

COMPARATIVE ANALYSIS OF THE COMPLETE MITOCHONDRIAL GENOME SEQUENCE OF AN ALPINE PLANT *TRIOSTEUM PINNATIFIDUM*

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*In this study, the complete mitochondrial genome (mt genome) of *Triosteum pinnatifidum* was investigated for the first time. The mt genome consisted of 803,609 bp, comprised of 62 genes including 19 tRNA genes, 3 rRNA genes and 40 protein-coding genes. We detected protein-coding genes and codon usage, RNA editing sites and repeat sequences. The protein-coding genes substitution rates and DNA segments migration were generated, the comparison of six species genomic features was performed. The phylogenetic analysis of 32 species was also taken. A total of 463 RNA editing sites were found in 40 protein-coding genes. Being slightly positive, the GC-skew and AT-skew were 0.0060 and 0.0004, respectively. Most of PCGs had Ka/Ks ratio less than 1, indicating the existence of purifying or negative selection in these genes. This is the first report of the mt genome in the Caprifoliaceae family and could provide a useful foundation for evolutionary analysis, molecular biology and taxonomy in genus *Triosteum* and other higher plants.*

Key words: mitochondrial genome; *Triosteum pinnatifidum*; structure and evolution characteristics; phylogeny.

ПОРІВНЯЛЬНИЙ АНАЛІЗ ПОВНОЇ ПОСЛІДОВНОСТІ МІТОХОНДРІАЛЬНОГО ГЕНОМУ АЛЬПІЙСЬКОЇ РОСЛИНИ *TRIOSTEUM PINNATIFIDUM*

У цьому дослідженні було вперше проведено вивчення повного мітохондріального геному (мт-геному) *Triosteum pinnatifidum*. Мт-геном складається з 803 609 п.н., 62 генів, включно з 19 тРНК генами, 3 рРНК генами та 40 білок-кодуючими генами. Ми виявили гени, що кодують білок, використання ко-

донів, участки редагування РНК і повторювані послідовності. Було згенеровано рівні заміщення генів, що кодують білок, міграцію сегментів ДНК і проведено порівняння шести видів геномних рис. Також було проведено філогенетичний аналіз 32 видів. Загалом у 40 генах, що кодують білок, було знайдено 463 участки редагування РНК. Будучи дещо позитивними, асиметричність GC та AT становить 0,0060 та 0,0004, відповідно. У більшості PCG баланс Ka/Ks був меншим ніж 1, що вказує на наявність очисного або негативного відбору в цих генах. Це перше повідомлення про мт-геном у сімействі Caprifoliaceae. Воно може стати корисним підґрунтям для еволюційного аналізу, молекулярної біології та таксономії роду *Triosteum* та інших вищих рослин.

Ключові слова: мітохондріальний геном; *Triosteum pinnatifidum*; характеристики структури та еволюції, філогенія.

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