

## FAT10单核苷酸多态性与肝细胞癌发生发展的关联

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### Relationship between Single Nucleotide Polymorphism of FAT10 Gene and Progression of Hepatocellular Carcinoma

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#### 摘要

#### 目的

探讨FAT10基因外显子和侧翼序列单核苷酸多态性(single-nucleotide polymorphism,SNP)与肝细胞癌发生和临床病理的关系。方法通过DNA测序分析方法,检测254例肝癌和268例健康对照人群的FAT10基因SNPs,并比较不同基因型与肝细胞癌的发生和临床病理的关系。采用Haploview统计软件分析研究对象的连锁不平衡和单体型。结果在肝癌组和对照组共检测到10个SNPs位点。其中-143 A/G,-121 A/G,+3476 T/C,+3607 T/C,+3620 C/G和+3809 G/T基因型与相应的野生型纯合子相比能明显降低肝癌发病的风险( $P<0.05$ ),但是这些多态性位点的基因型频率与肝癌的临床表型无关( $P>0.05$ )。进一步单体型分析发现,各变异等位基因在病例组和对照组内均存在遗传连锁不平衡现象,AATTTTCG、AATCTCG、GGCTCGT和AGCTCGT为四种常见的单体型。GGCTCGT和AGCTCGT单体型可能对肝癌的发病起保护性效应( $OR=0.41,95\%CI:0.24\sim0.70,P<0.05$ 和 $OR=0.43,95\%CI:0.22\sim0.983,P<0.05$ ),而AATTTTCG单体型可能增加肝癌的发病风险( $OR=1.64,95\%CI:1.24\sim2.17,P<0.05$ )。结论本研究首次发现中国汉族人群FAT10基因外显子和侧翼序列SNPs与肝癌的易感性相关,但需要不同种族的大样本和功能研究进一步验证。

关键词: FAT10基因 单核苷酸多态性 肝细胞癌

#### Abstract:

#### Objective

To study the association between single nucleotide polymorphism in exonic and flanking sequence of the human HLA-F adjacent transcript 10(FAT10) gene and susceptibility of hepatocellular carcinoma(HCC).MethodsA total of 522 subjects,including 268 healthy controls and 254 patients with HCC were recruited.Genotyping was done by DNA sequencing.The odds ratios(ORs) and 95% confidence intervals(CIs) were calculated by unconditional logistic regression model to estimate the risk of FAT10 SNPs to development of hepatocellular carcinoma.Haplotypes distribution was estimated by haploview software.ResultsWe identified 10 SNPs in both HCC and healthy subjects.The -143 A/G,-121 A/G,+3476 T/C,+3607 T/C,+3620 C/G and +3809 G/T genotypes were associated with a decreased risk for HCC(all  $P<0.05$ ),but no SNPs were associated with disease clinicopathology(all  $P>0.05$ ).Estimated by haploview software,genetic linkage disequilibrium existed both in the patients and the controls AATTTTCG,AATCTCG,GGCTCGT and AGCTCGT were four most common haplotypes.Haplotypes GGCTCGT and AGCTCGT were related to reduced HCC risk( $OR=0.41,95\%CI=0.24\sim0.70,P<0.05$  and  $OR=0.43,95\%CI:0.22\sim0.983,P<0.05$ ,respectively),while the haplotype AATTTTCG was involved into increased risk( $OR=1.64,95\%CI:1.24\sim2.17,P<0.05$ ).ConclusionThe FAT10 gene SNPs may be involved in the susceptibility of HCC,while further research is required to confirm this hypothesis both in large

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