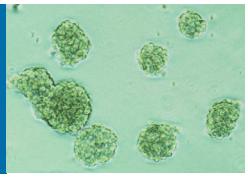
IDRAGON Management System

Idiscovery
Journal homepage: www.idiscovery.org.cn



Indication of Featured Biomarkers between Human Lung Adenocarcinoma and Inflammatory Pseudotumor Using Gene Expression microarray

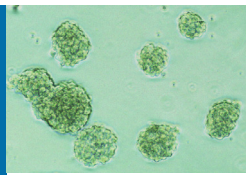
Ling Jiang[1],Yang Xu[*]
Department of Anesthesiology, West China Hospital, Sichuan University, Chengdu 610041, China

Abstract Background/Aim: To uncover the featured genes between lung adenocarcinoma (AC) and pulmonary inflammatory pseudotumor (IPT), we performed gene expression microarray to identify differentially expressed genes (DEGs) and bioinformatics analysis to unveil biological functions.**Methods:** DNA-microarray technology was used to analyze differentially expressed genes (DEGs) between samples from patients with lung AC and pulmonary IPT. Gene Ontology (GO) enrichment analysis, Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis and Protein-Protein interaction (PPI) networks analysis were used to explore biological functions of DEGs.**Results:** A total of 1351 genes were up-regulated and 1924 were down-regulated (Fold Change >= 2.0, P-value <= 0.05). The bioinformatics analysis showed for upregulated genes, the cell proliferation and metabolism were significantly enriched in biological process, the modulating genes replication was notably enriched in molecular function and intracellular part was dramatically enriched in cellular component, as well as Pyrimidine metabolism and Nucleotide excision repair were markedly enriched in KEGG pathway. For down-regualted genes, response to stimulus and immune system process were highly enriched in biological process, transmembrane receptor protein kinase activity and MAPK kinase tyrosine/ serine/threonine phosphate activity were notably enriched in molecular function and membrane part was significantly enriched in cellular component, as well as Staphylococcus aureus infection, Complement and coagulation cascades were dramatically enriched in KEGG pathway.**Conclusions:** We detect some candidate genes to distinguish lung AC with pulmonary IPT. Meanwhile, we hypothesize that the inhibition of inflammatory response and activation of mitotic cell cycle may be the molecular switch between lung AC and pulmonary IPT, which guides novel targeted therapies to inhibit the development of pulmonary IPT.

Key words: Lung ademocarcinoma; Pulmonary inflammatory pseudotumor; DNA-microarray technology; Bioinformatics.

IDRAGON Management System

Idiscovery
Journal homepage: www.idiscovery.org.cn



应用基因表达微阵列检测肺腺癌和炎性假瘤的特征生物标志物

蒋铃，徐杨 *

四川大学华西医院麻醉科，四川 成都 610041

［摘要］ 目的：为了揭示肺腺癌（AC）与肺部炎性假瘤（IPT）之间的特征基因，我们采用基因表达谱芯片进行差异表达基因的鉴定和生物信息学分析，揭示两者的生物学功能。**方法：**应用 DNA 微阵列技术对肺 AC 和肺 IPT 患者的 DEGs 进行分析。采用基因本体论（GO）富集分析、京都基因和基因组百科全书（KEGG）途径分析和蛋白质－蛋白质相互作用（PPI）网络分析，探讨 DEGS 的生物学功能。**结果：**与肺部炎性假瘤比，肺腺癌中共有 1351 个基因表达上调，1924 个基因表达下调（倍数变化≥2.0，P 值≤0.05）。生物信息学分析表明，上调基因在生物学过程中，细胞增殖和代谢显着增强，调控基因复制显着增强，分子功能显着增强，细胞成分显着增强，嘧啶代谢和核苷酸切除修复显着增强。对于下调基因，生物过程中刺激反应和免疫系统过程高度富集，分子功能中跨膜受体蛋白激酶活性和 MAPK 激酶酪氨酸／丝氨酸／苏氨酸磷酸活性显著富集，细胞成分中膜部分显著富集，金黄色葡萄球菌感染、KEGG 途径中补体和凝血级联显著富集。**结论：**我们检测到一些候选基因，可以区分肺 AC 和肺 IPT。同时，我们假设炎症反应的抑制和有丝分裂细胞周期的激活可能是肺 AC 和肺 IPT 之间的分子转换，这些发现可针对指导新的靶向治疗抑制肺部炎性假瘤的发展有一定价值。

［关键词］ DNA 微阵列技术；肺腺癌；肺部炎性假瘤；GO 分析