

双翅目昆虫线粒体基因组结构特点及其测序通用引物的设计 and 应用

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Structure characteristics of the mitochondrial genomes of Diptera and design and application of universal primers for their sequencing

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全文: PDF (7868 KB) HTML (1 KB) 输出: BibTeX | EndNote (RIS) 背景资料

摘要 研究双翅目昆虫线粒体基因组的结构特点, 并设计其测序的通用引物, 为今后双翅目昆虫线粒体基因组的研究提供参考和依据。利用比较基因组学和生物信息学方法, 分析了已经完全测序的26个双翅目昆虫线粒体基因组的结构特点、碱基组成和保守区, 并据此设计了双翅目昆虫基因组测序的通用引物。结果表明: 双翅目昆虫线粒体基因组长14 503~19 517 bp, 其结构保守, 含有37个编码基因, 包括13个蛋白质编码基因, 22个tRNA编码基因和2个rRNA编码基因, 此外还包含一段长度差异很大的非编码区(AT富含区)。基因组内基因排列次序稳定, 除个别基因外, 其余都与黑腹果蝇*Drosophila melanogaster*基因排列次序一致。基因组的碱基组成不均衡, AT含量在72.59%~85.15%之间, 碱基使用存在偏向性, 偏好使用AC碱基。全基因组的核苷酸和氨基酸序列保守, 共鉴定了11个保守区。在保守区内共设计了26对双翅目线粒体基因组测序通用引物, 扩增的目标片段都在1 200 bp以内。将该套通用引物用于葱蝇*Delia antiqua*线粒体全基因组测序, 结果证明其高效、合用。

关键词: 双翅目 葱蝇 线粒体基因组 基因结构 保守区域 通用引物

Abstract: The study aims to investigate the structural characteristics of Diptera mitochondrial genomes and design universal primers for sequencing of Diptera mitochondrial genomes so as to establish an overall framework of information for further study of Diptera mitochondrial genomes. We analyzed the structural characteristics, base composition and conserved regions of dipteran mitochondrial genome based on the known 26 full length mitochondrial genome sequences of Diptera using comparative genomics and bioinformatics methods, and designed a set of universal primers for mitochondrial genome sequencing of Diptera. The results show that the mitochondrial genomes of Diptera are 14 503-19 517 bp in length, and their structure are quite conservative with 37 coding genes, including 13 protein-coding genes, 22 tRNA genes and two rRNA coding genes. In addition, there is a non-coding region (AT-rich region) with various lengths. The individual gene location order on these genomes is quite stable, consistent with that on the mitochondrial genome of *Drosophila melanogaster* with only a few exceptions. The base composition on these genomes is not balanced with the AT content (72.59%-85.15%) significantly higher than the GC content, and base usage bias exists with A (50.91% of AT content) and C (57.79% of GC content) base usage significantly higher than T and G. We identified 11 conservative regions based on the nucleotide and amino acid sequence conservation analysis of whole genome, and designed 26 pairs of universal primers for mitochondrial genome sequencing of Diptera with each pair of primers anchored to identify conservative regions. The target fragment amplified with each pair of primers is less than 1 200 bp in length. This set of primers was applied for sequencing *Delia antiqua* mitochondrial genome, and the results prove that the set of primers is efficient and operable.

Key words: Diptera *Delia antiqua* mitochondrial genome gene structure conservative regions universal primers

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