Whole-transcriptome sequencing of *Pinellia ternata* using the Illumina platform

X. Huang, Y. Jing, D.J. Liu, B.Y. Yang, H. Chen and M. Li

Ministry of Education Key Laboratory of Standardization of Chinese Herbal Medicine, College of Pharmacy, Chengdu University of Traditional Chinese Medicine, Chengdu, Sichuan, China

Corresponding author: M. Li
E-mail: 028limin@163.com

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ABSTRACT. *Pinelliae rhizoma* is the dried tuber of *Pinellia ternata* (Thunb.) Breit., and has been used for thousands of years as a traditional Chinese medicine. However, its genomic background is little known. With the development of high-throughput genomic sequencing, it is now easy and cheap to obtain genomic information. In this study, 193,032,910 high-quality clean reads were generated using the Illumina Hiseq 2000 platform. A total of 53,544 unigenes were identified from the contigs assembled. Functional annotation analysis annotated 37,318, 27,697, 23,043, 22,869, 23,328, and 27,415 unigenes. KEGG analysis revealed that five pathways (169 genes) were associated with alkaloid synthesis, 201 unigenes were related to fatty acid biosynthesis (ko00061), and 133 unigenes were involved in the biosynthesis of unsaturated fatty acids (ko01040). In addition, 6703 simple sequence repeats were designed based on the unigene sequences for screening germplasm resources in the future. These data are a valuable resource for genomic studies on *Pinellia* plants.

Key words: *Pinellia ternata*; Next-generation sequencing; Organic acids; Alkaloid