[1]吴立强,陈建平,何念海,等.TIM-3基因多态性与儿童咳嗽变异性哮喘的关系[J].第三军医大学学报,2012,34(22):2302-2305.
Wu Liqiang,Chen Jianping,He Nianhai,et al.Relationship between TIM-3 polymorphism and childhood cough variant asthma[J].J Third Mil Med Univ,2012,34(22):2302-2305.

TIM-3基因多态性与儿童咳嗽变异性哮喘的关系(PDF)

《第三军医大学学报》[ISSN:1000-5404/CN:51-1095/R] 卷: 34 期数: 2012年第22期 页码: 2302-2305 栏目: 论著 出版日期: 2012-11-30

Title: Relationship between TIM-3 polymorphism and childhood cough variant asthma

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关键词: 儿童咳嗽变异性哮喘; 单核苷酸多态性; TIM-3; 单体型

Keywords: childhood cough variant asthma; single nucleotide polymorphism; TIM-3; haplotype

分类号: R394.4;R441.5;R725.622.5

DOI: -

文献标识码: A

摘要: 目的 探讨重庆地区汉族人群中哮喘免疫调节基因TIM-3启动子区3个单核苷酸多态性（SNP）位点与儿童咳嗽变异性哮喘（CVA）易感性的关联性。 方法 选取本科就诊CVA儿童200例，平均年龄6.8岁，作为CVA组，对照组儿童215例平均年龄6.9岁；采用（PCR-RFLP）聚合酶链反应-限制性片段长度多态性检测所有研究对象TIM-3基因启动子区Rs1051746、Rs4704853、Rs10053538三个多态性位点基因多态性，进行病例对照研究分析。 结果 PCR-RFLP检测结果显示， Rs1051746位点单核苷酸多态性(single nucleotide polymorphism, SNP)在哮喘组和对照组相比差异有统计学（*OR*=3.405，95%*CI* 1.214～9.551，*P*<0.05），CVA患儿组T等位基因频数（4%）显著高于健康组（1%）； Rs4704853、Rs10053538位点基因型频数及等位基因频数分布差异均无统计学意义（*P*>0.05）；单体型T-C-G在两组中差异有统计学意义（*P*=0.029，*OR*=3.232，95%*CI* 1.066～9.796)；分别比较各位点CVA患儿不同基因型的皮肤点刺、总IgE、EOS水平，并未发现有统计学差异的指标（*P*>0.05）。 结论 TIM-3启动子区的Rs1051746与儿童咳嗽变异性哮喘易感性相关，携带T-C-G单体型的人群罹患CVA的风险性可能较正常人群高，各位点基因多态性可能与皮肤点刺、总IgE、EOS水平无关。

Abstract: Objective To elucidate the relationship between the single nucleotide polymorphism (SNP) of the asthma immune regulator gene TIM-3 and the susceptibility of childhood cough variant asthma (CVA) in Han population in Chongqing. Methods PCR-restriction fragment length polymorphism (RFLP) was used to test the genotypes of the polymorphism loci of Rs1051746, Rs4704853 and Rs10053538 in TIM-3 promoter region among 200 CVA children (CVA group, 6.8

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years old on average) and 215 controls (control group, 5.9 years old on average). Results The results of PCR-RFLP showed that the SNP of the Rs1051746 in TIM-3 gene was significantly different between the CVA group and the control group (*OR*=3.405, 95% *CI* 1.214-9.551, *P*<0.05), and the frequency of allele T in the CVA group was significantly higher than that in the control group (*P*<0.05), suggesting the SNP of the Rs1051746 was associated with childhood CVA. The genotype and allele frequencies of the Rs4704853 and Rs10053538 showed no significant difference between the CVA group and the control group, suggesting the SNP of the Rs4704853 and Rs10053538 were not associated with childhood CVA (*P*>0.05). There was statistically significant difference of the haplotype T-C-G between the CVA group and the control group (*P*<0.05), but the differences of skin prick test (SPT) and the levels of total IgE (TIgE) and eosinophils (EOS) among the CVA children with different genotypes at Rs1051746, Rs4704853 and Rs10053538 were not statistically significant (*P*>0.05). Conclusion The SNP of Rs1051746 in the TIM-3 gene is associated with childhood CVA, and the children with haplotype T-C-G may be more likely affected by CVA compared with those without haplotype T-C-G. There may be no relationship between the SNP of Rs1051746, Rs4704853 and Rs10053538 and the levels of SPT, TIgE and EOS.

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备注/Memo: -

更新日期/Last Update: 2012-11-20