

Dissection of additive, dominant, epistatic roles of allelic variation within heat shock factor genes in Chinese indigenous poplar (*Populus simonii*)

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Abstract Heat shock transcription factors (Hsfs) play a crucial role in plant growth and development, but the significance of *Hsfs* is not clearly understood in long-lived perennial plants. Here, two class A *Hsf* members (*PsHsfA1c1* and *PsHsfA7a1*) were identified in *Populus simonii*, an important and pioneering species in northern China, using bioinformatics analysis and molecular cloning. Tissue-specific expression profiling showed that both *Hsfs* contained high transcript abundance in mature leaf, mature xylem, and root; also, their expression patterns varied in response to multiple abiotic stresses, such as temperature, drought, salt, hormone, and sugar, suggesting that *Hsfs* are essential in plant responses to diverse abiotic stresses. Based on nucleotide diversity ($\pi_T = 0.00772$, $\theta_w = 0.01519$ and $\pi_T = 0.00392$,

$\theta_w = 0.00899$) and linkage disequilibrium tests (LD, $r^2 \geq 0.1$, within 1200 and 700 bp, respectively) within *PsHsfA1c1* and *PsHsfA7a1* in a *P. simonii* association population (607 unrelated individuals), we identified 45, 49, and 26 associations consistent with additive, dominant, and epistatic effects, conferred by multiple variants within both genes across 12 morphological and physiological traits. In which, three significant SNPs (*PsHsfA1c1*_2273, *PsHsfA7a1*_308, and *PsHsfA7a1*_2595) exhibited significant differences of transcript abundance among their genotypic classes in the association population. The results observed here will be useful to understand their potential roles in tree growth, development, and response to environmental stresses.

Qingzhang Du and Zunzheng Wei contributed equally to this work.

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Introduction

Unique among terrestrial organisms, trees have large sizes, long lifespans, and woody, perennial growth; trees also regularly experience changing climatic fluctuations in their widely distributed populations. Many tree species natively occur in environments that harbor a wealth of diversity arising from both genetic and environmental factors. Also, tree survival and reproduction depend upon an array of protective mechanisms that involve the activation of a network of interconnected cellular stress response systems (Ahuja et al. 2010; Giorno et al. 2012). In plants, a wide range of transcription factors and their products play central roles in the response to extreme conditions (Giorno et al. 2012). For example, members of the heat shock transcription factor (*Hsf*) family function as