**ABSTRACT**

*Eranthis stellate* belong to Ranunculaceae, which is interest in phylogenetic research because it has often been considered one of the most basal eudicots families. However, there are few chloroplast genome data of Ranunculaceae available. Here, to provide available genomic data for the phylogenetic of Ranunculaceae, we determined the complete chloroplast genome of *E. stellate*. The complete chloroplast sequence is 158,817 bp, including a large single-copy (LSC) region of 87,137 bp, a small single-copy (SSC) region of 16,834 bp, a pair of inverted repeats (IR) regions of 27,424 bp. Plastid genome contain 129 genes, 84 protein-coding genes, 36 tRNA genes, and 8 rRNA genes. Phylogenetic analysis based on 14 chloroplast genomes indicates that *E. stellata* is sister to *Aconitum austrokoreense* clade in Ranunculaceae.

*Eranthis stellate* is a perennial early spring ephemeral herb, always distributing in the shade of forest or forest edge grassland of in northern China, North Korea and Russia (Li and Michio 2001). *E. stellate* belong to Ranunculaceae, which is interest in phylogenetic research because it has often been considered one of the most basal eudicots families and thus has been studied by many plant systematists using various taxonomic characters (Ghimire et al. 2015; Byng et al. 2016). However, morphological-based classification is susceptible to environmental influences, and there are few genome data of Ranunculaceae available. Herein, in order to provide available genomic data for the phylogenetic of Ranunculaceae, we reported the complete chloroplast genome of *E. stellate* based on Illumina sequencing data. The complete chloroplast genomic data will be helpful to study the origin, evolution and the relationship between the phenotype and environment of *E. stellate* (Xiang et al. 2019).

Although the chloroplast genome is small, it is prone to gene duplication, and significant differences in the molecular level of the intergenic spacers, providing a wealth of information for comparative evolution and phylogenetic studies (Green 2011).

The plant material of *E. stellata* comes from Wangou Forestry Bureau, Baishan city, Jilin province, China (126°47′—127°17′E, 41°51′—42°23′N). The voucher specimen is kept at the Herbarium of College of Forestry, Fujian Agriculture and Forestry University (specimen code FAFU07013).

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phylogenetic analysis was performed based on eight complete chloroplast genomes of Ranunculaceae and six other species as outgroup. Them all downloaded from NCBI GenBank. To reveal the phylogenetic location of *E. stellata*, the sequences were aligned by MAFFT v7.307 (Katoh and Standley 2013), and phylogenetic tree constructed by RAxML (Stamatakis 2014). The phylogenetic tree showed that *E. stellata* was sister to *A. ciliare* - *A. austrokoreense* clade with strong support (Figure 1).

**Disclosure statement**

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**Figure 1.** Phylogenetic analysis of 8 species of Ranunculaceae and 6 other species as outgroup based on chloroplast genome sequences by RAxML, bootstrap support value near the branch.