

论著

多药抗药基因1 C3435T在中国佤族、白族和藏族人群中的基因多态性

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摘要 目的 了解中国佤族、白族和藏族人群中多药抗药基因1 (MDR1) C3435T位点突变频率, 并与其他种族比较, 了解种族差异。方法 使用聚合酶链反应-限制性片段长度多态性方法并用直接测序法对中国143名佤族、138名白族和257名藏族健康个体进行MDR1 C3435T基因分型。结果 野生CC型在佤族、白族和藏族的频率分别为31.5%, 29.7%和25.7%, 突变杂合子CT型频率分别为44.7%, 50.7%和56.8%, 而突变纯合子TT型频率则分别为23.8%, 19.6%和17.5%, 分布符合Hardy-Weinberg平衡。MDR1 C3435T等位基因T在佤族、白族和藏族的频率分别为46.2%, 44.9%和45.9%, 与非洲裔美国人的比较有明显差异。佤族和藏族与汉族的比较有差异。结论 中国佤族、白族和藏族人群MDR1 C3435T位点的突变发生情况有自己的特点, 在临床应用相关药物时, 进行该位点基因型检测, 将有助于指导临床个体化用药。

关键词 [基因](#), [MDR](#) [基因型](#) [等位基因](#) [多态性](#), [单核苷酸](#)

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Genetic polymorphism of multidrug resistance gene 1 C3435T in Chinese Wa, Bai and Zang Nationalities

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Abstract

AIM To investigate the allele and genotype frequencies of multidrug resistance gene 1(MDR1) C3435T in Chinese Wa, Bai and Zang nationalities, and compare with other ethnics. **METHODS** The number of the healthy volunteers from Chinese Wa, Bai and Zang were 143, 138 and 257, respectively. The PCR-RFLP method, which was verified by direct sequencing, was applied to genotype MDR1 C3435T. **RESULTS** The MDR1 C3435T in Chinese Wa, Bai and Zang was: CC(31.5%, 29.7% and 25.7%), CT(44.7%, 50.7% and 56.8%) and TT(23.8%, 19.6% and 17.5%), which met Hardy-Weinberg equilibrium. The frequencies of allele T in Chinese Wa, Bai and Zang were 46.2%, 44.9% and 45.9%, that were significantly different from those in African-American, and Chinese Wa and Zang significantly different from those in Chinese Han. **CONCLUSION** The MDR1 C3435T gene distribution in Chinese Wa and Bai and Zang population Mutation occurred in the situation has its own characteristics. Genotyping of MDR1 C3435T will be helpful in guiding rational and individualized medication for individuals from Chinese Wa, Bai and Zang using drugs that are substrates of P-gp.

Key words [genes](#) [MDR](#) [genotype](#) [allele](#) [polymorphism](#) [single nucleotide](#)

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