excellent-genetic quality.

Finally, we selected 12 families which were in the former ranked 43 as pulpwood fine families based on principles of short rotation of pulpwood. Tree height and volume growth defined the selection indexes, under the selection ratio of 10%, and with flowering and fruit settings of the clonal seed orchard considered.

Acknowledgements This study was financially supported by the National "Tenth Five-Year Plan" (Grant No. 2004BA515B0102). The authors wish to thank postgraduates Wang Jian, Gong Jia and Mao Tao for their assistance work on translation.

References

- Chen J D (2000). Analysis on effect of thinning for tending to clonal seed orchard of *Pinus massoniana*. *China For Sci Tech*, 14(4): 19–20 (in Chinese)
- Fan L Y, Lai H L, Ji K S, Wang Z R, Wang R R (2004). Breeding value estimation and family selection for seedling seed orchard of masson pine. *J Northeast For Univ*, 32(4): 3–11 (in Chinese)
- Guan L H, Pan H X, Huang M R (2005). Research on growth and wood properties joint genetic improvement of new clones of *Populus deltoids* (I 69) × *P. euramericana* (I 45). *J Nanjing For Univ*, 29(2): 6–10 (in Chinese)
- Hui D F, Jiang C J (1996). *The Practical Tutorial for Software of Statistical Analysis System-SAS*. Beijing: Beijing University of Aeronautics and Astronautics Publishing House (in Chinese)
- Ji K S (2001). *Cultivation Techniques for Artificial Forest of Pinus massoniana*. Beijing: China Agriculture Publishing House, 14 (in Chinese)
- Li H G, Wang Z R, Chen T H (1993). Wood trait variation between *Pinus massoniana* individuals from different provenance stand. In: Tu Zhongyu, Shen Xihuan, eds. *Progress in Genetics Improvement of Forest Tree in China*. Beijing: Sci and Tech Documents Publishing House, 27–32 (in Chinese)
- Long G S, Li W P, Ge Y H, Tang X R (2002). Selective breeding of fine half-sib families of masson pine. *J Central South For Univ*, 22(1): 17–22 (in Chinese)
- Loo J A, Tauer C G, van Buijtenen J P (1984). Juvenile-mature relationships and heritability estimates of several traits in loblolly pine (*Pinus taeda*). *Can J For Res*, 14: 822–825
- Qiu G L (1991). Hereditary variation of wood density of freely pollinated progenies of fine trees in natural Masson pine forest. In: *Proceedings of forest trees improvement (Chinese fir, Masson pine, and so on)*. Beijing: Genetics and Breeding Association, China Forestry Society, 222–227
- The National Subject Cooperation Group of *P. massoniana* Seed Orchard (1990). *Symposium on techniques for establishing seed orchards of masson pine*. Beijing: Academic Book and Periodicals Press, 155–203, 275–313 (in Chinese)
- Wang Z R (1998). Masson pine genetic improvement for pulpwood. *China For Sci Tech*, 12(2): 6–8 (in Chinese)
- Wang Z R, Chen T H, Zhou Z C (1999). Experiment on natural population variation of pulping properties and pulp abilities of *Pinus massoniana* Lamb. *Chem Ind For Prod*, 19(1): 64–68 (in Chinese)
- Xu L A, Chen T H, Wang Z R (1997). Variation of provenance progenies in wood property and provenance selection for pulpwood of masson pine. *J Nanjing For Univ*, 21(2): 1–6 (in Chinese)
- Xu L A, Wang Z R, Cao H Y (1999). A study on variations of plus tree open-pollinated progenies of masson pine in Fujian province. *J Fujian Coll For*, 19(2): 114–117 (in Chinese)
- Zheng R H, Cai T G, Chen G J (1998). Studies on the plus tree progeny test and the fast-growing fine family selection of *Pinus massoniana*. *Fujian Coll For*, 25(3): 11–16 (in Chinese)
- Zhou Z C, Jing G Q, Zhou S S (1994). Genetic analysis and combined selection for growth and wood quality of open-pollinated families of masson pine. *For Res*, 36(2): 110–115 (in Chinese)
- Zhou Z C, Li G R, Huang G L, Chen B X, Lin Y K (2000). Genetic control of wood chemical compositions and its implication for wood breeding of masson pine. *Sci Silv Sin*, 7(3): 253–257 (in Chinese)
- Zobel B J, van Buijtenen J P (1989). *Wood Variation: Its Causes and Control*. Berlin: Springer-Verlag, 249–290