

International Master Program of Agriculture

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National Chung Hsing University

國立中興大學

Master thesis

香杉開放式授粉家系的幼年期與成熟期性狀的相

關性  
Juvenile-Mature Correlation for Early Selection of  
Open-Pollinated Families of China Fir

(*Cunninghamia lanceolata* (Lamb.) var. *konishii*)

Advisor: Dr. Israel Bau-Jen Jiang (姜保真 博士)

Student: Yu-Chun Yen (顏仔君)

Date: 15 July, 2012

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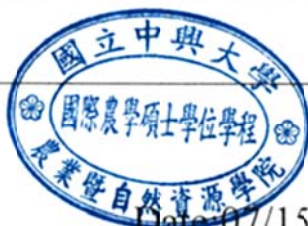
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## 摘要

本研究分析了兩個香杉的後裔檢定族群在不同年齡的性狀相關性。這兩個族群來自同一個開放式授粉的香杉無性系種子園，種子園建立於 1972 年，位於台灣中部山區，園內一共有 25 個家系。年齡較大 (25 年生) 的後裔檢定族群簡稱為 A，A 族群生長在野外，共量測到 232 棵樹，由種子園中當年所採集到的 18 個開花結實家系組成。另一族群簡稱為 B，生長於溫室環境，總共約有 15,000 棵小苗，由採自種子園中完整的 25 個家系組成，本研究使用其中 1,500 棵為樣本。由 A 族群所量測到的性狀包含有 2 年、6 年及 25 年生的樹高、胸高直徑、地際直徑、材積及年平均生長高度，另外於 27 年量測了木材密度。B 族群則是量測了 5 個月、7 個月、9 個月及 13 個月的根徑、根長、地下部及地上部各自的鮮重與乾重，根梢部的重量比、苗木的健壯指數及狄克森品質指數。調查結果顯示兩個族群在家系間都有顯著的遺傳變異，多數性狀的個體遺傳率都相當高(分別是  $h^2=0.35\sim 0.62$  及  $0.25\sim 1$ )。本篇研究主要發現 A 族群自身的 25 年性狀間相關性非常高( $r=0.61\sim 0.97$ ,  $P<.0001$ )，表示最初種子園的優樹選拔有效，子代同時具有高生長及橫向質量生長優勢；而 A 族群在不同年齡間的性狀相關性則顯示當兩年齡時間間隔較短時相關性會比較高(2 年及 6 年間:  $r=0.5$ ,  $P<.0001$ ; 6 年及 25 年間:  $r=0.4$ ,  $P<.0001$ )。而 B 族群在 5、7、9 月齡時的多數性狀都與 A 族群的 25 年樹高及材積有一定的相關性存在( $|r|=0.4\sim 0.7$ )。這樣的結果提示了香杉族群的一年以下幼年性狀有極大的潛力作為早期選拔的指標。

**關鍵字:** 香杉，種子園，後裔試驗，早期選拔，年齡間相關性

## ABSTRACT

Two groups of progeny trials China-fir populations are used for study age-age phenotypic correlation in this thesis. Both of them are single tree family from a same clonal seed orchard which composed of 25 clones established in 1972 in the central mountain area of Taiwan. The elder progeny test population, A, is composed of 232 trees from 18 maternal families which grown in wild field; the juvenile population, B, is composed of 15,000 seedlings from all the 25 families, grown in nursery garden, this study use only 1,500 seedlings for analysis. The A population are measured in 2, 6, and 25 years for height, diameter breast height and volume as well as annual height growth between age intervals, 27 years wood density is also involved; for B population, the acquired traits are root diameter, root length, fresh and dry biomass, height and ratio of shoot-root biomass as well as sturdiness quotient and Dickson quality index from 5, 7, 9, 13 months seedlings. Results show that both population in field and greenhouse have very high individual heritability for most of the traits ( $h^2=0.35\sim 0.62$  and  $0.25\sim 1$  respectively), and among all the family appear significant variance. Core finding on the correlation demonstrate that self-correlation within population A has strong trait-trait correlation ( $r=0.61\sim 0.97$ ,  $P<.0001$ ) in 25 years, and age-age correlation within A exist higher relationship between shorter age intervals (2 & 6 years:  $r=0.5$ ,  $P<.0001$ ; 6 & 25 years:  $r=0.4$ ,  $P<.0001$ ). The age-age correlations between two populations reveal that most of the traits in seedling age 5, 7, 9 months have correlations with height and volume in 25 years group ( $|r|=0.4\sim 0.7$ ), which indicate that China-fir juvenile traits can serve as indicators for the early selection in a very early growing period.

**Key words:** China-fir, seed orchard, progeny test, early selection, age-age correlation

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# CHAPTER 1 INTRODUCTION

## 1.1 General Introduction

In the tree breeding industry, foresters had long been faced the challenge by dealing with tree's long rotation period, which can causes 10 to 100 years, and its breeding cycle is usually as long as 8 to 20 years (Lantz, 2008). Therefore, the study on early prediction and optimal selection age on forest tree has become an integral part of silviculture. An efficient early selection project can help us to shorten the period on deciding which tree family or individual entity has better genetic component and we can easily choose before rotation age. To figure out whether our research trees contain the genetic combination that we favored, progeny testing is wildly applied in tree improvement program. By measuring the performance from trees' clonal or seedling progeny, one can better predict the genetic component of the trees and keep the good parents for future breeding, usually can serve as seed providers and thus results in the idea and methods for the develop of seed orchard. The research intention of this paper is also belongs part of the seed orchard strategy.

The main concept of juvenile-mature correlation is use the growth traits of younger age, usually under 3 years, which have higher correlation response with the senior growth traits that we are interested in. Numerous juvenile-mature correlation researches on conifer tree had been conducted, according to Cook (1991), conifers is one of the highest genetic variety species of the world, it reveals that selection from conifers tree can much easily acquire the traits we need.

The purpose of this study is to evaluate the age-age correlation between two groups of China-fir single parent families; and trying to find out if there have any positive

age-age correlations between these two China-fir populations. Furthermore, to decide which traits at which ages can be used as indicators for early selection of the mature phenotype that has economic value.

Many previous studies on age-age correlation were focused on “partial-whole correlation”, which implies the genetic correlation of the same individual tree’s younger age with its older age; however, in the study of this thesis, we will discuss the correlation between two groups of China-fir single parent families. These two groups of China-fir populations came from a same seed orchard, and from the same open-pollinated families, our study is going to use their family means to discuss the correlations between traits and ages.

## **1.2 Introduction of Genetic Material-- China-fir**

Tree species used in this study is China-fir, which also known as Formosan China-fir, konishii-fir or Luanta-fir, scientific name is *Cunninghamia lanceolata* (Lamb.) var. *konishii*, belongs to Taxodiaceae genus. China-fir is a subspecies of *Cunninghamia lanceolata* variety in Taiwan. This species is naturally distributed in north and central mountain area of Taiwan, and its favored altitude is between 1,300 and 2,800 meters height, usually growth with other conifer and broad leaf trees. Most of them located among Basianshan, Luatashan, and Taipingshan districts. The rotation age of China-fir is as long as 40 years. China-fir is a valuable wood sources often used as material on construction, furniture and coffin. According to the surveyed in 2002, the China-fir wood production ranked number five in Taiwan (台灣省林務局, 2002). Records also showed that large scale forestation of China-fir conducted during 1993 to 1998.

### **1.3 Seed Orchard**

Seed orchard is a breeding technique long been used in a lot of kinds of tree species. Combining with working of collection and phenotypic selection from nature population, progeny testing and finally keep the tree family what meet our breeding needs. Its aim is to provide a suitable seed resources for forestation, and maintain forestry biodiversity in chosen places. Before the era without seed orchard, foresters collect seed direct from natural forest tree, this work has disadvantages like risk of working in tough wild places, high costs, to harm maternal trees, production is unstable from year to year, and the seed material collected are unimproved etc. The establishment of seed orchard has two kinds, one is seedling seed orchard; another one is clonal seed orchard. In this experiment, the two populations we surveyed are progeny test trials of a clonal seed orchard established by grafting ramet in 1972, located in Chuyunshan, composed by 25 clones, 2475 trees (徐, 1983). Most of the planted graft had seed produce in 3 years after planting; in 1993, the production of seed in this orchard had exceeded to more than 30 liters.

This seed orchard is open-pollinated, we can only know the mother tree of seeds and therefore it is called “half-sib families”.

### **1.4 Progeny Test & Early Selection**

Those trees planted in seed orchards are mostly came from direct selection of phenotypic performance of natural forest, since the tree is a giant creature and located in wild environment, it is hard to surveyed and estimate the variety among them. In order to improve the genetic component of the seed orchard, we use mother trees' open-pollinated progenies to conduct evaluation, which known as progeny testing.

Those progenies from same maternal family have good average performance can be thought possessed better general combination ability (GCA), which implies their open-pollinated family's additive traits, such as height, volume, wood density are more close to the select direction we want.

However, the reproductive maturity year for tree average cost 5 to 20 years, the cost time for measuring of rotation traits is even longer. In consequence, early selection can help as a solution to diminish the time to pick up which seems suitable in terms of having considerable correlation with rotation age.

In Dean *et al.* (2005) study, they indicate the optimal selection age for Douglas-fir's height is 7 to 8 years, individual heritability around 0.18 to 0.22, and for diameter is from 0.07 to 0.10. Bouvet *et al.* (2007), research on *Eucalyptus* suggest that at 54 months selection for volume is better than other period, narrow sense heritability is as high as 0.70 for male and 0.90 for female.

### **1.5 Age-Age Correlation and Family Mean Correlation**

When predict on the future performance of the target traits, markers with high juvenile-mature correlation are commonly used and numerous studies already spot light on this topic for different tree species. In an idea experiment trial, usually we will analysis different age traits of a same individual group, which can diminish the factors from one individual to another and minimize the environmental effect from different sites as well. Numerous study has practice on this method, like (Hansen, Wellendo, & Kjare, 2005) study on a costal Douglas-fir at age 9 and 10 years; (Hogberg, Persson, Hallingback, & Jansson, 2010) study on 36 years old rotation wood of Scot pine with its juvenile traits; (Gwaze, Woolliams, & Kanowski, 1997) study on age-age genetic correlation for height of a *Pinus taeda* L. population at 1.5, 9.5, 13.5 and 22.5 years.

Nevertheless, in this study, age-age correlations of two populations in different location are used to analysis the relevance. We aim to exam if two populations from same maternal family in separate area can also have certain correlation between them. There are also studies on this type of cross site age-age correlation. Three series of jack pine were examined for their traits of height and volume from age 4 to age 20 (Weng, Tosh, Park, & Fullarton, 2007), the results showed that height and volume at different age show that the heritability has increase trend to age 20, however cross site correlation test is lower than single site test; (Kumar, Dungey, & Matheson, 2005) study on stiffness in radiate pine from a open-pollinated and a control-pollinated family, it suggested that selection at age 6-7 years is a good choice; (Rweyongeza, Yeh, & Dhir, 2005) examined on correlation of biomass from two white progeny trials, he indicated that different characteristics between juvenile and mature population have poor correlations.

### **1.6 Estimate of Genetic Parameter**

In a tree improving program, we will like to tell the real genetic components of an organism from its phenotypic and to ascertain our selection can be efficiently pass to the advanced generation. The parameter of heritability is an important signal that can show us the genetic component within the performance of organism. Furthermore, the genetic component can be divided into additive genetic variance and non-additive genetic variance, in which additive variance decide the performance of additive phenotype and can effectively fixed by programmatic selection.

The model used to calculate heritability in our study is from aspect of half-sib family, since male parent is unknown in open-pollinated environment and we can only estimate from maternal family. Besides, this research trying to select plus tree family



among seed orchard, family is counted as fixed effect when estimate family mean; on the other hand family is treated as random effect to acquire heritability of traits.

Most research on progeny test have examined on these parameters, Stonecypher *et al.* (1996) study on Douglas-fir pointed out individual heritability for height in age 6 and age 8 is 0.13; surveyed on green weight of white spruce found individual heritability ranged from 0.2 to 0.3 (Rweyongeza *et al.*, 2005); on Kumar's experiment in radiate pine for stiffness found that corewood ( $h^2=0.5-0.7$ ) has higher heritability than outwood ( $h^2=0.15-0.3$ ) (Kumar *et al.*, 2005); (Hawkins & Stoehr, 2009) study on 32 Douglas-fir family found that heritability for height in one-year-old height is around 0.03-0.09, and for root collar diameter is 0.11-0.28.



## CHAPTER 2 MATERIALS AND METHODS

### 2.1 Genetic Material and Sites

The surveyed parameters of the China-fir used in this study came from two different groups of trial places, both of them were established for progeny test of a China-fir vegetative seed orchard which located in central mountain area of Taiwan—, started in 1967. In the other word, these two groups of China-fir family came from same maternal family, which also called half-sib family. This seed orchard located in Chuyunshan nursery's Dongshih forestry working circle No. 40 and No. 41 components, elevation among 1,000 meters height. This garden belongs to Dongshih Forest District Office of Taiwan Forestry Bureau. The seed orchard is composed by 32 blocks and each block contains 25 China fir clones, totally has 800 trees(徐, 1971). Later in this paper we will use Group A as a symbol of first trial population, which is older and composed of less sample; group B represent another population, which is younger and much more traits are being examined.

Group A, one of this China-fir progeny test in which lied in Basianshan working circle No.12 and No.13 compartments established in 1977. Its elevation is around 1,300 meters height—under the auspices of Dongshih Forest District office of Taiwan Forestry Bureau. Seed material came from open pollinated progeny of the orchard mentioned above. However, only 18 families out of 25 were acquired, 231 trees were available and being surveyed (Su, 2004). The phenotype reviewed in this trial included tree height from 2, 6, and 25 years; diameter of breast height (DBH) from 25 years; basal stem diameter (DBA) from 25 years; wood volume (VOL) from 25 years; wood density (WD) from 27 years; and annual tree height growth (GH) between 2 to 6 years as well as 6 to

25 years.

Another set of parameter, group B is from the progeny trial conducted in 2003. In this year, all the 25 China-fir families in the same seed orchard had produced seed and were collected in this experiment. The seedling of this test grown in greenhouse which located in Chuyunshan nursery elevation is among 1,000 meters height, the same as seed orchard. This design had 14 blocks, each block randomly planted seedlings with 25 families, totally contained about 15,000 trees (14\*25\*42). The measuring was conducted in 5 months, 7 months, 9 months and 13 months after planting. Growth traits surveyed in this experiment included shoot height (HT); root collar diameter (RD); shoot length (RL); shoot biomass—fresh weight and dry weight (AFWT and ADWT); root biomass—fresh weight and dry weight (BFWT and BDWT); shoot -root ratio of fresh weight and dry weight (T1 and T2); sturdiness quotient (SQ), which is ratio of shoot height to rood diameter (HT/ RD); and Dickson quality index (DQI) (Wu, 2005).

Sturdiness quotient can help us to exam the structure of a tree from its root diameter and shoot height, thus geneticist can eliminate seedlings which are too weak to resist from physical damage. The T1, T2 can provide us overall growth information about plant, a good shoot-root biomass ratio usually range from 1:1 to 1:2, this character is especially hard to be practiced since it need to conduct numerous destructive sampling.

Dickson quality index is usually used to estimate early growth of shoot, which combined by parameter of shoot's total dry matter (TDM), shoot height (SH), shoot base diameter (SBD), and sturdiness quotient—stem dry matter (SDM)/ root dry matter (RDM). DQI is believed to be a good indicator for seedling healthiness as it takes into account several physical criterion (Binotto, Lúcio, & Lopes, 2010).

$$DQI = \frac{TDM(g)}{\frac{SH(cm)}{SBD(mm)} + \frac{SDM(g)}{RDM(g)}}$$

(Formula 1)

If we transform this DQI formula into the abbreviation used in this study, it will look like this:

$$DQI = \frac{ADWT(g) + BDWT(g)}{\frac{HT(cm)}{RD(cm)} + \frac{ADWT(g)}{BDWT(g)}}$$

(Formula 1.1)

Some of these growth traits measured in each of group are common in the most study of the progeny trial and age-age correlation, such as height, volume and basal stem diameter; however, some of these traits are seldom studied in the early test study, like shoot-root ratio, sturdiness quotient and Dickson quality index.

In the study of this thesis, we will analysis correlations between all these different traits of two populations and look for those which in junior age have considerable correlations with the older population.

## 2.2 Experimental Design

Our target China-fir seed orchard can trace back to 1960s. Plus trees are selected from nature forest, the criterion are tree height, DBA, age and straightness, flowering and fruiting rate, etc. 25 clones are chosen, each clones has 32 replications, the orchard is composed of 800 (25\*32) trees, land area has 3 hectares. It is arranged by shifting clone design to increase the probability of cross pollination; distance between rows is 6 meters (徐, 1971).

The population A is located in a steep slope land, divided into two blocks according to the slope. Plots within a block are located in the same elevations which apply the row-plot design, edged trees are deleted; each row contains 5 replications of a family. Overall, each family has 15 to 20 open-pollinated progenies used in this analysis and totally contains 232 trees. The distance between rows and trees are 2 meters. Block one has missing family and therefore it is the incomplete block design.

The trial B was planted in a nursery garden which located in the same elevation as seed orchard. The medium soil is the 1 to 1 mixed of peat soil and vermiculite. China-fir seed starts to germinated 3weeks after planting; the age evaluated in this experiment is started from the end of germination which takes about one and half months. Those seedlings are then transplant to tubing plate, in each plate has 42 tubing (tube diameter is 8 cm, tube length is 8 cm). One family planted in one plate, and further separated into 3 plots, 25 families are randomly arranged in a block, totally has 14 blocks; generally has around 15,000 ( $14 \times 25 \times 42$ ) seedlings. Only part of seedlings had been used as destructive evaluation in this study in each season, totally has about 3,300 samples. However, to mach up with the families in population A for the correlation analysis, some of the families were eliminated when calculation. Overall, each family has about 20 open-pollinated progenies in each study seasons and for all the 18 families, they added up to about 1,500 ( $20 \times 18 \times 4$ ) seedlings.

## **2.3 Statistical Analysis**

### **2.3.1 Test of Homogeneity**

Both data from A and B group were examined by Hartley's  $F_{\max}$  -test before analysis of variance (沈, 2010). The purpose is to make sure the data can fit in the

principle of ANOVA. Some of them were transferred by natural log treatment.

$$F_{\max} = \frac{\max(S_i^2)}{\min(S_i^2)} \quad (\text{Formula 2})$$

$\max(S_i^2)$  : Maximum estimated variation value among all treated mean of square

$\min(S_i^2)$  : Minimum estimated variation value among all treated mean of square

### 2.3.2 One way ANOVA:

We applied one way ANOVA to study if different growth traits among families were different or not.

$$Y_{ijk} = \mu + B_i + f_j + Bf_{ij} + \varepsilon_{ijk}$$

(model 1)

$Y_{ijk}$  : The individual tree's phenotypic value

$\mu$  : The mean value of the trait observed

$B_i$  : The effect of the  $i$ th block or plot. Where  $i=1,2$  in trial A;  $i=1\sim 4$  in trial B

$f_j$  : The effect of the half-sib family. Where  $j$  representing the  $j$ th female parent

$Bf_{ij}$  : The effect of the interactions between  $i$ th block and  $j$ th family

$\varepsilon_{ijk}$  The residual error.  $k$ = the replicated number of each family within a block

When we take family as random effect, the REML (restricted maximum likelihood) option is used to estimate the variance component, since data from both group A and group B are unbalanced (Hawkins & Stoehr, 2009; Johnson, Snizeko, & Mandel, 1997). To dealing with the missing value exist in data, Henderson's method III were used to estimate components of variance in a mixed model.

### 2.3.3 Estimate of individual heritability:

It is the estimation of additive genetic variance ( $\sigma_A^2$ ) over the total phenotypic variance ( $\sigma_P^2$ ) among individual trees.

$$h^2 = \frac{\sigma_A^2}{\sigma_P^2} = \frac{4\sigma_F^2}{\sigma_F^2 + \sigma_B^2 + \sigma_{B*F}^2 + \sigma_\varepsilon^2}$$

(Formula 3)

$h^2$ : Heritability

$\sigma_P^2$ : The total phenotype variance

$\sigma_A^2$ : The additive genetic variance

$\sigma_F^2$ : The variance among half-sib (poly-cross and open pollinated) families

$\sigma_B^2$ : The variance of block or plot

$\sigma_{B*F}^2$ : The variance of family by block interactions

$\sigma_\varepsilon^2$ : The variance of error

### 2.3.4 Analysis of Correlations between Traits

To estimate the correlation of traits parameters within and between two trial locations, we apply both Pearson product-moment correlation coefficient and Spearman's rank-order correlation coefficient to analysis the mean value of the traits. For all of the correlation conducted, we used family mean of the 18 families to calculate the phenotypic correlation between A, B groups.

Pearson product-moment correlation coefficient is to make direct correlation from the data we got. See from Formula 3. :

$$r_p = \frac{\sum(X_i - \bar{X})(Y_i - \bar{Y})}{\sqrt{[\sum(X_i - \bar{X})^2 \sum(Y_i - \bar{Y})^2]}}$$

(Formula 4)

$X_i$  : The trait X's observation value of a family

$Y_i$  : The trait Y's observation value of a family

$\bar{X}$  : The total mean of trait X

$\bar{Y}$  : The total mean of trait Y

Spearman's rank-order correlation coefficient can help us to examine the ranking correlation from two groups of family.

$$r_s = \frac{\sum(R_i - \bar{R})(S_i - \bar{S})}{\sqrt{[\sum(R_i - \bar{R})^2 \sum(S_i - \bar{S})^2]}}$$

(Formula 5)

$R_i$  : The trait X's ranking within a family

$S_i$  : The trait Y's ranking within a family

$\bar{R}$  : The trait X's ranking mean within families

$\bar{S}$  : The trait Y's ranking mean within families

### 2.3.5 Regression Model for the Correlated Traits

For those traits which have highly age-age correlation, we will use simple linear regression model to further testing the correlation strength between them. The model applied is:

$$Y = \beta_0 + \beta_1 + \varepsilon$$

(Formula 6)

Y: Family mean of the trait in population A



$\beta_0$  : Y- intercept of the regression line

$\beta_1$  : Slope of the regression line

X: Family mean of the trait in population B

$\varepsilon$  : The residual error



## CHAPTER 3 RESULTS

A number of interesting findings came out from this practice, but since this report focuses on the discussion of age-age correlation of two groups of single parent family. Furthermore, the A, B populations were already respectively studied by former research fellows, some preliminary results like variances of family and heritability had been published. Here we will also show some of them as a support for continuing our working.

### 3.1 Analysis of Variance and Heritability

Table 1 show the result of the variance component and the heritability of population A, which is the elder group grown in the field. Most of the traits have high individual narrow-sense heritability ( $h^2=0.35\sim0.62$ ) Tree height in 25 years and annual height growth from 6 to 25 years have higher heritability compare to height in 2 and 6 years. This result is resembled to other studies that heritability of tree height will increase with age after a certain period (Dean & Stonecypher, 2005; Hodge & White, 1991). Furthermore, in (Riemenschneider, 1988) study in Jack pine also demonstrated that heritability for tree height was highest at 1-year-old and lowest at 2-year-old during the period of 1, 2, 3, 5 and 7 years surveyed, which give us a notice that individual heritability may fluctuate at different growing stage.

**Table 1 Variance component and narrow-sense heritability of population A**

(partially quote from Su, 2004)

VARCOMP	HT2	HT6	HT25	DBH25	DBA25	VOL25	WD27	GH25_6	GH6_2
<b>FAMILY</b>	0	0.06253	2.35126	3.32324	5.72574	0.002843	0	0.005477	0.00289
Percentage	0%	9.91%	15.55%	8.70%	9.74%	10.66%	0%	15.07%	8.87%
<b>BLOCK</b>	0	0.02229	0.70874	3.14223	1.65749	0.001977	0	0.001192	0.001039
Percentage	0%	3.53%	4.69%	8.23%	2.82%	7.53%	0%	3.28%	3.19%
<b>F*B</b>	0.006653	0	1.79787	0	0.60151	0	0	0.004348	0
Percentage	25.56%	0%	11.89%	0%	1.02%	0%	0%	11.97%	0%
<b>ERROR</b>	0.01938	0.5459	10.26674	31.72702	50.7985	0.02145	0.003319	0.02532	0.02864
Percentage	74.44%	86.55%	67.88%	83.07%	86.40%	81.65%	100%	69.68%	87.94%
<b>TOTAL</b>	0.026033	0.63072	15.12461	38.19249	58.78324	0.02627	0.003319	0.036337	0.032569
<b>HERITABILITY</b>	0	0.396563	0.621837	0.348052	0.389617	0.432915	0	0.602921	0.354965

Footnote.: **HT-N**: height in N years; **DBH**: diameter breast height; **VOL**: volume; **WD**: wood density; **GH-N\_n**: annual height growth from n years to N years

For the juvenile population, B, some of the individual heritability has exceeds 1 (see Table 2), it may cause by the over-estimate on additive genetic variance. In this condition, usually we will set the upper limit of heritability at 1 (Buijtenen & Yeiser, 1989).

Since those seeds were the open-pollinated progeny, we can only identify their maternal trees, under this half-sib hypothesis that heritability was enhanced.

Furthermore, in this nursery experiment the environment is much homogenized, however, family and environment interaction may still exist and lead to the bias of the estimation. In spite of that, its family variance component trend and heritability can still provide as the overall information of the population.

(Matziris, 2005) study in black pine seedling and(Hawkins & Stoehr, 2009) study in Douglas-fir also point out that greater site homogeneity will cause the increase of additive genetic variance and heritability.

**Table 2 Variance component of population B (partially quote from Wu, 2005)**

<b>RD</b>	<b>5 months</b>		<b>7 months</b>		<b>9 months</b>		<b>13months</b>	
	Variance	%	Variance	%	Variance	%	Variance	%
FAMILY	0.0165	45.73%	0.0084	30.53%	0.0192	37.35%	0.0030	23.79%
PLOT	0.0013	3.53%	0	0%	0	0%	0.0005	4324%
ERROR	0.0184	50.74%	0.0190	69.47%	0.03227	62.65%	0.0090	71.96%
TOTAL	0.0362		0.0274		0.05151		0.0124	
HERITABILITY	1		1		1		0.9517	
<b>RL</b>	Variance	%	Variance	%	Variance	%	Variance	%
FAMILY	0.07808	33.14%	0.0085	20.31%	0.0816	11.36%	5.2494	7.49%
PLOT	0.0012	0.49%	0.0002	0.05%	0.0162	2%	0.1252	0.18%
ERROR	0.1562	66.34%	0.3313	79.64%	0.6205	86.39%	64.6853	92.33%
TOTAL	0.2354		0.4160		0.7184		70.0599	
HERITABILITY	1		0.8125		0.4542		0.2997	
<b>AFWT</b>	Variance	%	Variance	%	Variance	%	Variance	%
FAMILY	0.01801	44.66%	0.0249	31.41%	0.0363	36.81%	0.048	18.41%
PLOT	0.0014	3.37%	0	0%	0	0%	0.0055	2.12%
ERROR	0.0210	51.97%	0.0543	68.59%	0.0623	63.19%	0.2072	79.47%
TOTAL	0.0403		0.0792		0.0986		0.2608	
HERITABILITY	1		1		1		0.7362	
<b>BFWT</b>	Variance	%	Variance	%	Variance	%	Variance	%
FAMILY	0.01373	46.99%	0.0206	33.93%	0.0332	27.50%	0.4641	18.36%
PLOT	0.0010	3.45%	0	0%	0	0%	0.0223	0.88%
ERROR	0.0145	49.56%	0.0401	66.07%	0.0877	72.50%	2.0412	80.76%
TOTAL	0.0292		0.0607		0.1209		2.5275	
HERITABILITY	1		1		1		0.7344	
<b>ADWT</b>	Variance	%	Variance	%	Variance	%	Variance	%
FAMILY	0.0037	43.41%	0.0080	35.81%	0.0114	35.30%	0.0091	18.19%
PLOT	0.0003	3.20%	0	0%	0	0%	0.0018	3.58%
ERROR	0.0045	53.39%	0.0144	64.19%	0.0208	64.70%	0.0392	78.24%
TOTAL	0.0084		0.0224		0.0322		0.0501	
HERITABILITY	1		1		1		0.7274	
<b>BDWT</b>	Variance	%	Variance	%	Variance	%	Variance	%
FAMILY	0.0014	45.37%	0.0041	43.65%	0.0062	28.48%	0.0076	16.86%
PLOT	0.0001	3.22%	0	0%	0	0%	0.0006	1.31%
ERROR	0.0016	51.41%	0.0053	56.35%	0.0157	71.52%	0.0370	1.83%

	5 months		7 months		9 months		13months	
TOTAL	0.0031		0.0095		0.0219		0.0452	
HERITABILITY	1		1		1		0.6745	
<b>HT</b>	Variance	%	Variance	%	Variance	%	Variance	%
FAMILY	2.1595	39.27%	1.5432	19.36%	2.5681	29.30%	1.9786	20.17%
PLOT	0.1270	2.31%	0	0%	0.0498	0.57%	0.3542	3.61%
ERROR	3.2123	58.42%	6.4300	80.64%	6.1467	70.13%	7.4768	76.22%
TOTAL	5.4987		7.9730		8.7645		9.8096	
HERITABILITY	1		0.7742		1		0.8068	
<b>T1</b>	Variance	%	Variance	%	Variance	%	Variance	%
FAMILY	0.0052	20.56%	0.0062	32.84%	0.0036	16.28%	0.0013	6.37%
PLOT	0.0008	2.95%	0.0001	0.62%	0	0%	0	0%
ERROR	0.0195	76.49	0.0127	66.54%	0.0185	83.71%	0.0197	93.63%
TOTAL	0.0255		0.0190		0.0220		0.0210	
HERITABILITY	0.8224		1		0.6513		0.2547	
<b>T2</b>	Variance	%	Variance	%	Variance	%	Variance	%
FAMILY	0.0024	7.15%	0.0030	13.09%	0.0042	15.43%	0.0063	12.53%
PLOT	0	0%	0.00008	0.36%	0	0%	0	0%
ERROR	0.0314	92.85%	0.0198	86.55%	0.0228	84.57%	0.0439	87.47%
TOTAL	0.0338		0.0229		0.0269		0.0501	
HERITABILITY	0.2858		0.5235		0.6172		0.5013	
<b>SQ</b>	Variance	%	Variance	%	Variance	%	Variance	%
FAMILY	0.0029	17.15%	0.0013	14.77%	0.0005	31.44%	0.1243	12.22%
PLOT	0.00003	0.18%	0	0%	0.00002	1.14%	0.0134	1.32%
ERROR	0.0142	82.67%	0.0076	85.23%	0.0011	67.42%	0.8793	86.45%
TOTAL	0.0171		0.0089		0.0016		1.0171	
HERITABILITY	0.6861		0.5908		1		0.4889	
<b>DQI</b>	Variance	%	Variance	%	Variance	%	Variance	%
FAMILY	0.0006	47.55%	0.0015	42.50%	0.0027	32.62%	0.0021	20.23%
PLOT	0.00005	4.07%	0	0%	0	0%	0.0002	2.28%
ERROR	0.0006	48.37%	0.0020	57.50%	0.0055	67.38%	0.0079	77.49%
TOTAL	0.0012		0.0034		0.0082		0.0101	
HERITABILITY	1		1		1		0.8092	

Footnote:: **RD**: root diameter; **RL**: root length; **AFWT**: fresh shoot biomass; **DFWT**: fresh root biomass; **ADWT**: dry shoot biomass; **BDWT**: dry root biomass; **HT**: shoot height; **T1**: fresh shoot-root biomass ratio; **T2**: dry shoot-root biomass ratio; **SQ**: sturdiness quotient; **DQI**: Dickson quality index

## 3.2 Age-age Correlation

### 3.2.1 Self Age-age Correlation within Group A

From the results showed from Table 1., it revealed that the traits between two closer ages have higher and positive correlation, such as HT2 and HT6 ( $r=0.61$ ,  $P=0.076$ ); HT6 and HT25 ( $r=0.51$ ,  $P=0.03$ ). However, the 2 years traits have poor correlations with the traits of 25 years, in which implies 2 year-old traits is not suitable for serving as indicators. This is consistency with the study of *Eucalptus* by (Bouvet *et al.*, 2007), their research demonstrated that the correlation become higher after 36 months ( $r > 0.8$ ). The study of jack pine from (Weng *et al.*, 2007) also said that from age 5 to 7 have better correlations for early selection.

HT6 has higher correlation with annual height growth between 6 years to 25 years (GH25\_6) ( $r=0.98$ ,  $P < 0.0001$ ) than with annual growth between 6 years to 25 years ( $r=0.38$ ,  $P=0.12$ ), which is understandable that interval from 6 to 25 years is longer than from 2 to 6 years. On the other hand, it may reveal the correlation of juvenile to mature became much stable when the population reached to certain age.

**Table 3 Phenotypic correlation within group A—from family mean of the trait, N=18.**

	HT2	HT6	HT25	DBH25	DBA25	VOL25	GH25_6	GH6_2
HT2	1.00000	<b>0.60681</b> ( <b>0.0076</b> )	0.10595 (0.6756)	-0.10274 (0.6850)	-0.05351 (0.8330)	-0.09205 (0.7164)	0.01266 (0.9602)	<b>0.44838</b> ( <b>0.0620</b> )
HT6	<b>0.63604</b> ( <b>0.0045</b> )	1.00000	<b>0.51078</b> ( <b>0.0303</b> )	0.10944 (0.6655)	0.13308 (0.5986)	0.24181 (0.3337)	0.38221 (0.1175)	<b>0.98255</b> ( <b>&lt;.0001</b> )
HT25	0.15170 (0.5479)	0.33970 (0.1678)	1.00000	<b>0.46767</b> ( <b>0.0503</b> )	<b>0.49271</b> ( <b>0.0378</b> )	<b>0.71649</b> ( <b>0.0008</b> )	<b>0.98966</b> ( <b>&lt;.0001</b> )	<b>0.54961</b> ( <b>0.0181</b> )
DBH25	-0.03406 (0.8933)	0.10325 (0.6835)	0.38906 (0.1105)	1.00000	<b>0.95367</b> ( <b>&lt;.0001</b> )	<b>0.93963</b> ( <b>&lt;.0001</b> )	<b>0.48442</b> ( <b>0.0416</b> )	0.14711 (0.5602)
DBA25	-0.00103	0.04337	0.35397	<b>0.95666</b>	1.00000	<b>0.90803</b>	<b>0.50740</b>	0.16218

	HT2	HT6	HT25	DBH25	DBA25	VOL25	GH25_6	GH6_2
	(0.9968)	(0.8643)	(0.1496)	(<.0001)		(<.0001)	<b>(0.0316)</b>	(0.5203)
<b>VOL25</b>	-0.05057	0.15488	<b>0.73787</b>	<b>0.85552</b>	<b>0.77503</b>	1.00000	<b>0.72979</b>	0.29347
	(0.8421)	(0.5395)	<b>(0.0005)</b>	<b>(&lt;.0001)</b>	<b>(0.0002)</b>		<b>(0.0006)</b>	(0.2372)
<b>GH25_6</b>	0.06089	0.28394	<b>0.98762</b>	<b>0.42208</b>	0.38906	<b>0.77296</b>	1.00000	0.42686
	(0.8103)	(0.2535)	<b>(&lt;.0001)</b>	<b>(0.0810)</b>	(0.1105)	<b>(0.0002)</b>		(0.0773)
<b>GH6_2</b>	0.47575	0.94579	0.48813	0.28380	0.18473	0.36017	<b>0.44479</b>	1.00000
	(0.0460)	(<.0001)	(0.0399)	(0.2538)	(0.4631)	(0.1421)	<b>(0.0644)</b>	

Footnote: Data with white net bottom is the Pearson correlation coefficients; data with gray net bottom is Spearman Correlation Coefficients. Data within brackets are the P-value.

**Table 4 Phenotypic correlations within group A—from all the 232 individual (partially quote from Su, 2004)**

	HT2	HT6	HT25	DBH25	DBA25	VOL25	GH25_6	GH6_2
<b>HT2</b>	1.00000	<b>0.51718</b>	0.18646	0.0877	0.06369	0.10353	0.0838	0.34223
		<b>(&lt;.0001)</b>	(0.0044)	(0.1832)	(0.3341)	(0.1158)	(0.2035)	(<.0001)
<b>HT6</b>	<b>0.44465</b>	1.00000	<b>0.40162</b>	0.25628	0.23955	0.29587	0.20594	<b>0.98119</b>
	<b>&lt;.0001</b>		<b>(&lt;.0001)</b>	(<.0001)	(0.0002)	(<.0001)	(0.0016)	<b>(&lt;.0001)</b>
<b>HT25</b>	0.17659	<b>0.42039</b>	1.00000	0.34989	0.327	<b>0.61049</b>	<b>0.97889</b>	<b>0.39886</b>
	(0.007)	<b>(&lt;.0001)</b>		<b>(&lt;.0001)</b>	<b>(&lt;.0001)</b>	<b>(&lt;.0001)</b>	<b>(&lt;.0001)</b>	<b>(&lt;.0001)</b>
<b>DBH25</b>	0.1142	0.30271	0.35034	1.00000	<b>0.92608</b>	<b>0.92175</b>	0.31667	0.26157
	(0.0826)	(<.0001)	(<.0001)		<b>(&lt;.0001)</b>	<b>(&lt;.0001)</b>	(<.0001)	(<.0001)
<b>DBA25</b>	0.08055	0.30699	0.33664	<b>0.89786</b>	1.00000	<b>0.85442</b>	0.29595	0.24862
	(0.2216)	(<.0001)	(<.0001)	<b>(&lt;.0001)</b>		<b>(&lt;.0001)</b>	(<.0001)	(0.0001)
<b>VOL25</b>	0.15174	<b>0.40514</b>	<b>0.66822</b>	<b>0.91558</b>	<b>0.83375</b>	1.00000	<b>0.58629</b>	0.30147
	(0.0208)	<b>(&lt;.0001)</b>	<b>(&lt;.0001)</b>	<b>(&lt;.0001)</b>	<b>(&lt;.0001)</b>		<b>(&lt;.0001)</b>	(<.0001)
<b>GH25_6</b>	0.07772	0.24594	<b>0.97348</b>	0.31563	0.30775	<b>0.63226</b>	1.00000	0.20719
	(0.2383)	(0.0002)	<b>(&lt;.0001)</b>	(<.0001)	(<.0001)	<b>(&lt;.0001)</b>		(0.0015)
<b>GH6_2</b>	0.245	<b>0.96725</b>	<b>0.40959</b>	0.30393	0.31126	<b>0.40522</b>	0.23957	1.00000
	(0.0002)	<b>(&lt;.0001)</b>	<b>(&lt;.0001)</b>	(<.0001)	(<.0001)	<b>(&lt;.0001)</b>	(0.0002)	

Footnote: Data with white net bottom is the Pearson correlation coefficients; data with gray net bottom is Spearman Correlation Coefficients. Data within brackets are the P-value.

### 3.2.2 Age-age Correlations between Two Populations

From Table 5 to Table 12 are the results of age-age correlations between the A population and the B population. Compare to self-correlation within population A, the nursery-field correlations is lower ( $|r| = 0.4 \sim 0.71$ ), in Weng *et al.* (2008) study on white spruce also point out that correlation within field will larger than between fields. In Table 5 and Table 6, we can found that most of the growth traits in group B, such as root diameter (RD), root length (RL), fresh and dry shoot biomass (AFWT & ADWT) as well as root biomass (BFWT & BDWT), and Dickson quality index in 5-month-old all have considerable correlations with tree height (HT), volume (VOL), and annual growth of group A. Although most of them are negative correlations, the values are high enough for us to serve as indicators ( $|r| = 0.40 \sim 0.71$ ). The result from Pearson correlation coefficient is in tune with Spearman rank-order correlation coefficient.

According to this result, we can conclude that most growth traits in 5 months old are contrary to the performance in 25 years. The traits height, volume and annual growth from 6 to 25 years (GH25) in population A are correlated to juvenile traits, these three phenotype all share the same physical characteristic—tree height, which make this result reasonable. It apparently in this study case, 5 months old growth criteria and can reveal the trend in elder population, and it would not become significant until the mature group reached 25 years.

Dickson quality index (DQI) also shows similar results from other growth traits, from formula 1.1 we can tell that DQI is the combination of dry shoot biomass (ADWT, BDWT), shoot height (HT), and root diameter (RD), dry shoot-root biomass ratio (T2); however it is difficult to differentiate directly from the formula that on which factors



inside DQI leads to this result. We can only conclude that DQI is a potential indicator as well, and this situation is in compatible with 7 and 9 months (see Table 7 to Table 10).

One more finding we should pay attention from Table 5 and Table 6 is that the fresh shoot-root biomass ratio (T1) has positive correlation with 25 years traits; moreover, this circumstance continued to 7 month and 9 month, too. This may implicate that different traits have different strength to serve as criteria for indirect selection in different growth periods.

**Table 5 Pearson Correlation Coefficients of Group A with 5 Months Group B  
(from family mean of 18 families)**

	HT2	HT6	HT25	DBH25	DBA25	VOL25	GH25_6	GH6_2
<b>RD5</b>	0.05280 (0.8352)	0.00859 (0.9730)	<b>-0.62825</b> <b>(0.0052)</b>	-0.32314 (0.1909)	-0.29854 (0.2288)	<b>-0.43693</b> <b>(0.0698)</b>	<b>-0.67672</b> <b>(0.0020)</b>	-0.00270 (0.9915)
<b>RL5</b>	0.11049 (0.6625)	0.01415 (0.9556)	<b>-0.60649</b> <b>(0.0076)</b>	-0.20282 (0.4196)	-0.16305 (0.5180)	-0.35482 (0.1485)	<b>-0.65426</b> <b>(0.0032)</b>	-0.00995 (0.9687)
<b>AFWT5</b>	0.07077 (0.7802)	0.09988 (0.6933)	<b>-0.57547</b> <b>(0.0125)</b>	-0.37159 (0.1289)	-0.36428 (0.1372)	<b>-0.44101</b> <b>(0.0670)</b>	<b>-0.63522</b> <b>(0.0046)</b>	0.09576 (0.7054)
<b>ADWT5</b>	0.07879 (0.7560)	0.08517 (0.7369)	<b>-0.59772</b> <b>(0.0088)</b>	-0.35667 (0.1463)	-0.34519 (0.1606)	<b>-0.44430</b> <b>(0.0647)</b>	<b>-0.65668</b> <b>(0.0031)</b>	0.07734 (0.7603)
<b>BFWT5</b>	0.03541 (0.8891)	0.06377 (0.8015)	<b>-0.60545</b> <b>(0.0078)</b>	-0.32585 (0.1870)	-0.33671 (0.1718)	<b>-0.42575</b> <b>(0.0781)</b>	<b>-0.66142</b> <b>(0.0028)</b>	0.06343 (0.8026)
<b>BDWT5</b>	0.06116 (0.8095)	0.07542 (0.7661)	<b>-0.58829</b> <b>(0.0102)</b>	-0.25667 (0.3039)	-0.25250 (0.3121)	-0.37224 (0.1282)	<b>-0.64491</b> <b>(0.0039)</b>	0.07050 (0.7810)
<b>HT5</b>	0.10964 (0.6649)	0.04997 (0.8439)	<b>-0.61343</b> <b>(0.0068)</b>	-0.35138 (0.1528)	-0.31025 (0.2102)	<b>-0.45017</b> <b>(0.0608)</b>	<b>-0.66769</b> <b>(0.0025)</b>	0.03053 (0.9043)
<b>T15</b>	0.06804 (0.7885)	0.02218 (0.9304)	0.38228 (0.1174)	0.02210 (0.9306)	0.11391 (0.6527)	0.16392 (0.5157)	<b>0.40720</b> <b>(0.0935)</b>	0.00902 (0.9717)
<b>T25</b>	0.22837 (0.3621)	-0.05431 (0.8305)	0.23701 (0.3437)	-0.14123 (0.5762)	-0.10061 (0.6912)	-0.02070 (0.9350)	0.26381 (0.2902)	-0.11451 (0.6509)
<b>SQ5</b>	-0.02031 (0.9362)	0.09811 (0.6985)	0.36852 (0.1324)	0.13231 (0.6007)	0.07550 (0.7659)	0.21221 (0.3979)	0.37975 (0.1201)	0.11508 (0.6493)
<b>DQI5</b>	0.04423 (0.8617)	0.06093 (0.8102)	<b>-0.60959</b> <b>(0.0072)</b>	-0.30391 (0.2202)	-0.30460 (0.2191)	<b>-0.41367</b> <b>(0.0879)</b>	<b>-0.66540</b> <b>(0.0026)</b>	0.05816 (0.8187)

Footnote: Data within brackets are the P-value.

**Table 6 Spearman Correlation Coefficients of Group A with 5 Months Group B**

(from family mean of 18 families)

	HT2	HT6	HT25	DBH25	DBA25	VOL25	GH25_6	GH6_2
<b>RD5</b>	-0.02993 (0.9062)	0.11151 (0.6596)	<b>-0.53148</b> <b>(0.0232)</b>	-0.24871 (0.3196)	-0.22394 (0.3717)	<b>-0.42415</b> <b>(0.0794)</b>	<b>-0.55005</b> <b>(0.0180)</b>	0.01135 (0.9643)
<b>RL5</b>	-0.00722 (0.9773)	-0.05266 (0.8356)	<b>-0.53560</b> <b>(0.0220)</b>	-0.12900 (0.6099)	-0.04438 (0.8612)	-0.37874 (0.1212)	<b>-0.55418</b> <b>(0.0170)</b>	-0.14964 (0.5534)
<b>AFWT5</b>	-0.05263 (0.8357)	0.07228 (0.7756)	<b>-0.54180</b> <b>(0.0202)</b>	-0.33953 (0.1681)	-0.31889 (0.1971)	<b>-0.46749</b> <b>(0.0504)</b>	<b>-0.56450</b> <b>(0.0147)</b>	-0.03612 (0.8869)
<b>ADWT5</b>	-0.05263 (0.8357)	0.05576 (0.8261)	<b>-0.56037</b> <b>(0.0156)</b>	-0.35191 (0.1521)	-0.33127 (0.1793)	<b>-0.47575</b> <b>(0.0460)</b>	<b>-0.57895</b> <b>(0.0118)</b>	-0.05470 (0.8293)
<b>BFWT5</b>	-0.08772 (0.7293)	0.07228 (0.7756)	<b>-0.59546</b> <b>(0.0091)</b>	-0.27761 (0.2647)	-0.26729 (0.2836)	<b>-0.45924</b> <b>(0.0552)</b>	<b>-0.60991</b> <b>(0.0072)</b>	-0.03199 (0.8997)
<b>BDWT5</b>	-0.04231 (0.8676)	0.06298 (0.8039)	<b>-0.53973</b> <b>(0.0208)</b>	-0.17234 (0.4941)	-0.15377 (0.5424)	-0.38700 (0.1126)	<b>-0.55418</b> <b>(0.0170)</b>	-0.01548 (0.9514)
<b>HT5</b>	-0.01961 (0.9384)	0.05472 (0.8292)	<b>-0.60165</b> <b>(0.0083)</b>	-0.29618 (0.2327)	-0.27967 (0.2610)	<b>-0.46336</b> <b>(0.0528)</b>	<b>-0.61197</b> <b>(0.0070)</b>	-0.06295 (0.8040)
<b>T15</b>	0.14345 (0.5701)	0.12081 (0.6330)	0.39319 (0.1065)	-0.13519 (0.5927)	-0.13313 (0.5985)	0.12487 (0.6215)	<b>0.42208</b> <b>(0.0810)</b>	0.11662 (0.6449)
<b>T25</b>	0.08978 (0.7231)	0.04233 (0.8675)	0.27348 (0.2722)	-0.31269 (0.2065)	-0.28173 (0.2574)	0.00722 (0.9773)	0.27761 (0.2647)	-0.03199 (0.8997)
<b>SQ5</b>	0.02993 (0.9062)	0.00103 (0.9968)	0.30237 (0.2226)	0.04644 (0.8548)	-0.00310 (0.9903)	0.21156 (0.3994)	0.33746 (0.1708)	0.04025 (0.8740)
<b>DQI5</b>	-0.07534 (0.7664)	0.06505 (0.7976)	<b>-0.55418</b> <b>(0.0170)</b>	-0.25903 (0.2993)	-0.24252 (0.3322)	<b>-0.44066</b> <b>(0.0672)</b>	<b>-0.57688</b> <b>(0.0122)</b>	-0.02580 (0.9191)

Footnote: Data within brackets are the P-value

Results in 7 months appear to be consistent with 5 months (see Table 7 and Table 8), the correlations between 7-month-old traits of population B and population A are happened. Most of the especially centralized on the traits like height, volume and annual growth from 6 to 25 years of A site with most of trait in site B ( $|r| = 0.43 \sim 0.71$ ).

Shoot-root biomass ratio's correlation with elder population become more clear, what is

different from 5 months is that here it shift from fresh shoot-root ratio (T1) into dry ratio (T2) ( $r = 0.48 \sim 0.60$ ).

**Table 7 Pearson Correlation Coefficients from Group A with 7 Months Group B**  
(from family mean of 18 families)

	HT2	HT6	HT25	DBH25	DBA25	VOL25	GH25_6	GH6_2
<b>RD7</b>	-0.12715	-0.22569	<b>-0.64416</b>	-0.38884	-0.32806	<b>-0.50980</b>	<b>-0.65474</b>	-0.22404
P-value	(0.6151)	(0.3679)	<b>(0.0039)</b>	(0.1108)	(0.1838)	<b>(0.0307)</b>	<b>(0.0032)</b>	(0.3715)
<b>RL7</b>	0.08892	-0.00831	-0.33336	-0.26210	-0.19748	-0.36011	-0.35693	-0.03015
	(0.7257)	(0.9739)	(0.1764)	(0.2934)	(0.4322)	(0.1421)	(0.1459)	(0.9055)
<b>AFWT7</b>	-0.02519	-0.17125	<b>-0.63664</b>	<b>-0.44451</b>	<b>-0.41209</b>	<b>-0.52416</b>	<b>-0.65574</b>	-0.18668
	(0.9210)	(0.4969)	<b>(0.0045)</b>	<b>(0.0646)</b>	<b>(0.0893)</b>	<b>(0.0256)</b>	<b>(0.0031)</b>	(0.4583)
<b>ADWT7</b>	0.04203	-0.14869	<b>-0.66867</b>	<b>-0.43563</b>	<b>-0.40981</b>	<b>-0.53564</b>	<b>-0.69393</b>	-0.17704
	(0.8685)	(0.5560)	<b>(0.0024)</b>	<b>(0.0708)</b>	<b>(0.0912)</b>	<b>(0.0220)</b>	<b>(0.0014)</b>	(0.4822)
<b>BFWT7</b>	-0.07278	-0.06625	<b>-0.64988</b>	-0.37091	-0.33310	<b>-0.50239</b>	<b>-0.68749</b>	-0.05747
	(0.7741)	(0.7940)	<b>(0.0035)</b>	(0.1297)	(0.1768)	<b>(0.0336)</b>	<b>(0.0016)</b>	(0.8208)
<b>BDWT7</b>	0.04919	-0.11413	<b>-0.68265</b>	<b>-0.39978</b>	-0.37926	<b>-0.52467</b>	<b>-0.71473</b>	-0.13986
	(0.8463)	(0.6520)	<b>(0.0018)</b>	<b>(0.1002)</b>	(0.1206)	<b>(0.0254)</b>	<b>(0.0009)</b>	(0.5799)
<b>HT7</b>	0.15930	-0.09690	<b>-0.64163</b>	-0.31733	-0.26960	<b>-0.44337</b>	<b>-0.67350</b>	-0.14624
	(0.5278)	(0.7021)	<b>(0.0041)</b>	(0.1994)	(0.2793)	<b>(0.0653)</b>	<b>(0.0022)</b>	(0.5626)
<b>T17</b>	0.00394	-0.17985	0.28423	0.04007	0.01979	0.18264	0.33551	-0.20317
	(0.9876)	(0.4752)	(0.2530)	(0.8746)	(0.9379)	(0.4682)	(0.1735)	(0.4188)
<b>T27</b>	-0.11738	-0.01414	<b>0.55460</b>	0.18273	0.20347	0.34814	<b>0.59848</b>	0.01157
	(0.6427)	(0.9556)	<b>(0.0169)</b>	(0.4680)	(0.4180)	(0.1568)	<b>(0.0087)</b>	(0.9637)
<b>SQ7</b>	0.43065	0.19576	0.23086	0.19811	0.15824	0.23605	0.21549	0.11936
	(0.0744)	(0.4363)	(0.3567)	(0.4307)	(0.5306)	(0.3457)	(0.3905)	(0.6371)
<b>DQI7</b>	-0.00558	-0.15406	<b>-0.68688</b>	<b>-0.43810</b>	<b>-0.40998</b>	<b>-0.55457</b>	<b>-0.71260</b>	-0.17195
	(0.9825)	(0.5416)	<b>(0.0016)</b>	<b>(0.0690)</b>	<b>(0.0911)</b>	<b>(0.0169)</b>	<b>(0.0009)</b>	(0.4951)

Footnote: Data within brackets are the P-value

**Table 8 Spearman Correlation Coefficients of Group A with 7 Months Group B**

(from family mean of 18 families)

	HT2	HT6	HT25	DBH25	DBA25	VOL25	GH25_6	GH6_2
RD7	-0.17553 (0.4860)	-0.20764 (0.4084)	<b>-0.52556</b> <b>(0.0251)</b>	-0.19618 (0.4353)	-0.08157 (0.7476)	<b>-0.43676</b> <b>(0.0699)</b>	<b>-0.54517</b> <b>(0.0193)</b>	-0.25297 (0.3112)
RL7	0.05882 (0.8167)	0.01652 (0.9481)	<b>-0.44892</b> <b>(0.0617)</b>	-0.38493 (0.1147)	-0.27761 (0.2647)	<b>-0.57895</b> <b>(0.0118)</b>	<b>-0.46336</b> <b>(0.0528)</b>	-0.08359 (0.7416)
AFWT7	-0.02580 (0.9191)	-0.05163 (0.8388)	<b>-0.50258</b> <b>(0.0335)</b>	-0.34778 (0.1573)	-0.25697 (0.3033)	<b>-0.51290</b> <b>(0.0295)</b>	<b>-0.56244</b> <b>(0.0151)</b>	-0.15377 (0.5424)
ADWT7	0.02580 (0.9191)	-0.05989 (0.8134)	<b>-0.52735</b> <b>(0.0245)</b>	-0.34985 (0.1547)	-0.25284 (0.3114)	<b>-0.53354</b> <b>(0.0226)</b>	<b>-0.58720</b> <b>(0.0104)</b>	-0.16615 (0.5100)
BFWT7	-0.11868 (0.6390)	-0.01239 (0.9611)	<b>-0.57895</b> <b>(0.0118)</b>	-0.27967 (0.2610)	-0.19298 (0.4429)	<b>-0.54386</b> <b>(0.0196)</b>	<b>-0.61197</b> <b>(0.0070)</b>	-0.08566 (0.7354)
BDWT7	-0.00722 (0.9773)	-0.05059 (0.8420)	<b>-0.58308</b> <b>(0.0111)</b>	-0.29825 (0.2293)	-0.22394 (0.3717)	<b>-0.52941</b> <b>(0.0239)</b>	<b>-0.63880</b> <b>(0.0043)</b>	-0.14345 (0.5701)
HT7	0.15583 (0.5369)	-0.04027 (0.8740)	<b>-0.55418</b> <b>(0.0170)</b>	-0.28173 (0.2574)	-0.17441 (0.4888)	<b>-0.51909</b> <b>(0.0273)</b>	<b>-0.62023</b> <b>(0.0060)</b>	-0.17028 (0.4993)
T17	0.05263 (0.8357)	-0.21270 (0.3968)	0.26935 (0.2798)	-0.08153 (0.7478)	-0.09598 (0.7048)	0.21156 (0.3994)	0.27554 (0.2684)	-0.27141 (0.2760)
T27	0.01961 (0.9384)	0.08983 (0.7230)	<b>0.55418</b> <b>(0.0170)</b>	0.10423 (0.6806)	0.03406 (0.8933)	<b>0.47575</b> <b>(0.0460)</b>	<b>0.58927</b> <b>(0.0101)</b>	0.10217 (0.6867)
SQ7	0.47162 (0.0482)	0.32112 (0.1938)	0.20330 (0.4184)	0.04438 (0.8612)	0.01754 (0.9449)	0.18266 (0.4682)	0.18060 (0.4733)	0.22807 (0.3627)
DQI7	-0.07327 (0.7726)	-0.11151 (0.6596)	<b>-0.57688</b> <b>(0.0122)</b>	-0.28999 (0.2431)	-0.21569 (0.3900)	<b>-0.51496</b> <b>(0.0287)</b>	<b>-0.62848</b> <b>(0.0052)</b>	-0.19505 (0.4380)

Footnote: Data within brackets are the P-value

In Table 9 and Table 10, we can found that some correlations start to disappear, which mainly in the 9-month-old traits with 25 years height and its annual growth from 6 to 25 years. Furthermore, 25-year-old diameter breast height (DBH) and basal stem diameter (DBA) start to show up correlations with shoot and root biomass (AFWT,

ADWT, BFWT, and BDWT). It might infer that the phenotypic performance has changed to crosswise from height growth.

The same as 5 and 9 months, ratio of shoot-root biomass (T1 & T2) are positive related with 25 years population.

**Table 9 Pearson Correlation Coefficients of Group A with 9 Months Group B**  
(from family mean of 18 families)

	HT2	HT6	HT25	DBH25	DBA25	VOL25	GH25_6	GH6_2
RD9	0.40666 (0.0940)	0.13778 (0.5856)	-0.26774 (0.2828)	-0.26217 (0.2933)	-0.16485 (0.5133)	-0.28776 (0.2469)	-0.31077 (0.2094)	0.05977 (0.8137)
RL9	0.21386 (0.3941)	0.14724 (0.5599)	0.01348 (0.9577)	-0.27182 (0.2752)	-0.30649 (0.2161)	-0.19814 (0.4306)	-0.01008 (0.9683)	0.11553 (0.6480)
AFWT9	0.24946 (0.3181)	0.08065 (0.7504)	-0.18963 (0.4511)	<b>-0.40989</b> <b>(0.0912)</b>	-0.35087 (0.1534)	-0.33311 (0.1768)	-0.21728 (0.3864)	0.03232 (0.8987)
ADWT9	0.28385 (0.2537)	0.12676 (0.6162)	-0.19470 (0.4388)	<b>-0.42690</b> <b>(0.0773)</b>	-0.37000 (0.1307)	-0.34873 (0.1561)	-0.23042 (0.3576)	0.07613 (0.7640)
BFWT9	0.11044 (0.6627)	0.00247 (0.9923)	-0.31439 (0.2039)	<b>-0.45995</b> <b>(0.0548)</b>	<b>-0.42754</b> <b>(0.0768)</b>	<b>-0.42913</b> <b>(0.0756)</b>	-0.33834 (0.1697)	-0.02307 (0.9276)
BDWT9	0.14220 (0.5735)	-0.00946 (0.9703)	-0.35562 (0.1475)	<b>-0.47452</b> <b>(0.0466)</b>	<b>-0.46249</b> <b>(0.0533)</b>	<b>-0.44655</b> <b>(0.0632)</b>	-0.38067 (0.1191)	-0.04392 (0.8626)
HT9	0.30084 (0.2251)	-0.02012 (0.9368)	-0.20781 (0.4080)	<b>-0.41482</b> <b>(0.0870)</b>	-0.31051 (0.2098)	-0.38852 (0.1111)	-0.22002 (0.3803)	-0.09303 (0.7135)
T19	0.36572 (0.1356)	0.35301 (0.1507)	0.33907 (0.1687)	0.22038 (0.3795)	0.36967 (0.1311)	0.30851 (0.2129)	0.30557 (0.2175)	0.31139 (0.2084)
T29	0.27278 (0.2735)	0.36249 (0.1393)	<b>0.43538</b> <b>(0.0709)</b>	0.32432 (0.1892)	<b>0.51674</b> <b>(0.0281)</b>	<b>0.40839</b> <b>(0.0925)</b>	<b>0.40751</b> <b>(0.0932)</b>	0.34380 (0.1624)
SQ9	-0.20592 (0.4123)	-0.23278 (0.3526)	0.09643 (0.7035)	0.27912 (0.2620)	0.13966 (0.5805)	0.27472 (0.2699)	0.14248 (0.5728)	-0.21359 (0.3948)
DQI9	0.28594 (0.2500)	0.09742 (0.7006)	-0.33531 (0.1738)	<b>-0.42149</b> <b>(0.0815)</b>	<b>-0.38869</b> <b>(0.1109)</b>	<b>-0.40322</b> <b>(0.0971)</b>	-0.37667 (0.1234)	0.04264 (0.8666)

Footnote: Data within brackets are the P-value

**Table 10 Spearman Correlation Coefficients of Group A with 9 Months Group B  
(from family mean of 18 families)**

	HT2	HT6	HT25	DBH25	DBA25	VOL25	GH25_6	GH6_2
RD9	0.23438 (0.3492)	0.01963 (0.9384)	-0.22303 (0.3737)	-0.18069 (0.4731)	-0.08054 (0.7507)	-0.29220 (0.2393)	-0.24161 (0.3341)	-0.07124 (0.7788)
RL9	0.08772 (0.7293)	0.10015 (0.6925)	-0.00929 (0.9708)	-0.20330 (0.4184)	-0.17028 (0.4993)	-0.15789 (0.5315)	-0.05676 (0.8230)	0.04850 (0.8484)
AFWT9	0.05882 (0.8167)	0.11668 (0.6448)	-0.32508 (0.1881)	-0.33953 (0.1681)	-0.26109 (0.2953)	-0.34365 (0.1626)	-0.32921 (0.1822)	-0.06502 (0.7977)
ADWT9	0.03818 (0.8804)	0.16830 (0.5044)	-0.28380 (0.2538)	-0.30650 (0.2161)	-0.24045 (0.3365)	-0.30650 (0.2161)	-0.28586 (0.2502)	0.01754 (0.9449)
BFWT9	-0.12487 (0.6215)	0.02891 (0.9093)	-0.34572 (0.1600)	-0.25077 (0.3155)	-0.19505 (0.4380)	-0.31682 (0.2002)	-0.33333 (0.1765)	-0.05470 (0.8293)
BDWT9	-0.02580 (0.9191)	0.10325 (0.6835)	-0.34572 (0.1600)	-0.35191 (0.1521)	-0.27967 (0.2610)	-0.39732 (0.1025)	-0.35810 (0.1445)	-0.00310 (0.9903)
HT9	0.14345 (0.5701)	0.08157 (0.7476)	-0.38493 (0.1147)	-0.36429 (0.1372)	-0.25284 (0.3114)	<b>-0.45924</b> <b>(0.0552)</b>	<b>-0.39938</b> <b>(0.1006)</b>	-0.13313 (0.5985)
T19	0.30857 (0.2128)	0.37377 (0.1265)	0.30237 (0.2226)	-0.03818 (0.8804)	-0.00516 (0.9838)	0.14757 (0.5590)	0.28793 (0.2466)	0.28380 (0.2538)
T29	0.28793 (0.2466)	0.45225 (0.0595)	0.36017 (0.1421)	0.13519 (0.5927)	0.17853 (0.4784)	0.25490 (0.3073)	0.36842 (0.1325)	0.35604 (0.1470)
SQ9	-0.33333 (0.1765)	-0.14249 (0.5727)	-0.05470 (0.8293)	-0.06089 (0.8103)	-0.08359 (0.7416)	0.04644 (0.8548)	-0.01548 (0.9514)	-0.19711 (0.4331)
DQI9	0.02786 (0.9126)	0.13216 (0.6011)	-0.36223 (0.1396)	-0.35810 (0.1445)	-0.29412 (0.2361)	-0.40144 (0.0987)	-0.37668 (0.1234)	0.00929 (0.9708)

Footnote: Data within brackets are the P-value

The trend of correlation has dramatic change when it comes to 13 months of B population. Most of correlations exist in 5, 7, 9 months had faded away (Table 8. & Table 9.), only few correlation emerged in between the 13 months traits and the 2 years and the 6 years height of population A, which is the early year data of A. Not like most of the results from 5, 7, 9 months correlations, the 13 months' correlation which have

significant outcomes ( $P=0.04\sim 0.09$ ) were positive. Specifically, they appear in the correlations of root length (RL13), shoot height (HT13), sturdiness quotient (SQ13) with the 2 years and 6 years height (HT2 & HT6) of A. According to previous researcher (Wu, 2005), population B was planted in tubing inside a nursery, when it comes to 13 months, most of the shoot root was reached out of the tubing. It may effects the growth performance and the measure parameter, and probably it is the reason for inconsistency of the outcome from previous months.

In conclusion, these results were favorable to us, it demonstrated that we can possibly predict the performance of 25 years population especially from 5, 7, 9 months old population. Through the juvenile traits like root diameter, root length, fresh and dry shoot biomass, as well as Dickson quality index, we can envision the future growth in 25 years.

When we look into the detail, it is obvious that most of the juvenile-mature correlations in our model are negative, that is to say, when we applied the results for the selection, we should select from the opposite direction.

**Table 11 Pearson Correlation Coefficients from Group A to 13 Months Group B  
(from family mean of 18 families)**

	HT2	HT6	HT25	DBH25	DBA25	VOL25	GH25_6	GH6_2
RD13	0.02903 (0.9090)	-0.27713 (0.2656)	-0.29310 (0.2378)	-0.06474 (0.7986)	-0.12300 (0.6268)	-0.10108 (0.6898)	-0.26881 (0.2808)	-0.31845 (0.1978)
RL13	0.37743 (0.1226)	<b>0.44935</b> <b>(0.0614)</b>	0.20865 (0.4060)	-0.02932 (0.9081)	-0.08853 (0.7268)	0.01362 (0.9572)	0.14932 (0.5543)	<b>0.41699</b> <b>(0.0851)</b>
AFWT13	0.33893 (0.1689)	0.27100 (0.2767)	-0.05820 (0.8186)	-0.21366 (0.3946)	-0.16308 (0.5179)	-0.13348 (0.5975)	-0.10777 (0.6704)	0.22544 (0.3684)
ADWT13	0.26679 (0.2845)	0.12879 (0.6105)	-0.14391 (0.5689)	-0.17614 (0.4845)	-0.17671 (0.4830)	-0.11985 (0.6357)	-0.17617 (0.4844)	0.08240 (0.7451)
BFWT13	0.29907	0.27274	0.00079	-0.30584	-0.23101	-0.19452	-0.04465	0.23672

	HT2	HT6	HT25	DBH25	DBA25	VOL25	GH25_6	GH6_2
	(0.2280)	(0.2735)	(0.9975)	(0.2171)	(0.3564)	(0.4393)	(0.8604)	(0.3443)
BDWT13	0.18905 (0.4525)	0.15232 (0.5463)	-0.20063 (0.4247)	-0.37477 (0.1254)	-0.33751 (0.1708)	-0.30297 (0.2217)	-0.24106 (0.3352)	0.12705 (0.6154)
HT13	<b>0.48454</b> <b>(0.0416)</b>	0.33394 (0.1756)	-0.09323 (0.7129)	-0.20658 (0.4108)	-0.09093 (0.7197)	-0.19534 (0.4373)	-0.15591 (0.5367)	0.26215 (0.2933)
T113	0.05370 (0.8324)	-0.10400 (0.6813)	-0.17405 (0.4897)	0.30040 (0.2258)	0.33622 (0.1725)	0.21711 (0.3868)	-0.16973 (0.5007)	-0.12952 (0.6085)
T213	-0.05731 (0.8213)	-0.26090 (0.2957)	-0.20592 (0.4123)	0.03252 (0.8981)	0.04491 (0.8596)	-0.08202 (0.7463)	-0.17782 (0.4802)	-0.27999 (0.2605)
SQ13	0.33813 (0.1699)	<b>0.46296</b> <b>(0.0530)</b>	0.16798 (0.5052)	-0.09221 (0.7159)	0.06772 (0.7895)	-0.05259 (0.8358)	0.10333 (0.6833)	<b>0.44149</b> <b>(0.0666)</b>
DQI13	0.04432 (0.8614)	-0.04266 (0.8665)	-0.21564 (0.3901)	-0.23687 (0.3440)	-0.26405 (0.2897)	-0.16843 (0.5041)	-0.22467 (0.3701)	-0.05834 (0.8181)

Footnote: Data within brackets are the P-value

**Table 12 Spearman Correlation Coefficients from Group A to 13 Months Group B  
(from family mean of 18 families)**

	HT2	HT6	HT25	DBH25	DBA25	VOL25	GH25_6	GH6_2
RD13	0.02786 (0.9126)	-0.08673 (0.7322)	-0.33746 (0.1708)	-0.14138 (0.5758)	-0.21569 (0.3900)	-0.11042 (0.6627)	-0.31682 (0.2002)	-0.13725 (0.5871)
RL13	0.31063 (0.2096)	<b>0.43056</b> <b>(0.0745)</b>	0.15583 (0.5369)	0.08359 (0.7416)	0.11662 (0.6449)	0.05057 (0.8421)	0.09804 (0.6987)	<b>0.41589</b> <b>(0.0861)</b>
AFWT13	0.23013 (0.3583)	0.33660 (0.1720)	-0.08772 (0.7293)	-0.09391 (0.7109)	-0.03818 (0.8804)	-0.06914 (0.7851)	-0.08978 (0.7231)	0.22188 (0.3762)
ADWT13	0.04231 (0.8676)	0.08983 (0.7230)	-0.22188 (0.3762)	0.00103 (0.9968)	0.04231 (0.8676)	-0.03199 (0.8997)	-0.23839 (0.3408)	0.00103 (0.9968)
BFWT13	0.17028 (0.4993)	<b>0.35003</b> <b>(0.1545)</b>	-0.07740 (0.7602)	-0.17028 (0.4993)	-0.11662 (0.6449)	-0.11042 (0.6627)	-0.08566 (0.7354)	0.21981 (0.3808)
BDWT13	-0.04025 (0.8740)	0.13010 (0.6069)	-0.29205 (0.2396)	-0.30444 (0.2193)	-0.27141 (0.2760)	-0.29618 (0.2327)	-0.30031 (0.2260)	0.02580 (0.9191)
HT13	0.34159 (0.1653)	0.28394 (0.2535)	-0.11455 (0.6508)	-0.11042 (0.6627)	0.01135 (0.9643)	-0.21156 (0.3994)	-0.14138 (0.5758)	0.18060 (0.4733)
T113	0.12281 (0.6273)	0.10842 (0.6685)	-0.28793 (0.2466)	0.10630 (0.6746)	0.02993 (0.9062)	-0.05057 (0.8421)	-0.29412 (0.2361)	0.10836 (0.6687)



	HT2	HT6	HT25	DBH25	DBA25	VOL25	GH25_6	GH6_2
T213	0.14551 (0.5645)	-0.13216 (0.6011)	0.00929 (0.9708)	0.18266 (0.4682)	0.15583 (0.5369)	0.16409 (0.5153)	-0.01548 (0.9514)	-0.08566 (0.7354)
SQ13	0.26522 (0.2875)	0.37481 (0.1254)	0.18060 (0.4733)	0.01342 (0.9579)	0.15170 (0.5479)	-0.05882 (0.8167)	0.14345 (0.5701)	0.33333 (0.1765)
DQI13	-0.12693 (0.6157)	-0.10325 (0.6835)	-0.34985 (0.1547)	-0.18473 (0.4631)	-0.19711 (0.4331)	-0.15789 (0.5315)	-0.34159 (0.1653)	-0.17647 (0.4836)

Footnote: Data within brackets are the P-value

### 3.3 Indirect Selection from Family Ranking of Highly Correlated

#### Traits

After the analysis of correlation from A and B population, we set up a standard that correlation value higher than 0.4 ( $|r| > 0.4$ ), and P value lower than 0.1 ( $P < 0.1$ ) than we will treat these two traits as correlated. We picked up those correlated traits and ranking those traits by their family means, later on we select half of the family by rankings and compare the percentage of the same family were chosen between two traits.

For example, in Table 13 is the ranking of the family means of the trait height in 25 years (HT25) and other traits in 7 months from population B. Those data are the family number and are sorted by ranking from top to bottom. We select from the middle of the population, for traits which have negative correlation with HT25, than we choose from the bottom, and those have positive correlation we choose from top side. Next, we can acquire the ratio of same family number between testing population and target population.

Table 13 Percentage of the same family number from the family mean ranking— take HT25 with traits in 7 months population B as an example

	HT25	RD7	RL7	AFWT7	ADWT7	BFWT7	BDWT7	HT7	T27	SQ7	DICKSON7
High	20	18	14	8	8	6	8	8	4	11	8
	17	8	19	18	18	8	18	6	17	9	18
	24	16	6	6	6	18	6	18	9	6	6
	4	14	18	10	10	14	14	10	23	20	14
	11	10	25	14	14	19	10	14	22	10	10
	16	6	10	16	16	10	5	25	20	4	16
	22	25	22	5	5	16	16	11	16	17	5
	9	24	16	24	24	5	19	5	11	22	24
	19	19	5	19	19	25	24	19	10	14	19
	Low	18	5	17	11	25	24	25	24	5	23
6		23	8	25	11	22	11	16	24	8	11
7		22	7	23	9	7	7	9	18	5	7
10		4	24	4	23	11	9	23	8	25	23
25		7	9	9	4	4	23	4	19	19	4
23		11	20	22	7	23	4	22	7	7	9
8		9	11	7	22	9	22	7	25	24	22
5		17	23	17	17	17	17	17	6	18	17
14		20	4	20	20	20	20	20	14	16	20
		67%	67%	67%	67%	78%	67%	78%	78%	67%	67%

From Table 14 to Table 17 are the results of the same family ration from the selection between population A and B, only those traits which have high correlations ( $|r| > 0.4, P < 0.1$ ) are calculated.

In the tree breeding program, we hope our selection can include most of the economic traits in the same time. Use Table 14 as an example, when we take root diameter in 5 months as criterion to select the plus tree family, we can efficiently acquire family with good performance on tree height and volume in 25-year-old population.

In general, from the outcomes shown in Table 14 to Table 17, most of the percentage values are very high, it implies that use these traits in juvenile population as indicators can acquire good performance families for advanced population.

**Table 14 Selection from Family Ranking—Use 5 months population B as Indicators**

	HT2	HT6	HT25	DBH25	DBA25	VOL25	GH25_6	GH6_2
<b>RD5</b>	--	--	67%	--	--	67%	67%	--
<b>RL5</b>	--	--	56%	--	--	--	44%	--
<b>AFWT5</b>	--	--	67%	--	--	67%	67%	--
<b>ADWT5</b>	--	--	67%	--	--	67%	67%	--
<b>BFWT5</b>	--	--	78%	--	--	67%	67%	--
<b>BDWT5</b>	--	--	78%	--	--	67%	78%	--
<b>HT5</b>	--	--	78%	--	--	67%	78%	--
<b>T15</b>	--	--	78%	--	--	--	33%	--
<b>T25</b>	--	--	--	--	--	--	--	--
<b>SQ5</b>	--	--	--	--	--	--	--	--
<b>DQI5</b>	--	--	78%	--	--	67%	67%	--

Footnote: Data with gray net bottom implies the correlation between these two traits is positive.

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**Table 15 Selection from Family Ranking—Use 7 months population B as Indicator**

	HT2	HT6	HT25	DBH25	DBA25	VOL25	GH25_6	GH6_2
<b>RD7</b>	--	--	67%	--	--	67%	67%	--
<b>RL7</b>	--	--	67%	--	--	67%	67%	--
<b>AFWT7</b>	--	--	67%	56%	56%	67%	67%	--
<b>ADWT7</b>	--	--	67%	56%	56%	67%	67%	--
<b>BFWT7</b>	--	--	78%	--	--	78%	78%	--
<b>BDWT7</b>	--	--	67%	56%	--	67%	67%	--
<b>HT7</b>	--	--	78%	--	--	78%	78%	--
<b>T17</b>	--	--	--	--	--	--	--	--
<b>T27</b>	--	--	78%	--	--	78%	78%	--
<b>SQ7</b>	67%	--	67%	--	--	--	--	--
<b>DQI7</b>	--	--	67%	56%	56%	67%	67%	--

Footnote: Data with gray net bottom implies the correlation between these two traits is positive.

**Table 16 Selection from Family Ranking—Use 9 months population B as Indicator**

	HT2	HT6	HT25	DBH25	DBA25	VOL25	GH25_6	GH6_2
<b>RD9</b>	--	--	--	--	--	--	--	--
<b>RL9</b>	--	--	--	--	--	--	--	--
<b>AFWT9</b>	--	--	--	56%	--	--	--	--
<b>ADWT9</b>	--	--	--	56%	--	--	--	--
<b>BFWT9</b>	--	--	--	44%	56%	56%	--	--
<b>BDWT9</b>	--	--	--	44%	56%	56%	--	--
<b>HT9</b>	--	--	--	56%	--	67%	--	--
<b>T19</b>	--	--	--	--	--	--	--	--
<b>T29</b>	--	--	67%	44%	44%	--	--	--
<b>SQ9</b>	--	--	--	--	--	--	--	--
<b>DQI9</b>	--	--	--	44%	56%	67%	--	--

Footnote: Data with gray net bottom implies the correlation between these two traits is positive.

**Table 17 Selection from Family Ranking—Use 13 months population B as Indicator**

	HT2	HT6	HT25	DBH25	DBA25	VOL25	GH25_6	GH6_2
<b>RD13</b>	--	--	--	--	--	--	--	--
<b>RL13</b>	--	89%	--	--	--	--	--	78%
<b>AFWT13</b>	--	--	--	--	--	--	--	--
<b>ADWT13</b>	--	--	--	--	--	--	--	--
<b>BFWT13</b>	--	--	--	--	--	--	--	--
<b>BDWT13</b>	--	--	--	--	--	--	--	--
<b>HT13</b>	56%	--	--	--	--	--	--	--
<b>T113</b>	--	--	--	--	--	--	--	--
<b>T213</b>	--	--	--	--	--	--	--	--
<b>SQ13</b>	--	44%	--	--	--	--	--	44%
<b>DQI13</b>	--	--	--	--	--	--	--	--

Footnote: Data with gray net bottom implies the correlation between these two traits is positive.

### 3.4 Simple Linear Regression of Population A and B

Since we already knew the juvenile and mature populations in our experiment indeed have correlation, the regression between these two populations is further examined. From Table 18 to Table 25 are the results of simple regression between traits, only those pairs which have significant correlations are taken to conduct in this step.

Nevertheless, all of the simple regression model show up has very poor power to explain the relation between two populations ( $r^2 < 0.5$ ), which implies the correlations are exist but may not be fitted in the regression model we used.

Among all of the models in Table 18 to Table 25, we can found that those in which have higher R-square values ( $r^2 > 0.4$ ) are gather up at HT25 and GH25\_6 with growth trait in 5 and 7 months, it is accordance with the discussion above that tree height in 25 years has significant correlation with juvenile period.

In Appendix 6 are parts of the simple regression figures from HT25. From the trend of the figures, they may help us to predict better regression models that can fit with our China-fir population.

Table 18 Simple regression models to estimate HT2 and the correlated traits of population B

Model	Regression equation	R square	DF
1	HT2=-0.05276+0.68595*( SQ7)	0.1928	17
2	HT2=0.27881+0.02030*(HT13)	0.2348	17

Table 19 Simple regression models to estimate HT6 and the correlated traits of population B

Model	Regression equation	R square	DF
1	HT6=3.18589+0.03746*( RL13)	0.2019	17
2	HT6=1.71184+1.13188*(SQ13)	0.2228	17

Table 20 Simple regression models to estimate HT25 and the correlated traits of population B

Model	Regression equation	R square	DF
1	HT25=23.91884-8.7702 *(RD5)	0.3844	17
2	HT25=28.91322-4.1029*(RL5)	0.3648	17
3	HT25=20.32634-8.08193*(AFWT5)	0.3504	17
4	HT25=20.38586-18.24616*(ADWT5)	0.3725	17
5	HT25=19.97066-10.14337*(BFWT5)	0.3825	17
6	HT25=19.75811-30.14016*(BDWT5)	0.3693	17
7	HT25=21.34509-0.74020 *(HT5)	0.3652	17
8	HT25=19.61928-46.99506*(DICKSON5)	0.3841	17
9	HT25=30.45042-12.04768 *(RD7)	0.4079	17
10	HT25=23.74447-2.19986 *(RL7)	0.1112	17
11	HT25=22.02028-6.58035 *(AFWT7)	0.3871	17
12	HT25=21.3089-12.267 *(ADWT7)	0.4200	17
13	HT25=21.03656-7.46516 *(BFWT7)	0.3988	17
14	HT25=20.28824-18.16605 *(BDWT7)	0.4496	17
15	HT25=26.28506-0.86218 *(HT7)	0.4406	17
16	HT25=6.54885+16.87627 *(T27)	0.3142	17
17	HT25=5.13347+11.30836 *(SQ7)	0.0546	17
18	HT25=20.41552-30.35295 *(DICKSON7)	0.4457	17
19	HT25=11.58907+11.08386 *(T29)	0.1736	17

Table 21 Simple regression models to estimate DBH25 and the correlated traits of population B

Model	Regression equation	R square	DF
1	DBH25=33.73453-5.79974*( AFWT7)	0.1738	17
2	DBH25=32.80231-10.18729*( ADWT7)	0.1674	17
3	DBH25=31.53992-13.570*( BDWT7)	0.1449	17
4	DBH25=31.95388-24.57193*( DICKSON7)	0.1688	17
5	DBH25=34.30498-5.66636*( AFWT9)	0.1775	17
6	DBH25=33.89977-10.13957*( ADWT9)	0.1823	17
7	DBH25=35.46152-6.99064*(BFWT9)	0.2315	17
8	DBH25=34.50829-16.01491*(BDWT9)	0.2392	17
9	DBH25=37.22808-0.6956 *(HT9)	0.1870	17
10	DBH25=24.63097+9.50071*(T29)	0.0737	17
11	DBH25=33.14726-21.35968*( DICKSON9)	0.1958	17

Table 22 Simple regression models to estimate DBA25 and the correlated traits of population B

Model	Regression equation	R square	DF
1	DBA25=41.48849-7.06669*( AFWT7)	0.0888	17
2	DBA25=40.42094-12.55255*( ADWT7)	0.1402	17
3	DBA25=39.38240-30.31789*( DICKSON7)	0.1418	17
4	DBA25=44.06515-8.95027*(BFWT9)	0.2094	17
5	DBA25=43.24369-21.46047*(BDWT9)	0.2370	17
6	DBA25=27.3428+20.65498 *(T29)	0.1923	17
7	DBA25=40.86942-26.41299 *( DICKSON9)	0.1652	17

Table 23 Simple regression models to estimate VOL25 and the correlated traits of population B

Model	Regression equation	R square	DF
1	VOL25=0.52216-0.21944*(RD5)	0.1819	17
2	VOL25=0.44787-0.22738*(AFWT5)	0.2096	17
3	VOL25=0.44732-0.50534*(ADWT5)	0.2159	17
4	VOL25=0.42794-0.26375*(BFWT5)	0.1954	17
5	VOL25=0.41332-0.72201*(BDWT5)	0.1601	17
6	VOL25=0.46821-0.01980*(HT5)	0.1976	17
7	VOL25=0.41602-1.19159 *(DICKSON5)	0.1866	17
8	VOL25=0.73282-0.33905 *(RD7)	0.2442	17
9	VOL25= 0.63022-0.08439*(RL7)	0.1237	17
10	VOL25=0.5016-0.19109*(AFWT7)	0.2467	17
11	VOL25=0.47733-0.34887*(ADWT7)	0.2567	17
12	VOL25= 0.46568-0.20719*(BFWT7)	0.2321	17
13	VOL25=0.44272-0.49621*(BDWT7)	0.2535	17
14	VOL25=0.57689-0.02122*(HT7)	0.2017	17
15	VOL25= 0.10912+0.38074*(T27)	0.1209	17
16	VOL25= 0.45256-0.86699*(DICKSON7)	0.2748	17
17	VOL25=0.50608-0.18234*(BFWT9)	0.2060	17
18	VOL25=0.48170-0.41887*(BDWT9)	0.2140	17
19	VOL25=0.53961-0.01722 *(HT9)	0.1498	17
20	VOL25=0.44660-0.56067*(DICKSON9)	0.1765	17

Table 24 Simple regression models to estimate GH25\_6 and the correlated traits of population B

Model	Regression equation	R square	DF
1	GH25_6=1.03908-0.46139*(RD5)	0.4437	17
2	GH25_6=1.30450-0.21665*(RL5)	0.4243	17
3	GH25_6=0.85527-0.43355*(AFWT5)	0.4206	17
4	GH25_6=0.85756-0.97554*(ADWT5)	0.4441	17
5	GH25_6=0.83426-0.53993*(BFWT5)	0.4520	17
6	GH25_6=0.82384-1.61038*(BDWT5)	0.4397	17
7	GH25_6=0.90891-0.03958*(HT5)	0.4356	17
8	GH25_6=0.89645-0.55963*(T15)	0.1435	17
9	GH25_6=0.81569-2.50299 *(DICKSON5)	0.4544	17
10	GH25_6=1.34037-0.60011*(RD7)	0.4221	17
11	GH25_6=1.03116-0.11606 *(RL7)	0.1291	17
12	GH25_6=0.92606-0.33328*(AFWT7)	0.4142	17
13	GH25_6=0.89265-0.62669*(ADWT7)	0.4572	17
14	GH25_6= 0.88386-0.38805*(BFWT7)	0.4494	17
15	GH25_6=0.84175-0.93256*(BDWT7)	0.4941	17
16	GH25_6=1.14201-0.04366*(HT7)	0.4713	17
17	GH25_6= 0.13364+0.87172*(T27)	0.3496	17
18	GH25_6=0.84645-1.54729 *(DICKSON7)	0.4831	17

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Table 25 Simple regression models to estimate GH6\_2 and the correlated traits of population B

Model	Regression equation	R square	DF
1	GH6_2=0.69835+0.00773*( RL13)	0.1739	17
2	GH6_2=0.37908+0.24049*(SQ13)	0.2035	17



## CHAPTER 4 DISCUSSION AND CONCLUSION

The premise conditions for estimate a population's viability for early selection are its heritability, family variance, and age-age correlation. In the results present in this paper, both of juvenile and elder populations are possessed these provisions. The target population, A, has very high individual heritability ( $h^2 = 0.35 \sim 0.62$ ) on most of its traits, two exceptions appear in 2 years height and 27 years wood density. It reveals that in this China-fir family, the genetic effect of tree height become much stronger after 6 years; but for the wood density, 27 years may still be too young to reach its genetic performance age. Aside from these, the others of population A are beneficial for the discussion of our selection, the significant of family variance and high-reaching of individual heritability are indispensable to the efficiently selection for next generation.

For the future establish of second generation seed orchard, the family No. 11, 20, 22, 24 have good average performance on mature tree height, DBA, and DBH; on the other side, family No. 5, 6, 10, 18, 23 are relatively poor on their average growth traits and can be eliminate.

Seldom studies has been conducted on the juvenile-mature correlations in the age under 1 year, most of the study indicate that heritability of growth traits tend to become stable after certain age and the value is usually higher then. In the case of age-age correlation has the same circumstances, usually the optimal age for early selection are suggested after 5 years plantation, some cases can lead to 10 years. In this study, the preliminary results had suggested that it would be optimistic for these two populations to conduct further testing on their correlation since our juvenile population has very good result on its heritability and between family variance.

The core finding demonstrated that these two single parent populations, which originated from a same China-fir clonal seed orchard, do have considerable age-age phenotypic correlations. Most excitingly, their correlation can trace back to 5, 7, 9 months old. In the 13 months, those fragmentary showed up correlations are needed for further survey. According to previous study on population B, the root of 13 months shoot had exposure from tubing, this is the uncertain factor for us to explain that whether in 13 months is truly lacking of correlation or not. If our outcome in 13 months is trustable, than it pointed out an important message, that is, from 9 months to 13 months the physical performance has tremendous change and it result in the transform of correlations with the target population. Moreover, its conversion is from negative correlation with elder age (25 years) of target group into positive correlation with parameter measured in younger age (2 and 6 years).

Although our attempt on using regression model to explain the correlation trend between two populations seems to be very weak, it may give us a hint that this model is unsuitable under this situation, or probably a bigger sample data is needed for the further estimation.

No matter the relationship within a population or between two populations, tree height and volume in mature age seems to be the most easily and earlier traits to be predict, Johnson et al.(1997) study on age-age correlation in Douglas-fir finds it consonant with the result here. From our working results, most of juvenile traits in shoot stage are useful to serve as criteria in China-fir family. The reliability of different traits may differ from populations and can be further examined by similar practice.

Some juvenile-mature correlation implications can be drawn from this study. First, the progeny testing can be carrying on in shoot period. Second, even though they are two different entity bodies, genetic effects within family are strong enough to control

the phenotype. With this information, we can start out selection in a very young age—5 to 9 months, which is far shorter compare to common early selection year, usually 2 to 10 years, not to mention the direct selection from rotation age.



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## CHAPTER 6 APPENDIX

**Appendix 1 ANOVA Table of A population**

<b>2H</b>	D.F.	S.S.	M.S.	F value	P value
Family	17	0.90466314	0.05321548	2.75	0.0004
Block	1	0.03698565	0.03698565	1.91	0.1687
F*B	16	1.13511192	0.07094450	3.66	<.0001
Error	197	3.81854931	0.01938350		
Total	231	5.97230862			
<b>6H</b>	D.F.	S.S.	M.S.	F value	P value
Family	17	19.08993131	1.12293714	2.03	0.0114
Block	1	3.08055234	3.08055234	5.56	0.0193
F*B	16	7.13698500	0.44606156	0.81	0.6784
Error	197	109.0843916	0.5537279		
Total	231	141.4872414			
<b>H25</b>	D.F.	S.S.	M.S.	F value	P value
Family	17	844.4983355	49.6763727	4.89	<.0001
Block	1	97.6038810	97.6038810	9.60	0.0022
F*B	16	360.9940550	22.5621284	2.22	0.0058
Error	197	2002.413076	10.164533		
Total	231	3242.764510			
<b>DBH25</b>	D.F.	S.S.	M.S.	F value	P value
Family	17	1130.495045	66.499709	2.05	0.0102
Block	1	371.852632	371.852632	11.48	0.0008
F*B	16	353.417655	22.088603	0.68	0.8098
Error	197	6379.683177	32.384179		
Total	231	8386.459138			
<b>DBA25</b>	D.F.	S.S.	M.S.	F value	P value
Family	17	1910.236455	112.366850	2.25	0.0043
Block	1	291.570123	291.570123	5.84	0.0166
F*B	16	961.418158	60.088635	1.20	0.2685
Error	197	9842.50145	49.96194		
Total	231	13195.17720			
<b>VOL25</b>	D.F.	S.S.	M.S.	F value	P value

Family	17	1.02117217	0.06006895	2.89	0.0002
Block	1	0.25757767	0.25757767	12.39	0.0005
F*B	16	0.45494303	0.02843394	1.37	0.1611
Error	197	4.09633295	0.02079357		
Total	231	5.76040427			
<b>WD27</b>	D.F.	S.S.	M.S.	F value	P value
Family	17	0.0417951	0.00245854	0.74	0.7606
Block	1	0.00102246	0.00102246	0.31	0.5801
F*B	16	0.07432022	0.00464501	1.40	0.1468
Error	197	0.65576296	0.00332875		
Total	231	0.76662990			
<b>GH6_2</b>	D.F.	S.S.	M.S.	F value	P value
Family	17	0.94937336	0.05584549	1.92	0.0179
Block	1	0.15265307	0.15265307	5.26	0.0229
F*B	16	0.38153726	0.02384608	0.82	0.6603
Error	197	5.71855891	0.02902822		
Total	231	7.33698481			
<b>GH25_6</b>	D.F.	S.S.	M.S.	F value	P value
Family	17	2.00715545	0.11806797	4.71	<.0001
Block	1	0.18283804	0.18283804	7.29	0.0075
F*B	16	0.88923714	0.05557732	2.22	0.0059
Error	197	4.93777439	0.02506484		
Total	231	7.86751994			

**Appendix 2 ANOVA Table of B population in 5 months**

<b>RD5</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	7.60680479	0.31695020	17.27	<.0001
Position	20	0.90031179	0.04501559	2.45	0.0005
Error	394	7.23286146	0.01835752		
Total	438	15.72662080			
<b>RL5</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	38.46934467	1.60288936	10.27	<.0001
Position	20	3.68031037	0.18401552	1.18	0.2685
Error	394	61.4852828	0.1560540		
Total	438	103.3965516			
<b>AFWT5</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	8.47874342	0.35328098	16.86	<.0001
Position	20	0.98532455	0.04926623	2.35	0.0010
Error	394	8.25566643	0.02095347		
Total	438	17.67764510			
<b>BFWT5</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	6.41098863	0.26712453	18.44	<.0001
Position	20	0.71473740	0.03573687	2.47	0.0005
Error	394	5.70768442	0.01448651		
Total	438	12.78897555			
<b>ADWT5</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	1.73114561	0.07213107	16.04	<.0001
Position	20	0.20271661	0.01013583	2.25	0.0017
Error	394	1.77143908	0.00449604		
Total	438	3.69577575			
<b>BDWT5</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	0.67429070	0.02809545	17.63	<.0001
Position	20	0.07391731	0.00369587	2.32	0.0012
Error	394	0.62779321	0.00159338		
Total	438	1.36935485			
<b>HT5</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	1031.243466	42.968478	13.39	<.0001
Position	20	117.719937	5.885997	1.83	0.0160
Error	394	1271.084201	3.209809		
Total	438	2419.455510			



<b>T15</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	2.62676043	0.10944835	5.62	<.0001
Position	20	0.70156379	0.03507819	1.80	0.0187
Error	394	7.66644635	0.01945799		
Total	438	11.00246244			
<b>T25</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	1.81598490	0.07566604	2.40	0.0003
Position	20	0.58497689	0.02924884	0.93	0.5531
Error	394	12.43527190	0.03156160		
Total	438	14.79303953			
<b>SQ5</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	1.54273505	0.06428063	4.53	<.0001
Position	20	0.28392807	0.01419640	1.00	0.4603
Error	394	5.59003337	0.01418790		
Total	438	7.42425137			
<b>DQI5</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	0.27521945	0.01146748	19.42	<.0001
Position	20	0.03275688	0.00163784	2.77	<.0001
Error	394	0.23269477	0.00059060		
Total	438	0.53810906			

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**Appendix 3 ANOVA Table of B population in 7 months**

<b>RD7</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	3.67646688	0.15318612	7.98	<.0001
Position	20	0.31417143	0.01570857	0.82	0.6918
Error	357	6.85595821	0.01920436		
Total	401	10.88917261			
<b>RL7</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	42.49904719	1.77079363	5.33	<.0001
Position	20	6.65942723	0.33297136	1.00	0.4577
Error	357	118.5142182	0.3319726		
Total	401	167.9458355			
<b>AFWT7</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	11.11704368	0.46321015	8.46	<.0001
Position	20	0.92156652	0.04607833	0.84	0.6625
Error	357	19.55314643	0.05477072		
Total	401	31.53700024			
<b>BFWT7</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	9.49953619	0.39581401	9.72	<.0001
Position	20	0.58291024	0.02914551	0.72	0.8101
Error	357	14.53166188	0.04070494		
Total	401	24.58961159			
<b>ADWT7</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	3.55861362	0.14827557	10.20	<.0001
Position	20	0.24292113	0.01214606	0.84	0.6696
Error	357	5.18877912	0.01453440		
Total	401	8.97987622			
<b>BDWT7</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	1.82072023	0.07586334	13.98	<.0001
Position	20	0.07272487	0.00363624	0.67	0.8556
Error	357	1.93737272	0.00542681		
Total	401	3.83480176			
<b>HT7</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	776.4027532	32.3501147	5.00	<.0001
Position	20	116.3071119	5.8153556	0.90	0.5885
Error	357	2315.371371	6.467518		
Total	401	3207.773648			

<b>T17</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	2.93942426	0.12247601	9.65	<.0001
Position	20	0.29319277	0.01465964	1.16	0.2913
Error	357	4.52950455	0.01268769		
Total	401	7.75509125			
<b>T27</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	1.70296026	0.07095668	3.56	<.0001
Position	20	0.41996952	0.02099848	1.05	0.3970
Error	357	7.10881320	0.01991264		
Total	401	9.23064194			
<b>SQ7</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	0.64572496	0.02690521	3.54	<.0001
Position	20	0.14245021	0.00712251	0.94	0.5398
Error	357	2.71307291	0.00759964		
Total	401	3.52814354			
<b>DQI7</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	0.63345049	0.02639377	13.28	<.0001
Position	20	0.03428639	0.00171432	0.86	0.6359
Error	357	0.70976163	0.00198813		
Total	401	1.37891995			

**Appendix 4 ANOVA Table of B population in 9 months**

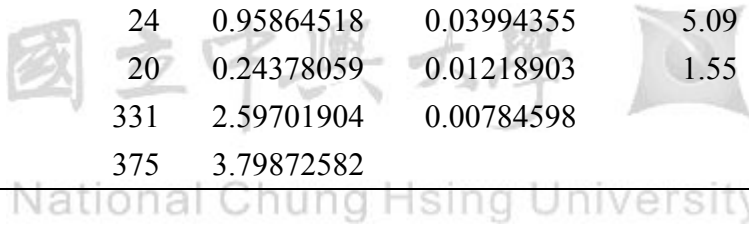
<b>RD9</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	8.11720801	0.33821700	10.37	<.0001
Position	20	0.54314347	0.02715717	0.83	0.6734
Error	319	10.40614103	0.03262113		
Total	363	19.29512178			
<b>RL9</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	44.36280715	1.84845030	2.96	<.0001
Position	20	17.40012574	0.87000629	1.39	0.1229
Error	319	199.2057263	0.6244694		
Total	363	261.9307786			
<b>AFWT9</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	14.27998006	0.59499917	9.46	<.0001
Position	20	1.07531487	0.05376574	0.85	0.6451
Error	319	20.06198504	0.06289024		
Total	363	35.76820780			
<b>BFWT9</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	14.08927562	0.58705315	6.62	<.0001
Position	20	1.44022781	0.07201139	0.81	0.6992
Error	319	28.29854759	0.08871018		
Total	363	44.16912786			
<b>ADWT9</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	4.54347535	0.18931147	9.03	<.0001
Position	20	0.36915956	0.01845798	0.88	0.6123
Error	319	6.68627361	0.02096011		
Total	363	11.70062689			
<b>BDWT9</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	2.67159066	0.11131628	6.97	<.0001
Position	20	0.22573181	0.01128659	0.71	0.8197
Error	319	5.09745002	0.01597947		
Total	363	8.05937792			
<b>HT9</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	1026.975718	42.790655	6.96	<.0001
Position	20	139.854125	6.992706	1.14	0.3093
Error	319	1967.025662	6.146955		
Total	363	3161.545041			

<b>T19</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	1.73073420	0.07211393	3.87	<.0001
Position	20	0.32626230	0.01631311	0.88	0.6183
Error	319	5.94104697	0.01862397		
Total	363	8.03046100			
<b>T29</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	2.05698542	0.08570773	3.71	<.0001
Position	20	0.37146890	0.01857344	0.80	0.7093
Error	319	7.37297950	0.02311279		
Total	363	9.83545183			
<b>SQ9</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	0.23157594	0.00964900	9.16	<.0001
Position	20	0.02774826	0.00138741	1.32	0.1649
Error	319	0.33585515	0.00105284		
Total	363	0.59660047			
<b>DQI9</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	1.13627731	0.04734489	8.44	<.0001
Position	20	0.08984299	0.00449215	0.80	0.7121
Error	319	1.78842648	0.00560635		
Total	363	3.04284269			

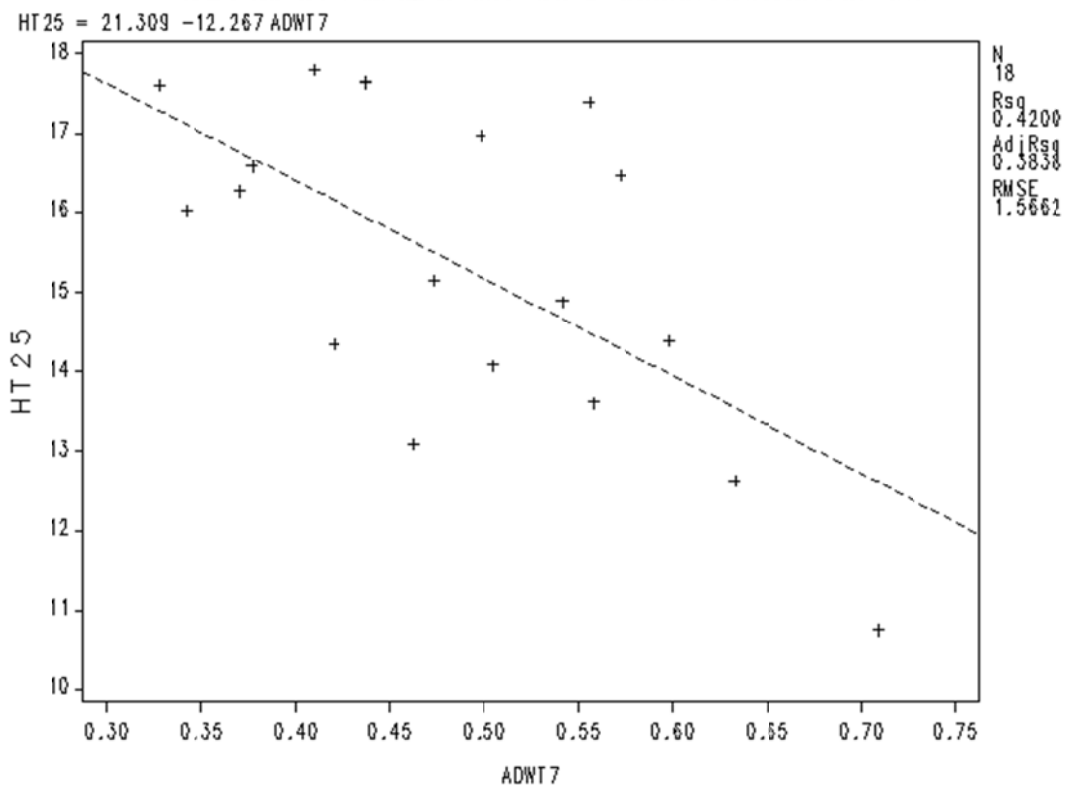
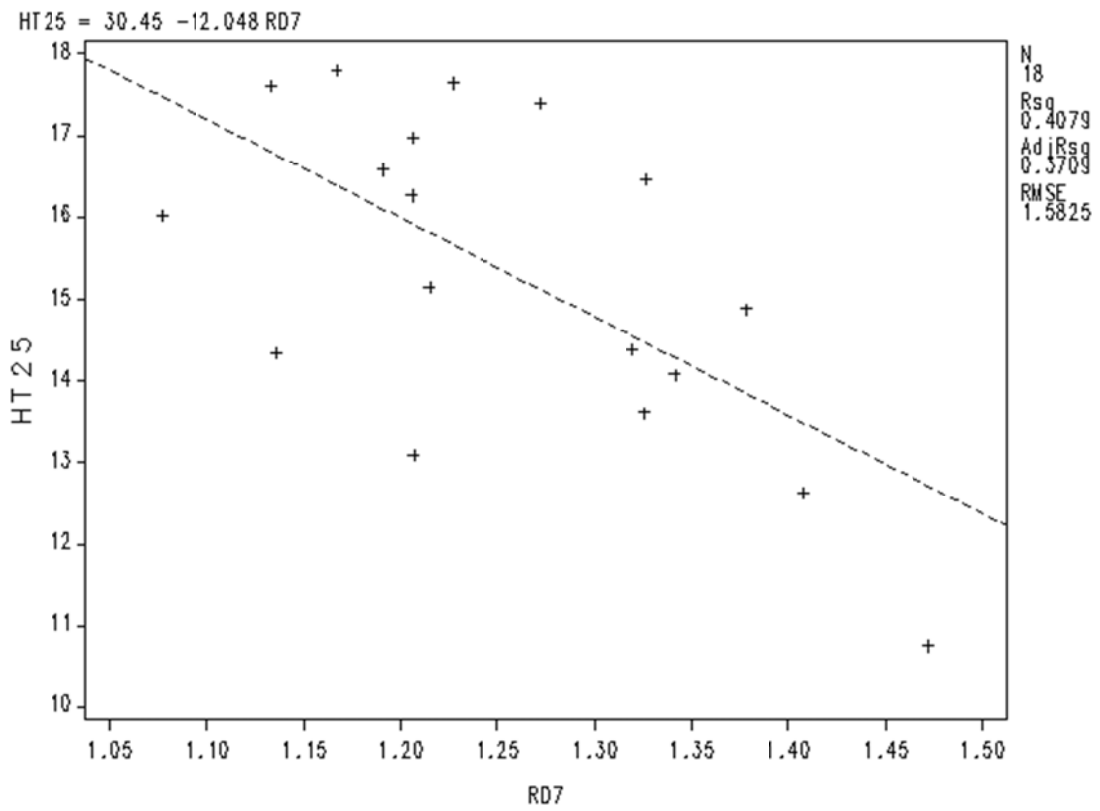
**Appendix 5 ANOVA Table of B population in 13 months**

<b>RD13</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	1.26195026	0.05258126	5.87	<.0001
Position	20	0.36742005	0.01837100	2.05	0.0055
Error	331	2.96677153	0.00896306		
Total	375	4.61582515			
<b>RL13</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	3392.790014	141.366251	2.19	0.0013
Position	20	1342.693975	67.134699	1.04	0.4139
Error	331	21364.25084	64.54456		
Total	375	26150.95338			
<b>AFWT13</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	22.61244148	0.94218506	4.56	<.0001
Position	20	6.30128948	0.31506447	1.52	0.0707
Error	331	68.41654891	0.20669652		
Total	375	97.03666928			
<b>BFWT13</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	221.3268093	9.2219504	4.52	<.0001
Position	20	49.9663986	2.4983199	1.23	0.2305
Error	331	674.8819617	2.0389183		
Total	375	945.3228500			
<b>ADWT13</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	4.27556786	0.17814866	4.55	<.0001
Position	20	1.45055788	0.07252789	1.85	0.0151
Error	331	12.95427402	0.03913678		
Total	375	18.62444539			
<b>BDWT13</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	3.74717180	0.15613216	4.22	<.0001
Position	20	0.97301023	0.04865051	1.31	0.1664
Error	331	12.24821475	0.03700367		
Total	375	16.92992761			
<b>HT13</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	858.7978585	35.7832441	4.79	<.0001
Position	20	276.3453626	13.8172681	1.85	0.0154
Error	331	2474.117681	7.474676		
Total	375	3610.260000			

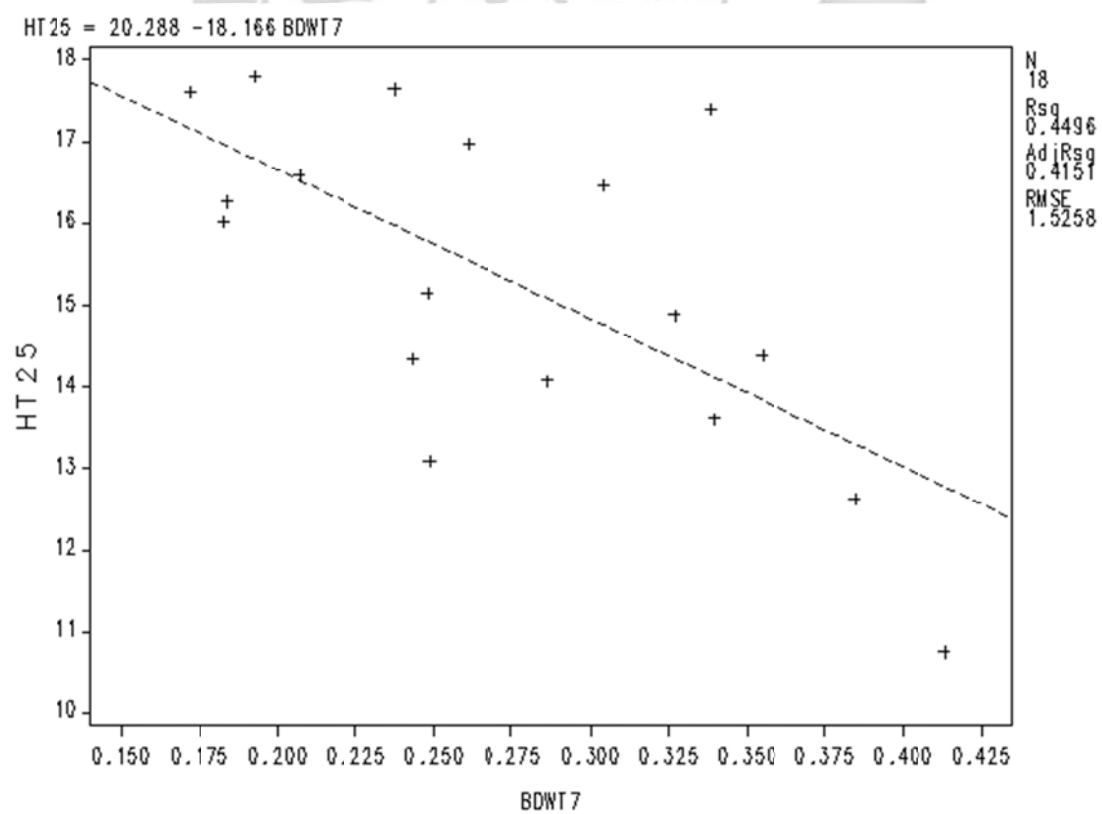
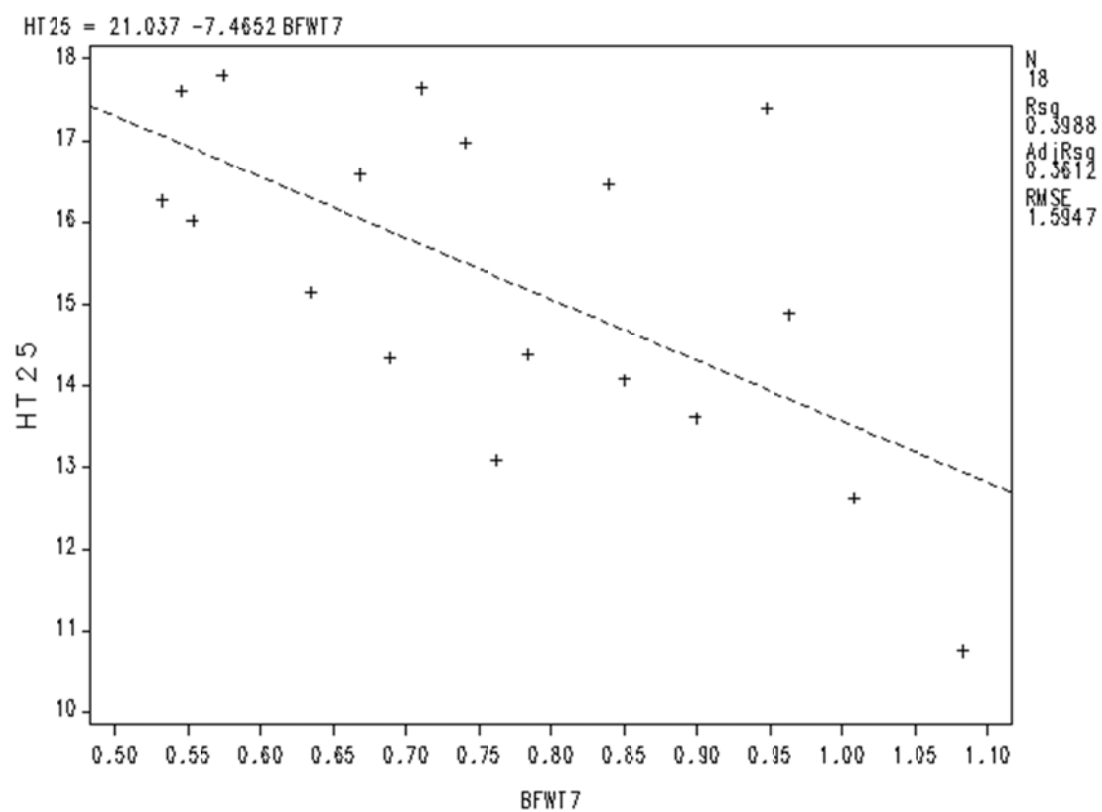
<b>T113</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	0.94468575	0.03936191	1.93	0.0062
Position	20	0.19794457	0.00989723	0.49	0.9712
Error	331	6.74815614	0.02038718		
Total	375	7.89782287			
<b>T213</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	3.09775430	0.12907310	2.88	<.0001
Position	20	0.51365368	0.02568268	0.57	0.9301
Error	331	14.83561777	0.04482060		
Total	375	18.47215444			
<b>SQ13</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	83.63606409	3.48483600	3.96	<.0001
Position	20	24.27365364	1.21368268	1.38	0.1261
Error	331	420.3544045	0.8794025		
Total	375	528.3020355			
<b>DQI13</b>	D.F.	S.S.	M.S.	F value	P value
Family	24	0.95864518	0.03994355	5.09	<.0001
Position	20	0.24378059	0.01218903	1.55	0.0622
Error	331	2.59701904	0.00784598		
Total	375	3.79872582			



**Appendix 6 Figure of Simple regression models of HT25 and the correlated traits of population B**







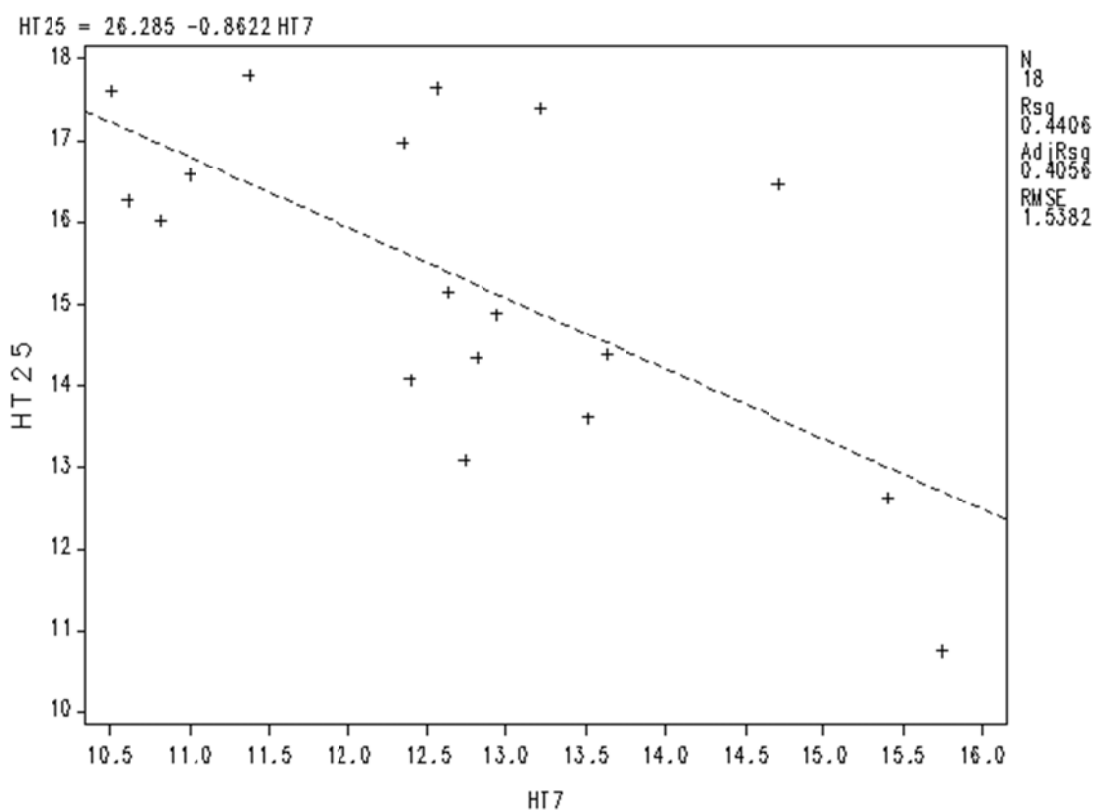


圖 2 訂正後之件

