山东临朐胃癌高发人群和北京人群Lewis血型抗原相关SE基因多态性分析 Analysis of Polymorphisms on Lewis Blood Group Antigen Related SE Gene in the Populations in Shandong with High-risk of Gastric Cancer and Beijing

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摘要 为探讨宿主的遗传背景和幽门螺杆菌(Helicobacter pylori, H. pylori)相关胃癌的易感性之间的关系,本文采用PCR产物直接测序和PCR-RFLP的方法,检测142例山东临朐县胃癌高发人群个体(包括69例癌症患者和73例非癌个体)和93例北京正常对照个体SE基因多态性的分布特点。结果显示: sew/sew基因型在山东非癌个体和北京人群之间的分布差异具有统计学意义(P<0.01, 0R=3.06, 95% CI, 1.28~7.30),sew/sew基因型在山东癌症病人和非癌个体之间分布频率无显著性差异,H. pylori感染状况与SE基因型的分布也无关联性。提示: sew/sew纯合突变在山东临朐人群中分布频率较高,可能为临朐人群的遗传标记之一。

Abstract:To study the relation between host genetic backgroud and the susceptibility to H. pylori associated gastric cancer, PCR-sequencing and PCR-RFLP were used to screen SECRETOR gene polymorphisms in 142 subjects including 69 cancer patients and 73 non-cancer individuals from highrisk area of gastric cancer in Shandong and 93 control individuals from Beijing. Results showed that the difference in sew/sew distribution between non-cancer individuals and Beijing population was significant (P<0.01, OR is 3.06, 95% CI, 1.28~7.30), but that between cancer patients and non-cancer individuals was not with significance. SE gene polymorphism was not relevant to H. pylori infection. We concluded that Shandong population from high-risk area of gastric cancer shared a high distribution of sew/sew genotype, which could be considered as one of the genetic markers.

关键词 <u>胃癌 Lewis血型抗原 SECRETOR基因 基因多态性 Key words gastric cancer Lewis blood group antigen SECRETOR gene gene polymorphism</u>

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