

人癌细胞线粒体DNA控制区序列特征分析 Sequence Feature Analysis of Mitochondrial DNA Control Region in Human Carcinoma Cells

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摘要 为了探讨癌细胞mtDNA控制区序列的变化特征, 采用PCR产物限制性片段长度多态性(PCR-RFLP)分析与直接测序相结合的方法, 对比分析6株人癌细胞系、6例癌患者及4例健康成人白细胞mtDNA控制区序列。发现第16519位T→C、16 534位A→G、46位T→G和49位A→C突变, 在癌细胞系和癌患者白细胞mtDNA中分别占50%(3/6)和33.3%(2/6), 健康成人白细胞mtDNA中未见此类型突变; 第16 278位C→T突变, 在癌细胞系mtDNA中占50%(3/6), 显著高于正常人群mtDNA中此位点的多态性变异。表明癌细胞和癌患者白细胞mtDNA重链复制起点及其相邻D环区的特征性突变可能与细胞癌变/或癌的易感性有关。

Abstract: To explore the sequence feature of mitochondrial DNA(mtDNA) control region in human carcinoma cells, polymerase chain reaction-restriction fragment length polymorphism(PCR-RFLP) and direct sequence techniques were used to analyze the sequence of mtDNA control region of 6 human carcinoma cell lines versus white blood cells which from 6 tumor patients and 4 normal adults. The T to C mutation at np 16 519, A to G mutation at np 16 534, T to G mutation at np 46, and A to C mutation at np 49 was found in 50% (3/6 cases) of carcinoma cell lines and in 33.3%(2/6 cases) of tumor patients, but it was not found in normal adults. The C to T mutation at np 16 278 was found in 50%(3/6 cases) of carcinoma cell lines, it was significantly higher than that of the polymorphism of normal population. These findings suggest that the typical mutation in the starting area of heavy-strand replication and the first half of D-loop region might probably be associated with carcinogenesis or susceptibility of carcinoma.

关键词 [人癌细胞系](#) [线粒体DNA](#) [控制区](#) [核苷酸序列](#) [突变](#) **Key words** [Human carcinoma cell line](#) [mtDNA](#) [Control region](#) [Nucleotide sequence](#) [Mutation](#)

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