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Differentiation and authentication of *Panax ginseng* (Korea and China), *Panax quinquefolius*, and development of genetic marker by AFLP analysis

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Objectives

In this study, convenient and reproducible method for the identification of various kinds of ginseng (Korean cultivated and wild ginseng, Chinese wild ginseng, American cultivated and wild ginseng) was developed by amplified fragment length polymorphism (AFLP) analysis.

Materials and Methods

1. Plant materials : *Panax ginseng* {Korea (wild and cultivar) and China (wild)}, *Panax quinquefolius* (Wild and cultivar)
2. Isolation of genomic DNA : the genomic DNA was extracted from leaves or roots according to Plant DNeasy Mini kit (Qiagene) protocol.
3. Digestion of genomic DNA and adapter ligation : 2 μg of DNA was digested with 10 units of two restriction enzymes (*EcoR* I and *Mse* I) for 7 h and ligatied with adapter for 12 h.
4. PCR and acrylamide gel electrophoresis : PCR reaction were preformed using Ex-*Taq* polymerase (TaKaRa) and 4 μl of the reaction were separated in a 6% denaturing polyacrylamide gel. The DNA bands were visualized by silver staining method.
5. Statistical analysis : similarity matrix were analysis using the NTSYS-PC program with UPGMA.

Results and Discussion

The genetic distance coefficients between the *P. ginseng* and *P. quinquefolius* were high, ranging from 0.573 to 0.692, whereas samples of *P. ginseng* (cultivated and wild type) from the different area in Korea and China were very low, ranging from 0.056 to 0.164. By detailed AFLP analysis, some important different bands between wild type of *P. ginseng* from Korea and China were obtained. These results support that this approach could be applied to distinguish Korean ginseng (*Panax ginseng*) from others (Chinese and American ginseng) and to authenticate cultivated and wild ginseng at the molecular level.

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