论著

利用苯肾上腺素诱导新生大鼠心肌细胞肥大基因表达谱构建其调控网络

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摘要

目的：　利用心肌肥大病理过程中基因表达谱的变化，构建基因/蛋白质调控网络。方法：以苯肾上腺素诱导新生大鼠心肌细胞肥大为模型，在分析肥大心心肌细胞基因表达谱变化的基础上，进一步利用Pathwaystudio和Agilent Literature Search软件结合文献挖掘方法，构建基因/蛋白质相互作用网络。结果：构建的网络包含450个相互作用的基因/蛋白质（节点）以及592个它们之间相互作用的关系（边）。拓扑分析表明该网络具有无尺度特性，同时分析确定14个基因/蛋白质是网络的关键节点。通过GO (gene ontology)分析，发现在苯肾上腺素诱导新生大鼠心肌细胞肥大的过程中，与物质代谢、细胞信号转导及细胞骨架等密切相关的基因可能发挥了重要作用。结论：构建基因/蛋白质网络为研究心肌肥大的分子机制提供了有用的信息和方法。

关键词　心脏；心肌肥大；基因表达谱

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Construction of a genomic regulatory network based on gene expression profile of neonatal hypertrophic cardiomyocytes induced by phenylephrine

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Abstract

<FONT face=Verdana>AIM: To construct a genomic regulatory network based on gene expression profiling of hypertrophic cardiomyocytes induced by phenylephrine in neonatal rats. METHODS: Cultured neonatal hypertrophic cardiomyocytes were induced by phenylephedrine. The gene expression profiles of these cells were assessed by using a cDNA microarray, and the microarray data were further analyzed by Pathwaystudio and Agilent Literature Search software. RESULTS: A genes/proteins interaction network was constructed with 450 nodes and 592 edges by analyzing the gene expression in hypertrophic cardiomyocytes and literature mining. The network belongs to scale-free network by topological analysis, and 14 genes/proteins as key nodes, including PTPN11, TRAF6, HSPA8, VIM, RPS6KA3, PTHRP, GRB2 and PI3K, were predicted. Based on GO analysis, the genes/proteins associated with metabolism, signal transduction and cytoskeleton may play important roles in the process of cardiomyocytes hypertrophy induced by phenylephedrine in neonatal rat. CONCLUSION: The genomic regulatory network based on gene expression profiling and literature mining may provide integrated clue to elaborate hypotheses about the evolution of cardiomyocyte hypertrophy.</FONT>

Key words　Heart　Myocardial hypertrophy　Gene expression profiling

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