

论著

应用基因表达谱芯片研究MNNG诱致小鼠胚胎畸形肢体基因表达的变化

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摘要 背景与目的: 研究N-甲基-N'-硝基-N-甲基亚硝基胍(N-methy-N'-nitro-N-nitrosoguanidine,MNNG)诱致小鼠胚胎畸形肢体基因表达的变化,筛选肢体畸形相关基因。材料与方法: 应用含有8 192条小鼠基因的cDNA表达谱芯片,对MNNG诱致的孕14 d胎鼠畸形肢体组织及正常肢体组织的基因表达谱进行分析。结果: 畸形肢体组织共筛到差异表达基因287条,其中下调214条,上调73条。结论: MNNG诱致的小鼠胚胎肢体短肢、少趾畸形可引起很多基因的表达改变,涉及与凋亡有关的基因、与生长因子或生长因子样物质有关的基因、结构基因及很多功能未知的相关基因,差异表达基因中以下调基因居多,这些结果可为进一步研究肢体短肢、少趾畸形的形成机制提供依据。

关键词 [N-甲基-N'-硝基-N-甲基亚硝基胍](#); [肢体畸形](#); [基因表达谱](#); [聚类分析](#); [小鼠](#)

Investigation on the Gene Expression Pattern of Abnormal Limb of Mouse Embryo Following Exposure to MNNG

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Abstract **BACKGROUND & AIM:** To analyse the gene expression profiles in abnormal and normal developmental limbs of GD14 embryo mice. **MATERIAL AND METHODS:** A series of expression microarray analysis of abnormal limb were initiated by cDNA microarray which representing a set of 8 192 mice genes. **RESULTS:** By applying this cDNA microarray we identified 287 differentially expressed genes, among which 73 upregulated and 214 downregulated. **CONCLUSION:** cDNA microarray for analysis of gene expression patterns is a powerful method to identify teratogenicity-related gene. Further analysis of these differentially expressed genes will be helpful for understanding the molecular mechanism of teratogenicity.

Keywords [N-methy-N'-nitro-N-nitrosoguanidine](#) [gene expression profiles](#) [abnormal limb](#) [cluster analysis](#) [mouse](#)

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