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IFN-γ基因多态性与HBV感染及原发性肝细胞癌易感性的研究

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Study on Susceptibility of HBV Infection and Primary Hepatocellular Carcinoma with Gene Polymorphism of IFN-gamma

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摘要 目的

探讨细胞因子IFN-γ基因-1615C/T和+5171A/G位点单核苷酸多态性在广西人群中的分布及其对原发性肝细胞癌(HCC)发生、乙型肝炎病毒(HBV)感染的影响。方法设计以医院为基础的病例对照研究，对375名HCC患者、377名HBV携带者和406健康对照进行频数匹配，采用TaqMan MGB实时荧光定量PCR技术对上述位点进行分型。应用Logistic回归模型分析基因型在三组中的分布差异及基因环境交互作用，并进行连锁不平衡和单倍型分析。结果-1615C/T和+5171A/G位点的基因多态性在三组中分布差异无统计学意义($P>0.05$)。Logistic回归分析结果显示，吸烟、饮酒和肝癌相关家族史与基因存在交互作用；饮酒联合-1615C/T位点突变型基因T能增加HBV感染风险(OR=1.72，95%CI:1.11~3.26)；两个位点的突变型基因T和G联合肝癌相关家族史能增加HCC患病风险（OR:29.24、52.03，95%CI:6.91~123.6、7.02~385.4）。IFN-γ的-1615C/T和+5171A/G位点存在连锁不平衡($D'=0.976$，$P=2.22^{-16}$)，但单倍型分布在HCC组与总对照组（HBV携带者对照和健康对照）间无统计学差异。 结论IFN-γ的-1615C/T和+5171A/G位点的突变型基因可能不是广西人患HCC和感染HBV的直接危险因素，但环境危险因素对HCC发生和HBV感染有协同作用。

关键词： 原发性肝细胞癌；HBV感染；IFN-&gamma ；基因多态性

Abstract： Objective

To explore the distribution of cytokines IFN-gamma gene (-1615C/T and +5171A/G)single nucleotide polymorphisms in Guangxi people，and the impact of hepatitis B virus (HBV)infection and primary hepatocellular carcinoma(HCC)occurrence.MethodsA case-control study based on hospital was carried out and all the objects were frequency matched by 375 HCC patients - 377 HBV carriers-406 healthy control.TaqMan MGB Real-Time fluorescence quantitative PCR technology was applied to detect the SNPs of the two loci.The distribution of the genotype and the interaction of gene-environment in the three groups were analyzed by Logistic regression model.The linkage disequilibrium and haplotype of IFN-gamma gene were analyzed.ResultsThere was no significant statistically difference in the polymorphisms of -1615C/T and +5171A/G loci among the three groups ($P>0.05$).There were gene-environment interactions in smoking，alcohol consumption，liver cancer related family history with IFN-gamma gene according to logistic regression analysis.Alcohol consumption combined -1615 locus mutant gene G increased HBV infection risk(OR=1.72，95%CI:1.11~3.26).The two loci mutant genes combined with liver cancer related family history also enhanced HCC risk (OR:29.24，52.03，95%CI:6 91~123.6, 7.02~385.4, respectively).-1615C/T and +5171A/G sites on IFN-gamma had linkage disequilibrium($D'=0.976$, $p=2.22^{-16}$)，but the haplotypes between HCC groups and the total controls (HBV carriers and healthy control) had no significant statistically difference.ConclusionThe mutant genes of -1615C/T and +5171A/G loci might not influence the occurrence of HCC and HBV infection directly in the population of Guangxi，however they enhanced the risk interacted with the environment risk factors.

Key words:

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