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Comparative analysis of *Paeonia suffruticosa* based on the ITS sequences of nuclear ribosomal DNA

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Moutan Cortex is the cortex radicis of *Paeonia suffruticosa*. The internal transcribed spacer (ITS) sequences of nuclear ribosomal DNA sequence were compared by using fresh leaf and dried root of Moutan cortex. The result of comparing the ITS regions of ITS1 and ITS4 in Moutan Cortex by using PCR, there were same sequences between fresh leaf and dried root cortex, and the analyzed 11 samples that was collected from Korea and China did show 99% of homology. By comparing the base sequence of *Paeonia suffruticosa* on to the ITS region of NCBI (National Center for Biotechnology Information) GenBank, the samples from 3 regions showed 1 bp difference with U27692, and C base in 448 bp was deleted. The base sequence showing the identical result as the current study result was newly registered in GenBank (bankit019310). Although the dry root cortex showed the same result as the fresh leaf, and the most similar plants to Moutan Cortex were found to *be P. lutea, P. delavayi*, and *P. coriacea*. It was possible to identify *P. suffruticosa*, and it could be used in the differentiation of Moutan Cortex.
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A Phylogenetic Comparison of *Phellodendron* species using *rbcL* intergenic space and ITS sequence

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Phellodendron amurense Ruprecht or *P. chinense* Schneider (*Rutaceae*) is used as a herbal medicine. For the base sequence analysis for *Phellodendron* species, the fresh leaves of it was collected in Korea and China, and the dried *Phellodendri* cortex medicine was collected to be used in total 20 samples. In the result of analyzing the base sequence of *rbcL* intergenic space of chloroplast DNA, 17 samples revealed to show 99% homology to *P. amurense* (AF066804) that is registered in the NCBI (National Center for Biotechnology information), and 16 samples excluding 1 sample revealed 100% identity. However, the specific-site detection by analyzing the *rbcL* intergenic space was difficult by showing 100% identity of base sequence in all of *P. amurense, P. amurense* Ruprecht var. *latifoliatum* and *P. sacharinensis*. The base sequence of ITS 1 and 2 regions in nuclear DNA was corresponded to the base sequence of fungi or to other bacterial base sequence disabling the comparison analysis of *Phellodendron* species. For future identification of *Phellodendron* species, the chloroplast DNA or others has to be used for the analysis.
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