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论著

ACE基因缺失多态性与中国人妊娠高血压综合征发病易感性的Meta分析

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摘要: 目的: 探讨中国人群中血管紧张素转化酶(angiotensin-converting enzyme, ACE)基因缺失多态性与妊娠高血压综合征发病的相关性。方法: 利用网络数据库检索中国知网、万方、VIP和PubMed, 检索时间从建库至2012年3月, 收集有关ACE基因缺失多态性与中国人群妊娠高血压综合征发病关系的病例-对照研究。在评价纳入文献质量, 提取有效数据后, 采用Stata11.0软件进行Meta分析。结果: 共纳入11篇病例-对照研究, 含806个病例, 900个对照, Meta分析显示各基因型合并后的OR值与95% CI, 其中D等位基因vs I等位基因: OR=2.73, 95% CI (1.64, 4.24); 基因型DD+DI vs 基因型II: OR=3.11, 95% CI (1.98, 4.90); 基因型DD vs 基因型II: OR=5.00, 95% CI (2.30, 10.88); 基因型DI vs II基因型II: OR=1.97, 95% CI (1.53, 2.53), 差异均有统计学意义($P<0.001$)。结论: 中国人中携带ACE基因缺失多态性D等位基因型个体妊娠高血压综合征的发病风险升高。

关键词: 血管紧张素转化酶 妊娠高血压综合征 基因多态性 Meta分析

Meta analysis of correlation of angiotensin-converting enzyme gene deletion/insertion polymorphism and risk of pregnancy-induced hypertension in Chinese women

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Abstract: Objective: To investigate the association of the polymorphism of angiotensin-converting enzyme (ACE) gene and pregnancy-induced hypertension (PIH) in Chinese Women.

Methods: We systematically searched CNKI, Wanfang database, VIP and PubMed from database construction to March 2012 to collect case-control studies. Stata 11.0 was used for meta analysis after evaluating the quality of studies and collecting the data. The association was assessed by odds ratio (OR) with 95% confidence intervals (CIs). Publication bias was analyzed by Begg's funnel plot and Egger's regression test.

Results: We identified 11 case-control studies on association between ACE gene polymorphism and PIH, which included 806 PIH patients and 900 controls. Overall, significant association was found between ACE gene polymorphism and PIH risk [for D vs I: OR=2.73, 95% CI (1.64, 4.24), $P<0.001$; for DD+DI vs II: OR=3.11, 95% CI (1.98, 4.90), $P<0.001$; for DD vs II: OR=5.00, 95% CI (2.30, 10.88), $P<0.001$; for DI vs II: OR=1.97, 95% CI (1.53, 2.53), $P<0.001$].

Conclusion: Chinese women with D allele gene deletion have a higher risk of suffering pregnancy-induced hypertension syndrome.

Keywords: angiotensin-converting enzyme pregnancy-induced hypertension gene polymorphism Meta analysis

收稿日期 2012-06-29 修回日期 网络版发布日期

DOI: 10.3969/j.issn.1672-7347.2013.06.013

基金项目:

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