



Northeastern

Department of Civil and Environmental Engineering

Toxicogenomics-enabled Technology Platform For Water Toxicity Assessment and Monitoring

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Thursday, December 5, 2013

**12pm-1pm
105 Shillman Hall**

Abstract

The contaminants of emerging concern (CECs), such as endocrine disrupting compounds (EDCs), pharmaceuticals, personal care products (PPCPs) and nanomaterials, are anticipated to greatly increase the demands for their toxicity, ecological effects and risk assessments. Current whole animal/organism exposures-based methods used for regulatory decision-making in ecotoxicology are resource and time-intensive and, they provide little information on toxicity mode of action (MOA) and cellular level sub-lethal impact. Alternative and/or complimentary toxicity screening methods, which are less costly, yet with informative endpoints are needed. Recently, we have explored the application of a toxicogenomics approach for toxicity assessment and screening of CECs, using a comprehensive GFP-infused bioluminescent whole cell array. Compared with traditionally microarray technology, this method is simpler and faster, and therefore is feasible for screening a large number of chemicals. Furthermore, it provides multi-dimensional transcriptional level effect information, by adding a temporal dimension to the gene expression data, and therefore can more accurately reflect the chemical-induced cell responses that are time-dependent. We demonstrated that toxicogenomic data could also be used to potentially identify and classify compounds with similar MOAs (mode of action) while gaining diagnostic insights into the causal agents. One of the main challenges in applying toxicogenomics for environmental monitoring is the lack of a quantitative method to convert the rich toxicogenomic information into a readily usable and transferable format that can potentially link to regulation endpoints and be incorporated into ecological risk assessment and regulatory framework. We proposed a new transcriptional effect level index (TELI) that exhibited a dose-response relationship and allowed for linking (“phenotype anchoring”) the transcriptional level effects to conventional toxicity endpoints. Cross-species comparison and extrapolation is another key aspect related to predictive and mechanistic toxicity assessment to overcome the limitation of data generation ability. We have compared genotoxicity across three different species for variety of compounds and demonstrated the possibility of cross-species extrapolation with stress-response pathway ensemble based toxicity assessment.

Bio

Dr. Gu is an associate professor in Civil and Environmental Engineering Department, faculty and track leader for Interdisciplinary Bioengineering Program within the College of Engineering and affiliated faculty for Biotechnology Program with Bouve College of Health Sciences at Northeastern University in Boston. She obtained her B.S. in Environmental Engineering and Science from Tsinghua University in Beijing, China and a Ph.D. in Civil and Environmental Engineering, jointly in Microbiology, from the University of Washington in Seattle. Her expertise and area of research interest include application of biotechnology for water and wastewater treatment, water quality monitoring and toxicity assessment, biosensors, biological wastewater treatment processes and modeling, microbial ecology, bioavailability of nutrients in aquatic systems and bioremediation. She is an Editorial Board member for Water Environmental Research Journal, Frontiers of Toxicogenomics, and Associate Editor for Water Science And Technology Journal. She serves on a number of international and national committees for IWA, WEF and AWWA. She was a NSF CAREER awardee in 2009 and received Søren Buus Outstanding Research Award from the College of Engineering at Northeastern University in 2011. She was invited speaker for Gordon Conference-Environmental Nanotechnology 2013, and Gordon Conference – Water Science in 2012.