The role of environmental contaminants in human disease has been well established. However, the biological mechanisms through which these diverse and prevalent substances cause toxicity are not completely understood. Here, we used \textit{in silico} analyses of data available from the Comparative Toxicogenomics Database to explore known chemical-gene-disease interactions for 83 high-priority chemicals, as ranked by the Agency for Toxic Substances and Disease Research. Hierarchical clustering revealed that similar substances had impacts on similar biological pathways. Rankings of the associations identified the MAPK pathway as associated with the highest proportion of chemicals, and demonstrated that numerous contaminants act on the same genes within pathways. Understanding how environmental contaminants perturb biological pathways to result in disease states is of tremendous interest in public health and medicine. These results present a novel approach to identify and prioritize biological pathways of particular relevance to numerous high-priority environmental contaminants.

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