

论著

粤东客家地区乙型肝炎病毒S基因序列多态性分析

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摘要 目的: 探讨广东客家地区乙型肝炎病毒(HBV) S基因序列的多态性, 了解该地区S基因的流行病学特征。方法: 运用基因扩增技术对40例来自广东客家地区的乙肝表面抗原阳性及HBVDNA阳性的HBV感染者S基因进行扩增, 再对扩增产物进行DNA测序, 将该地区S基因序列与标准序列对比分析。结果: 40例样本中, adw型36例, adr型4例。36例adw型中, 第131位天冬酰胺(Asn)均被苏氨酸(Thr)替代, 其它位点也不不同程度存在着氨基酸密码的差异: 第127位脯氨酸(Pro)被Thr替代, 第133位蛋氨酸(Met)被亮氨酸(Leu)或Thr替代, 第134位苯丙氨酸(Phe)被酪氨酸(Tyr)替代, 第143位Thr被Met替代, 更多位点的遗传密码存在着简并性。而4例adr型的氨基酸序列高度同源。结论: HBV亚型的分布具有明显的域性, 广东客家人感染的HBV亚型主要为adw型, 只有少数为adr型。与参照序列相比, adw型存在较明显的多态性。

关键词 [肝炎病毒,乙型;](#) [基因;](#) [变异\(遗传\)](#)

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S-gene polymorphism of hepatitis B virus in Hakka area of Guangdong

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Abstract

AIM: To examine the surface (S) gene variability of hepatitis B virus (HBV) in Hakka area of Guangdong province in China. METHODS: The S genes from 40 HBsAg and HBV DNA positive patients in Hakka area of Guangdong province were amplified and sequenced directly for its molecular characterization, then these sequences were compared with the consensus sequences. RESULTS: In all 40 patients, 36 patients belongs to subtype adw and 4 patients to subtype adr. In 36 patients of subtype adw, it was found that at the position 131 all amino acid residues were Thr not Asn, at the position 127, 133, 134 and 143 all were also substituted by other amino acids. In 4 patients of subtype adr, amino acid residues were found to be highly conservative. CONCLUSION: The different HBV subtypes have different patterns of geographic distribution. Subtype adw is the major type in Hakka area of Guangdong. S gene sequence of HBV has its variability, especially in subtype adw.

Key words [Hepatitis B virus](#) [Genes](#) [Variation \(genetics\)](#)

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