

Highly variable chloroplast genome from two endangered Papaveraceae lithophytes *Corydalis tomentella* and *C. saxicola*

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Abstract

The increasingly wide application of chloroplast(cp) genome super-barcode in taxonomy and the recent breakthrough in cp genetic engineering make the development of new cp gene resources urgent and significant. *Corydalis* is recognized as the most genotypes complicated and taxonomically challenging plant taxa in Papaveraceae. However, no complete cp genome for this genus has been reported to date. In this study, we sequenced four complete cp genomes of two endangered lithophytes *Corydalis saxicola* and *C. tomentella* in *Corydalis*, conducted a comparative genomics study on them, and a highly variable cp genome structure was found. The cp genomes have a large genome size of 189,029 to 190,247 bp, possessing a quadripartite structure and with two highly expanded inverted repeat (IR) regions (length: 41,955 to 42,350 bp). Comparison between the cp genomes of *C. tomentella*, *C. saxicola* and Papaveraceae species, five NADH dehydrogenase-like genes (*ndhF*, *ndhD*, *ndhL*, *ndhG*, *ndhE*) with *psaC*, *rpl32*, *ccsA* and *trnL-UAG* normally located in the SSC region have migrated to IRs, resulting in IR expansion and gene duplication. An up to 9 kb inversion involving five genes (*rpl23*, *ycf2*, *ycf15*, *trnI-CAU* and *trnL-CAA*) was found within IR regions. The *accD* gene was found to be absent and the *ycf1* gene has shifted from the IR/SSC border to the SSC region as a single copy. Phylogenetic analysis based on the sequences of common CDS showed that the genus *Corydalis* is quite distantly related to the other genera of Papaveraceae, it provided a new clue for recent advocacy to establish a separate Fumariaceae family. Our results revealed one special cp genome structure in Papaveraceae, provided a useful resources for classification of the genus *Corydalis*, and will be valuable for understanding Papaveraceae evolutionary relationships.

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