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Track:
1st: Aquatic Toxicology and Ecology
2nd: Ecological Risk Assessment
Session:
1st: Advancing the OMICS in aquatic ecotoxicology and ecology
2nd: How do we incorporate nontraditional endpoints into the regulation of environmental contaminants?

Abstract title:
Utility of gene expression and ex vivo steroid production in a 96 h assay for predicting impacts of endocrine active chemicals on fish reproduction.

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Development of efficient test methods that can generate reliable data to inform risk assessment is an on-going challenge in the field of ecotoxicology. In the present study we evaluated whether a 96 h in vivo assay focused on a small number of quantitative real-time polymerase chain reaction (QPCR) and ex vivo steroid production assays, using ovary tissue, may have utility for predicting longer term reproductive outcomes in fish. Eight endocrine active chemicals (EACs) that were previously tested in a short term fathead minnow reproduction assay (i.e., fadrozole, flutamide, haloperidol, ketoconazole, prochloraz, 17β-trenbolone, trilostane, vincolozolin) were subsequently evaluated in shorter term exposures. Ex vivo estradiol and testosterone production and expression of 14 genes coding for proteins with putative roles in adverse outcome pathways associated with impaired fish reproduction or hypothesized to have specificity for specific endocrine modes of action were evaluated. Responses were compared with no observed effect concentrations (NOECs) and lowest observed effect concentrations (LOECs) determined in 21 d reproduction assays. Additionally, for a subset of six gene transcripts, fathead minnow responses were compared with those in zebrafish exposed under similar conditions. Fourteen of the 16 endpoints evaluated were significantly altered by at least one of the EACs that produced reproductive impairment. However, there were no responses that were consistently significant at EAC concentrations that impaired reproduction and consistently absent at EAC concentrations that did not. Additionally, among the subset of genes analyzed in both zebrafish and fathead minnow, there was little conservation of 96h molecular response between species. Analyses are on-going to determine whether predictive power of short term in vivo assays could be enhanced by focusing on other time points, utilizing high-content data (e.g., transcriptomic, metabolomic), and/or developing biologically-based concentration-duration-response models to aid data interpretation. *The contents of this abstract neither constitute nor reflect official US EPA policy.*