

Inbreeding in Chinese fir: Insights into the adaptive growth traits of selfed progeny from mRNA, miRNA and copy number variation view

Houyin Deng^{1,2}, Rong Huang², Ruping Wei², Runhui Wang², Shu Yan², Yousry A. El-Kassaby³, Yuhan Sun¹, Yun Li^{1,†}, Huiquan Zheng^{2,†}

(1. State Key Laboratory of Tree Genetics and Breeding, National Engineering Research Center of Tree Breeding and Ecological Restoration, College of Biological Sciences and Technology, Beijing Forestry University, Beijing 100083, People's Republic of China; 2. Guangdong Provincial Key Laboratory of Silviculture, Protection and Utilization; Guangdong Academy of Forestry, Guangzhou 510520, People's Republic of China; 3. Department of Forest and Conservation Sciences Faculty of Forestry, The University of British Columbia, 2424 Main Mall, Vancouver, BC V6T 1Z4, Canada;)

Abstract: **【Objective】** The impact of inbreeding on biological processes is well-documented in severely depressed individuals. However, the biological processes influencing the adaptive growth of selfed normal individuals are unknown. Here, we aimed to investigate how inbreeding affects gene expression for adaptive growth of selfed normal seedlings (NS) from a self-fertilizing parent in Chinese fir (*Cunninghamia lanceolata* (Lamb.) Hook.). **【Method】** Using RNA-seq data from above- and under-ground tissues of selfed abnormal seedlings (AS) and NS, we conducted GO biological processes network analyses. We also performed small RNA-Seq on the above-ground tissues and measured the copy number variations (CNV) of the hub genes. **【Result】** Phenotypic fitness analysis revealed that NS were more adapted than their AS counterparts. The up-regulated differentially expressed genes (DEGs) were associated with development processes, while the down-regulated DEGs were mainly enriched in fundamental metabolism and stress response. mRNA-miRNA parallel sequencing revealed up-regulated target genes predominantly associated with development, highlighting their crucial role of phosphorylation in signal transduction networks. Additionally, we discovered moderate correlation ($0.1328 < R^2 < 0.6257$) between CNV and gene expression levels for three hub genes (TMKL1, GT2, and RHY1A). **【Conclusion】** We uncovered the key biological processes underpinning the growth of selfed normal seedlings and established the relationship between CNV and the expression levels of hub genes in selfed seedlings. Understanding the candidate genes involved in the growth of selfed seedlings will help us comprehend the genetic mechanisms behind inbreeding depression in the evolutionary biology of plants.