人类与医学遗传学

高低转移卵巢癌细胞株差异表达基因在染色体定位及其功能

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摘要

用基因芯片技术研究高(H)、低（L）转移卵巢癌细胞株（HO-8910PM和HO-8910）和正常卵巢上皮(C)基因表达谱差异，筛选与卵巢癌转移相关的基因，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：高、低转移卵巢癌细胞株比较表达差异2倍以上共有 409个基因，其中表达上调（信号比的对数值[SLR]≥1) 有271 个，表达下调（SLR ≤-1) 有 138个。从表达差异的基因在染色体定位分析，发现除1个基因未知其定位外，其余所有差异表达基因散在分布于各条染色体上，但以1号染色体最多有43个（占10.7%）。其次是6号染色体有39个（占9.6%），第三是2号染色体有29个（占7.1%）。第四是17号染色体有28个（占6.9%）。第五是3号染色体有25个（占6.2%）。第6是5号和11号染色体各有24个（各占5.9%）。而差异表达的基因发生在染色体短臂（q）的有264个（占64.7%），在13，14，15，21和22号仅发现在q都有异常表达。从表达差异基因的分子功能分类看，属于酶和酶调控子基因为最多（104个，占25.4%），其次是信号传导基因（43个，占10.5%）。第3类是核酸结合基因（42个，占10.3%）。第4类是蛋白结合基因（34个，占8.3%）。以上4大类共占基因总数54.5%。还有功能未知的基因有76个，占18.6%。高、低转移卵巢癌细胞株差异表达基因散在分布在各条染色体上，但以1、6、2、17、3、5和 11号染色体差异表达基因居多。肿瘤的转移是多基因共同作用的结果。4大类（酶和酶调控子、信号传导、核酸结合和蛋白结合）相关基因异常是我们今后研究卵巢癌转移的重要基因。

关键词　　卵巢癌细胞株；转移相关基因表达谱；染色体定位；分子功能

分类号

Identification of Differentially Expressed Genes in the High and Low Metastatic Human Ovarian Cancer Cell Lines and Analyses of Their Chromosomal Localizations and Functions

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Abstract

<P>Oligonucleotide microarrays were used to study the differences of gene expressions in high (H) and low (L) metastatic ovarian cancer cell lines and in normal ovarian tissues (C). Bioinformatics was used to identify novel genes and their functions as well as chromosomal localizations. A total of 409 genes were differentially expressed between the high and low metastatic ovarian cancer cell lines. Of them, 271 genes were up regulated (Signal Log Ratio[SLR] ≥1), and 138 genes were down regulated (SLR≤-1). Except one gene whose location was unknown, all these genes were localized randomly on all the chromosomes, with a majority of them localized to Chromosomes 1, 6, 2, 17, 3, 5 and 11. Chromosome 1 contained, 43 of them (10.7%), the most for a

single chro-mosome. A total of 264 genes (64.7%) were localized on the short arm of the chromosome (q). Functional classification showed that the 104 (25.4%) genes coding for enzymes and enzyme regulators made up the largest functional group, followed by signal transduction activity genes (43, 10.5%), nucleic acid binding activity genes (42, 10.3%), and proteins binding activity genes (34, 8.3%). These four groups accounted for 54.5% of all the differentially expressed genes. In addition, the functions of 76 genes (18.6%) were unknown. Tumor metastasis is the result of a number of genes acting in concert. The four functional groups of genes classified among these genes and their abnormalities would be the focus of further studies on ovarian cancer metastasis.</P>

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