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Comparative analysis of complete chloroplast genome sequence of two *Aconitum* species and in the family Ranunculaceae

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Aconitum species are well known herbaceous medicinal ingredient as well as toxic material and has great economic value in Asian countries. However, genomic information is still limited in Ranunculaceae. In this study, we completed chloroplast genome sequence of two *Aconitum* species, *A. coreanum* and *A. carmichaelii*, based on the Illumina MiSeq platform. The gene order, gene content and orientation of two *Aconitum* chloroplast genomes exhibit the general structure of flowering plants and are similar to other *Aconitum* species. The two *Aconitum* chloroplast genomes are 155,880 and 157,040 bp in length, respectively and contain 131 unique functional genes including 86 protein coding gene, 8 rRNA and 37 tRNA. We established genetic relationship of *Aconitum* species and Ranunculaceae through phylogenetic tree based on 71 protein coding genes of 19 angiosperms. Comparison of the chloroplast genome structure and gene order to those of *Aconitum* species revealed general contraction and expansion of the inverted repeat region (IR) and single copy boundary regions. We obtained barcoding target sequence and developed SCAR marker helpful for discrimination of the *Aconitum* species. These results suggest that the sequence variables of chloroplast genome could provide the useful genetic information and development of molecular marker for discrimination to identify *Aconitum* species.

Biography

Inkyu Park is a Senior Research Scientist at the Korea Institute of Oriental Medicine (KIOM), South Korea. He has completed his PhD from Chungnam National University, Republic of Korea. His research has centered upon chloroplast genome study with development molecular marker and plastid evolution.

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