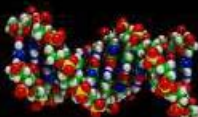


Molecular Methods in Contaminants Studies:

Profiling of gene induction in response to contaminants or other
treatments

Natalie Karouna-Renier
USGS-PWRC



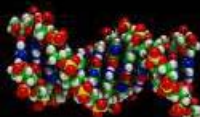
The “-omics” and toxicology

- Tools for screening for toxic effects and gaining mechanistic insight
 - **Genomics** (transcriptomics) – mRNA, DNA
 - Toxicogenomics, ecotoxicogenomics
 - **Proteomics**- proteins
 - **Metabolomics** – intermediary metabolites, small molecules, peptides



Traditional vs. “-omic” Toxicology

- Identify chemicals of potential concern
 - doses used to determine adverse effects
 - selected to ensure that tissue level or whole animal toxic responses can be identified
 - molecular/biochemical changes
- Limited vs. multiple endpoints
 - Traditional methods = whole-organism responses (mortality, growth, reproduction)
 - minimal understanding of the mechanisms



Traditional vs. “-omic” Toxicology

- Genomics technologies simultaneously examine a number of response pathways
 - Offers the opportunity to understand possible mode(s) of action
 - Improve mixtures analysis
- Extrapolation from sentinel species
- Standardization
 - Handling and interpreting large amounts of data



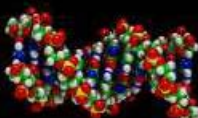
Biomarkers vs. signature profiles

- Biomarkers

- e.g. HSPs, MT, Cyt P450, GSH

- Signature profiles

- cellular receptors, modifying enzymes, repair enzymes, cell cycle control factors, regulators of cell division and death



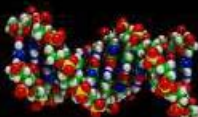
Toxicogenomic Methods

- Combination of toxicology, genetics, and molecular biology
- Expression – DNA microarrays, qRT-PCR, expression libraries (SSH)
- Genetic variations – sequencing, qPCR (SNPs).....

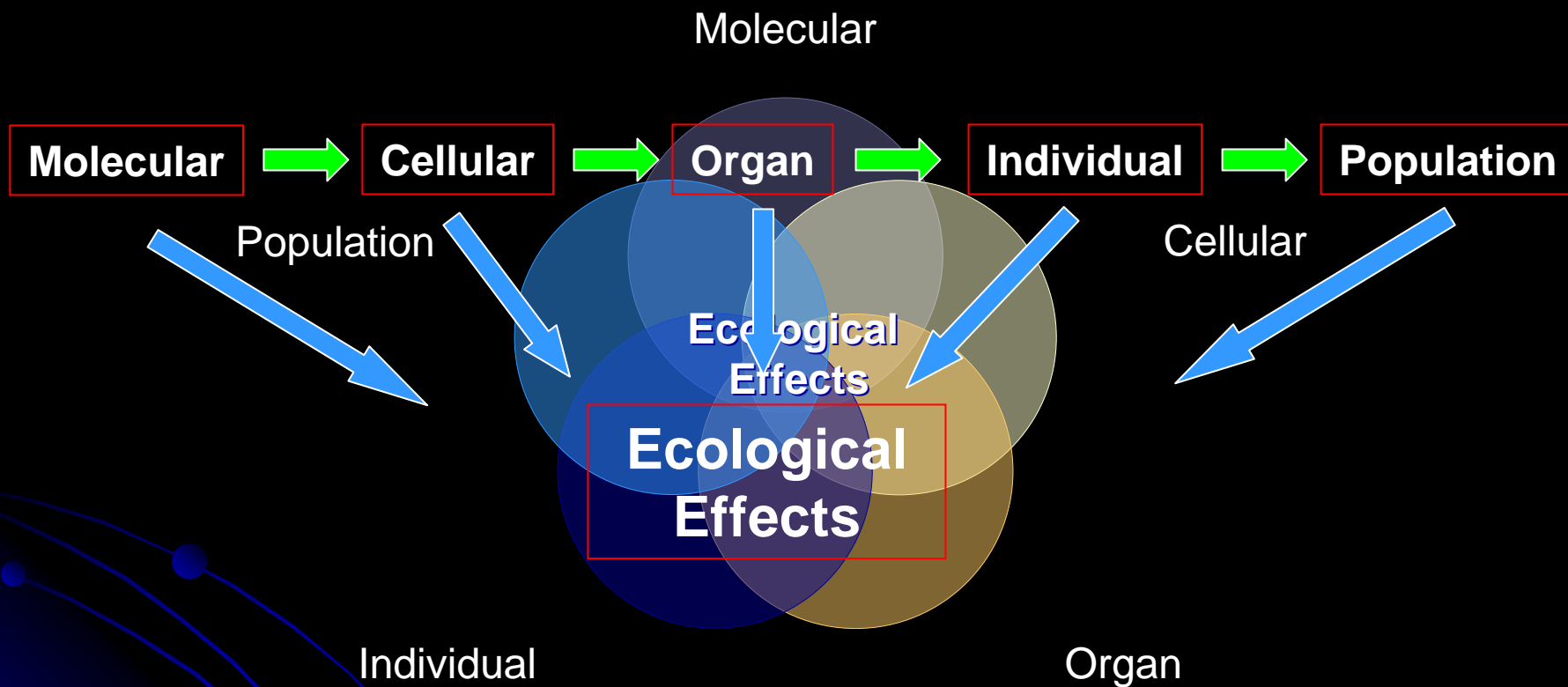


Why measure at the molecular level?

- Total concentrations in tissues are insufficient criteria for making toxicologically relevant judgments (Scheuhammer et al. 1998)
 - susceptible populations and life stages
 - effects of mixtures
- Tissue concentrations do not always reflect the susceptibility of a species to a contaminant
 - more efficient repair systems = higher resistance
 - sensitive species = detrimental effects at significantly lower levels of exposure



Can we predict ecological effects?



Applications for Genomics Data

- Genomics technologies are likely to contribute significantly to defining a chemical's mode of action, in evaluating effects on susceptible populations and life stages, and in assessing exposure to and effects of chemical mixtures
- Genomics will not fundamentally alter risk assessment process but will serve as a more powerful tool for evaluating the exposure to, and effects of stressors



Role for Genomics

- Genomics data alone are currently insufficient as a basis for risk assessment and management decisions
 - Links between molecular events and adverse ecological outcomes are not yet established
- Useful in a weight-of-evidence approach for wildlife, human health and ecological risk assessments



Current Research

- Profiling Mercury Responsive Genes in Bird Embryos as an Indicator of Species Sensitivity
- Genotoxicity In Avian Species Inhabiting a Mercury-contaminated River System



Profiling Mercury Responsive Genes

- CalFed – Gary Heinz, Dave Hoffman
 - provide information that will lead to a reduction of mercury in resident fish tissues to protect humans and wildlife
- Previous analyses conducted at Patuxent found that embryos of different bird species vary in their sensitivity to methylmercury (Heinz, 2003).
- Minimal information available on molecular mechanisms that account for sensitivity differences



Profiling Mercury Responsive Genes

- Challenge – predicting responses across phylogenetic groups
 - extrapolate from a limited set of test species
- Are observed residue levels harmful?
- What causes differences in sensitivity?



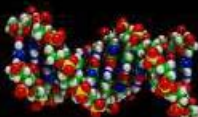
Species-specific toxicity

- Genetic variability (polymorphisms) - associated with altered efficiency of a biological pathway and with risk for adverse effects
 - affects sensitivity to contaminants
- Certain genes have a greater than average influence over susceptibility
- Study of toxic effects cannot be separated from the study of the genetic mechanisms underlying variations in individual susceptibilities.



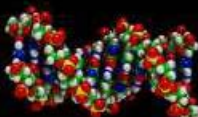
Previous Studies

- Alterations in gene expression due to Hg
 - immune response
 - nervous system function
 - reproduction, including egg fertilization and development
 - mammals, fish, and amphibians



Profiling Mercury Responsive Genes

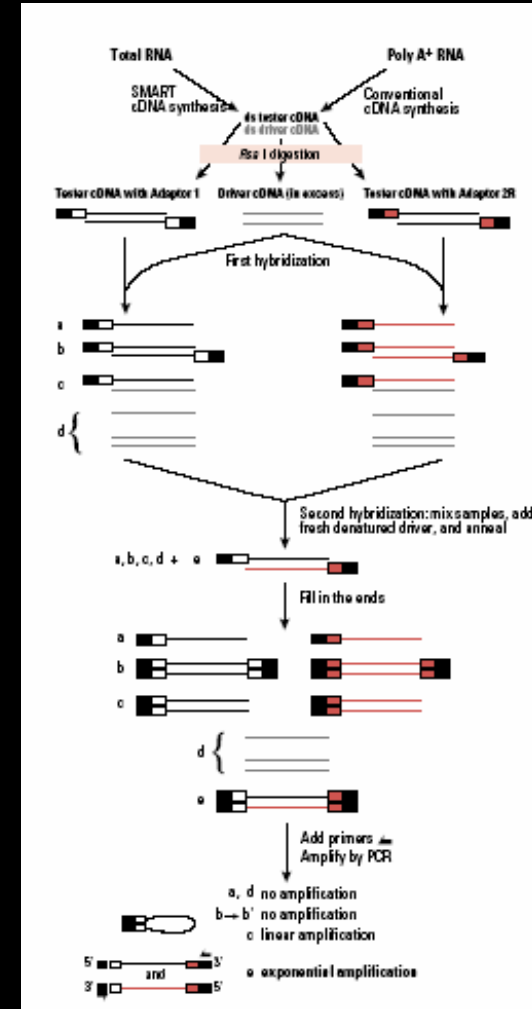
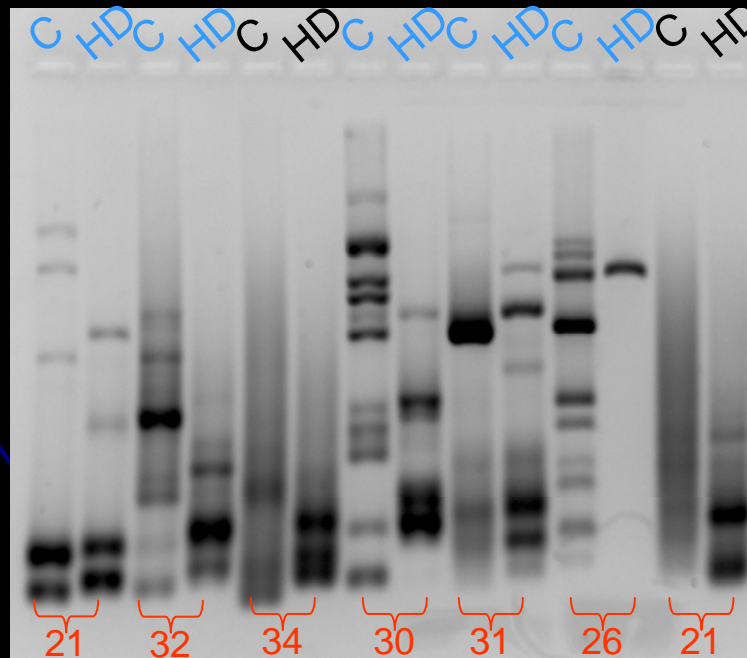
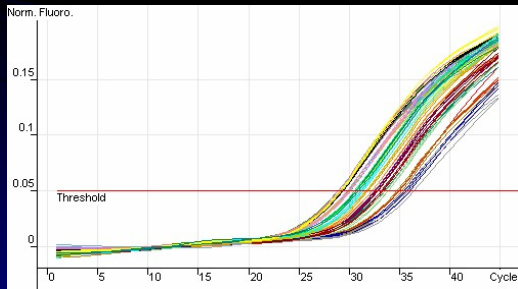
- Dosing of wild bird eggs with MeHg
 - measuring each species' sensitivity to mercury
 - laughing gulls, grackles, kestrels, osprey, tree swallows
- Objectives
 - Identify differentially expressed genes in embryos exposed to methyl mercury
 - Compare gene profiles in liver, brain, and kidney from control and dosed embryos
 - Evaluate association between gene expression, mercury dose, and the level or types of deformities observed
 - Future studies? Compare profiles in highly sensitive with less sensitive sp., SNPs



Mercury responsive genes

- mRNA Profiling

- Subtractive Hybridization
- Differential Display PCR
- qRT-PCR



Genotoxicity In a Mercury-Contaminated River System

- The potential of a stressor to cause damage to a cell's DNA
 - not limited to exogenous environmental pollutants
- Genotoxins may bind directly to DNA or act indirectly, leading to DNA damage by affecting enzymes involved in DNA replication or repair
 - genotoxic substances are not necessarily carcinogenic
- Genotoxic Disease Syndrome
 - genetic changes that are detrimental to the fitness of an individual exposed to xenobiotics



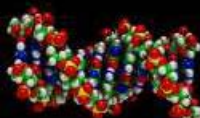
Genotoxicity In a Mercury-Contaminated River System

- Weight of evidence approach
- Multiple end points important for understanding the magnitude of injury
 - Are the levels of Hg in birds having genotoxic effects?
- Provides mechanistic data in the assessment of bird health
 - Improves totality of injury assessment



Comet Assay

- Sensitive single cell assay that detects DNA strand breaks and unwinding via electrophoresis.
- ‘Comet tail’ visualized under fluorescence microscopy.
 - damaged DNA migrates during electrophoresis from the nucleus towards the anode forming a head (cell nucleus with intact DNA) and a tail (relaxed and broken DNA).



Other Genetic Methods

- Polymorphic variants (SNPs)
 - individual susceptibility
- Population/Community Analysis
 - Microsatellites, mtDNA, AFLP, TRFLPs, RAPDs



Acknowledgements

- David Hoffman, Gary Heinz
- David Evers (BRI)
- John Schmerfeld (USFWS)

