Novel mitochondrial gene content and gene arrangement indicate illegitimate inter-mtDNA recombination in the chigger mite, *Leptotrombidium pallidum*

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**ABSTRACT** : To better understand the evolution of mitochondrial (mt) genomes in the Acari (mites and ticks), we sequenced the mt genome of the chigger mite, *Leptotrombidium pallidum* (Arthropoda: Acari: Acariformes). This genome is highly rearranged relative to that of the hypothetical ancestor of the arthropods and the other species of Acari studied. The mt genome of *L. pallidum* has two genes for large subunit rRNA, a pseudogene for small subunit rRNA, and four nearly identical large noncoding regions. Nineteen of the 22 tRNAs encoded by this genome apparently lack either a T-arm or a D-arm. Further, the mt genome of *L. pallidum* has two distantly separated sections with identical sequences but opposite orientations of transcription. This arrangement cannot be accounted for by homologous recombination or by previously known mechanisms of mt gene rearrangement. The most plausible explanation for the origin of this arrangement is illegitimate inter-mtDNA recombination, which has not been reported previously in animals. In light of the evidence from previous experiments on recombination in nuclear and mt genomes of animals, we propose a model of illegitimate inter-mtDNA recombination to account for the novel gene content and gene arrangement in the mt genome of *L. pallidum*.
再編成によっては説明できない。最も真実味のある説明は、動物では報告されていない非正統的なミトコンドリアDNA間組換えである。以前からの動物の核およびミトコンドリアゲノムの組換えについての研究から、我々はフタゲツツガムシのミトコンドリアゲノムについての新規な遺伝子配列および遺伝子編成の説明に非正統的なミトコンドリア間組換えモデルを提案する。

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