

专题研究

# 十三种化合物诱导的小鼠原代培养肝细胞基因表达谱的聚类分析

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**摘要** 背景与目的: 利用基因芯片技术研究13种化合物所诱导的小鼠原代培养肝细胞基因表达谱, 通过对基因表达谱的聚类分析, 对化合物在基因组反应水平上进行分类的尝试, 使化合物的分类与其诱导的基因表达谱联系起来。材料与方法: 用30%的致死剂量染毒原代培养的小鼠肝细胞, 24 h后提取RNA, 用芯片进行检测。结果: 聚类分析结果表明, 13种化合物分成了三类。结论: 用基因表达谱来对化合物进行分类, 使其分类结果与毒性作用相联系, 进而探讨其作用机制、预测未知毒性化合物的毒性是可行的, 是很有价值与希望的研究方向。

**关键词** [基因芯片](#); [毒理基因组学](#); [基因表达谱](#); [聚类分析](#)

## Clustered Analysis of Gene Expression Profiles of Primary Mouse Hepatocyte Culture Induced by 13 Chemicals

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**Abstract** **BACKGROUND & AIM:** We investigated the gene expression profiles of primary mouse hepatocyte culture induced by 13 chemicals by using DNA microarray. We then used clustered analysis on the gene expression profiles, and then tried to classify chemicals based on the level of the genome response, so that a relation could be made between the classification of chemicals and its gene expression profiles. **MATERIAL AND METHODS:** Primary mouse hepatocyte culture was treated with 30% of the lethal dose of 13 chemicals. 24 hours after treatment, RNA was extracted and reverse transcribed to cDNA. The cDNA were detected by DNA microarray. **RESULTS:** By using average-linkage hierarchical clustered analysis, 13 chemicals were classified into 3 groups. **CONCLUSION:** Classifying chemicals by gene expression profiles, so as to classify them relative to their toxic action then to study their toxicity mechanism and to predict the toxicity of unknown chemicals is a worthwhile and promising research direction.

**Keywords** [DNA microarray](#) [gene expression profiles](#) [toxicogenomics](#) [clustered analysis](#)

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