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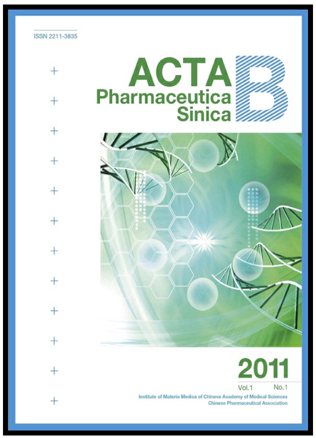

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ORIGINAL ARTICLE

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Genome-wide characterization and analysis of bHLH transcription factors in *Panax ginseng*

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Abstract Ginseng (*Panax ginseng* C.A. Meyer) is one of the best-selling herbal medicines, with ginsenosides as its main pharmacologically active constituents. Although extensive chemical and pharmaceutical studies of these compounds have been performed, genome-wide studies of the basic helix-loop-helix (bHLH) transcription factors of ginseng are still limited. The bHLH transcription factor family is one of the largest transcription factor families found in eukaryotic organisms, and these proteins are involved in a myriad of regulatory processes. In our study, 169 bHLH transcription factor genes were identified in the genome of *P. ginseng*, and phylogenetic analysis indicated that these PGbHLHs could be classified into 24 subfamilies. A total of 21 RNA-seq data sets, including two sequencing libraries for jasmonate (JA)-responsive and 19 reported libraries for organ-specific expression analyses were constructed. Through a combination of gene-specific expression patterns and chemical contents, 6 PGbHLH genes from 4 subfamilies were revealed to be potentially involved in the regulation of ginsenoside biosynthesis. These 6 PGbHLHs, which had distinct target genes, were further divided into two groups depending on the absence of MYC-N structure. Our results would provide a foundation for understanding the molecular basis and regulatory mechanisms of bHLH transcription factor action in *P. ginseng*.

1. Introduction

Ginseng (*Panax ginseng* C.A. Meyer), belonging to the order Apiales and family Araliaceae, has been widely used as a medicinal and functional food for over 5000 years in East Asia. The genus name “*Panax*” means

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