# 基于生物信息数据挖掘对卵巢浆液性癌差异表达基因筛选及分析

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| **Title:** | Screening and analysis of differentially expressed genes in serous ovarian carcinoma based on bioinformation data mining |

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**摘要:** 目的：利用生物信息学对卵巢浆液性癌的差异表达基因进行筛选及分析，探索浆液性卵巢癌的潜在治疗靶点。方法：从GEO数据库下载卵巢癌数据集GSE10971、GSE54388、GSE14407，用GEO2R筛选差异表达基因，DAVID数据库进行GO及KEGG富集分析，String数据库构建蛋白互作网络，同时利用Cytoscape获取关键基因，GEPIA数据库分析关键基因的表达情况，UCSC Xena对关键基因进行分层聚类分析，并通过cBioPortal分析关键基因的共表达网络。结果：筛选获得114个差异表达基因，包括41个下调基因及73个上调基因。主要涉及调整细胞周期、有丝分裂、染色体分离等细胞学过程，富集于细胞周期、p53信号通路、细胞衰老等信号通路。从差异表达基因筛选出49个关键基因，在卵巢癌中均呈高表达，其中21个基因的表达与卵巢癌分期相关，BIRC5基因的表达与卵巢癌患者的总生存期相关。结论：利用生物信息学对卵巢浆液性癌差异表达基因功能及信号通路的相关研究，为改善卵巢浆液性癌的预后提供了治疗靶点。

**Abstract:** Objective：To screen and analyze differentially expressed genes in serous ovarian carcinoma using bioinformatics，and to explore potential therapeutic targets for serous ovarian cancer.Methods：We download the ovarian cancer databases GSE10971，GSE54388，and GSE14407 from the GEO database.GEO2R was used to screen differentially expressed genes，DAVID database was used for GO and KEGG enrichment analysis.String database was used to construct protein interaction network，and Cytoscape was used to obtain critical genes.The GEPIA database analyzed the expression of essential genes，and the UCSC Xena performed hierarchical cluster analysis of crucial genes and analyzed the co-expression network of essential genes through the cBioPortal.Results：We obtained a total of 114 differentially expressed genes，including 41 down-regulated genes and 73 up-regulated genes.It mainly involved cytological processes such as cell cycle，mitosis，and chromosome separation，and enriched in signal pathways such as cell cycle，p53 signaling pathway，and Cellular senescence.We got forty-nine essential genes from differentially expressed genes，which highly represented in ovarian cancer.The expression of 21 genes was associated with ovarian cancer stage.The expression of BIRC5 gene was associated with the overall survival of ovarian cancer patients.Conclusion：The use of bioinformatics to study the differentially expressed gene function and signaling pathway in serous ovarian carcinoma provides a therapeutic target for improving the prognosis of ovarian serous carcinoma.

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