中国病理生理杂志 2008 24 (12): 2391-2395 ISSN: 1000-4718 CN: 44-1187/R

论著

TNF-α基因单核苷酸多态性与肺炎的相关性研究

袁伟锋[1,2],黄文杰[2△],梁坤[2]

1南方医科大学研究生学院,广东 广州 510515;2广州军区广州总医院呼吸内科,广东 广州 510010

收稿日期 2007-12-5 修回日期 2008-7-8 网络版发布日期 2009-2-22 接受日期 2008-7-8

摘要 目的: 以中国南方汉族人群为研究对象，探讨肿瘤坏死因子-α(tumor necrosis factor-alpha,TNF-α)基因启动子区单核苷酸多态性(single-nucleotide polymorphisms,SNPs)与肺炎易感性以及肺炎严重程度的相关性。

方法: 以67例肺炎患者和50例健康人群为研究对象，应用聚合酶链反应-限制性片段长度多态性(PCR-RFLP)方法对TNF-α基因启动子区5个位点(-1 031、-863、-857、-308、-238)进行基因分型，用SPSS统计软件分析各多态性位点与肺炎严重程度的相关性。

结果: TNF-α基因启动子区总突变频率在肺炎患者中高于健康体检者(56.7%，38.0%，P<0.05)，-863A在重症肺炎患者与非重症肺炎患者中出现频率分别为〖JP2〗44.4%与15.5%，P<0.05；-308A在重症肺炎患者与非重症肺炎患者中出现频率分别为44.4%与12.1%，P<0.05，〖JP〗在死亡与存活病例中的频率分别为75.0%与12.7%，P<0.01。

结论: TNF-α基因启动子区多态性可能是肺炎易感以及肺炎进展为重症肺炎、增加重症肺炎患者死亡率的因素。

关键词 肺炎 基因,肿瘤坏死因子 单核苷酸多态性

分类号 R363

Single-nucleotide polymorphisms of tumor necrosis factor-alpha gene are associated with severe adult community acquired pneumonia in Chinese

YUAN Wei-feng[1,2],HUANG Wen-jie[2],LIANG Kun[2]

1Postgraduate Institute of the Southern Medical University,Guangzhou,510515,China;2Department of Respiratory Medicine,Liuhuaqiao Hospital,Guangzhou 510010,China.E-mail: Huangyelu1029@VIP.163.com

Abstract

<FONT face=Verdana>AIM: Tumor necrosis factor-α (TNF-α) participates in the establishment of inflammatory lesions in pneumonia.High production of TNF-α may relate to the severity of pneumonia.There have already been several studies examining the association between pneumonia and single nucleotide polymorphisms (SNPs) that affect cytokine productivity.SNPs of TNF-α,-1 031,-863,-857,-308 and -238 have been identified.The variant alleles of these SNPs have suggested to be related to high TNF-α production and the severity of pneumonia.Therefore,the aim of this study 〖JP2〗is to examine the association between the severity of pneumonia 〖JP3〗in Chinese and the following SNPs: five in the TNF-α〖JP〗 gene promoter (-1 031,-863,-857,-308,-238).
METHODS: A total of 117 Chinese individuals were enrolled in this study.They were 67 patients with pneumonia and 50 healthy subjects.TNF-α was genotyped by polymerase chain reaction-restriction fragment length polymorphism for all subjects.The frequency distributions of genotypes in different groups were analyzed by SPSS 11.5 program.
RESULTS: Frequency of subjects who carried at least one variant allele in TNF-α-1 031,-863,-857,-308,-238 SNPs among pneumonia patients was significantly higher than that in healthy subjects.And frequency of subjects who carried variant allele in TNF-α-863,and -308 SNPs among severe adult community acquired pneumonia patients was significantly higher than that in common pneumonia patients.
CONCLUSION: TNF-α -863 and -308 SNPs appear to be associated with severe adult community acquired pneumonia in Chinese populations.
</FONT>

Key words Pneumonia Genes tumor necrosis factor Single-nucleotide polymorphisms

DOI: 1000-4718

通讯作者 黄文杰 Huangyelu1029@VIP.163.com