

论著

辽宁省未经治疗HIV-1感染者耐药变异本底研究

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摘要 摘要: 目的 研究辽宁省未经抗病毒治疗的人类免疫缺陷病毒(HIV)感染人群中耐药突变的发生和流行情况。方法 提取辽宁省91例HIV-1感染者外周血基因组DNA, 巢式PCR方法扩增pol区蛋白酶基因全序列与逆转录酶基因部分序列, 直接进行序列测定。序列拼接后, 递交HIVdb-Drug Resistance Algorithm进行耐药性分析。结果 3株毒株在蛋白酶编码区含有M46I变异, 在蛋白酶编码区次要变异普遍存在, 由高到低依次为L63P(60.4%)及V77I(60.4%)、M36I/V(31.9%)、A71V/T(22.0%)、L10I(8.8%)和K20R(6.6%)。1株毒株在逆转录酶编码区含有M184I变异。结论 约4.4%的感染者对至少一种我国现有的抗病毒药物耐药。辽宁省未经抗病毒治疗的HIV-1感染人群绝大部分为抗病毒治疗敏感人群, 但应加强监测, 防止耐药株流行。

关键词 [人类免疫缺陷病毒](#) [耐药](#) [基因型](#)

分类号

Background Study of HIV-1 Drug Resistant Mutations in Treatment-naïve Patients in Liaoning Province

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Abstract ABSTRACT: Objective To collect background information on drug resistance mutations in treatment-naïve HIV-1 infected individuals in Liaoning Province. Methods Samples from 91 antiretroviral therapy-naïve patients were collected. The entire protease gene and 1-290 amino acids of the reverse transcriptase gene were amplified by nested PCR from provirus DNA and sequenced. The results were analyzed with HIVdb-Drug Resistance Algorithm, and genotypic resistance mutations were determined to particular anti-HIV drugs. Results Totally 91 sequences were obtained, 3 of which displayed M46I mutations in the protease gene. Minor resistance mutation rate to protease inhibitors was 100%, including types of L63P (60.4%), V77I (60.4%), M36I/V(31.9%), A71V/T (22.0%), L10I(8.8%), and K20R (6.6%). Only one sequence carried reverse transcriptase related resistance mutations M184I. Conclusions About 4.4% of HIV-1 infected individuals in Liaoning Province carried strains with drug resistance mutations. Most treatment-naïve HIV-1 infected individuals in Liaoning Province were sensitive to the currently available antiviral medicines, but antiviral treatment must be in accordance with the strict procedures to keep better adherence and avoid the prevalence of drug-resistant strains.

Key words [human immunodeficiency virus](#) [drug resistance](#) [genotype](#)

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