论著

四川彝族人群HIV-1辅助受体CX3CR1基因多态性分析

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收稿日期 2006-3-28 修回日期 2006-7-6 网络版发布日期:

背景与目的:了解四川省彝族人群中HIV-1辅助受体CX3CR1基因多态性在正常人和HIV-1感染者中的 分布特点,探讨此辅助受体多态性对HIV感染的影响。 材料与方法: 从202份外周血中提取基因组DNA(正常人 115份,HIV-1感染者87份)。用PCR-限制性片段长度多态性(PCR-RFLP)技术检测V249I和T280M两种变体,检测 结果用行列表χ2检验法进行统计学分析。 结果: 在检测的115例正常人样品中,249I和280M等位基因频率分别 为8.3%和5.7%;HIV感染者中,两种等位基因频率分别为7.5% 和5.7%。2491和280M间存在明显的连锁关系。 正常人和感染者的两种等位基因频率的差异无统计学意义(P>0.05)。结论: 所获得的四川彝族人群HIV-1辅助受体 CX3CR1基因多态性资料有助于进一步分析四川彝族人群HIV感染和艾滋病病程的影响因素。

HIV-1; 受体,CX3CR1; 等位基因; 遗传多态性; 突变

Genetic Polymorphism of HIV Coreceptor CX3CR1 Allele in Chinese Yi Ethnic Group in Sichuan

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Abstract BACKGROUND & AIM: To explore the CX3CR1 genetic polymorphisms in HIVinfected and uninfected Chinese Yi Ethnic Groups in Sichuan. MATERIALS AND METHODS: The genomic DNA of 202 Yi subjects (115 HIV-1 uninfected, 87 HIV-1 infected) was extracted 秦光明 邢辉 李 克 邵一鸣 from PBMCs. The V249I and T280 M allelic frequencies were identified by PCR-RFLP. All data were tested by χ^2 analysis. RESULTS: Allelic frequencies of 249I and 280M in HIV-1 uninfected group were 8.3% and 5.7%, respectively. The frequencies in HIV-1 infected group were 7.5% and 5.7%, respectively. There was no significant difference between HIV-1 infected group and HIV-1 uninfected group, and both groups were in accordance with Hardy-Weinberg equilibrium. There are strong linkage disequilibrium between 249I and 280M of CX3CR1. CONCLUSION: Polymorphism of CX3CR1 allele from Chinese Yi Ethnic Group was found, this would be helpful for the risk analysis of HIV infection and the rate of HIV disease progression in Chinese Yi Ethnic Group in Sichuan.

Keywords HIV-1 receptors CX3CR1 alleles genetics polymorphism mutation DOI

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