

人类与医学遗传学

胃癌差异表达基因在染色体上的定位及其功能分析

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摘要

利用标准化的Affymetrix公司生产的U133A基因芯片检测胃癌(T)与切缘正常胃黏膜(C)基因表达谱差异, 并利用生物信息学方法对检测结果进行差异基因在染色体定位和功能分析。结果表明: 胃癌与正常胃黏膜比较差异8倍以上共有 270个基因, 其中表达上调 [信号比的对数值(SLR) ≥ 3] 有157个, 表达下调(SLR ≤ -3)有113个。从表达差异的基因在染色体定位分析, 发现除4个基因未知其定位外, 其余所有差异表达基因散在分布在各条染色体上, 但以1号染色体为最多, 有26个(占9.8%), 其次是11和19号染色体上分别有24个(各占9.1%)。而差异表达的基因发生在染色体短臂(q)上有173个(占65%)。从表达差异的基因功能分类看, 属于酶和酶调控子基因最多(67个, 24.8占%), 其次是信号传导基因(43个, 占15.9%), 第3类是核酸结合基因(17个, 占6.3%), 第4类是转运子基因(15个, 占5.5%), 第5类是蛋白结合基因(12个, 占4.4%), 还有功能未知的基因有50个, 占18.5%。以上5大类共占基因总数56.9%。胃癌差异表达基因散在分布在各条染色体上, 但以1、11、19号染色体差异表达基因居多。这5大类(酶和酶调控子、信号传导、核酸结合、转运子、蛋白结合)相关基因异常是今后研究胃癌的重要基因。

关键词 [胃癌; 基因表达谱; 染色体定位; 分子功能](#)

分类号

Function and Chromosome Location of Differentially Expressed Genes in Gastric Cancer

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Abstract

<P>Using Affymetrix U133A oligonucleotide microarrays, screening was done for genes that were differentially expressed in gastric cancer (T) and normal gastric mucosa (C), and their chromosome location was characterized by bioinformatics. A total of 270 genes were found to have a difference in expression levels of more than eight times. Of them 157 were up-regulated (Signal Log Ratio [SLR] ≥ 3), and 113 were down-regulated (SLR ≤ -3). Except for, four genes with unknown localization, a vast majority of the genes were sporadically distributed over every chromosome. However, chromosome 1 contained the most differentially expressed genes (26 genes, or 9.8%), followed by chromosomes 11 and 19 (both 24 genes, or 9.1%). These genes were also more likely to be on the short-arm of the chromosome (q), which had 173 (65%). When these genes were classified according to their functions, it was found that most (67 genes, 24.8%) belonged to the enzymes and their regulators groups. The next group was the signal transduction genes group (43 genes, 15.9%). The rest of the top three groups were nucleic acid binding genes (17, 6.3%), transporter genes (15, 5.5%), and protein binding genes (12, 4.4%). These made up 56.9% of all the differentially expressed genes. There were also 50 genes of unknown function (18.5%). Therefore it was concluded that differentially expressed genes in gastric cancer seemed to be sporadically distributed across the genome, but most were found on chromosomes 1, 11 and 19. The five groups associated genes abnormality were important genes for further study on gastric cancer.</P>

Key words [gastric cancer; gene expression profile; chromosomal localization; molecular](#)

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“胃癌; 基因表达谱; 染色体定位; 分子功能”	
的 相关文章	
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