

论著

恶性疟原虫海南分离株裂殖子表面蛋白1基因的分型研究

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摘要

目的 了解海南省恶性疟原虫裂殖子表面蛋白 1(PfMSP1)等位基因型的分型特征。方法 采用套式PCR方法,用几对PfMSP1特异引物扩增疟原虫株PfMSP1基因第 2区与第 3区部分片段,并对等位基因型代表株的基因片段进行序列分析。结果 39份血样中有 36份恶性疟患者共扩增出 44个PfMSP1基因片段,以MAD2 O型为主导型(占 75%),K1型为次要型,未检出RO33型。两种不同等位基因型的混合感染率为 19.4%。序列分析表明,海南省恶性疟原虫虫株的MAD2 O型和K1型第 2区序列与MAD2 O和K1原型序列具有高度同源性。结论 海南省恶性疟原虫虫株存在MAD2 O型和K1型两种等位基因型,以MAD2 O型为优势虫株。

关键词 [恶性疟原虫](#) [裂殖体表面蛋白1](#) [基因分型](#) [序列分析](#)

分类号

Gene Typing of Merozoite Surface Protein 1 of Plasmodium falciparum isolates from Hainan Province

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Abstract

Objective To identify the genotype of merozoite surface protein 1 (MSP1) of Plasmodium falciparum isolates from Hainan Province. Methods Nested PCR was applied to amplify the MSP1 of Blocks 2 and 3 Plasmodium falciparum isolates from Hainan Province. Two allelic family representative gene fragments were sequenced. Results From 36 out of 39 blood samples from Plasmodium falciparum patients, 44 gene fragments of blocks 2 and 3 of the MSP1 were amplified, of which the MAD20 type allele was dominant(75%). followed by K1 type allele. No RO33 type allele was found. The mixed infection rate of the two different allelic type was 19.4%. Sequence analysis showed that the sequences of MAD20 and K1 type isolates from Hainan Province were highly homologous to that of the MAD20 and K1 allelic prototypes. Conclusion Two principal allelic types of MSP1 gene, MAD20 and K1 type, exist in malaria endemic areas in Hainan Province, the MAD20 type being the dominant.

Key words [Plasmodium falciparum](#) [MSP1](#) [genotyping](#) [sequence analysis](#)

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