

研究论文

# 用基因芯片筛选高转移卵巢癌细胞系转移相关基因

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摘要 用标准化的Affymetrix公司生产U133A基因芯片技术研究高(H)转移卵巢癌细胞株(HO-8910PM)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及其在染色体的定位和功能。结果发现高转移卵巢癌细胞株和正常卵巢上皮比较表达差异8倍以上共有1,237个基因, 其中表达上调(信号比的对数值SLR≥3)有597个, 表达下调(SLR ≤-3)有640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分散在各条染色体上, 但以1号染色体最多, 有115个(9.3%)。其次是2号染色体有94个(7.6%), 第三是12号染色体有88个(7.1%)。第四是11号染色体有76个(6.1%)。第五是X染色体有71个(5.7%)。第6是17号染色体有69个(5.6%)。而差异表达的基因发生在染色体短臂(q)上有805个(占65.1%), 在13, 14, 15, 21和22号仅发现在q上有差异表达基因。从表达差异的基因分子功能分类看, 属于酶和酶调控子基因最多(306个, 占24.7%), 其次是核酸结合基因(144个, 占11.6%)。第三类是信号传导基因(137个, 占11.1%)。第四类是蛋白结合基因(116个, 占9.4%)。以上4大类共占基因总数56.8%。还有功能未知的基因有207个, 占16.7%。结论: 高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、2、12、11、17和 X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(酶和酶调控子活性、核酸结合活性、信号传导活性、蛋白结合活性)差异表达基因是我们今后研究卵巢癌转移相关的重要基因。

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

## Screening of the Metastasis-Associated Genes by Gene Chip in High Metastatic Human Ovarian Cancer Cell Lines

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### Abstract

Affymetrix U133A oligonucleotide microarrays were used to study the differences of gene expressions between high (H) metastatic ovarian cancer cell line, HO-8910PM, and normal ovarian tissues (C). Bioinformatics was used to identify their chromosomal localizations. A total of 1,237 genes were found to have a difference in expression levels more than eight times. Among them 597 were upregulated [Signal Log Ratio (SLR) ≥3], and 640 genes were downregulated (SLR ≤-3). Except one gene, whose location was unknown, all these genes were randomly distributed on all the chromosomes. However, chromosome 1 contained the most differentially expressed genes (115 genes, 9.3%), followed by chromosome 2 (94 genes, 7.6%), chromosome 12 (88 genes, 7.1%), chromosome 11 (76 genes, 6.1%), chromosomes X (71 genes, 5.7%), and chromosomes 17 (69 genes, 5.6%). These genes were localized on short-arm of chromosome (q), which had 805 (65.1%) genes, and the short arms of No.13, 14, 15, 21, and 22 chromosomes were the only parts of the chromosomes where the differentially expressed genes were localized. Functional classification showed that most of the genes (306 genes, 24.7%) belonged to the enzymes and their regulator groups. The subsequent group was the nucleic

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acid binding genes (144 genes, 11.6%). The rest of the top two groups were signal transduction genes (137 genes, 11.1%) and proteins binding genes (116 genes, 9.4%). These comprised 56.8% of all the differentially expressed genes. There were also 207 genes whose functions were unknown (16.7 %). Therefore it was concluded that differentially expressed genes in high metastatic ovarian cancer cell were supposed to be randomly distributed across the genome, but the majority were found on chromosomes 1, 2, 12, 11, 17, and X. Abnormality in four groups of genes, including in enzyme and its regulator, nucleic acid binding, signal transduction and protein binding associated genes, might play important roles in ovarian cancer metastasis. Those genes need to be further studied.

**Key words** [ovarian cancer cell line](#) [metastatic associated gene](#) [chromosomal localization](#) [molecular function](#)

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