

Development of Molecular Tools for Stressor Identification in Sediment Toxicity Tests

Steven M. Bay

*Southern California Coastal Water
Research Project*

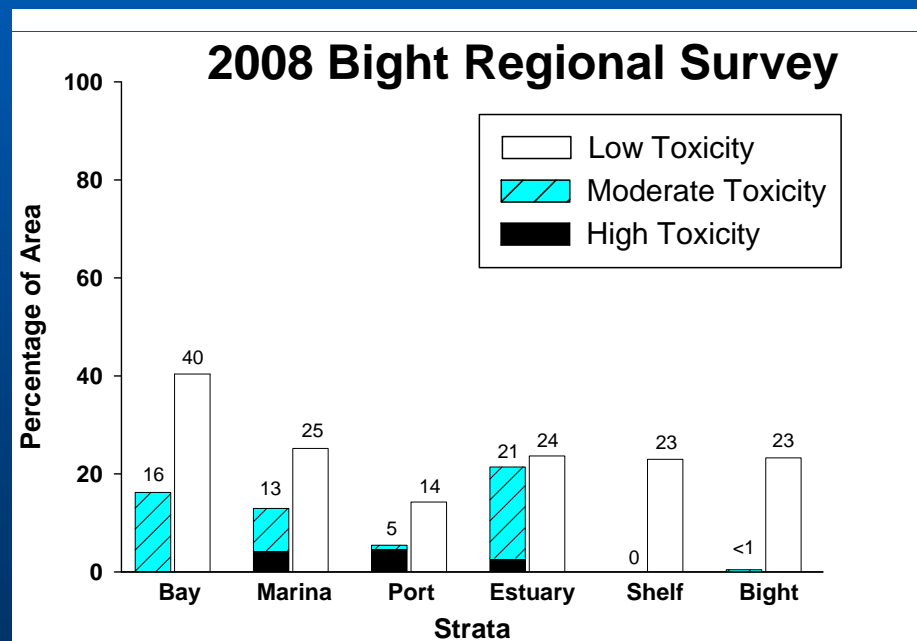
Chris Vulpe

University of California Berkeley



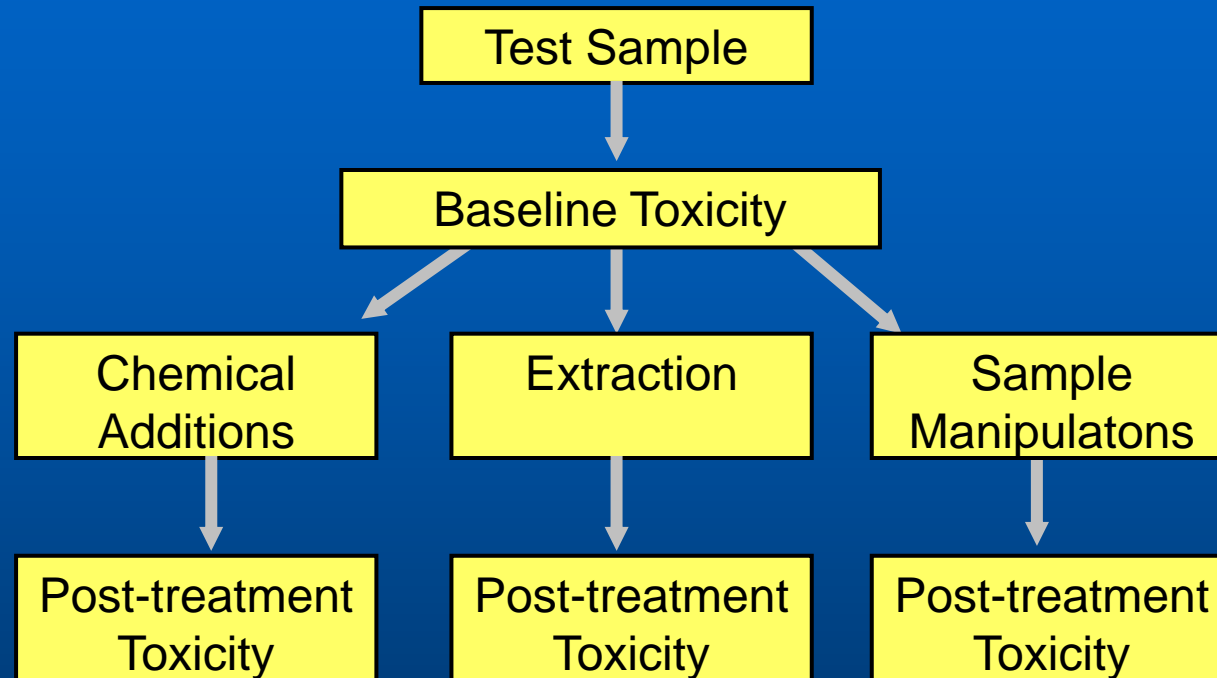
Understanding Sediment Toxicity is Essential

- Sediment toxicity is an important factor in sediment quality assessment in bays and estuaries
 - Cleanup targets are often based on reducing toxicity
- Identifying the cause of toxicity is difficult
 - Complex mixtures of contaminants are present
 - Ammonia, pesticides, and PAHs often present at levels of concern
 - Response characteristics (mortality, growth) not toxicant-specific



Toxicant Identification Evaluation (TIE)

Traditional Approach



Various contaminant-specific treatments applied to sample

Changes in toxicity following sample treatments indicates type of toxicant

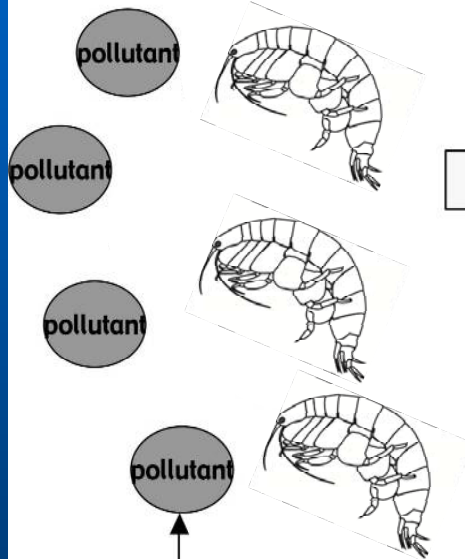
Better Stressor Identification Methods Are Needed

- TIE results are frequently inconclusive or nonspecific
 - Chemical treatments have limited specificity
 - Chemical extraction/fractionation alters bioavailability
- Limited range of application
 - Require highly toxic sediments
- Limited ability to identify new types of stressors
 - Have to determine chemical characteristics first
 - Stressor-specific treatments may not be available
- TIEs not applicable to resident organisms
 - Rely on laboratory manipulations of sediment

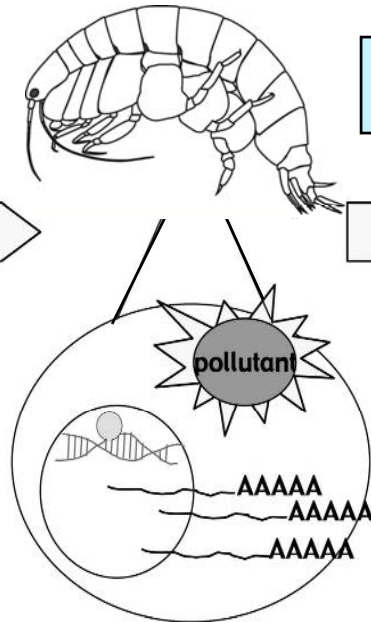
Can molecular methods provide a better tool?

Molecular TIE Approach

Organism is exposed to pollutant and it causes stress



At the cellular level, the organism responds to the stress by turning on/off certain genes (transcription)



The genes responding will indicate the kind of stress the organism is experiencing

AAAAA
AAAAA
Direct cellular damage

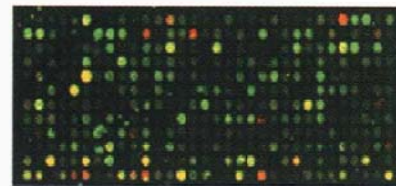
AAAAA
AAAAA
Detoxification

AAAAA
AAAAA
Damage repair

Greater Relevance

Greater Specificity

Greater Sensitivity



Microarray/qPCR/NextGenSequencing

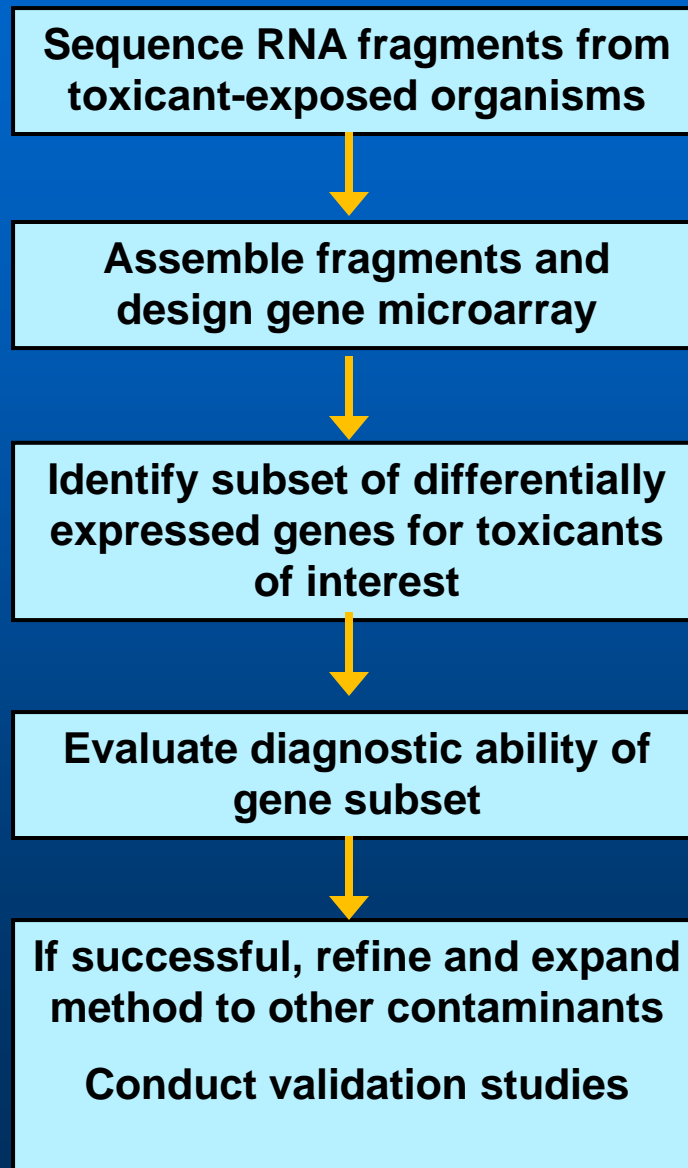
Molecular TIE Development Program

- Focus on amphipod *Eohaustorius estuarinus*
 - Benchmark test species for Canada and U.S. monitoring programs
- Goal is to develop and evaluate a new approach for TIE based on gene expression
 - Use existing test methods (10-day survival)
 - Reduce need for manipulations and iterations
- Multiple partners
 - San Francisco Estuary Institute
 - UC Berkeley
 - Environment Canada
 - NOAA (Hollings Marine Laboratory)
 - UC Davis Marine Pollution Studies Laboratory



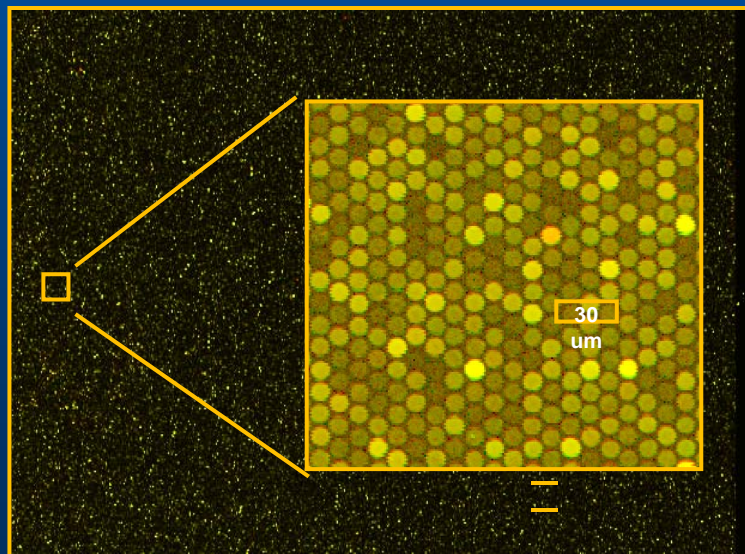
Research Program

- **Substantial progress so far**
 - Developed amphipod gene microarray
 - Initial demonstration of effectiveness
- **Additional studies needed**
 - Refinement and validation
 - Interlaboratory comparison



Microarray Analysis

- 8,610 amphipod gene sequences in array
- 8 samples analyzed simultaneously



RNA extracted from preserved sample

Converted to cDNA & labeled with dye

Hybridization to DNA probes



Measure dye intensity per probe

Calculate differential gene expression relative to controls

Preliminary Evaluation of Molecular TIE

- Does micorarray “work”?
 - Binding of *E. estuarius* RNA to probes
- Are measurements precise?
 - Replicate analyses of same sample
- Can we detect differences among toxicants?
 - Compare samples exposed to different types of toxicants
- Can we identify toxicants in test samples?
 - Predict toxicant type in blind samples

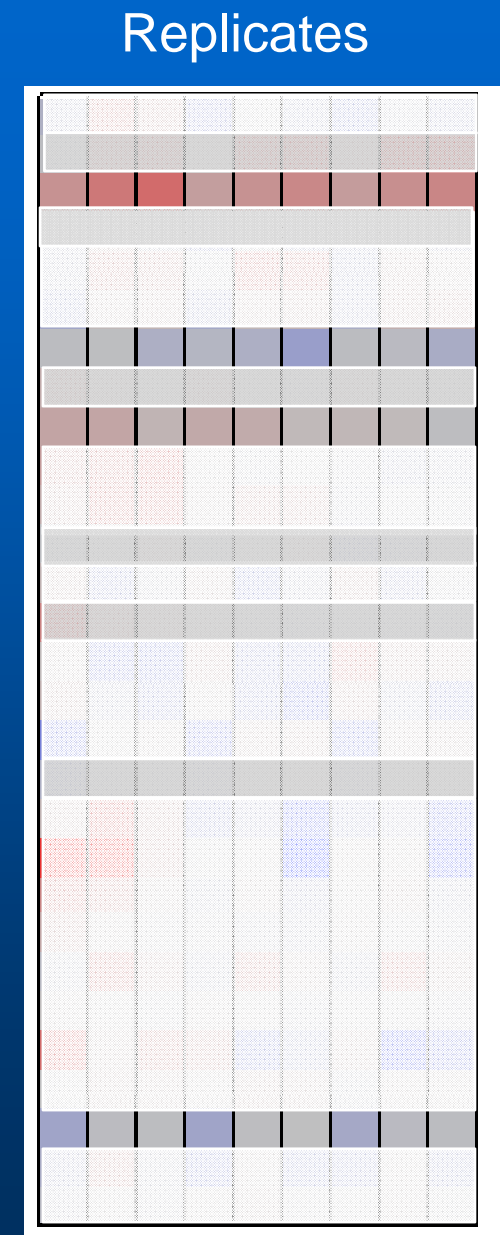
Training Data Set

- **Diverse toxicants and mechanisms of action**
 - Current use pesticides
 - Chlorinated pesticides
 - PAHs
 - Ammonia
 - Metals
- **Focus on pyrethroid pesticides**
- **Doses near LOEC**
- **Different exposure matrices and durations**
 - Matched controls
- **2-3 replicates**
 - 5 amphipods/replicate

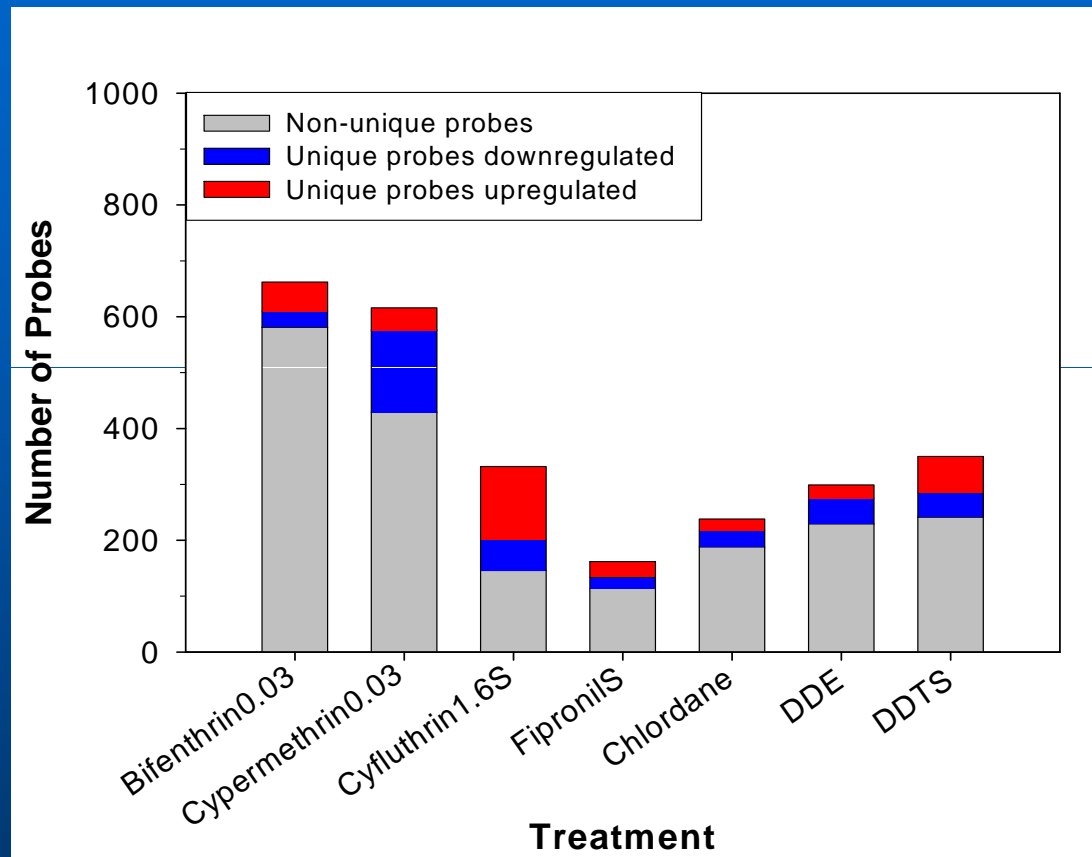
Treatment	Concentration	Matrix	Survival (% of Control)
Bifenthrin	0.01 ug/L	Water	80
Bifenthrin	0.03 ug/L	Water	55
Cypermethrin	0.01 ug/L	Water	100
Cypermethrin	0.03 ug/L	Water	87
Cyfluthrin	0.8 ug/kg	Sediment	88
Cyfluthrin	1.6 ug/kg	Sediment	60
Fipronil	10 ug/kg	Sediment	80
Chlordane	100 ug/L	Water	58
DDE	4 ug/L	Water	80
DDT	2400 ug/kg	Sediment	58
Pyrene	10 ug/L	Water	38
Pyrene	25000 ug/kg	Sediment	90
Ammonia	100000 ug/L	Water	100
Copper	250 ug/L	Water	100
Copper	750 ug/L	Water	98
Cd	10000 ug/l	Water	83

Candidate Gene Selection

- Identify genes most likely to represent toxicant-specific response
- Consistent response among replicates
- Significant differential expression relative to control
- Calculated mean to minimize effect of outliers



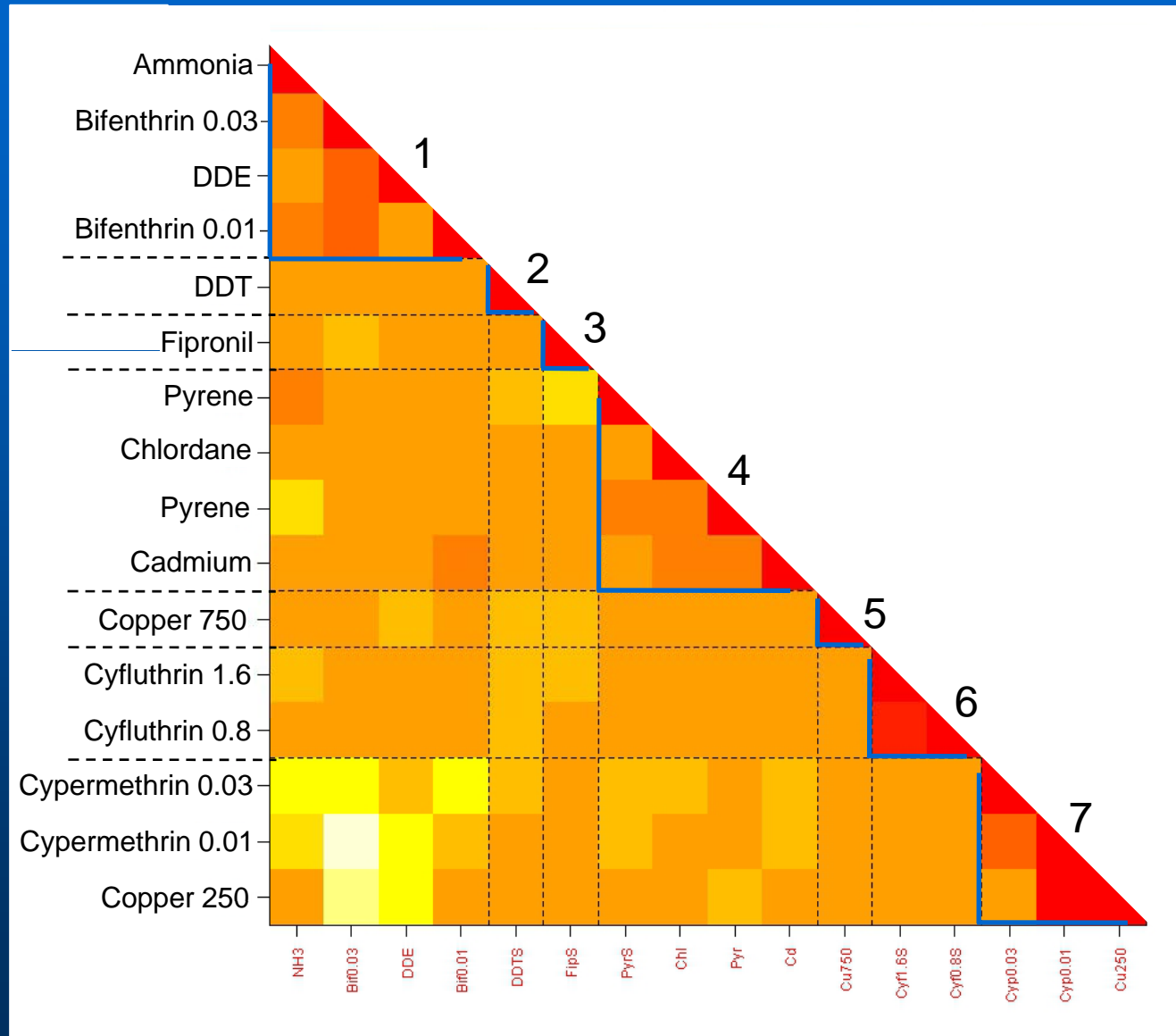
Candidate Genes: Pesticides



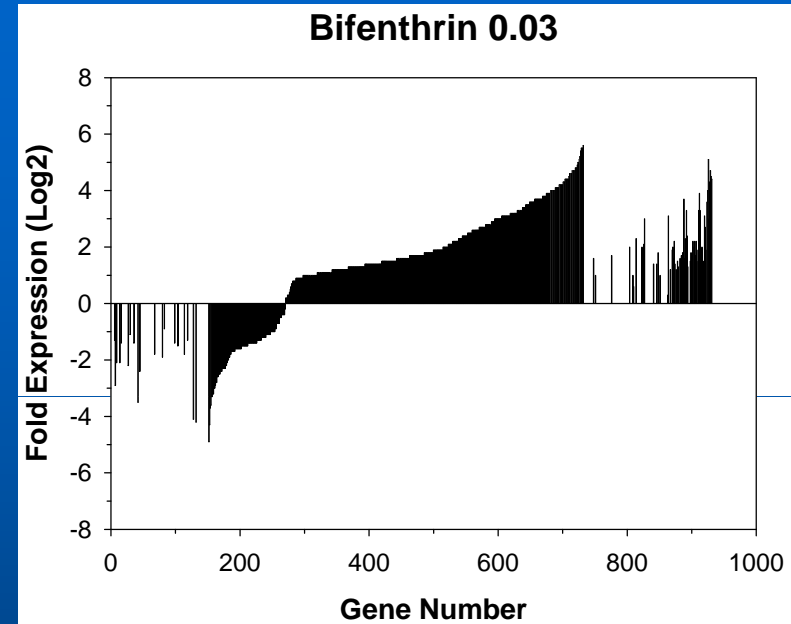
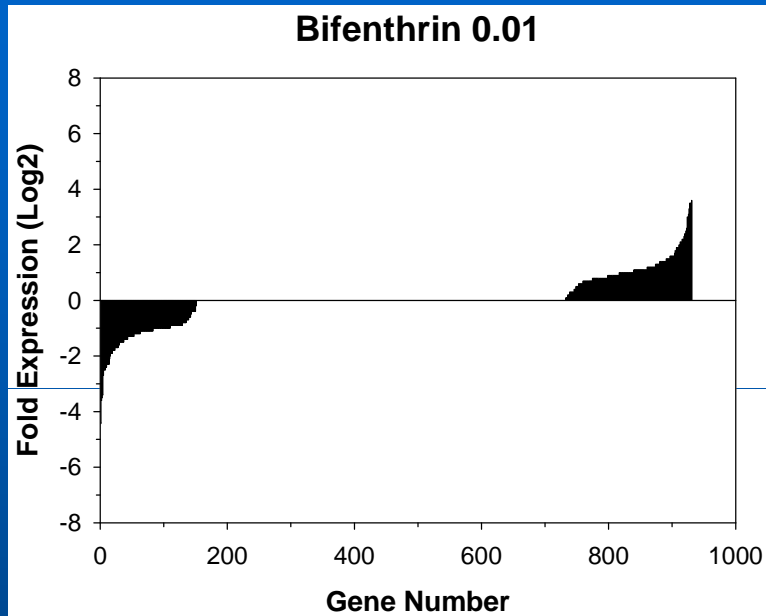
- Approx. 100 uniquely expressed probes for each chemical

Cluster Analysis

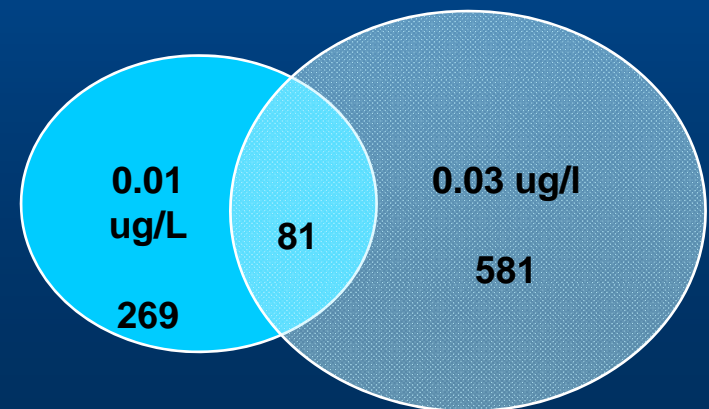
- Distinctive expression patterns for many contaminants
- Different dose levels group together (usually)
- Clusters show little relationship to toxicant type



Dose Response: Bifenthrin



- Relatively few candidate genes in common
- Greater differential expression at higher dose

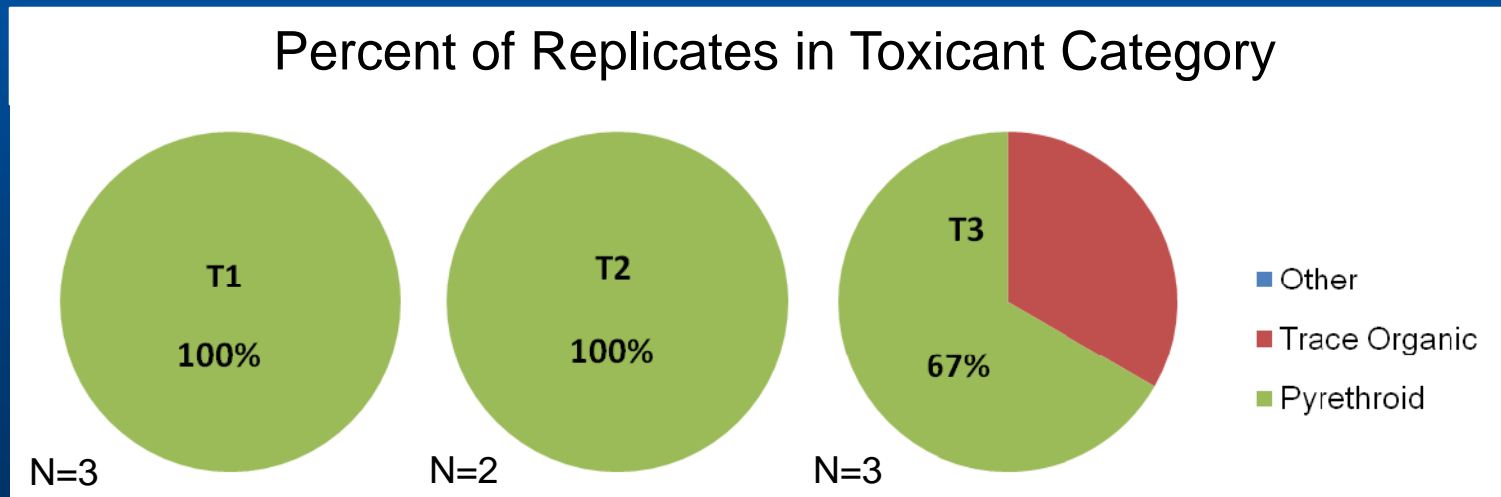


Evaluation of Toxicant Identification Ability

- **3 independent evaluation samples**
 - Not used for training, identity unknown to analyst
 - T1: sediment spiked with cyfluthrin (pyrethroid)
 - T2: LA field sediment with toxicity due to pyrethroids
 - T3: toxic field sediment from SF Bay RMP BA41 (cause of toxicity not known)
- **Developed classification model**
 - 3 classes of toxicants: Pyrethroids, Trace Organics, Other
 - Multivariate method: Random Forest
 - Selected 73 predictor genes
 - Used training data to develop prediction “trees” for each class

Evaluation Results

- Encouraging prediction results
 - Correct classification for 2 samples with identified cause of toxicity
 - SF Bay sample (T3) results cannot be verified
 - Small sample size



Summary

- **Substantial progress so far**
 - Successful amphipod RNA sequencing
 - Microarray available for use/evaluation
- **Initial results encouraging**
 - Probes bind amphipod RNA successfully
 - Distinctive expression patterns apparent for different contaminant treatments
 - Dose or method variations may influence results
- **Initial evaluation of classification potential encouraging**
 - Additional refinement and validation needed
 - Specifics of approach likely to evolve with further development

Acknowledgments

- **Vulpe Laboratory**

- Don Pham
- Alex Loguinov
- Audrey Arai
- Leona Scanlan

- **SCCWRP**

- Doris Vidal-Dorsch
- Darrin Greenstein
- Diana Young
- Monica Mays
- Blythe Layton

- **Support**

- San Francisco Estuary Institute
- Environment Canada