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论著

弱精症患者精子基因表达谱的建立及分析

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摘要 背景与目的: 应用基因芯片技术建立弱精症患者精子基因表达谱。 材料与方法: 收集30份弱精症患者精液标本和20份成年健康有生育能力男性的精液标本,提取精子RNA,制备生物素标记的cDNA探针,与含有30 968个探针的Phalanx OneArrayTM芯片杂交,分析弱精症患者与健康有生育能力成年男性精子中基因的表达情况。 结果: 高活力精子和低活力精子共1 995个基因存在表达差异,上调基因394个,下调基因437个。功能聚类分析结果提示,弱精症患者精子中表达上调的基因集中在物理化学刺激、压力应激、炎性反应等聚类,或一些催化酶聚类,这些因素可能是导致精子活力降低的重要诱因;而弱精症患者精子中表达下调的基因主要集中在一些与精子发生和抗凋亡相关的基因聚类中。 结论: 弱精症患者精子基因表达谱的建立对分析精子运动的分子机制和探讨弱精症的病因将会有所帮助。

关键词 弱精症 精子 基因芯片 mRNA 表达谱

Construction and Analysis of Gene-expression Profiles in the Sperms of Patients with Asthenospermia

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Abstract BACKGROUND AND AIM: To construct and analyze the gene-expression profiles in the sperms of asthenospermic patients. MATERIALS AND METHODS: 30 semen samples from asthenospermia patients and 20 semen samples from healthy normal adult men were collected; and total RNAs extracted to produce cDNAs probes. Hybridization with Phalanx OneArrayTM contained 30 968 probes was carried out after the labeled cDNAs were purified by PCR Product Purification Kit. RESULTS: Among the 30 968 probes; 394 genes were up-regulated; 437 genes were down-regulated; the others showed no different expressions. Functional cluster displayed that response to external stimulus; defense; stress and inflammation were the most important reasons leading to asthenospermia; and protease inhibitor could also lead to asthenospermia. Furthermore; genes associated with spermatogenesis and negative regulation of apoptosis were very important to maintain high sperm motility. CONCLUSION: Construction of gene-expression profiles in the sperms of asthenospermic patients could help to analyze the molecular mechanism of sperm motility and to study the etiopathogenisis of asthenospermia.

Keywords asthenospermia sperm microarrays gene-expression profiles

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