



Transcriptional regulation of chilling stress responsive long noncoding RNAs in *Populus simonii*

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Abstract

Key message We report genome-wide identification and functional prediction of lncRNAs under chilling stress, the present study deepened our understanding of the transcriptional regulation mechanism of poplar under chilling stress.

Abstract Chilling stress is a major threat to tree development and survival. Long noncoding RNAs (lncRNAs) are known to play a role in plant stress responses, but their transcriptional regulatory network remains elusive. We conducted genome-wide identification and functional prediction of lncRNAs under chilling stress in an ecologically important poplar species, *Populus simonii*. After the chilling treatment, we detected 30,769 genes and 10,186 putative lncRNAs, of which 13,172 genes and 5082 lncRNAs were differentially expressed under chilling stress in *P. simonii*. From these chilling-responsive transcripts, we hypothesized that five unique patterns of 21 lncRNAs acted directly on genes, and 617 lncRNAs affected gene expression by interacting with microRNAs (miRNAs). Additionally, the significantly differentially expressed genes were enriched to 198 gene ontology (GO) terms, which were prominently involved in photosynthesis and endogenous phytohormone synthesis pathways. Based on the physiological index, we found 48 genes with 15 lncRNAs, and 70 genes with 50 lncRNAs that were significantly differentially expressed in photosynthesis and endogenous phytohormone synthesis pathways, respectively. These findings improve our understanding of the potential functions of lncRNAs by refining the regulatory roles of lncRNAs in the photosynthesis and phytohormone synthesis pathways.

Keywords Chilling stress · Long noncoding RNA · Photosynthesis · Phytohormone synthesis · Regulatory network

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Introduction

In the long-term evolution of plants, temperature has always been a major environmental constraint, with severe effects on plant growth and development (Morison and Lawlor 1999). Chilling stress, exposure to extreme temperatures lower than 15 °C and higher than 0 °C, frequently occurs in many geographical areas and has captured the attention of researchers. Chilling stress is the main limiting environmental factor that has broad-spectrum effects on the productivity, quality, and viability of many plants. Its influences include, but are not limited to, cellular components (Xiong et al. 2002; Yan 2005), photosynthesis rates (Allen and Ort 2001), enzyme activity (Li et al. 2011), electron transport, and carbohydrate metabolism (Fryer et al. 1998). Additionally, gene expression levels often change significantly to adjust to extreme temperatures, performing a vital function in anti-stress physiological processes in plants.

Unlike coding genes, long noncoding RNAs (lncRNAs), which are non-coding and greater than 200 nucleotides (nt)