Linkage of Exposure and Effects using Genomics, Proteomics, and Metabolomics in Small Fish Models

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research & development

U.S EPA, ORD, Computational Toxicology Research Program

Specific Approach

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Science Question

· How can we improve extrapolation

levels of organization), species (including under-represented taxa) and

from the lab to field for single

chemicals and complex mixtures?

· Can we establish functional linkages between changes at the molecular level

risk assessment for multi-organ biological systems well conserved

among vertebrates?

· Can we develop integrated, biologically-based computational

Research Goals

· Identify novel molecular markers of

representing different mechanisms of

action (MOA) within the vertebrate hypothalamic-pituitary-gonadal (HPG)

effects of exposure to chemicals

· Link these biomarkers to responses

· Support development of integrated

as a basis for prediction of adverse

relevant to ecological risk assessment

modeling approaches that utilize MOA

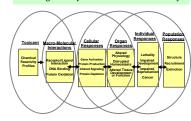
and phenotypic outcomes relevant for

models that use mechanism of action as a basis for predicting adverse

across life stages/endpoints (biological

- Investigate effects of chemical probes on the HPG axis using definitive tests in the fathead minnow to establish initial toxicity pathways and ecologically-relevant responses (Phase 1)
- Identify transcriptomic, proteomic, metabolomic, and other whole-animal responses to the same chemicals using short-term zebrafish exposures (Phase 2)
- Validate genomic markers in the fathead minnow with an emphasis on time-course of responses and/or compensation and recovery after exposure (Phase 3)
- Concurrently integrate data from above in a systems modeling context, as well as relevant population modeling

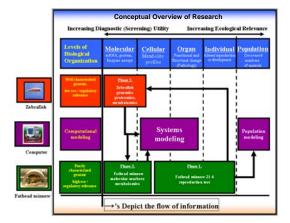
Defining Toxicity/Adverse Outcome Pathways

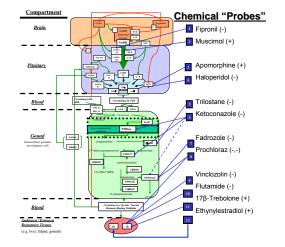


Overview of Fish Reproduction



Methods/Approach

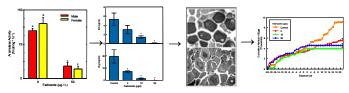




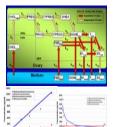
Results/Conclusions

Impact and Outcomes

Definition of Novel Toxicity/Adverse Outcome Pathways (Ankley et al. 2009)

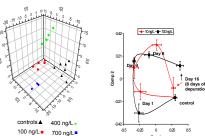


Computational Model of Vertebrate Steroidogenesis (Breen et al. 2007)



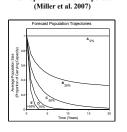
controls A 400 ng/L •

Metabolomics for Defining Pathways and Exposure Reconstruction (Ekman et al. 2008; 2009)



Physiologically-Based Model for Predicting Estrogen Effects on HPG Axis Function (Watanabe et al. 2009)

Translating Biochemical Alterations into Population-Level Responses



Gill: Chemical Uptake Brain: Signaling Liver VTG Production Other: Elimination Blood: Transport

