

COMPARATIVE ANALYSIS OF THE MITOCHONDRIAL GENOME OF ACCIPITER NISUS

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Accipiter nisus is a small to medium-sized raptor widely distributed across Eurasia and parts of Africa. In this study, we sequenced the complete mitochondrial genome of *A. nisus* from Mianyang using the Illumina platform. We then compared mitochondrial genome *A. nisus* variations across four regions and analyzed the phylogenetic relationship of this species within the genus *Accipiter*. The results indicate that the mitochondrial genome of *A. nisus* from Mianyang is 18,297 bp in length, which is smaller than those from Qufu (18,647 bp), Yeongyang-gun (18,352 bp), and Buk-Gu (19,417 bp). The genomes of all four individuals contain 37 genes, an A+T-rich control region, and a pseudo-control region, with the most notable length variation occurring in the pseudo-control region. Additionally, inconsistencies in the usage of start and stop codons were observed in some protein-coding genes (PCGs). Phylogenetic analysis based on 13 PCGs and CYTB genes revealed that *A. nisus* is phylogenetically related to *A. gentilis*. This study provides essential genetic data and scientific evidence for *A. nisus* conservation.

Key words: *Accipiter nisus*; complete mitochondrial genome; Comparative analysis; Phylogenetic relationship.

ПОРІВНЯЛЬНИЙ АНАЛІЗ МИТОХОНДРІАЛЬНОГО ГЕНОМУ ACCIPITER NISUS

Accipiter nisus — це хижий птах невеликих або середніх розмірів, широко розповсюджений в Євразії та деяких регіонах Африки. У цьому дослідженні ми

секвенували повний мітохондріальний геном *A. nisus* з округу Мяньян за допомогою платформи Illumina, порівняли варіанти мітохондріального геному *A. nisus* із чотирьох регіонів та проаналізували філогенетичні зв'язки цього виду в межах роду *Accipiter*. Результати продемонстрували, що мітохондріальний геном *A. nisus* з округу Мяньян має довжину 18 297 пн, що менше довжини геномів з округів Цюйфу (18 647 пн), Йон'ян (18 352 пн) та Бук-Гу (19 417 пн). Геноми всіх чотирьох особин містять 37 генів, контрольну ділянку, багату на А+Т та псевдоконтрольну ділянку, при цьому найзначніша варіація довжини міститься саме в псевдоконтрольній ділянці. Крім того, у деяких білок-кодуєчих генах (PCGs) спостерігали невідповідність використання старт та стоп-кодонів. Філогенетичний аналіз на основі 13 PCG та генів *CYTB* продемонстрував, що *A. nisus* філогенетично споріднений із *A. gentilis*. Це дослідження надає важливі генетичні дані та наукові докази для збереження *A. nisus*.

Ключові слова: *Accipiter nisus*; повний мітохондріальний геном; порівняльний аналіз; філогенетичний зв'язок.

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