中国寄生虫学与寄生虫病杂志 2000 18 (1): 1-4 ISSN: 1000-7423 CN: 31-1248/R

论著

不同疟区恶性疟原虫地理株谷氨酸富有蛋白基因R2区序列分析及分型

诸欣平,张新梅,周蕾,高欣

首都医科大学寄生虫学教研室!北京100054

收稿日期 修回日期 网络版发布日期 接受日期

摘要

[目的]测定云南与海南两省不同疟区恶性疟原虫分离株谷氨酸富有蛋白 (GLURP)基因的部分序列及了解其分型。[方法]采用套式PCR方法特异性扩增GLURP基因R2区片段 ,并将该基因片段克隆于T载体 ,用双脱氧末端终止法测定不同长度的阳性克隆核苷酸序列 ,并应用DNAStar软件对云南与海南两省分离株GLURP基因及蛋白序列进行比较和分析。[结果]首次发现云南与海南两省恶性疟原虫至少存有 7个大小不同的GLURP等位基因型虫株 ,其基因片段变化范围为 6 0 0～ 15 0 0bp。不同分离株的GLURP基因R2区具高度保守性 ,其由编码 19～ 2 0个氨基酸的碱基的基本重复单位构成 ,该基因具有长度的多态性 ,表现在碱基基本重复单位的数目不同。序列分析结果表明 ,我国不同分离株之间或同一地区不同株之间GLURP基因及氨基酸序列具有高度的同源性 ,无明显的地理差异。 [结论]不同分离株GLURP基因结构的高度保守性及碱基重复片段数目的多态性 ,对研究疫苗候选抗原和建立疟原虫基因分型方法具有一定理论价值。

关键词 恶性疟原虫 谷氨酸富有蛋白 R2区 疫苗 基因分型

分类号

SEQUENCE ANALYZING AND GENOTYPING OF THE GENE ENCODING GLUTAMATE RICH PROTEIN OF GEOGRAPHICALLY DIFFERENT PLASMODIUM FALCIPARUM ISOLATES OBTAINED FROM DIFFERENT MALARIA ENDEMIC AREAS

ZHU Xin ping,ZHANG Xin mei,ZHOU Lei,GAO Xin

Department of Parasitology;Capital University of Medical Sciences;Beijing 100054

Abstract

Objective] To sequence a gene encoding GLURP and identify the genotypes of geographically different Plasmodium falciparum isolates from Yunnan and Hainan Provinces, China. [Methods] The gene of R2 repeat region of GLURP was amplified by the nested polymerase chain reaction and cloned into T vector. The nucleotide sequence of the GLURP gene was determined using automatic sequencer (dideoxy chain termination method), and analyzed by DNA Star software. [Results] At least 7 different GLURP genotypes ranging from 600 bp to 1 500 bp were found in different P falciparum isolates from Yunnan and Hainan Provinces. R2 region of GLURP gene consisted of several repeat units, each was composed of 19～20 residues which were shown to be highly conserved. The GLURP gene was also size polymorphic due to differences in the number of repeat units, whereas the repeat sequence was conserved. Sequence analysis showed that DNA sequences and deduced amino acid sequences were highly homologous among the geographically dispersed isolates or various isolates from the same geographical region. No obvious differences were found in the GLURP gene sequences among geographically different isolates. [Conclusion] TheGLURP gene of geographically different P falciparum isolates is highly conserved and size polymorphic, being useful in searching for malaria vaccine candidate antigen and developing a genotyping method for malaria research.

Key words Plasmodium falciparum glutamate rich protein(GLURP) R2 region vaccine genotyping.

DOI:

通讯作者

作者个人主页 诸欣平;张新梅;周蕾;高欣