

研究论文

# 云南桔小实蝇(*Bactrocera dorsalis*)季节性分布区4个地理种群遗传结构

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**摘要** 对云南桔小实蝇季节分布区内六库、大理、昆明和曲靖4个典型地区桔小实蝇种群 (*Bactrocera dorsalis*), 共52个个体的线粒体DNA CO I 基因中的部分序列进行了测定分析。在获得的503 bp序列中, 共发现15个多态位点, 定义了14种单倍型, 其中种群间的共享单倍型有4个。通过对桔小实蝇4个地理种群的K2P遗传距离、Fst值, 种群间和种群内遗传差异平均数的统计检测, 以及4个种群之间基因流状况分析表明, 研究的各种种群间存在不同程度的遗传分化。六库种群与其余3个种群间的遗传分化最大, 遗传差异显著 ( $p < 0.05$ )。大理种群与曲靖种群之间存在一定程度遗传分化 ( $p < 0.10$ ), 但与昆明种群间的分化程度较低。昆明种群与曲靖种群间的遗传分化程度最低。简言之, 在桔小实蝇季节性分布区内, 位于西部的种群遗传分化程度最高, 由西向东, 遗传分化程度渐次下降, 位于东部的两个种群遗传结构相近。研究认为, 地理隔离是导致六库种群与其余3个种群遗传分化的主要原因, 而大理、昆明和曲靖种群之间遗传分化较低, 可能是这些种群来自相近或相同的虫源地。研究结果对于在桔小实蝇季节性分布区的不同地点制定桔小实蝇治理方案具有重要的参考价值。

**关键词** 桔小实蝇; 季节分布区; 地理种群; 线粒体DNA; 细胞色素氧化酶 I 基因; 遗传分化

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**Abstract** The partial section of mitochondrial cytochrome oxidase I (CO I) was sequenced. These sequences were in 52 individuals from four *Bactrocera dorsalis* geographic populations (Liuku, Dali, Kunming, Qujing) located in the seasonal occurrence zone of the fly in Yunnan Province. The 503bp sequences were obtained from mitochondrial cytochrome oxidase I DNA sequences. Fifteen nucleotide sites were substituted. Fourteen haplotypes were identified in all the sequences, with four shared. The genetic distances of the four populations were analyzed by K2P genetic distances and Fst value. Average number of pairwise genetic differences were obtained between and within 4 populations. Gene flow among four populations was also detected. All results showed that genetic differences existed among the four populations. The genetic differences between Liuku and other three populations were largest. The p value was  $< 0.05$ . There were some genetic differences between Dali and Qujing population. That p value  $< 0.01$ . But the genetic differences between Kunming and Qujing population were lowest. In a word, in seasonal occurrence zone of *Bactrocera dorsalis*, the genetic differences was larger in the western region. The genetic differences declined gradually from western to eastern region. The two populations located in eastern region have closer genetic structure. The results showed geographic isolation is the main reason of genetic differences between Liuku population and other three populations. The lower genetic differences among Dali, Kunming and Qujing population probably resulted from them having the same origin. The results of the study have important implications for the management and eventual elimination of *Bactrocera dorsalis* populations at different locations in the seasonal occurrence zone in Yunnan.

**Key words** [Bactrocera dorsalis](#); [geographic population](#) \_ [MtDNA](#) \_ [cytochrome oxidase I](#)

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