

论著

三种蚊虫COII基因的克隆与序列分析

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摘要

目的 测定和比较中华按蚊、白纹伊蚊和致倦库蚊细胞色素C氧化酶亚基II(COII)基因全序列,分析3种蚊虫之间及与其它几种蚊虫的COII基因序列的同源性。方法 运用T A克隆技术分别获得3种蚊虫的COII基因重组质粒,并进行DNA测序和结构分析。结果 3种蚊虫COII基因的核苷酸序列同源性为84.1%~87.9%,氨基酸序列的同源性为85.1%~89.5%;C+G含量为23.2%~24.9%,颠换频率高于转换频率。结论 基因序列同源性比较结果显示:在COII分子结构,白纹伊蚊与致倦库蚊具有更近的亲缘关系。

关键词 [中华按蚊](#) [白纹伊蚊](#) [致倦库蚊](#) [COII基因](#)

分类号

Cloning and Sequencing of Cytochrome c Oxidase II (COII) Gene of Three Species of Mosquitoes

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Abstract

Objective To determine and compare the complete sequence of COII gene from *Anopheles sinensis*, *Aedes albopictus* and *Culex quinquefasciatus* and to identify the molecular homology among these mosquitoes. Methods The recombinant plasmids including COII gene from the three species of mosquitoes were obtained by the T A cloning technique, and the COII genes were sequenced and analyzed. Results The homology of the COII gene nucleotide sequence and the deduced amino acid sequence of COII among the three species of mosquitoes varied from 84.1% to 87.9% and from 85.1% to 89.5%, respectively. The C+G content of COII gene was 23.2%-24.9%, the frequency of transversion higher than that of transition. Conclusion *Aedes albopictus* and *Culex quinquefasciatus* are closely related species at their COII molecular level according to COII gene.

Key words [Anopheles sinensis](#) [Aedes albopictus](#) [Culex quinquefasciatus](#) [cytochrome c oxidase subunit II gene](#)

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