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Toxicogenomic investigation of *Tetrahymena thermophila* exposed to organic pollutants and arsenic

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The organic pollutants such as Benzopyrene (BaP), dichlorodiphenyltrichloroethane (DDT), tributyltin (TBT), and 2,3,7,8-tetrachlorodibenzo-p-dioxin (TCDD) are persistent in the environment and capable of endocrine disruption within the reproductive system, the central nervous system, or the immune system. Arsenic contamination is also a serious risk to human health and affects millions of people across the world. The ciliate protozoan *Tetrahymena thermophila* has long been used a good unicellular eukaryotic model for toxicological studies. In this study, this organism was exposed to BaP, DDT, TBT, TCDD, and Arsenic for 24 hrs, respectively and then RNA-Seq of each toxicant exposure was performed to identify differentially expressed genes (DEGs). The functions of these DEGs were categorized using Gene Ontology enrichment analysis and the results suggested that the responses of *T. thermophila* were similar to those of multicellular organisms. For each toxicant, the involved gene-interaction network was constructed and the model of each toxicant effect on *T. thermophila* was inferred. In addition, based on analysis of the networks, key enzymes that are potentially responsive to the toxicant metabolism were also identified. Functional validation of these key enzymes is ongoing.

Biography

Wang have been well trained in bioinformatics and population genetics. Wang research interests focus on some basic questions using *Tetrahymena thermophila* as a model system. Based on professional skills in Bioinformatics and omics data analysis, he have made a direct contribution to reveal some important biological process or pathway in *Tetrahymena* and other ciliated protozoa through genome or transcriptome sequencing. Wang early publications have revealed that germline-limited sequences in *Tetrahymena* can encode genes with specific expression patterns and development-related functions during *Tetrahymena* MAC development. Wang also helps to demonstrate a facultative pathogen ciliate, *Pseudocohnilembus persalinus*, may gain its virulence through horizontal gene transfer. In addition, by integrating different kinds of omics data, and he helps to construct functional genomics database of *Tetrahymena*.

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