



PCR-RFLP检测输入性恶性疟原虫 Pfcrt基因多态性

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Analysis of Pfcrt Gene Polymorphism in Plasmodium falciparum from Imported Cases

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摘要 目的 了解来自不同流行区输入性恶性疟原虫Pfcrt基因K76T的点突变情况,探讨恶性疟原虫Pfcrt基因多态性。方法 采集2008-2012年从非洲(尼日利亚、赤道几内亚、刚果、利比里亚、安哥拉和马里)和东南亚(缅甸和印度尼西亚)等疟疾流行区回国人员恶性疟现症患者血样共72份,根据恶性疟原虫Pfcrt基因序列设计巢式PCR引物,以血样中的恶性疟原虫DNA为模板,进行巢式PCR,扩增产物经限制性内切酶Apo I酶切后鉴定。结果 72份输入性恶性疟现症患者血样中,71份扩增出目的条带。扩增产物酶切结果显示,突变型Pfcrt等位基因41份(57.7%, 41/71),野生型Pfcrt等位基因30份(42.3%, 30/71)。其中非洲6国50份血样中,野生型和突变型各25份(50%, 25/50);缅甸和印度尼西亚21份血样中,野生型5份(23.8%, 5/21),突变型16份(76.2%, 16/21)。结论 来自不同流行区的恶性疟原虫分离株Pfcrt基因突变出现率不同。

关键词: 输入病例 恶性疟原虫 Pfcrt基因 多态性

Abstract: Objective To identify the incidence of the K76T mutation in Pfcrt gene of imported Plasmodium falciparum and study the Pfcrt gene polymorphism in Plasmodium falciparum. Methods Seventy-two blood samples were collected from patients infected with P. falciparum returning from Africa (Nigeria, Equatorial Guinea, Congo, Liberia, Angora and Mali) and Southeast Asia (Myanmar and Indonesia) from 2008 to 2012. According to Pfcrt gene sequence of P. falciparum, nested PCR primers were designed, and the reaction was applied with P. falciparum DNA in the blood samples as templates. PCR products were identified by Apo I digestion. Results Among 72 blood samples of P. falciparum, mutant Pfcrt alleles were found in 41 samples (57.7%, 41/71) and wild type Pfcrt alleles were found in 30 samples (42.3%, 30/71). There were 25 samples (50%, 25/50) each with mutant Pfcrt alleles or wild type that were from Africa, while 16 samples (76.2%, 16/21) with mutant Pfcrt alleles and 5 samples (23.8%, 5/21) with wild type that were from Southeast Asia, respectively. Conclusion The incidence of Pfcrt gene mutation is different in P. falciparum isolates from different regions.

Keywords: Imported cases Plasmodium falciparum Pfcrt gene Polymorphism

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