ミトコンドリアゲノム (soft ticks) の遺伝子構成は 4億年を経てもなお変化を受けていない

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Insect Mol. Biol, 13 (3): 219-224 (2004)

The mitochondrial genomes of soft ticks have an arrangement of genes that has remained unchanged for over 400 million years.

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ABSTRACT: There are two major groups of ticks: soft ticks and hard ticks. The hard ticks comprise the prostriate ticks and t)he metastriate ticks. The mitochondrial (mt) genomes of one species of prostriate tick and two species of metastriate ticks had been sequenced prior to our study. The prostriate tick has the ancestral arrangement of mt genes of arthropods, whereas the two metastriate ticks have rearrangements of eight genes and duplicate control regions. However, the arrangement of genes in the mt genomes of soft ticks had not been studied. We sequenced the mt genomes of two species of soft ticks, *Carios capensis* and *Ornithodoros moubata*, and a metastriate tick, *Haemaphysalis flava*. We found that the soft ticks have the ancestral arrangement of mt genes of arthropods, whereas the metastriate tick, *H. flava*, shares the rearrangements of mt genes and duplicate control regions with the other two metastriate ticks that have previously been studied. Our study indicates that gene rearrangements and duplicate control regions in mt genomes occurred once in the most recent common ancestor of metastriate ticks, whereas the ancestral arrangement of arthropods has remained unchanged for over 400 million years in the lineages leading to the soft ticks and the prostriate ticks.

抄録 ダニは主にマダニ科とヒメダニ科から構成され、マダニ属はさらに二つのグループ (Metastriata と Prostriata) に分類される。 2種の soft tick, Carios capensis, Ornithodoros moubata と metastriata tickの Haemaphysalis flavaのミトコンドリアゲノム塩基配列解析し、遺伝子構成比較を行った。その結果、H. flavaでは、遺伝子再構成と制御領域の複製がおこっているが、2種の soft tick では節足動物に見られる遺伝子構成と同じであった。我々の結果は、節足動物のミトコンドリアゲノムの遺伝子構成は soft ticks と prostriate ticks の系統進化において4億年以上も変化がないままであるが、metastriata tickの最も近い共通祖先において、かつて1度だけ遺伝子再構成と制御領域の複製が起こったことを示している。

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