

Development of Molecular Tools for Stressor Identification in Sediment Toxicity Tests

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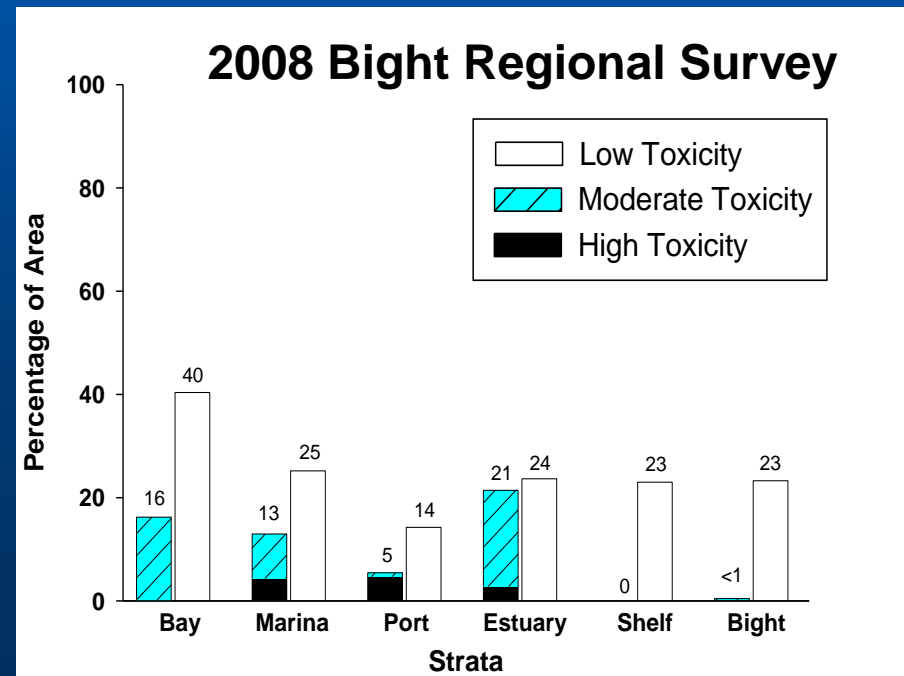
*Southern California Coastal Water
Research Project*

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Understanding Sediment Toxicity is Essential

- Sediment toxicity is an important factor in sediment quality assessment and management actions
 - 30-50% of sediments in urban embayments are toxic
- Identifying the cause of toxicity is difficult
 - Complex mixtures of contaminants are present
 - Test endpoints not toxicant-specific
 - Few hotspots with strong gradients of contamination

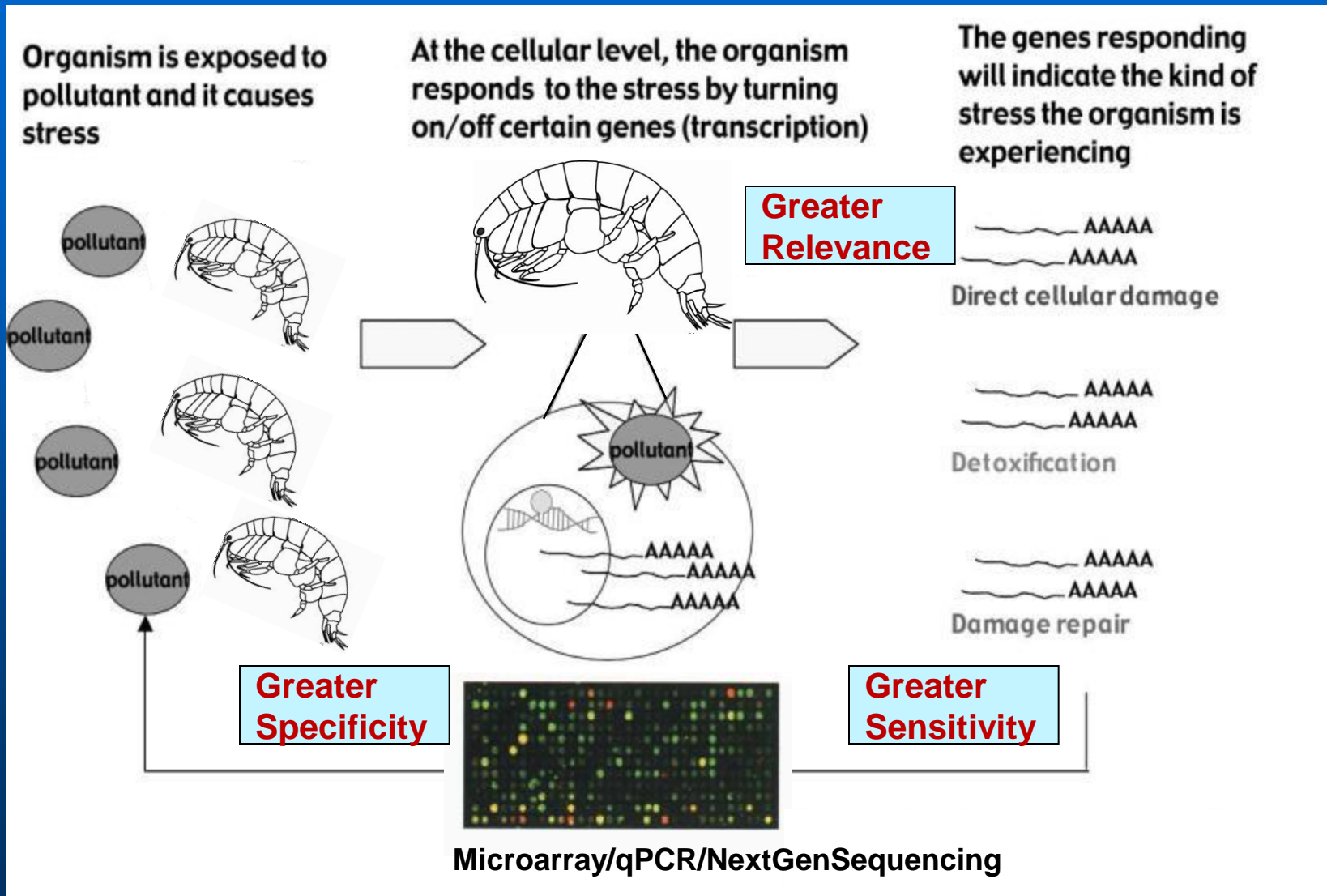


Better Stressor Identification Methods Are Needed

- 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



Molecular TIE Development Program

- Focus on amphipod *Eohaustorius estuarius*
 - 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 Bay Regional Monitoring Program (RMP)
 - UC Berkeley
 - Environment Canada
 - NOAA (Hollings Marine Laboratory)
 - UC Davis Marine Pollution Studies Laboratory



Study Questions and Design

1. **Can the microarray be used to measure amphipod gene expression?**
 - Binding of amphipod RNA to probes and variability
 - Identify consistent responses
2. **Does gene expression differ with exposure to different toxicants?**
 - Analyze training samples and compare patterns
3. **Is the information useful for stressor identification?**
 - Develop a statistical method to interpret the results
 - Analyze independent validation samples

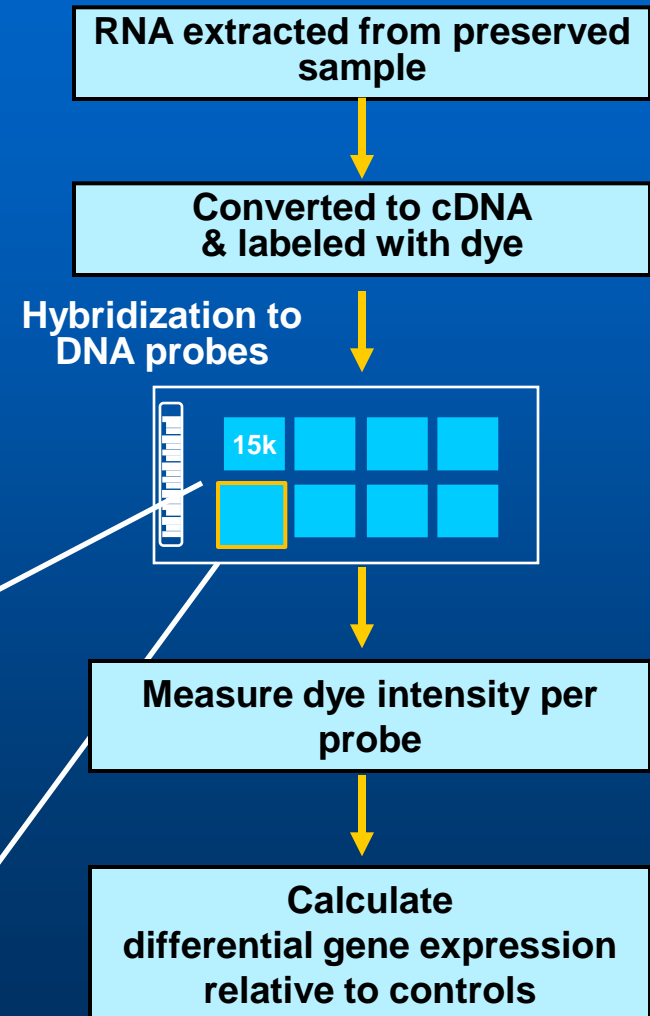
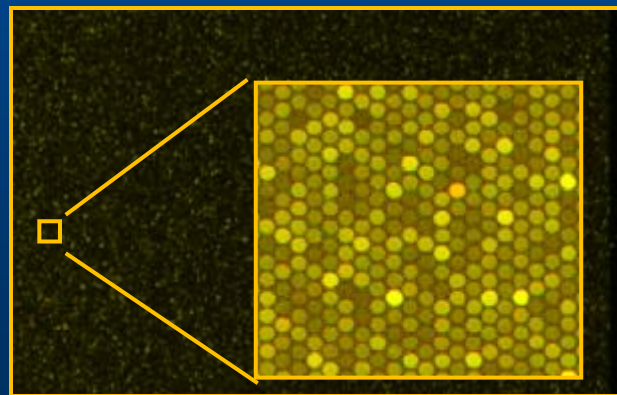
Microarray Analysis

- 8,610 amphipod gene sequences
- Compare sample to control

Differential expression

$$= \log_2(\text{sample/control})$$

2 = four-fold increase in gene expression



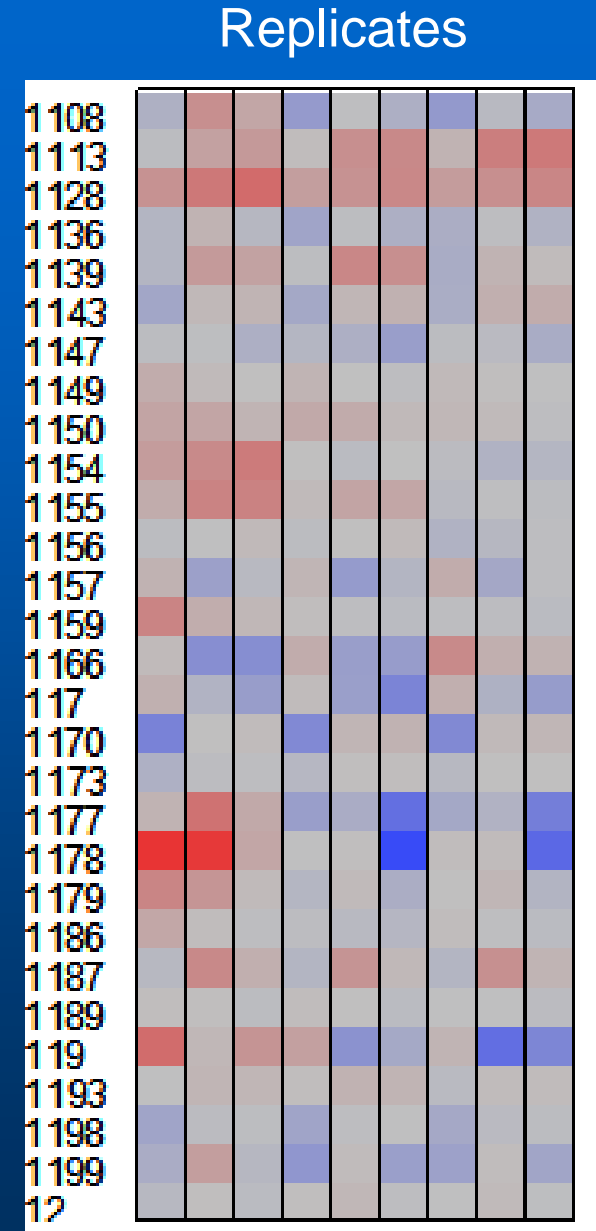
Training Data Set

- **Diverse toxicants and mechanisms of action**
 - Pyrethroid pesticides
 - Trace organics
 - Pesticides & PAHs
 - Other
 - 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

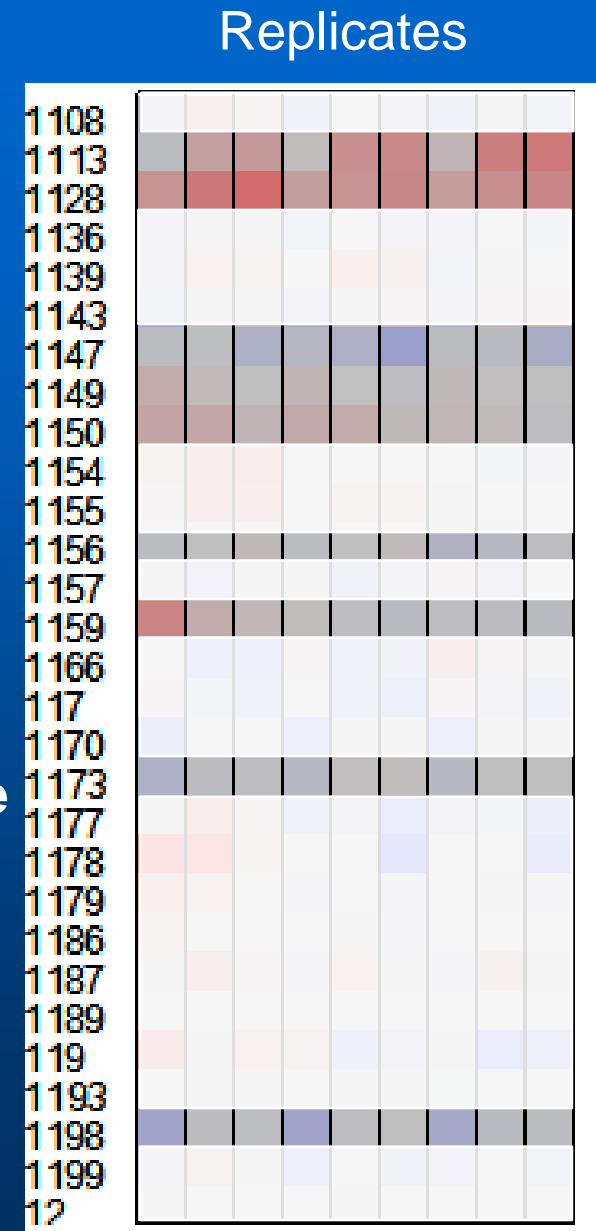
Candidate Gene Selection

- Not all gene probes provide consistent or relevant information
- Multistep process used to identify genes most likely to represent toxicant-specific response
 - Consistent response among replicates



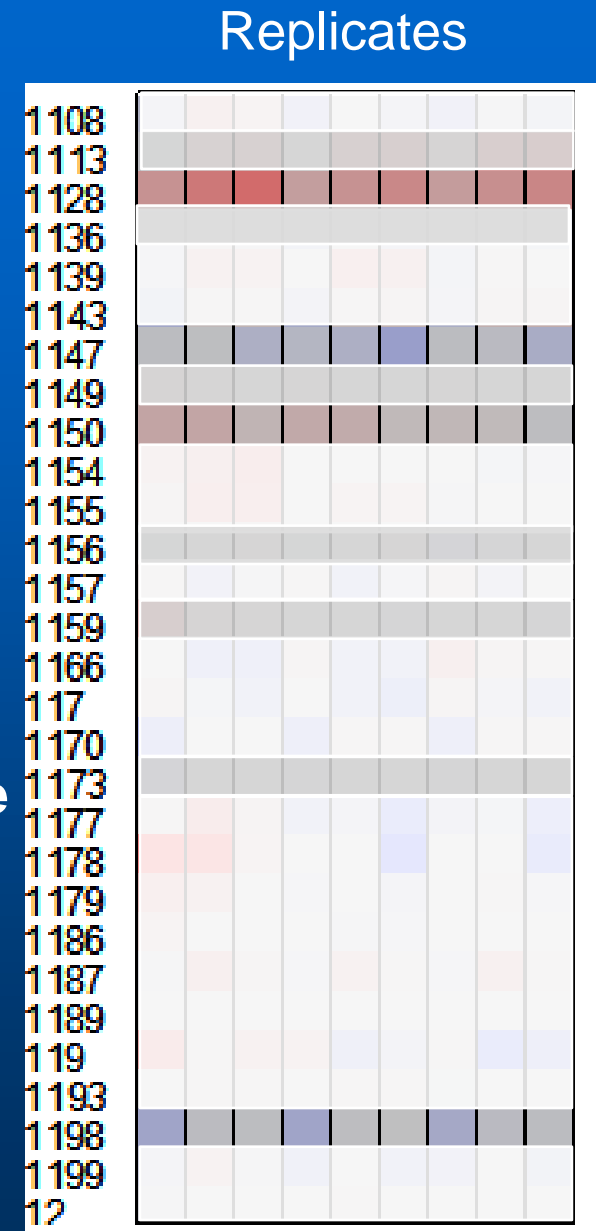
Candidate Gene Selection

- Not all gene probes provide consistent or relevant information
- Multistep process used to identify genes most likely to represent toxicant-specific response
 - Consistent response among replicates
 - Significant differential expression relative to control

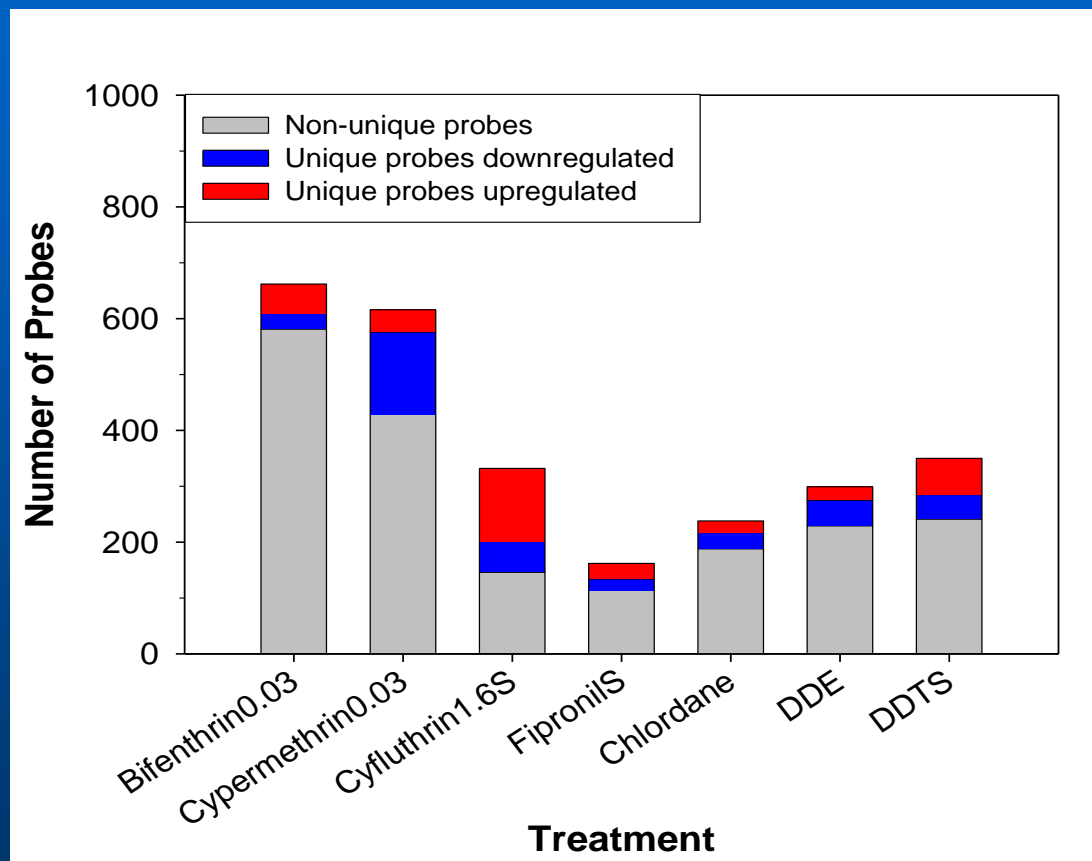


Candidate Gene Selection

- Not all gene probes provide consistent or relevant information
- Multistep process used to 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

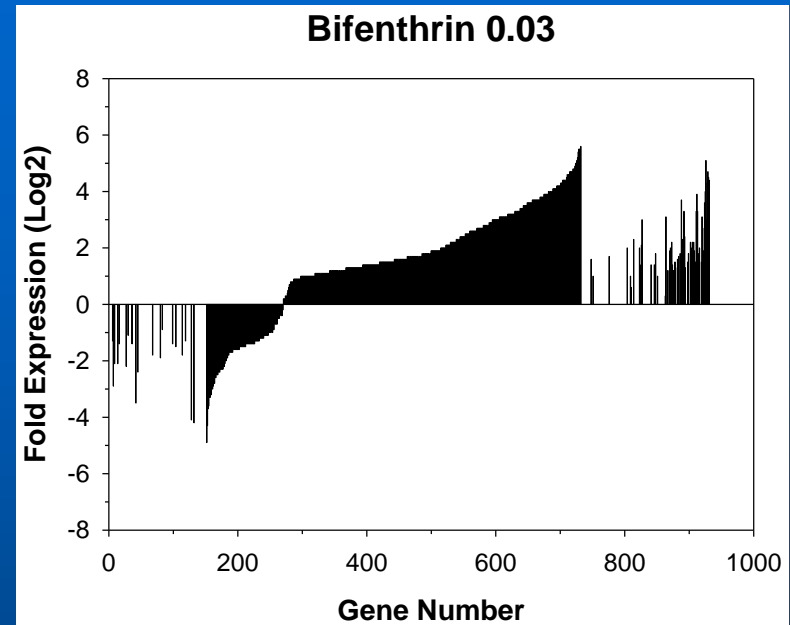
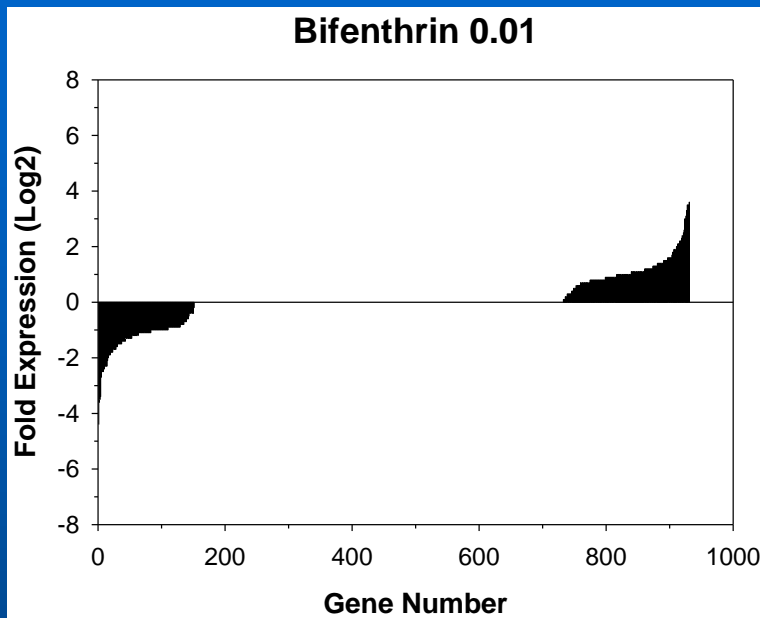


Gene Expression Differs Among Toxicant Types

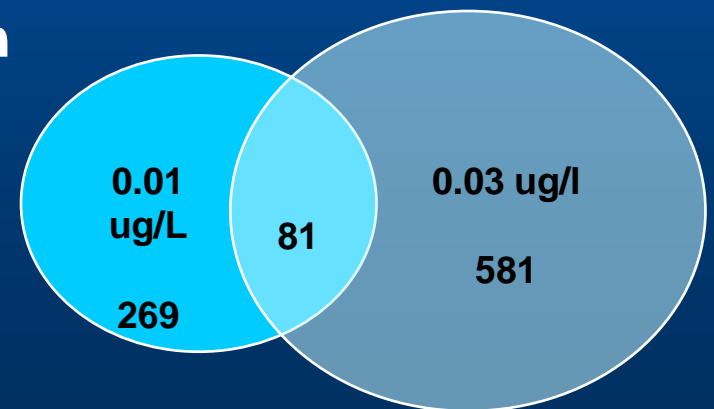


- 21-257 uniquely expressed probes for each chemical

Dose Response: Bifenthrin



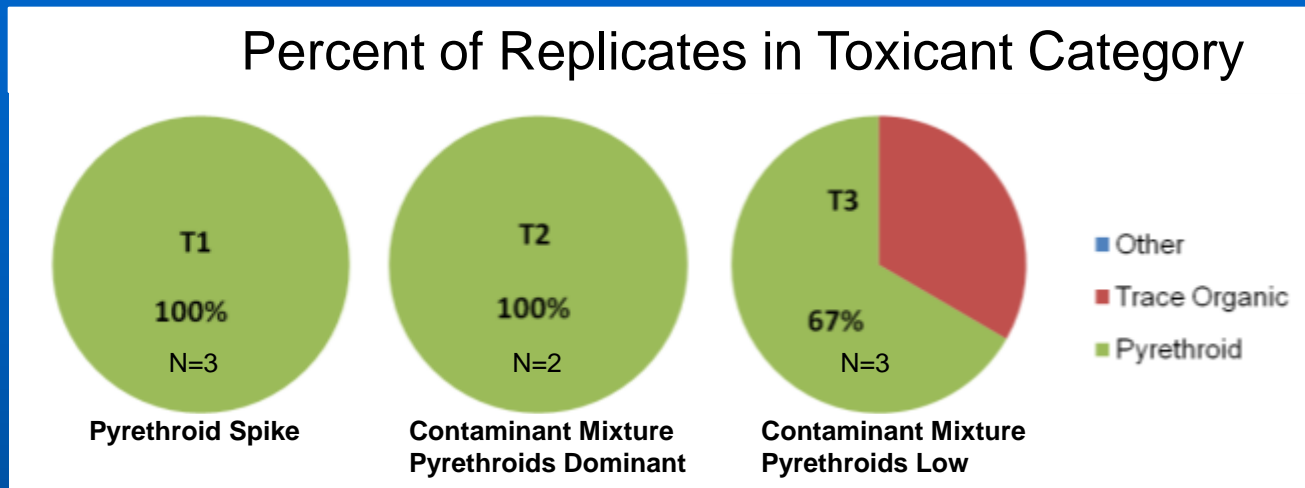
- Concentration, exposure time, and test matrix influence gene expression
- Relatively few candidate genes in common between concentrations
- Differences among control groups also present



Evaluation of Toxicant Identification Ability

- **Develop a statistical model to interpret (classify) results**
 - **Random Forest method used in initial studies**
 - Training sample data used to develop prediction “trees” for each class
 - Trees saved and used to classify evaluation samples
 - **Model developed for 3 classes of toxicants**
 - Pyrethroids, Trace Organics, Other
- **Applied model to independent evaluation samples**
 - **T1: Reference sediment spiked with cyfluthrin**
 - **T2: Ballona Creek estuary sediment (toxicity due to pyrethroids)**
 - **T3: San Francisco Bay sediment (cause of toxicity unknown)**

Evaluation Results



- **Encouraging prediction results**

- Correct classification for 2 samples with identified cause of toxicity
- No TIE data to verify SF Bay sample results
- Preliminary evaluation due to limited number and diversity of evaluation samples
 - Intentional emphasis on pyrethroids

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

Next Steps

- **Investigate interlaboratory comparability of microarray analysis**
 - Developing study design and partners
- **Refine and expand stressor identification approach**
 - Greater standardization of training samples
 - Additional stressors (e.g., PAHs, fine sediment)
 - Alternative data interpretation methods
- **Apply approach in focused stressor identification studies**
 - Compare to traditional TIE methods