

Article

Variation in the Growth Traits and Wood Properties of Chinese Fir from Six Provinces of Southern China

Hongjing Duan ¹, Sen Cao ¹, Huiquan Zheng ², Dehuo Hu ², Jun Lin ³, Huazhong Lin ⁴, Ruiyang Hu ¹, Yuhan Sun ¹ and Yun Li ^{1,*}

¹ National Engineering Laboratory for Tree Breeding, Key Laboratory of Genetics and Breeding in Forest Trees and Ornamental Plants, Ministry of Education, College of Biological Sciences and Technology, Beijing Forestry University, Beijing 100083, China; duan673356712@126.com (H.D.); sailingcs@163.com (S.C.); hury1102@163.com (R.H.); syh831008@163.com (Y.S.)

² Guangdong Provincial Key Laboratory of Bio-control for the Forest Disease and Pest, Guangdong Academy of Forestry, Guangzhou 510520, Guangdong, China; zhenghq@sinogaf.cn (H.Z.); hudehuo@163.com (D.H.)

³ The ex situ gene bank of Longshan State Forest Farm, Lechang 512221, Guangdong, China; m13902346498@163.com

⁴ Jiangle National Forest Farm, Sanming 353300, Fujian, China; fjsmllhz@sina.com

* Correspondence: yunli@bjfu.edu.cn; Tel./Fax: +86-10-6233-6094

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Abstract: To determine the phenotypic variation in 700 ten-year grafted Chinese fir collected from six provinces in southern China, 10 phenotypic traits were investigated: tree height, diameter at breast height, bark thickness, volume of timber, heartwood ratio, density of wood, hygroscopicity, tracheid length, tracheid diameter, and ratio of tracheid length to tracheid diameter. Abundant phenotypic variation was found among the six populations; the phenotypic variation coefficients all exceeded 10%, and the largest was for volume of timber. Significant variation ($p < 0.01$ or 0.05) in traits was found among the populations, except for diameter at breast height, heartwood ratio, and tracheid diameter, while all traits differed significantly ($p < 0.01$) within populations. The high value of repeatability (broad-sense heritability) suggested moderate genetic control of the traits. The 10 traits were strongly correlated within the entire population; strong positive correlations ($p < 0.01$) were observed between growth traits, and significant negative correlations ($p < 0.01$ or 0.05) were found between the density of wood and most other characteristics, except for heartwood ratio and ratio of tracheid length to tracheid diameter. Using diameter at breast height and density of wood as criteria, 98 relatively fast-growing genotypes with relatively high wood basic density were identified.

Keywords: Chinese fir; phenotypic variation; growth traits; wood properties; correlation

1. Introduction

The forest ecosystems on Earth provide about 82% of the continental biomass and more than 50% of terrestrial biodiversity [1,2], the economic and commercial values of which are affected directly by wood quality. The abundant variation in the traits of trees strengthens their ability to adapt to different environmental conditions and provides the potential for the selection of trees with desirable traits [3–5]. An important reason to breed trees is to increase the quantity and quality of wood. Wood properties are closely related to the complex biological processes of wood formation under cambial activity [6–8], and most traits are complex, quantitative, and associated and regulated by multiple genes [9,10]. A better understanding of the variation in these traits of trees can enhance the use of germplasm collection and elucidate the genetic basis of phenotypic variation [11]. In addition, to maximize the genetic gain in important traits, variation in and correlations between growth and wood quality must be assessed.