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基础研究

不同预后肺腺癌患者酪氨酸激酶信号传导通路异常的初步探讨

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Preliminary Analysis of Tyrosine Kinase Signaling Pathway in Different Prognosis Patients with Lung Adenocarcinoma

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摘要

目的 探讨不同预后肺腺癌患者在酪氨酸激酶信号传导通路上的具体差异。方法 选取生存期大于60个月和生存期仅9个月的两例患者，抽提其肺腺癌标本及其癌旁组织的总RNA，与含13824个基因的基因芯片进行杂交，计算机分析比较两种组织的差异表达基因。结果 两例不同预后的肺腺癌患者在酪氨酸激酶信号传导通路上存在明显差异。预后差的S病例高表达许多增殖相关基因，而与免疫相关的信号传导如干扰素7介导的信号传导通路受到抑制；预后好的L病例中干扰素7介导的信号传导通路激活，而某些在预后差的S病例中表达的增殖相关基因在预后最好的病例中处于低表达水平。结论 预后好的肺腺癌高表达抗增殖和免疫相关基因；预后差的肺腺癌高表达与增殖相关基因，同时抗增殖和免疫防御相关基因处于低表达水平。

关键词： 信号传递 酪氨酸激酶 基因表达谱 基因芯片 肺肿瘤

Abstract: Objective To study the abnormity of tyrosine kinase signaling pathway in different prognosis patients with lung adenocarcinoma. Methods We chose two patients , one’s survival time was more than 60 months , the other’s only 9 months. Total RNA was extracted form the two lung adenocarcinoma samples and their matched normal tissues , and then hybridized on the microarray with 13824 genes. At last their expression profiles of tyrosine kinase signaling pathway were analyzed by computer. Results The tyrosine kinase signaling pathway between L (the patient with the best prognosis) and S (the worse one) was very different . The most different was that S overexpressed some genes related to proliferation (such as fms、K-ras、myc and so on) while the genes related to immunity and anti-proliferation were in a low lever , for example , INFγ signaling pathways were inhibited , but which in L were activated. Some genes related to proliferation (PDGF and it s recepter , H-ras , MAPK,etc.) were overexpressed in S but low expressed in L. Conclusion In the complex system of tyrosine kinase signaling pathway in lung adenocarcinoma , different prognosis samples have different characteristic genes. In our research , the patient with the best prognosis overexpressed some genes related to immunity and anti-proliferation , and the worse one overexpressed some genes related to proliferation while the genes related to immunity and anti-proliferation were in a low lever.

Key words: Signaling Tyrosine kinase Gene-expression profiles Microarray Lung neoplasm

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