

Genome-wide identification of the *bHLH* transcription factor family and the regulatory roles of *PbbHLH74* in response to drought stress in *Phoebe bournei*

Ning-Ning Fu Li Wang Qing-Lin Sun Qi-Guang Wang Yu-Ting Zhang Xiao Han Qi Yang¹ Zai-Kang Tong* Jun-Hong Zhang*

(State Key Laboratory of Subtropical Silviculture, School of Forestry & Biotechnology, Zhejiang A&F University, Lin'an, Hangzhou 311300, Zhejiang, China)

Abstract: *Phoebe* species constitute a large portion of subtropical forestry, which are a key player in biomass resources. Basic helix-loop-helix (*bHLH*) as the second largest transcription factor family plays essential roles in response to multiple stresses in plants. However, little information of *bHLH* family is available in *Phoebe bournei*. In this study, 130 *PbbHLHs* were identified and classified into 24 subfamilies. The *bHLH* domain, conserved motifs and gene structures, evolutionary patterns and protein structural features were probed. The expression of 17 *PbbHLHs* was differentially induced by PEG and ABA, indicating that they may play essential roles in drought stress response. *PbbHLH74* was transcriptionally active and localized in the nucleus. *PbbHLH74* heterologous transformation of yeast improved cellular drought tolerance. Overexpressing *PbbHLH74* in *Arabidopsis* enhanced drought resistance by increasing the expression levels of stress-related genes. Transgenic *PbbHLH74 P. bournei* by hairy-rooting improved drought tolerance by enhancing root development and expression levels of genes involved in the ABA pathway and ROS scavenging. Moreover, *PbbHLH74* might positively regulate the expression of *PbPOD* by Y1H and dual-luciferase reporter assays. Overall, these results elucidated the structure and evolution of the *PbbHLH* family and *PbbHLH74* could be applied to molecular assisted breeding for drought tolerance in *P. bournei*.