

实验研究

西藏墨脱县疟疾流行区多斑按蚊复合体种型鉴定

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摘要

目的 鉴定西藏林芝地区墨脱县疟疾流行区多斑按蚊复合体的种型。方法 墨脱县捕获的5 190只按蚊经形态学鉴定为多斑按蚊复合体后, 随机取575只, 酚-氯仿法提取单蚊DNA作为模板, 根据伪威氏按蚊、多斑按蚊、威氏按蚊、达罗毗按蚊和塞沃按蚊分别设计5对特异性引物, PCR扩增rDNA第二转录间隔区(ITS2)片段, 进行种型鉴别。对目标片段进行测序、同源性比对, 并运用MEGA(3.1)软件构建多斑按蚊复合体的系统进化树。结果 575份DNA样本中有11份扩增出约231 bp的条带, 即威氏按蚊(1.9%); 564份扩增出约119 bp的条带, 为伪威氏按蚊(98.1%)。PCR种型鉴定结果与同源性比对及系统进化树的结果一致。结论 西藏林芝地区墨脱县疟疾流行区多斑按蚊复合体由伪威氏按蚊和威氏按蚊构成, 伪威氏按蚊为优势蚊种。

关键词 [西藏](#) [墨脱](#) [多斑按蚊复合体](#) [种型鉴定](#)

分类号

Species Identification of Anopheles maculatus Complex in Malaria Endemic Area Motuo County, Tibet

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Abstract

Objective To identify the species of Anopheles maculatus complex in malaria endemic area Motuo County, Linzhi Prefecture, Tibet Autonomous Region. Methods 5 190 adult mosquitoes were morphologically identified as An. maculatus complex, and 575 were randomly selected to extract DNA by phenol-chloroform method. According to the rDNA ITS2 variations of An. maculatus s. s., An. willmori, An. pseudowillmori, An. sawadwongporni and An. dravidicus, 5 pairs of specific primers were designed for PCR identification on the species of An. maculatus complex. The PCR products were sequenced in double directions, and homology searches were done over the Web using the program Blast. 22 ITS2 sequence of An. maculatus complex from GenBank was adopted to construct phylogenetic tree with UPGMA method by MEGA(3.1) software. Results 575 DNA samples were extracted. Among which, 11 were amplified 231 bp An. willmori fragment (1.9%) and 564 were amplified 119 bp An. pseudowillmori fragment (98.1%). PCR identification, Web homology blast and phylogenetic tree showed same results. Conclusion The predominant anopheline mosquitoes in Motuo County is An. pseudowillmori.

Key words [Tibet](#) [Motuo](#) [Anopheles maculatus complex](#) [Species identification](#)

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