**ABSTRACT**

*Salvia chanryoenica* is an endemic species, which locates on the ridges of mountains in South Korea. In this study, we determined the complete chloroplast (cp) genome sequence of *S. chanryoenica*. The cp genome of *S. chanryoenica* is 151,689 bp in length and consists of a large (82,903 bp) and small (17,634 bp) single-copy regions, separated by a pair of identical inverted repeats (25,576 bp). This genome contains unique 79 protein-coding genes, 30 tRNA, and 4 rRNA. The gene order and organization of the *S. chanryoenica* are consistent with those of other Lamiaceae cp genomes. The overall GC content of the whole genome was 37.9%. Phylogenetic analysis was conducted using a gene data matrix consisting of 71 protein-coding genes from 15 in Lamiaceae. *Erythranthe lutea* and *Paulownia tomentosa* were used as an outgroup. Maximum likelihood tree was constructed with RAxML (Stamatakis 2014) using the GTR + R + I model with 1000 bootstrap replicates. The genus *Salvia* was well-supported monophyletic (100% bootstrap values, BS) and *S. chanryoenica* was sister to *S. miltiorrhiza*. Our results, the cp genome sequence of *S. chanryoenica* may contribute to a better understanding of the evolution of *Salvia*. Also offers a useful resource for molecular marker and species conservation.

**Disclosure statement**

No potential conflict of interest was reported by the authors.
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