




## The complete chloroplast genome of *Aconitum coreanum* (H. Lév.) Rapaics (Ranunculaceae)

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### ABSTRACT

*Aconitum coreanum* (H. Lév.) Rapaics listed in the Korean Red List is a medicinal herb. We presented complete chloroplast genome, which is 157,024 bp long and has four subregions: 87,637 bp of large single-copy and 16,901 bp of small single-copy regions, which are separated by two 26,243 bp inverted repeat regions including 132 genes (86 protein-coding genes, 8 rRNAs, and 37 tRNAs). The overall GC content of the chloroplast is 38.0%. Phylogenetic trees show that *A. coreanum* occupied a basal position at subgenus *Aconitum* clade and two *A. coreanum* isolated from midwestern and eastern regions of Korea are clustered together.

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Genus *Aconitum* (Ranunculaceae), composing around 400 species in three subgenera *Aconitum*, *Lycotoxum*, and *Gymnaconitum* (Meng et al. 2018), usually used as medicinal herbs (Braca et al. 2003; Liou et al. 2005), is a perennial or pseudo-annual herb distributed in temperate regions of northern hemisphere (Kadota 1987). *Aconitum coreanum* (H. Lév.) Rapaics is perennial with thickened roots growing up to 100 cm and distributed in China, Mongolia, Russian Primorsky, and Korean peninsula as the southern limit (Kim et al. 2016) and has been used as a medicinal plant in Korea and China (Liang et al. 2012). The natural habitat of this species has been extremely reduced due to indiscriminate collecting for medicinal usage, and hence, has been listed in the Korean Red List as Vulnerable. To preserve its resources and to understand its genetic diversity, chloroplast genome of *A. coreanum* isolated in Namhansan Fortress in Korea was sequenced (Permission no. is 2019-41 by the Ministry of Environment, Korea).





Total genomic DNA (Shingu Botanic Garden; A2019-0215) was extracted from fresh leaves by using a DNeasy Plant Mini Kit (Qiagen, Hilden, Germany). Genome was sequenced using HiSeqX at Macrogen Inc., Korea, and *de novo* assembly and sequence confirmation were done by Velvet 1.2.10 (Zerbino and Birney 2008), SOAPGapCloser 1.12 (Zhao et al. 2011), BWA 0.7.17 (Li 2013), and SAMtools 1.9 (Li et al. 2009). Geneious R11 11.0.5 (Biomatters Ltd., Auckland, New Zealand) was used for chloroplast genome annotation based on *A. coreanum* chloroplast (NC\_031421).

*Aconitum coreanum* chloroplast genome (Genbank accession is MN400660) is 157,024 bp long (GC ratio is 38.0%) and has four

subregions: 87,637 bp of large single-copy (GC ratio is 36.0%) and 16,901 bp of small single-copy (SSC; GC ratio is 32.7%) regions are separated by 26,243 bp of inverted repeat (IR; GC ratio is 43.0%). It contains 132 genes (86 protein-coding genes, 8 rRNAs, and 37 tRNAs); 18 genes (seven protein-coding genes, four rRNAs, and seven tRNAs) are duplicated in IR regions. SSC region was inverted compared to previous chloroplast genomes, similar to those of *Salix koriyanagi* (Park, Kim, and Xi 2019) and *Hibiscus syriacus* (Kim et al. 2019).

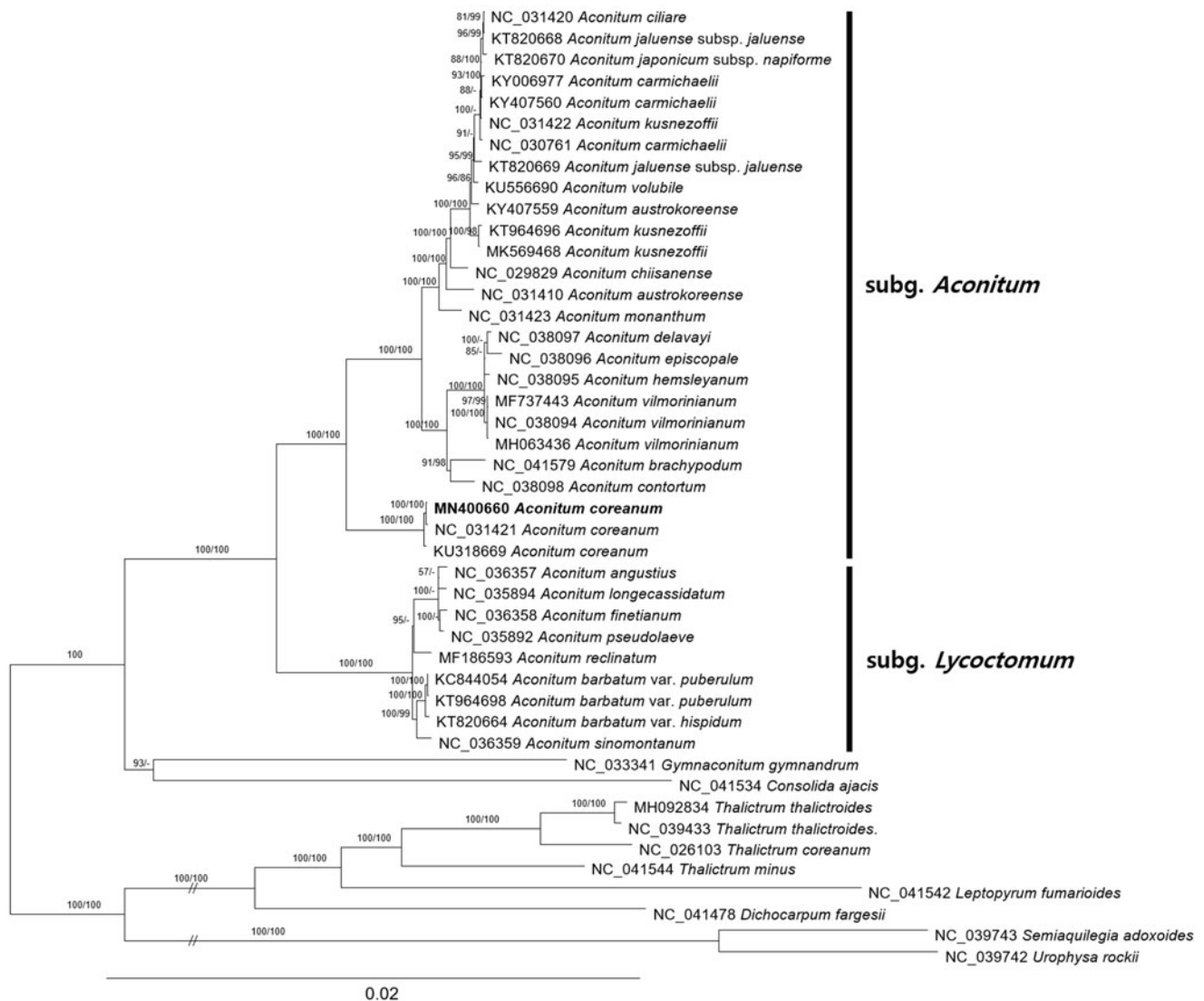
Based on alignments against two *A. coreanum* chloroplast genomes, 5 single nucleotide polymorphisms (SNPs) and 17 insertions and deletions (INDELs) with NC\_031421 were found, similar to those of *Nymphaea alba* (Park, Kim, Kwon, et al. 2019) and *Camellia japonica* (Park, Kim, Xi, Oh, et al. 2019); while 23 SNPs and 62 INDELs against KU318669 were identified, similar to that of *Coffea arabica* (Min et al. 2019). It presents enough intraspecies variations in *A. coreanum*, which can distinguish its origin inside Korea enough.

45 complete chloroplast genomes of *Aconitum* and its relative genera were aligned by MAFFT 7.388 (Katoh and Standley 2013) for constructing neighborjoining and maximum likelihood bootstrapped phylogenetic trees using MEGA X (Kumar et al. 2018) and IQ-TREE 1.6.6 (Nguyen et al. 2015), respectively. Phylogenetic trees show that *A. coreanum* occupied basal position at subg. *Aconitum* clade congruent with previous studies (Kong et al. 2017; Park et al. 2017) and it is clustered with that isolated from eastern part of Korea (Figure 1).

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**Figure 1.** Maximum likelihood (bootstrap repeat is 1,000) and neighbor joining (bootstrap repeat is 10,000) phylogenetic tree of 45 *Aconitum* and its relative genus complete chloroplast genomes: *Aconitum coreanum* (MN400660 in this study; NC\_031421; KU318669), *Aconitum ciliare* (NC\_031420), *Aconitum jaluense* subsp. *jaluense* (KT820668; KT820670), *Aconitum carmichaelii* (KY006977; KY407560; NC\_030761), *Aconitum kusnezoffii* (NC\_031422), *Aconitum jaluense* subsp. *jaluense* (KT820669), *Aconitum volubile* (KU556690), *Aconitum austrokoreense* (KY407559; NC\_031410), *Aconitum kusnezoffii* (KT964696; MK569468), *Aconitum chiisanense* (NC\_029829), *Aconitum monanthum* (NC\_031423), *Aconitum delavayi* (NC\_038097), *Aconitum episcopale* (NC\_038096), *Aconitum hemsleyanum* (NC\_038095), *Aconitum vilmorinianum* (MF737443; NC\_038094; MH063436), *Aconitum brachypodum* (NC\_041579), *Aconitum contortum* (NC\_038098), *Aconitum ciliare* (NC\_031420), *Aconitum angustius* (NC\_036357), *Aconitum longecassidatum* (NC\_035894), *Aconitum finetianum* (NC\_036358), *Aconitum pseudolaeve* (NC\_035892), *Aconitum reclinatum* (MF186593), *Aconitum barbatum* var. *puberulum* (KC844054; KT964698), *Aconitum barbatum* var. *hispidum* (KT820664), *Aconitum sinomontanum* (NC\_036359), *Gymnaconitum gymnandrum* (NC\_033341), *Consolida ajacis* (NC\_041534), *Thalictrum thalictroides* (MH092834; NC\_039433), *Thalictrum coreanum* (NC\_026103), *Thalictrum minus* (NC\_041544), *Leptopyrum fumarioides* (NC\_041542), *Dichocarpum fargesii* (NC\_041478), *Semiaquilegia adoxoides* (NC\_039743), *Urophysa rockii* (NC\_039742). Phylogenetic tree was drawn based on maximum likelihood phylogenetic tree. The numbers above branches indicate bootstrap support values of maximum likelihood and neighborjoining phylogenetic trees, respectively.

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The authors declare that they have no competing interests.

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