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论文

醛固酮合成酶基因及环境因素对高血压交互作用

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摘要:

目的 探讨汉族人群醛固酮合成酶基因(CYP11B2)启动子区-344C/T和第三外显因子K173R多态性位点与原发性高血压(EHT)关系。方法 按病例对照研究方法选择来自黑龙江省哈尔滨市的2组人群(210例EHT患者和391名对照及补充的182例EHT患者和189名对照),利用聚合酶链反应-限制性片段长度多态性及直接测序技术分别对其进行-344C/T与K173R基因型检测,问卷调查和实验室检查获取传统危险因素。结果 总人群和男性中,-344C/T基因型分布在高血压组和对照组间差异均有统计学意义($P<0.05$),而K173R基因型分布仅在女性高血压组和对照组间差异有统计学意义($\chi^2=11.16$,$P=0.003\ 8$);总人群中,-344C/T CC+TC、K173R KK分布与体质指数、腰围、血脂异常、高血糖对EHT均存在正交互作用,饮酒、吸烟与-344C/T CC+TC分布同时出现对EHT发生有促进作用;按性别分组的亚群中,除男、女血脂异常、女性血糖升高与-344C/T CC+TC分布同时存在对EHT存在负交互作用外,其余均为正交互作用。结论 -344C/T、K173R基因多态性分布在汉族EHT与正常人群中存在差异;-344 C/T CC+TC、K173R KK与传统危险因素联合作用可促进EHT发生。

关键词: 原发性高血压(EHT) 基因多态性 危险因素 交互作用

Effects genetic polymorphisms of CYP11B2 and enviromental factors on development of essential hypertension

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Abstract:

Objective To explore the relationship between genetic polymorphisms of -344C/T in the promoter region,K173R in the exon-3 of aldosterone synthase gene(CYP11B2) and essential hypertension (EHT),and to identify whether classical risk factors interact with genetic polymorphisms in the development of the disease.Methods We used a nested case-control design to investigate the relationship between genetic polymorphisms of -344C/T,K173R and the risk of EHT.The genetic polymorphisms were detected with polymerase chain reaction-restriction fragment length polymorphism (PCR-RELP) in 210 EHT patients and 391 normal controls(182 complemental cases and 189 matched controls) from Harbin city.Information on several classical risk factors were collected.Results The differences in 344C/T genotype frequency distribution between EHT patients and normal controls were statistically significant in men and all subjects($P<0.05$).The difference in K173R genotype frequency distribution between EHT patients and normal controls was statistically significant in women ($P<0.01$).Overall,there were several synergistic effects between the studied polymorphisms and classical risk factors,including overweight,abdomen obesity,hyperglycemia and dyslipidemia.The presence of -344C/T CC+TC(and also K173R KK) increased the odds of developing EHT when combined with the classical risk factors(synergism index>1).Alcohol drinking and smoking also increased the risk of EHT in the presence of -344C/T CC+TC.In the subgroup analyses,dyslipidemia interacted negatively with -344C/T CC+TC for both men and women,and hyperglycemia interacted negatively with -344C/T CC+TC in women.In addition,the risk factors interacted positively with -344C/T CC+TC as well as K173R KK.Conclusion The differences in -344C/T and K173R genotype frequency distributions between EHT patients and normal controls are statistically significant in Han people.Moreover,the combined effects of -344C/T CC+TC,K173R KK,and some classical risk factors significantly contribute to the development of the EHT.

Keywords: essential hypertension gene polymorphism risk factor interaction

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参考文献:

[1] 杨利婷,赵景波.高血压相关基因研究进展
[J].中国公共卫生,2009,25(1):18-19.

[2] Zhu HD,Sagnella GA,Dong Y,et al.Contrasting associations between aldosterone synthase gene polymorphisms and essential hypertension in blacks and in whites
[J].Hypertension,2003,21(1):87-95.

[3] Silvia RSF,Pedro HC,Rodrigo SMN,et al.Combined analysis of genetic and environmental factors on essential hypertension in a Brazilian rural population in the Amazon region
[J].Arq Bras Cardiol,2007,88(4):393-397.

[4] Guidelines Subcommittee,1999 World Health Organization-International Society of Hypertension.Guidelines for the Management of Hypertension
[J].Journal of Hypertension,1999,17(2):151-183.

[5] 中华人民共和国卫生部疾病控制司.中国成人超重和肥胖症预防控制指南(试行)
[S].北京:卫生部疾病控制司,2002.

[6] 董砚虎,孙黎明,李利.肥胖的新定义及亚太地区肥胖诊断的重新评估与探讨
[J].辽宁实用糖尿病杂志,2001,9(2):3-5.

[7] 中华心血管病杂志编辑委员会.血脂异常防治建议
[J].中华心血管病杂志,1997,25(3):169-172.

[8] World Health Organization,Diagnosis and classification of diabetes mellitus and its complications.Report of a WHO Consultation.Part I:Diagnosis and classification of diabetes mellitus.Geneva:World Health Organization,1999.

[9] 马冠生,孔灵芝,栾德春,等.中国居民吸烟行为的现状分析
[J].中国慢性病预防与控制,2005,13(5):195.

[10] 马冠生,朱丹红,胡小琪,等.中国居民饮酒行为现况
[J].营养学报,2005,27(5):363.

[11] Arias-Vásquez A,Sayed-Tabatabaei FA,Schut AFC,et al.Angiotensin converting enzyme gene,smoking and mortality in a population-based study
[J].Eur J Clin Invest,2005,35:444-449.

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