Microarray analysis of altered gene expression in diallyl trisulfide-treated HepG2 cells

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Abstract:
Diallyl trisulfide (DT) is a natural compound derived from garlic. Despite its reported lipid-lowering effects, the mechanisms of its actions are not clear yet. To further understand the molecular mechanisms of actions of this compound, microarray technology was used in the present study to investigate the lipid-lowering effects of DT on HepG2 cells. To optimize the concentration of DT treatment on HepG2 cells, a series of concentration of DT were incubated with HepG2 cells for 24 h. The data indicated that the concentrations of DT in the range from 20 to 50 μM were effective in lowering cellular total triglyceride and cholesterol, with no significant cytotoxicity. Using oligonucleotide microarrays and RT-PCR technology, the genes that were differentially regulated by DT were identified. The results showed that peroxisome proliferator-activated receptor α (PPAR-α) and hepatocyte nuclear factor-4α (HNF-4α) mRNA were up-regulated, and CYP7A1 mRNA was down-regulated following DT treatment, suggesting that the lipid-lowering effects of DT may be at least in part mediated through the regulation of PPAR-α dependent pathways.

Key words:
diallyl trisulfide, oligonucleotide microarray, gene expression, HepG2 cells