

## 应用微卫星标记分析不同桔小实蝇种群的遗传多样性

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Analysis of genetic diversity of different populations of *Bactrocera dorsalis* (Diptera: Tephritidae) using microsatellite markers

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### 摘要

为探究不同桔小实蝇*Bactrocera dorsalis* (Hendel)地理种群的遗传变异、入侵来源和扩散情况, 利用13对引物对中国南方10省区、泰国、夏威夷、菲律宾和老挝的30个桔小实蝇种群共180个个体的遗传多样性水平进行了研究。Popgene32和NTSYS-pc2.10e软件分析结果表明: 30个不同桔小实蝇种群的遗传相似度在0.3599~0.9153范围内。种群的Nei氏基因多样性指数平均为 $0.6464 \pm 0.1026$ , Shannon信息指数I平均为 $1.2845 \pm 0.2632$ , 提示桔小实蝇种群具有较丰富的遗传多样性。UPGMA聚类分析显示, 福建地区和海南地区分别独立一支, 广东地区和台湾地区种群聚成一支, 而广西、泰国、湖南、云南、老挝、四川、重庆和贵州地区聚为一大支系。据此提出泰国种群和老挝种群是最早入侵我国的种群, 云南地区是最早的入侵地, 广西地区可能为又一较早入侵地。

### 关键词:

### Abstract:

To explore the genetic variation, the source of invasion and the dispersal of different geographical populations of *Bactrocera dorsalis* (Hendel), the genetic diversity and relationships of 30 *B. dorsalis* populations consisting of 180 individuals collected from 10 provinces of South China, Thailand, Hawaii, Philippines, and Laos were analyzed with 13 microsatellite loci. The analysis results with the softwares of Popgene32 and NTSYS-pc2.10e showed that the Nei's genetic identity of 30 *B. dorsalis* populations was between 0.3599 and 0.9153. A relatively high level of genetic diversity was revealed:  $H=0.6464 \pm 0.1026$ ,  $I=1.2845 \pm 0.2632$ . UPGMA cluster analysis indicated that the populations from Fujian and Hainan gathered separately into two different clades, the populations from Guangdong and Taiwan gathered into one clade, while the populations from Guangxi, Thailand, Hunan, Yunnan, Laos, Sichuan, Chongqing and Guizhou formed the other one. So it is inferred that the populations from Thailand and Laos were the earliest ones to invade China, Yunnan was the region to be invaded earliest, and Guangxi was probably also among the regions to be invaded early by this pest.

### Key words:

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