遗传 2007 29 (5): 637-642 ISSN: 0379-4172 CN: 11-5450/R

研究报告

# 戊型肝炎病毒第4基因型中国株ORF2编码蛋白的抗原表位分析

张红梅[1,3]，戴星[2]，孟继鸿[1]，赵宇[1]，单祥年[3]

1. 东南大学医学院病原生物学和免疫学系, 南京 210009;
2. 东南大学医学院附属中大医院皮肤科, 南京 210009;
3. 东南大学医学院遗传学研究中心, 南京 210009

收稿日期 2006-11-19 修回日期 2007-1-15 网络版发布日期 2007-4-12 接受日期

摘要

以戊型肝炎病毒(HEV)第4基因型中国株ORF2编码蛋白p166Chn制备单克隆抗体(McAbs)，同时制备20个N端或C端逐渐截短的p166Chn截短蛋白，与7种不同基因型和亚型的p166蛋白一起，通过ELISA、免疫印迹(Western blot)以及竞争抑制实验对主要存在于我国的HEV第4基因型毒株进行抗原表位分析。结果发现所制备的McAbs与p166Chn截短蛋白的免疫反应有两种类型，以1G10为代表的McAbs能与N端不短于aa477、C端不短于aa613的截短蛋白反应，其针对的抗原表位是构象依赖型表位，依赖于aa477~aa613肽链区段；而McAb 2F11则能与N端不短于aa474、C端不短于aa617的截短蛋白反应，其针对的抗原表位也是构象表位，但需依赖于较长的肽链区段(aa474~aa617)。竞争抑制实验显示两类McAbs互不抑制，进一步证实了所发现的两个抗原表位在空间位置上的不同。更有意义的是，两类McAbs均能与其他不同HEV基因型和亚型来源的p166重组蛋白发生阳性反应，表明这两个抗原表位是HEV基因型共同性的，可以在世界各国分布的不同基因型HEV毒株中诱导交叉免疫。

关键词 戊型肝炎病毒 单克隆抗体 基因型 表位

分类号



# Characterization of antigenic epitopes of ORF2 encoded proteins of hepatitis E virus genotype 4 identified in China

ZHANG Hong-Mei[1,3], DAI Xing[2], MENG Ji-Hong[1], ZHAO Yu[1], SHAN Xiang-Nian[3]

1. *Department of Microbiology and Immunology, Southeast University School of Medicine, Nanjing* 210009, *China*;
2. *Department of Dermatology, Zhongda Hospital, Southeast University School of Medicine, Nanjing* 210009, *China*;
3. *Genetic Research Center, Southeast University School of Medicine, Nanjing* 210009, *China*

**Abstract**

<P>To characterize antigenic epitopes of hepatitis E virus (HEV) genotype 4 that was first identified in China a few years ago, a recombinant protein, p166Chn, encoded by HEV genotype 4 ORF2 was used to prepare anti-p166Chn McAbs. Simultaneously, twenty N- or C-terminal truncated p166Chn proteins were generated. Immunoreactivity between the McAbs and the truncated proteins as well as seven p166 recombinant proteins derived from different HEV genotypes and subgenotypes was detected by indirect ELISA, Western blot and competition inhibition ELISA. Two reactive profiles were observed with different McAbs and different truncated proteins. The McAbs, represented by 1G10, reacted with those N-terminal truncated proteins beginning at upstream of aa477 and those C-terminal truncated proteins ending at down-stream of aa613, suggesting that the epitope recognized by 1G10 relied on the region of aa477－aa613 and was conforma-tion-dependent. While McAb 2F11 was reactive to those truncated p166Chn proteins beginning at upstream of aa474 or ending at downstream of aa617, indicating that the epitope recognized by 2F11 was also conformation-dependent and relied on a longer peptide of aa474－aa617. However, the two

groups of McAbs didn't inhibit each other when tested by a compe-tition inhibition ELISA, which confirmed the different spatial positions of the two epitopes. Furthermore, when p166 pro-teins derived from different HEV genotypes and subtypes were applied, all of the McAbs prepared against pChn166 of genotype 4 identified in China could react with the proteins of genotype 1, 2 and 3 distributed worldwide. The data sug-gested that the two identified epitopes were HEV genotype-common and played significant effects on cross immunoreactiv-ity between different HEV genotypes.</P>

**Key words** Hepatitis E virus monoclonal antibodies genotype epitope

DOI: 10.1360/yc-007-0637

---

通讯作者 孟继鸿 jihongmeng@263.net