

Extensive Reorganization of the Chloroplast Genome of *Corydalis platycarpa*: A Comparative Analysis of their Organization and Evolution with other *Corydalis* plastomes

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The chloroplast (cp) is an autonomous plant organelle with an individual genome that codes for essential cellular functions. The architecture and gene content of the cp genome is highly conserved in angiosperms. The plastome of *Corydalis* belongs to the Papaveraceae family, and the genome is comprised of unusual rearrangements and gene content. Thus far, no extensive comparative studies have been carried out to understand the evolution of *Corydalis* chloroplast genomes. Therefore, the *Corydalis platycarpa* cp genome was sequenced, and wide-scale comparative studies were conducted using publicly available twenty *Corydalis* plastomes. Comparative analyses showed that an extensive genome rearrangement and IR expansion occurred, and these events evolved independently in the *Corydalis* species. In addition, the protein-coding genes *accD* and the *ndh* gene loss events occurred in the common ancestor of the *Corydalis* and sub-clade of the *Corydalis* lineage, respectively. The gene *ndh* lost in the *Corydalis*-sub clade species is distributed predominantly in the Qinghai-Tibetan plateau (QTP) region. The molecular clock analysis suggests that the divergence time of all the *ndh* gene lost *Corydalis* sub-clade species occurred in the 44.31 – 15.71 mya. These results coincide very well with the uplift of the Qinghai-Tibet Plateau in the Oligocene and Miocene periods, and maybe during this period, it probably triggered the radiation of the *Corydalis* species. To the best of the authors' knowledge, this is the first large-scale comparative study of *Corydalis* plastomes and their evolution. The present study may provide insights into the plastome architecture and the molecular evolution of *Corydalis* species.

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