

研究报告

云南四个瓜实蝇地理种群的遗传关系分析

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摘要

对云南4个不同地理区域的瓜实蝇种群(*Bactrocera cucurbitae*)共23个个体的线粒体DNA细胞色素b基因中的部分序列进行测定和分析,并以桔小实蝇(*B. dorsalis*)、番石榴实蝇(*B. correct*)和南瓜实蝇(*B. tau*)为外群种构建了不同单倍型的N-J分子系统树.在获得的426 bp序列中, A+T含量约占65.0%,有4个多态位点,无任何碱基插入和缺失.这些位点共定义5种单倍型,其中一种为共享单倍型.对4个瓜实蝇地理种群进行Fst值和基因流动统计, Fst值为0.16667~0.20000($P>0.05$), Nm值为2.00~2.50.5种单倍型共形成了3个聚类簇.可以认为,4个地理种群间均存在一定程度的遗传分化,但分化程度不高,导致遗传分化的主要因素是地理隔离,而种群遗传分化程度低与瓜实蝇所在环境条件相似有关.

关键词 [瓜实蝇,线粒体DNA,细胞色素b基因,遗传分化](#)

分类号

Genetic relationships among four *Bactrocera cucurbitae* geographic populations in Yunnan Province

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Abstract

In this study, the partial section of mitochondrial cytochrome b in 23 individuals of four *Bactrocera cucurbitae* geographic populations (Banna, Ruili, Yuanjiang, and Hekou) in Yunnan Province was sequenced, and the phylogenetic trees of all haplotypes were constructed by means of N-J method, using *B. dorsalis*, *B. correct* and *B. tau* as the out-group species. Of the 426 bp mitochondrial cytochrome b DNA sequences obtained, A%+T% was about 65.0%, four nucleotide sites were substituted, and no base composition of the sequences was inserted and lost. Five haplotypes were identified in all the sequences, with four showing polymorphism, and one shared. The genetic characters of the four populations were analyzed by Fst value and gene flow through Mega software. The Fst value was 0.16667~0.20000 ($P>0.05$), and the Nm value was 2.00~2.50. The N-J tree suggested that four haplotypes constructed three clades. All results showed that the genetic differences presented among the four populations, but with low degrees. The main reason causing the genetic differences among the four populations was supposed to be related to genetic isolation and ecological adaptation.

Key words [Bactrocera cucurbitae](#) [MtDNA](#) [Cytochrome b gene](#) [Genetic differentiation](#)

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