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CHARACTERIZATION OF THE COMPLETE CHLOROPLAST GENOME AND EVOLUTIONARY POSITION OF *CLEMATIS TOMENTELLA*

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Clematis tomentella 2001 (*Ranunculaceae*) is a typical drought-tolerant sand-fixing plant in desert ecosystem in northwest China. To elucidate the phylogenetic status of *C. tomentella* and its related species, we determined the complete chloroplast (*cp*) genome and analyzed their interspecific relationships. The result showed that the *cp* genome of *C. tomentella* was 159,816 bp in length, including two inverted repeats of 31,045 bp, a large single copy region of 79,535 bp, and a small single copy region of 18,191 bp. 136 genes were annotated across the whole *cp* genome, including 92 protein-coding genes, 8 rRNA genes, and 36 tRNA genes, as well as the GC content accounted for 38 %. Crucially, we found that the regions of *psbE-petL*, *trnG-UCC-atpA*, *ndhF-rpl32*, and *rps8-infA* were highly divergent, which could be marked as DNA barcodes for the identification of *C. tomentella* in *Ranunculaceae*. A maximum likelihood phylogenetic tree revealed that *C. tomentella* was closely related to *C. fruticosa*. Our results provide the references and implications for the phylogenetic study of *Clematis* in *Ranunculaceae* in the future.

Key words: *C. tomentella*; complete chloroplast genome; *Clematis*; gene; phylogenetic analysis

ХАРАКТЕРИСТИКА ПОВНОГО ХЛОРОПЛАСТНОГО
ГЕНОМУ ТА ЕВОЛЮЦІЙНЕ ПОЛОЖЕННЯ
CLEMATIS TOMENTELLA

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ІНЖЕНЕРІЇ НАН УКРАЇНИ, 2024

Clematis tomentella 2001 (*Ranunculaceae*) – це типова посухостійка рослина, яка укріплює пісок у пустельній екосистемі північно-західного Китаю. Щоб з'ясувати філогенетичний статус *C. tomentella* та споріднених видів, ми визначили повний хлоропластний (*cp*) геном і проаналізували їхні міжвидові відносини. Результати показали, що хлоропластний геном *C. tomentella* мав 159 816 п.н. у довжину, включно з двома інвертованими повторами по 31 045 п.н., велику малокопійну ділянку на 79 535 п.н. та невелику малокопійну ділянку на 18 191 п.н. 136 генів було анотовано по всьому хлоропластному геному, включно з 92 білок-кодуєчими генами, 8 рРНК генами та 36 тРНК генами, а вміст GC становив 38 %. Ми виявили, що ділянки *psbE-petL*, *trnG-UCC-atpA*, *ndhF-rpl32* та *rps8-infA* були значно дивергентними, що може вважатися ДНК штрих-кодом для ідентифікації *C. tomentella* у *Ranunculaceae*. Філогенетичне дерево на основі максимальної ймовірності показало, що *C. tomentella* тісно пов'язана з *C. fruticosa*. Наші результати дають підстави для подальшого вивчення філогенетичних відносин *Clematis* у *Ranunculaceae*.

Ключові слова: *C. tomentella*; повний хлоропластний геном; *Clematis*; ген; філогенетичний аналіз.

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