论著

原发性肝癌发病年龄的遗传方差分量模型研究

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摘要
目的 HBV感染对原发性肝癌的家庭聚集性有很重要的影响，本研究控制HBV感染的同时，研究原发性肝癌发病年龄的遗传方差分量。方法 家系资料来自2001-2002年江苏泰兴的一次原发性肝癌的病例对照家系调查，利用Cox遗传方差分量模型，分析满足方差分量模型要求的178个肝癌核心家系和184个肝癌扩展家系资料，MCMC方法用于协变量回归系数和随机效应方差分量的估计。结果 不包含家庭共享环境方差的简化模型最终收敛。核心家系和扩展家系资料的遗传方差分量模型得到相似的参数估计结果，扩展家系结果显示HBsAg阳性对肝癌发病年龄的HR值为12.13（95%CI: 6.94-23.03）；遗传加性效应方差分量为0.076（95%CI: 0.002-0.291），遗传显性效应方差分量为0.301（95%CI: 0.010-1.067）。结论 除HBV感染的作用外，原发性肝癌发病年龄的家庭相关还有遗传因素的作用，包括遗传加性效应和遗传显性效应/同胞共享环境因素影响肝癌的发病年龄。
关键词　　原发性肝癌；　发病年龄；　遗传方差分量模型
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The study on genetic variance components model of age at the onset of primary hepatocellular carcinoma

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Abstract
Objective Hepatitis B virus (HBV) infection has important influence on familial aggregation of primary hepatocellular carcinoma（HCC）. The specific aim of this study was to estimate genetic variance components of age at onset for HCC when HBsAg was taken into consideration. Methods We conducted a population-based case-control family study of liver cancer in Taixing, China, in 2001-2002. Genetic variance components method based on random-effects Cox proportional hazards model was used for 178 nuclear families and 184 extended families data, and MCMC was used to estimate parameters. Results Simplified model excluding shared common environmental variance was finally fitted. There was a resemblance on the results for estimated parameters between nuclear families and extended families data. The results from extended families data showed the hazards ratio for HBV associated with age at the onset of HCC was 12.13 （95% confidence interval: 6.94-23.03）, and additive genetic variance and dominance genetic variance were 0.076 (95% CI: 0.002-0.291) and 0.301 (95% CI: 0.010-1.067) respectively. Conclusions The additive genetic and dominance genetic factors (or shared sibling environmental factors) played an important role in the age at onset of HCC but that common environmental factors were negligible besides HBV infection.

Key words　　hepatocellular carcinoma　age at onset　genetic variance components

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