论著

湖北省间日疟原虫分离株环子孢子蛋白部分序列分析

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收稿日期 修回日期 网络版发布日期 接受日期

摘要

目的:为了确定湖北省间日疟原虫虫株环子孢子蛋白(CSP)的分型和探讨CSP 多态性的生物学特征。方法:采用常规的克隆和Sanger链终止法,首次对湖北省间日疟原虫的环子孢子蛋白(CSP)基因测序。结果:HB2 株CSP 基因的N-C-端非重复区包括重复区后可变区核苷酸序列与北朝鲜(NK)株和中国株(CH2-CH7)相同,而中央前后重复区则有较大变异。在HB2 CSP中央前后重复区,有8种变异型。与其它已发表的间日疟原虫CSP核苷酸序列相比,重复体GNGAGGQP/AA和重复后可变区有明显的地理学特征。此外同一份HB2 CSP基因PCR产物克隆后获得含两个大小不等插入片段的阳性克隆,分别为0.75kb和1.1kb。两者非重复区的核苷酸序列相同,在中央前后重复区除了重复数次不同外,仅有3处隐性核苷酸变异和1处显性核苷酸变异。结论:CSP基因变异,尤其是重复区的变异不仅与DNA聚合酶的自身作用有关,而且还可能牵涉到间日疟原虫潜伏期的改变。

关键词 <u>间日疟原虫</u> <u>环子孢子蛋白</u> <u>测序</u> <u>多态性</u> <u>自身作用</u> 分类号

ANALYSIS OF PARTIAL SEQUENCE OF CIRCUMSPOROZOITE PROTEIN OF *PLASMODIUM VIVAX* ISOLATES IN HUBEI PROVINCE

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Abstract

AIM: To identify circumsporozoite protein (CSP) genes of *Plasmodium vivax* in Hubei endemic areas and explore the biological features of CSP polymorphism. METHODS: Circumsporozoite protein (CSP) gene of *P. vivax* in Hubei was firstly sequenced by using routine cloning and Sanger Chain Terminal method. RESULTS: The N- and C- terminus sequences flanking the central tandem repeat, including post-repeat variable region of CSP gene of HB2 isolate were identical to those of North Korean (NK) isolate and Southern China isolates (CH2-7), while the central tandem repeat region existed extensive poly-morphism. Compared with the other CSP gene sequences published so far, the repeat form GNGAGGQP/AA and the post-repeat variable region had obvious geographical characteristics. Incidentally, one CSP gene PCR product of HB2 isolate produced two clones containing 0.75 kb and 1.1 kb DNA fragment, respectively. Their nucleotide sequences were almost the same except for three silent changes and one nonsilent change and the difference in the repeat number as well. CONCLUSION: The variation of CSP gene sequence, especially in the repeat and the post-repeat variable region, possibly involve the changes of latent period of *P. vivax*.

Key words <u>Plasmodium vivax</u> <u>circumsporozoite protein</u> <u>sequence</u> <u>polymorphism</u> <u>artefact</u>

DOI:

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