THE COMPLETE MITOCHONDRIAL GENOMES OF TWO APPLE CULTIVARS REVEAL THE HIGHLY CONSERVED STRUCTURE IN CULTIVATED APPLES

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Apples are as one of the most popular and economically important fruits worldwide, have the important nutritional and ornamental value. However, because of their complexity, studies on apple mitochondrial (mt) genomes have been limited. In this study, the mt genomes of Aksu Fuji and Ralls Janet cultivars were assembled, annotated, and analyzed based on a hybrid strategy using Illumina, and comprehensive comparisons of their structure, gene content, intercellular gene transfer, phylogeny, and RNA editing sites were performed. The mt genome length and gene structure of the two apple cultivars were identical (396,592 bp) and included 63 protein-coding genes (PCGs), 20 transfer RNA (tRNA) genes, and 4 ribosomal RNA (rRNA) genes. There were 44 and 31 mitochondrial plastid fragments (MTPTs) identified between the mt and plastid genomes of the Ralls Janet and Aksu Fuji cultivars, accounting for 1.98 and 2.19 % of their mt genomes, respectively. Furthermore, there were 419 and 421 RNA editing sites were detected in Aksu Fuji and Ralls Janet, respectively. Analyses of coding usage bias, nucleotide diversity, selection pressure, and genetic distance revealed that the mt genomes of the two cultivars were highly conserved. Phylogenetic analysis of 29 Rosaceae species showed that Aksu Fuji and Ralls Janet clustered with Malus baccata and M. kansuensis. This study provides new insights into the genetics, systematics, and evolution of apple mt genomes

***Key words*:** *cultivated apple, mitochondrial genome, mitochondrial plastid sequences, RNA editing sites, phylogenetic analysis.*

ПОВНІ МІТОХОНДРІАЛЬНІ ГЕНОМИ ДВОХ СОРТІВ ЯБЛУК ДЕМОНСТРУЮТЬ ВИСОКОКОНСЕРВАТИВНУ СТРУКТУРУ

Яблука є одними з найпопулярніших та економічно важливих фруктів у всьому світі і мають як харчову, так і декоративну цінність. Однак, дослідження мітохондріальних (mt) геномів яблук проводяться рідко через їхню складність. У цьому дослідженні було зібрано, анотовано та проаналізовано mt-геноми сортів Аксу Фуджі та Роллс Дженет на основі гібридної стратегії з використанням Illumina, а також проведено всебічне порівняння їхньої структури, вмісту генів, міжклітинного переносу генів, філогенезу та сайтів редагування РНК. Довжина геному mt і структура генів двох сортів яблук були ідентичними (396, 592 п.н.) і включали 63 гени, що кодують білки (PCG), 20 генів транспортних РНК (тРНК) і 4 гени рибосомних РНК (рРНК). Між mt і пластидними геномами сортів Роллс Дженет і Аксу Фуджі було виявлено 44 і 31 мітохондріально-пластидних фрагментів (MTPT), що становить 1,98 і 2,19 % від їхніх mt геномів, відповідно. Крім того, було виявлено 419 та 421 сайт редагування РНК у Аксу Фуджі та Роллс Дженет, відповідно. Аналіз зсуву використання кодування, нуклеотидного різноманіття, селекційного тиску та генетичної дистанції показав, що mt-геноми обох сортів є висококонсервативними. Філогенетичний аналіз 29 видів розоцвітих показав, що Аксу Фуджі та Роллс Дженет кластеризуються з *Malus baccata* та *M. kansuensis.* Це дослідження дає нові уявлення про генетику, систематику та еволюцію mt-геномів яблук.

Ключові слова: вирощувані яблука, мітохондріальний геном, послідовність мітохондріальних пластид, сайти редагування РНК, філогенетичний аналіз.

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