Analysis of genomic-wide expression profile for genotoxic chemicals using *Escherichia coli DNA microarray*

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Abstract

Toxicogenomic analysis for discriminating the effect of toxic chemicals to bacterial cells is studied. Impacts of chemicalsto bacterial cells were assigned and characterized according to bacterial gene expression patterns using *E. coli* 6K-oligo chip. To distinguish between general mechanisms of toxicity, 4 chemicals (Mitomycin C, N-methyl-N'-nitrosoguanidine, Nalidixic acid and 4-Nitroqinoline-oxide) that are known to affect bacterial genetic material were screened to generate toxic chemical-gene relation, based on their expression profiles. Mitomycin C, 4-NQO, Nalidixic acid and, in lesser extend, MNNG exposure increase expression of genes involved in the SOS-response as a primary response. Similar expression patterns for energy production and conversion genes were observed due to treatment with 4-nqo and nalidixic acid whereas transcription, aminoacid and transport and metabolism genes were induced by MMC and MNNG. Many genes down-regulated by both nalidixic acid and MMC are related with flagellar biosynthesis (fli and flg operons) and protein synthesis. According to hierarchical clustering, the degree of relativeness among chemicals was: Nalidixic acid>MMC>4nqo>MNNG. Furthermore, for nalidixic acid, time-dependent experiments were assessed to elucidate changes in *E. coli* transcriptional patterns. The primary response is induction of the SOS regulon, which amplifies with time concluding that this antibiotic triggers a time-dependent response. Up-regulated genes are related with energy production and conversion, cell envelope biogenesis as well as many genes with unknown function, whereas cell motility and secretion and amino acid transport and metabolism genes were down regulated.