

Molecular identification and phylogenetic analysis of important medicinal plant species in genus *Paeonia* based on rDNA-ITS, *mat*K, and *rbc*L DNA barcode sequences

W.J. Kim, Y. Ji, G. Choi, Y.M. Kang, S. Yang and B.C. Moon

K-herb Research Center, Korea Institute of Oriental Medicine, Yuseong-daero, Yuseong-gu, Daejeon, Republic of Korea

Corresponding author: BC Moon E-mail: bcmoon@kiom.re.kr

Genet. Mol. Res. 15 (3): gmr.15038472 Received January 20, 2016 Accepted March 11, 2016 Published August 5, 2016 DOI http://dx.doi.org/10.4238/gmr.15038472

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ABSTRACT. This study was performed to identify and analyze the phylogenetic relationship among four herbaceous species of the genus *Paeonia*, *P. lactiflora*, *P. japonica*, *P. veitchii*, and *P. suffruticosa*, using DNA barcodes. These four species, which are commonly used in traditional medicine as Paeoniae Radix and Moutan Radicis Cortex, are pharmaceutically defined in different ways in the national pharmacopoeias in Korea, Japan, and China. To authenticate the different species used in these medicines, we evaluated rDNA-internal transcribed spacers (ITS), *mat*K and *rbc*L regions, which provide information capable of effectively distinguishing each species from one another. Seventeen samples were collected from different geographic regions in Korea and China, and DNA barcode regions were amplified using universal primers. Comparative analyses of these DNA barcode

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sequences revealed species-specific nucleotide sequences capable of discriminating the four *Paeonia* species. Among the entire sequences of three barcodes, marker nucleotides were identified at three positions in *P. lactiflora*, eleven in *P. japonica*, five in *P. veitchii*, and 25 in *P. suffruticosa*. Phylogenetic analyses also revealed four distinct clusters showing homogeneous clades with high resolution at the species level. The results demonstrate that the analysis of these three DNA barcode sequences is a reliable method for identifying the four *Paeonia* species and can be used to authenticate Paeoniae Radix and Moutan Radicis Cortex at the species level. Furthermore, based on the assessment of amplicon sizes, inter/intra-specific distances, marker nucleotides, and phylogenetic analysis, rDNA-ITS was the most suitable DNA barcode for identification of these species.

Key words: DNA barcode; *Paeonia* species; rDNA-ITS; *mat*K; *rbc*L; Species discrimination

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