

A Computational Tool for Defining Conservation of Molecular Initiating Events Across Species

U.S. EPA
Carlie LaLone
8/22/13



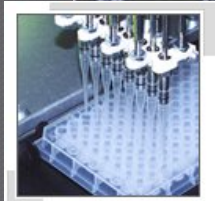
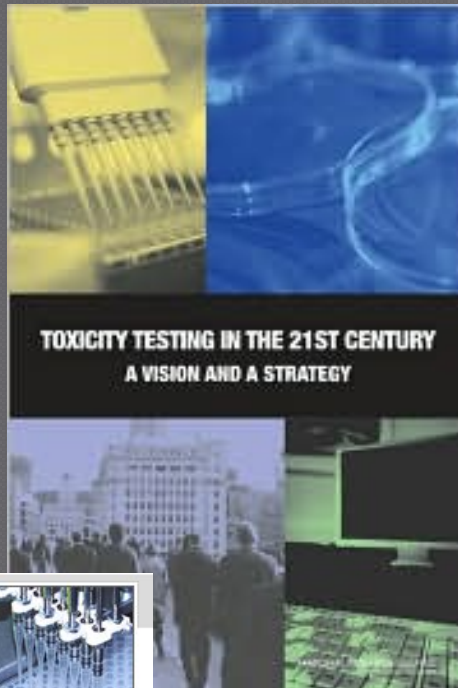
Chemical Safety for Sustainability

Problem Statement

Although chemicals are essential to modern life, **we lack innovative, systematic, effective, and efficient approaches and tools to inform decisions that reduce negative environmental and societal impacts of chemicals** while increasing economic value.

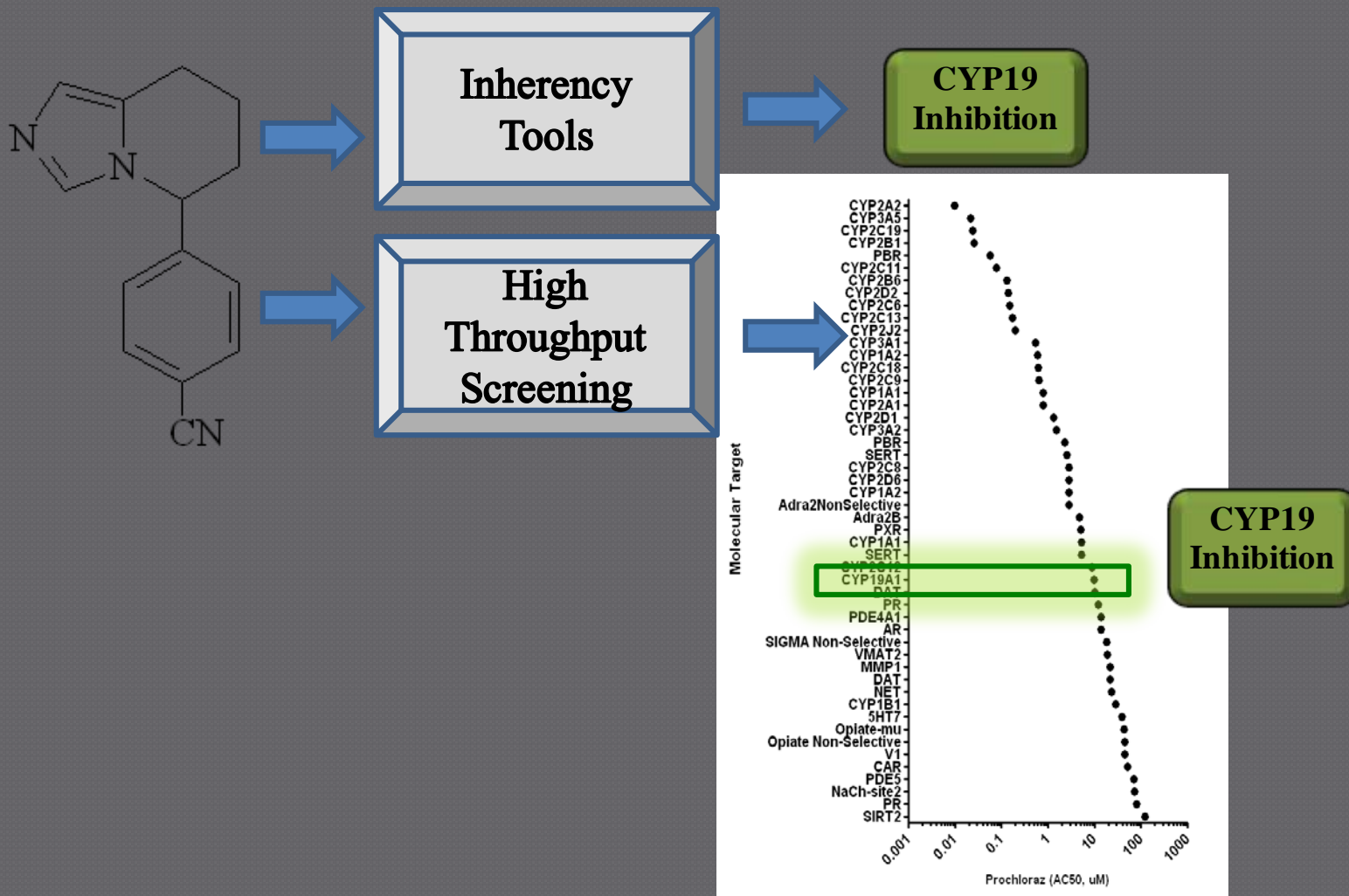


Toxicity Testing in the 21st Century

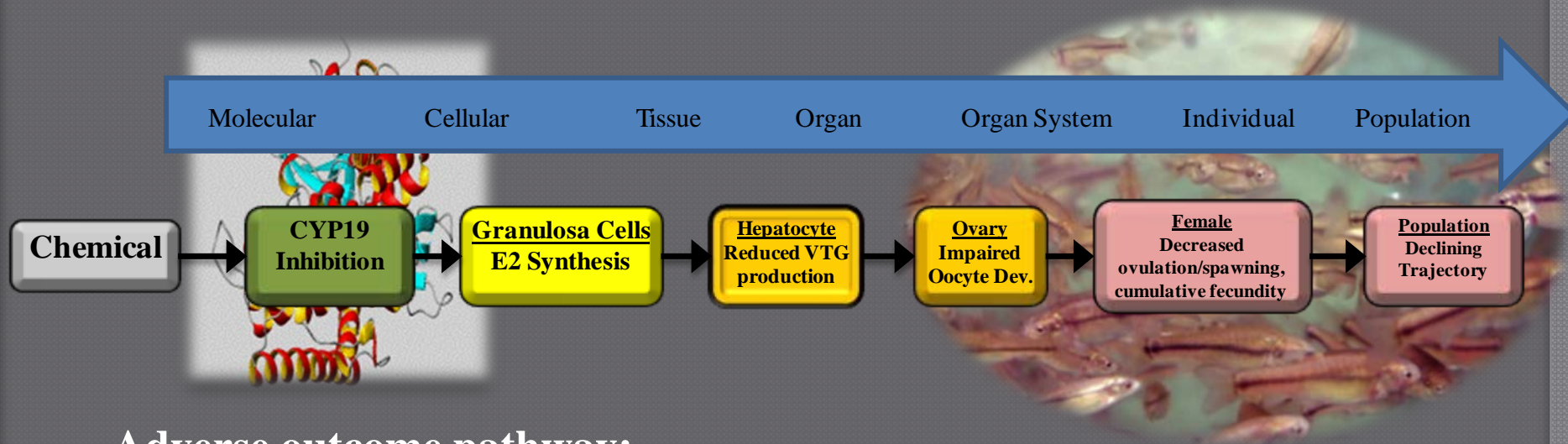


- “Transform toxicity testing **from a system based on whole-animal testing to one founded primarily on in vitro [or in silico] methods** that evaluate changes in biologic processes using cells, cell lines, or cellular components, preferably of human origin”
- “The vision emphasizes the development of **suites of predictive, high-throughput assays**” (p. 7)
- “The mix of tests in the vision include tests that **assess critical mechanistic endpoints involved in the induction of overt toxic effects rather than the effects themselves.**” (p. 121)

Increase the efficiency and speed of chemical evaluations



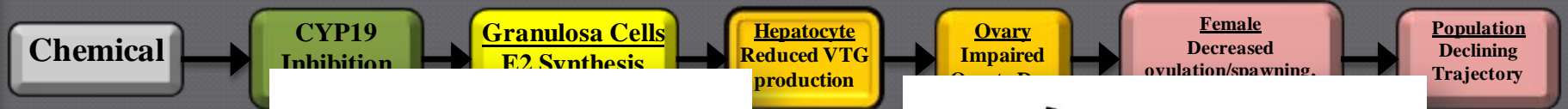
Identify putative molecular initiating events: chemical - biomolecule



Adverse outcome pathway:

- Links molecular initiating event to adverse outcome relevant to risk assessment
- Hazard prediction from inherency or toxicity-pathway data

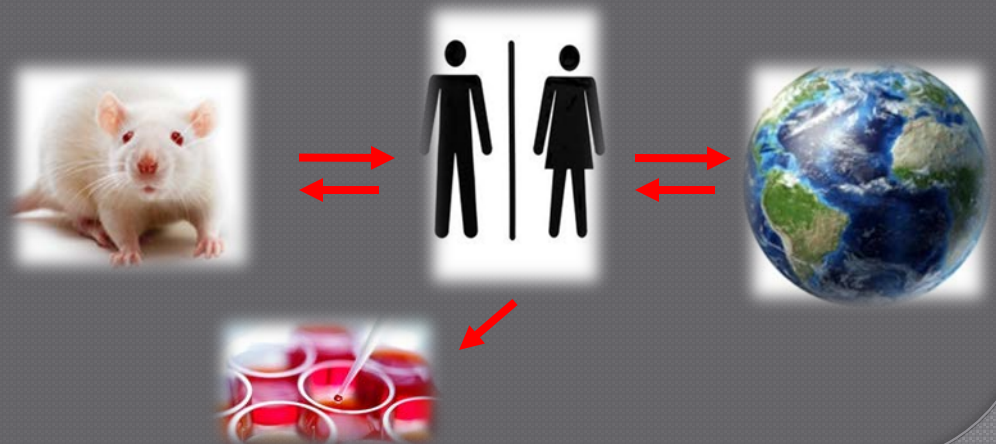
Application of 21st C Paradigm to Ecotoxicology – challenge of species extrapolation



Target Sequ...
 tes rapid...
 protein
 tion for predicting species applicability

Taxonomic applicability domain

- Inherency tools
- Molecular screening data
- AOPs (to some extent)



Chemicals with well defined MIEs

○ Pharmaceuticals and Pesticide

- Designed to act on specific molecular targets to provide therapeutic benefits or exterminate pests
 - Molecular targets
 - Genomic information and translated protein sequence information

○ How do we translate this knowledge to potential effects on ecological species?

○ Molecular Target Similarity– Species Extrapolation

Molecular

Cellular

Tissue

Organ

Organ System

Individual

Population

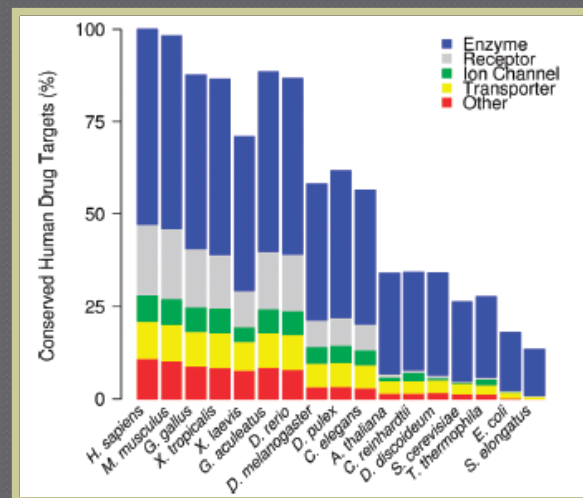
Ecosystem

Molecular Target Similarity: Species Extrapolation

- Ability to identify organism classes with differing sensitivity based on molecular target homology (Kostich and Lazorchak, *Science of the Total Environment*. 2008, 389, 329-339)

- Distribution of orthologs

(Gunnarsson et al. *Environ Sci Technol*. 2008; 42(15):5807-13)

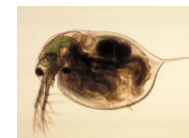


- Which proteins are conserved and to what degree?

Example Supporting Sequence-based Intrinsic Susceptibility Predictions

Estrogen Receptor (OW/ORD Emerging Contaminants Workgroup, 2008)

| Animal Kingdom | Genus | Common name | Chronic value (ng/L) |
|------------------------|---------------------|-------------------|----------------------|
| Vertebrates, aquatic | <i>Danio</i> | Zebrafish | <1.1 |
| | <i>Pimephales</i> | Fathead minnow | 1.5 |
| | <i>Oryzias</i> | Medaka | 3.2 |
| | <i>Oncorhynchus</i> | Rainbow trout | <16 |
| Invertebrates, aquatic | <i>Potamopyrgus</i> | Snail | 50 |
| | <i>Gammarus</i> | Freshwater shrimp | >7,600 |
| | <i>Daphnia</i> | Water flea | 45,000 |
| | <i>Tisbe</i> | Copepod | >100,000 |
| | <i>Chironomus</i> | Midge | 320,000 |
| | <i>Brachionus</i> | Rotifer | 800,000 |



Moving from qualitative understanding of molecular target conservation to quantitative measures

- New tools and technologies have emerged

Developing an Automated Computational Methodology



Protein Sequence Similarity Tool



Predict relative intrinsic susceptibility

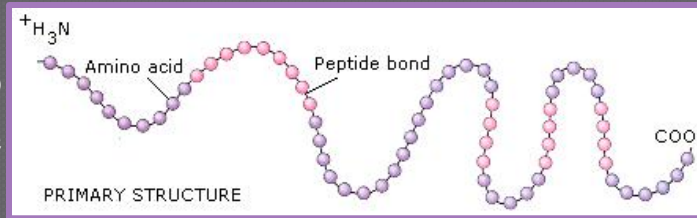
- Relative in that it is dependent on which species is selected as the target (query species)
- Intrinsic susceptibility can be defined as the vulnerability (or lack thereof) of an organism to chemical insult due to its inherent biological composition
 - Receptor/enzyme (protein) available for the chemical to act upon



Strategic Approach for Assessing Protein Similarity

Low Level of Complexity

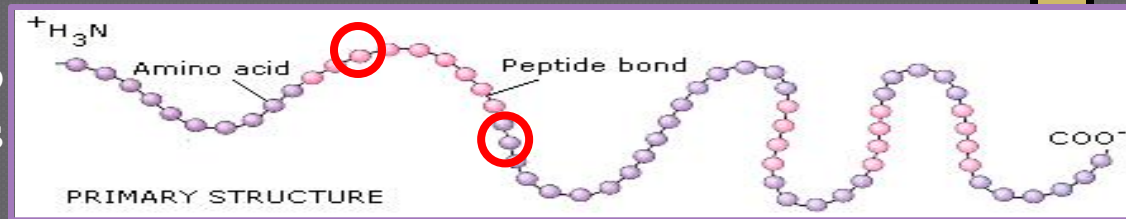
Primary Amino Acid Sequence



Conserved Functional Domains



Individual Amino Acid Residue Queries



Tertiary Protein Structure



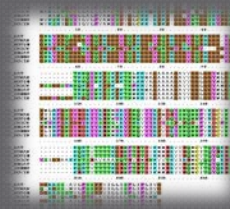
High level of Complexity

Computational Assessment of Protein Similarity: Quantitative Metrics

- ◉ Assume that presence of molecular target in non-target species is one critical route via which a chemical could cause adverse effects
- ◉ Target species vs. Non-target species (NCBI)
 - Align amino acid sequences and conserved domains
 - Assume greater similarity = greater likelihood
 - interact with molecular target in non-target species



vs.



**All Species in
NCBI Protein
Database**

Linking Data Sources

DRUGBANK
Open Data Drug & Drug Target Database

PPDB

VSDB

t3db

Toxin, Toxin-Target Database

- Pesticide Properties DataBase, T3DB, Veterinary Substances DataBase, & DrugBank : identifies molecular targets for pesticide/pharmaceutical
- Link to NCBI GenBank: Protein accession

 **BLAST**[®]

Basic Local Alignment Search Tool

Home

Recent Results

Saved Strategies

Help

- Molecular Target Similarity Tool
 - Automated BLASTp and Conserved domain database
 - Query target species protein accession against all organism classes for vertebrates, invertebrates, and plants

Output from Sequence Analysis

| Number of Proteins in NCBI Database | Organism Class | Species | NCBI Protein Accession | Protein Name | Bit score | E-value | % Similarity | Number of Conserved Domains |
|-------------------------------------|----------------|-------------------------------|------------------------|--|-----------|---------|--------------|-----------------------------|
| 35,859 | Insecta | <i>Aedes aegypti</i> | ACB37024.1 | voltage-gated para-like sodium channel | 4464 | 0 | 100.0 | 4 |
| 115 | Insecta | <i>Culex pipiens pallens</i> | BAI77918.1 | para-sodium channel | 3964 | 0 | 88.8 | 4 |
| 38,393 | Insecta | <i>Culex quinquefasciatus</i> | BAI77917.1 | para-sodium channel | 3963 | 0 | 88.8 | 4 |

Most similar to target species

| Species | NCBI Protein Accession | Protein Name | Bit score | E-value | % Similarity | Number of Conserved Domains |
|--------------------------------|------------------------|---|-----------|---------|--------------|-----------------------------|
| <i>Aedes aegypti</i> | ACB37024.1 | voltage-gated para-like sodium channel | 4464 | 0 | 100.0 | 4 |
| <i>Homo sapiens</i> | NP_066287.2 | sodium channel protein type 2 subunit alpha isoform 1 | 1639 | 0 | 36.7 | 2 |
| <i>Drosophila melanogaster</i> | EDV46862.1 | GG19319 | 3432 | 0 | 76.9 | 0 |
| <i>Drosophila virilis</i> | EDW65213.1 | paralytic | 3410 | 0 | 76.4 | 3 |

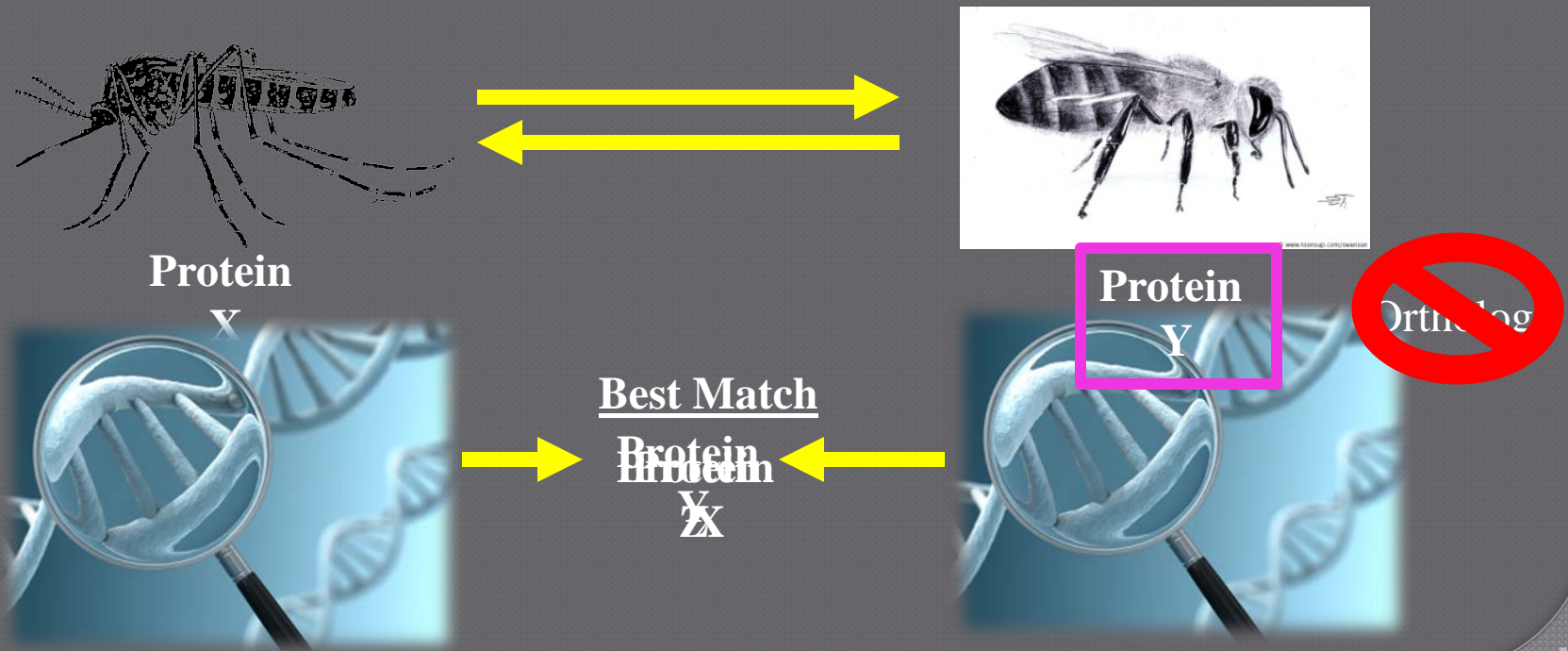
| Species | NCBI Protein Accession | Protein Name | Bit score | E-value | % Similarity | Number of Conserved Domains |
|--------------------------|------------------------|--|-----------|---------|--------------|-----------------------------|
| <i>Aedes aegypti</i> | ACB37024.1 | voltage-gated para-like sodium channel | 4464 | 0 | 100.0 | 4 |
| <i>Drosophila erecta</i> | EDV46862.1 | GG19319 | 3432 | 0 | 76.9 | 0 |

| | | | | | | | | |
|---------|--------------|------------------------------|----------------|---|------|---|------|---|
| 324 | Insecta | <i>Periplaneta americana</i> | ACX44801.1 | voltage-gated sodium channel Nav1 alpha subunit | 3218 | 0 | 72.1 | 4 |
| 16,324 | Insecta | <i>Danus plenippus</i> | EHD74501.1 | voltage-gated sodium channel alpha subunit | 3212 | 0 | 72.0 | 4 |
| 15,129 | Insecta | <i>Harpegnathos saltator</i> | EFN86793.1 | Sodium channel protein para | 3212 | 0 | 72.0 | 4 |
| 31,591 | Branchiopoda | <i>Daphnia pulex</i> | EFX81393.1 | hypothetical protein DAPPUDRAFT_50150 | 2652 | 0 | 59.4 | 3 |
| 20 | Malacostraca | <i>Cancer borealis</i> | ABL10360.2 | voltage-gated sodium channel | 2523 | 0 | 56.5 | 3 |
| 41,714 | Arachnida | <i>Rhodes scapularis</i> | EEC03677.1 | skeletal muscle sodium channel alpha subunit, putative | 2416 | 0 | 54.1 | 3 |
| 212 | Arachnida | <i>Haplopyema schmidtii</i> | ABH12275.1 | putative voltage-gated sodium channel | 2273 | 0 | 50.9 | 2 |
| 25,335 | Mammalia | <i>Callithrix jacchus</i> | XP_002749429.1 | PREDICTED: sodium channel protein type 2 subunit alpha isoform 2 | 1640 | 0 | 36.7 | 2 |
| 25,661 | Mammalia | <i>Macaca mulatta</i> | XP_001100011.1 | PREDICTED: sodium channel protein type 2 subunit alpha-like isoform 6 | 1639 | 0 | 36.7 | 2 |
| 596,962 | Mammalia | <i>Homo sapiens</i> | NP_066287.2 | sodium channel protein type 2 subunit alpha isoform 1 | 1639 | 0 | 36.7 | 2 |
| 40,939 | Mammalia | <i>Sus scrofa</i> | XP_003133492.1 | PREDICTED: sodium channel protein type 2 subunit alpha isoform 1 | 1639 | 0 | 36.7 | 2 |
| 39,590 | Mammalia | <i>Pan troglodytes</i> | XP_001153476.1 | PREDICTED: sodium channel protein type 2 subunit alpha isoform 1 | 1639 | 0 | 36.7 | 2 |

Least similar to target species

Setting the Susceptibility Cut-off

- Ortholog identification
 - Ortholog = A sequence diverged after a speciation event
- Reciprocal best hit BLAST



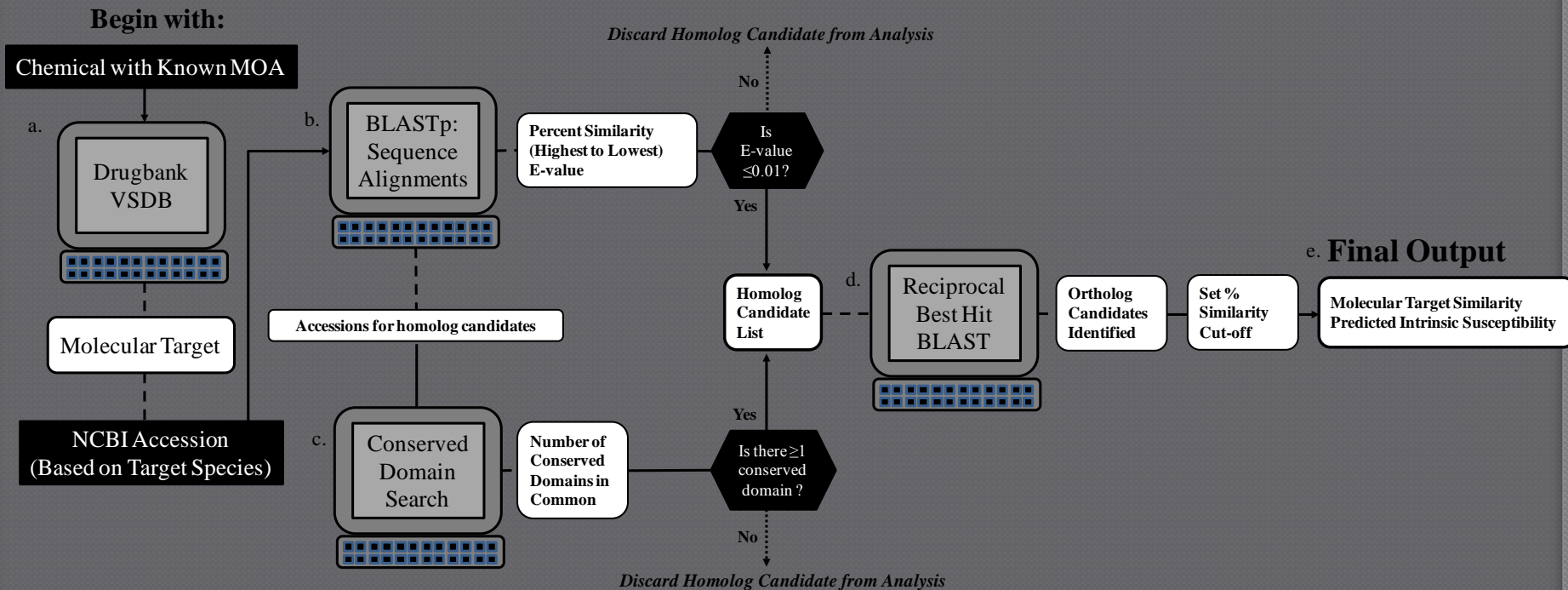
Orthologs Identified

◉ Set susceptibility cut-off

- Protein with lowest percent similarity that was identified as an ortholog

| Taxonomic Lineage | Species | Reciprocal Best Hit | NCBI Protein Accession | Protein Name | Bit score | E-value | % similarity |
|-------------------|-------------------------------|---------------------|------------------------|---|-----------|---------|--------------|
| Insecta | <i>Aedes aegypti</i> | Target Species | ACB37022 | voltage-gated para-like sodium channel | 4449 | 0 | 100 |
| Insecta | <i>Harpegnathos saltator</i> | Ortholog | EFN86793 | Sodium channel protein para | 3223 | 0 | 72.4 |
| Arachnida | <i>Ixodes scapularis</i> | - | XP_002407119 | skeletal muscle sodium channel alpha subunit, putative | 2417 | 0 | 54.3 |
| Insecta | <i>Solenopsis invicta</i> | Ortholog | EFZ17857 | hypothetical protein SINV_07049 | 1551 | 0 | 34.9 |
| Ascidiacea | <i>Ciona intestinalis</i> | - | XP_002123673 | similar to sodium channel, voltage-gated, type III, alpha | 1403 | 0 | 31.5 |
| Gastropoda | <i>Aplysia californica</i> | - | NP_001191637 | sodium channel alpha-subunit SCAP1 | 890 | 0 | 20.0 |
| Chondrichthyes | <i>Heterodontus francisci</i> | - | ADV73289 | voltage-dependent sodium channel 2 | 843 | 0 | 18.9 |

Analysis Overview



Case Examples: Illustration of Concept

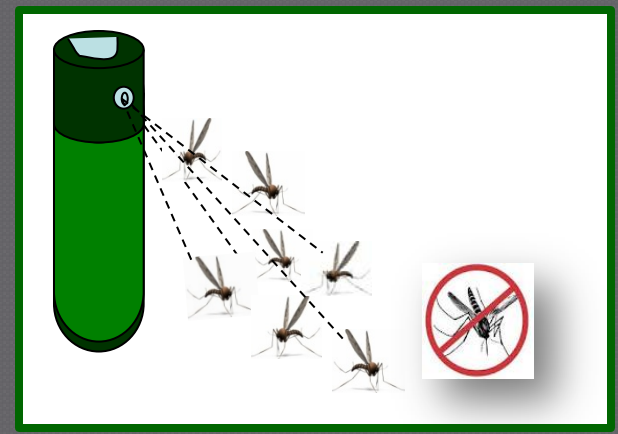
Ethinylestradiol



17 β -trenbolone



Permethrin

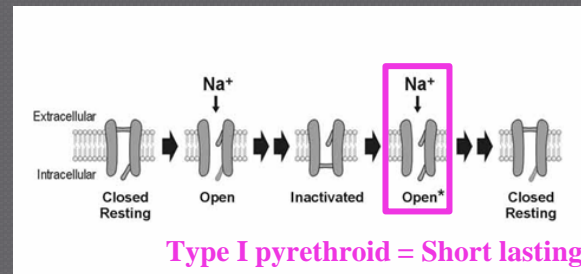
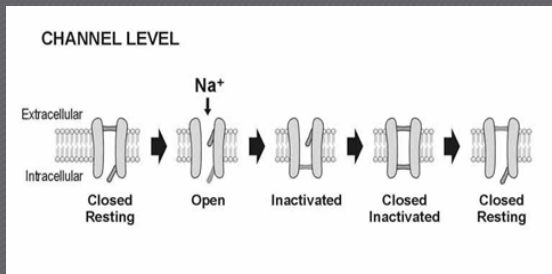
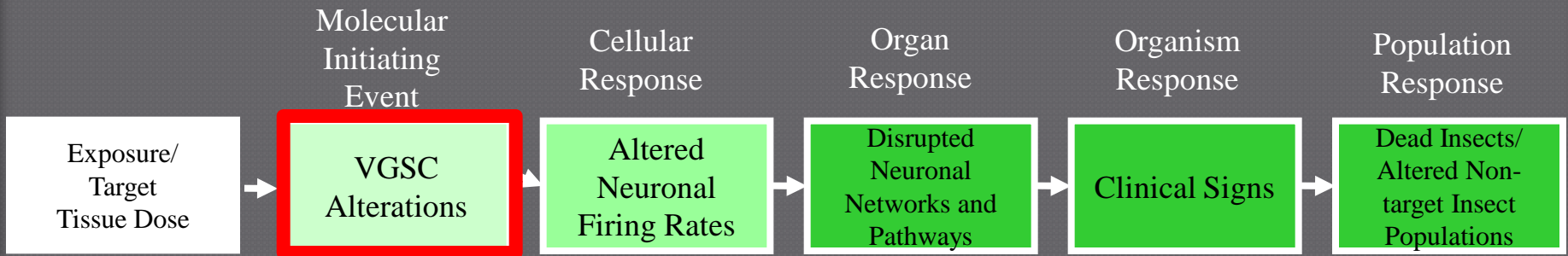


LaLone et al. Molecular Target Sequence Similarity as a Basis for Species Extrapolation to Assess the Ecological Risk of Chemicals with Known Modes of Action. 2013. Submitted.



Permethrin-Insecticide

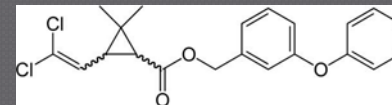
◉ Molecular Target: Voltage-gated sodium channel



VGSC Slide material: Ke Dong, Michigan State University

◉ Acute neurotoxicity: Muscle spasm, paralysis, death

- Target Species: Lice, ticks, fleas, mites, scabies (www.drugbank.ca), mosquitoes (U.S. EPA, Registration Eligibility Decision, RED)



Tool: Example Query

Protein Target 1:

Multiple Protein Targets [Click to Add more protein targets](#)

Protein Target 2:

Target Species :

Multiple Target Species [Click to Add more target species](#)

Target Species:

Choose Analysis:

Full Search My Species Program Office Species of Interest

[Click to Add more non- target species](#)

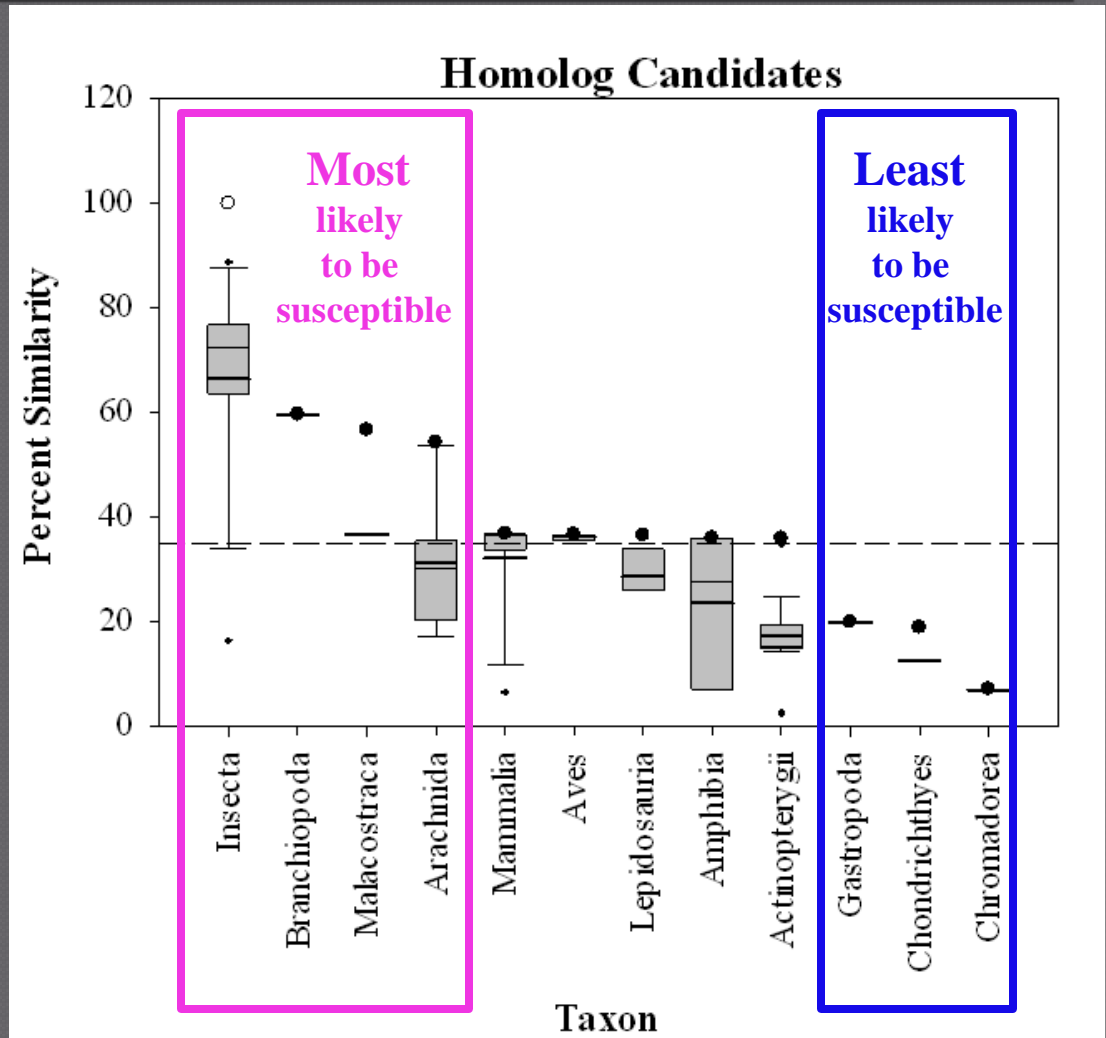
Align Sequences

Conservation Across Species



Target Species: *Aedes aegypti*
Molecular Target: Voltage-gated
para-like
sodium channel

Define
taxonomic
applicability
domain



Comparing Relative Intrinsic Species Susceptibility Predictions to Empirical Toxicity Data



Mining the ECOTOX database

Summarizes Toxicity Data for Individual Chemicals

Chemical (Analytical measurements, Chemical purity)

| <u>Chemical</u> | <u>CAS</u> |
|----------------------|------------|
| Permethrin | 52645-53-1 |
| (+)-cis-Permethrin | 61949-76-6 |
| (+)-trans-Permethrin | 61949-77-7 |
| (+)-cis-Permethrin | 54774-45-7 |
| (-)-cis Permethrin | 54774-46-8 |
| (+)-trans Permethrin | 51877-74-8 |
| (-)-trans Permethrin | 54774-47-9 |

Species (Exclude Resistant/Susceptible Strains, Pesticide exposed)

- All **Aquatic** Taxa (Identify Life Stage)

Endpoint (Desired Acute Response in Target Species = Death)

- **EC50/LC50**
- **Mortality / Survivability**
- Acute durations (48 hr invertebrate/96 hr vertebrate)
- Water Exposure (No feeding or diet)



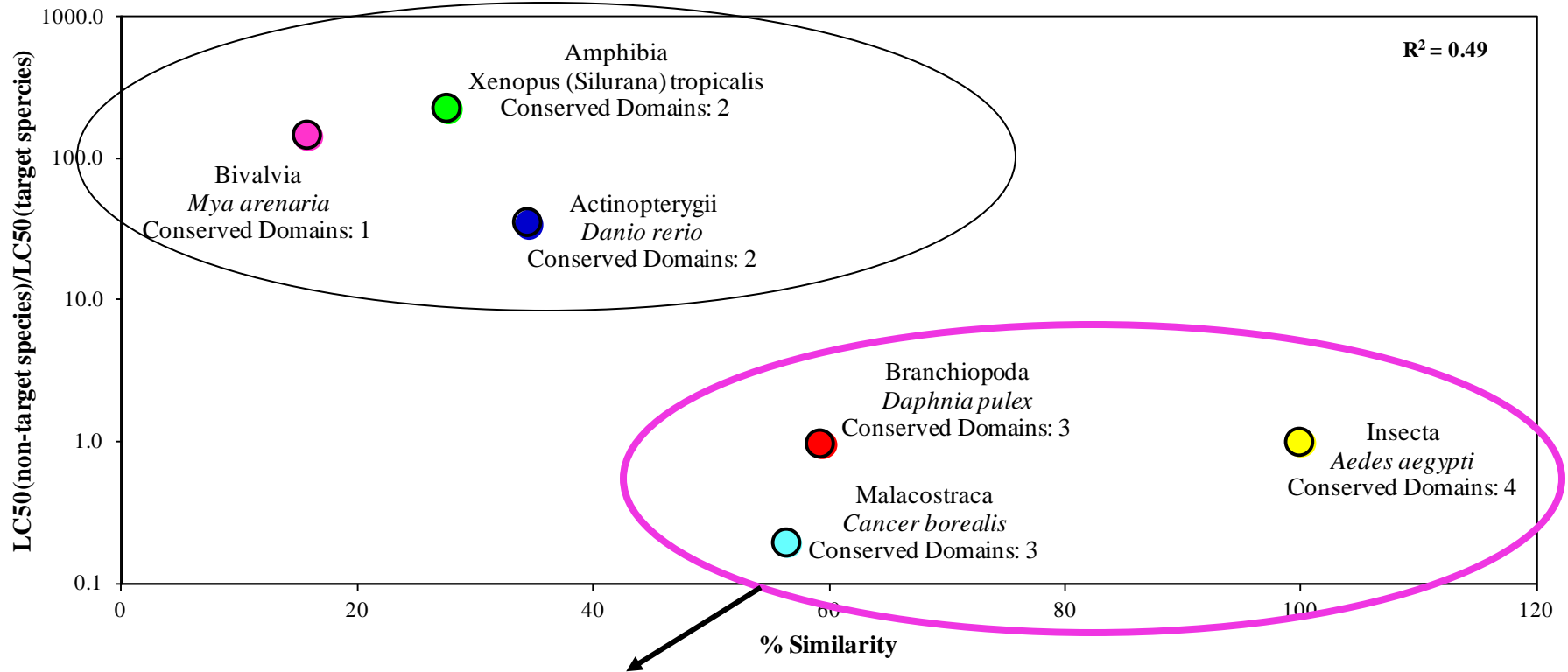
**Quick
Database
Query**



**Advanced
Database
Query**

Compare to Homology Data

Test of concept



MIE likely to be relevant

Exposure/
Target
Tissue Dose

VGSC
Alterations

Altered
Neuronal
Firing Rates

Disrupted
Neuronal
Networks and
Pathways

Clinical Signs

Dead Insects/
Altered Non-
target Insect
Populations

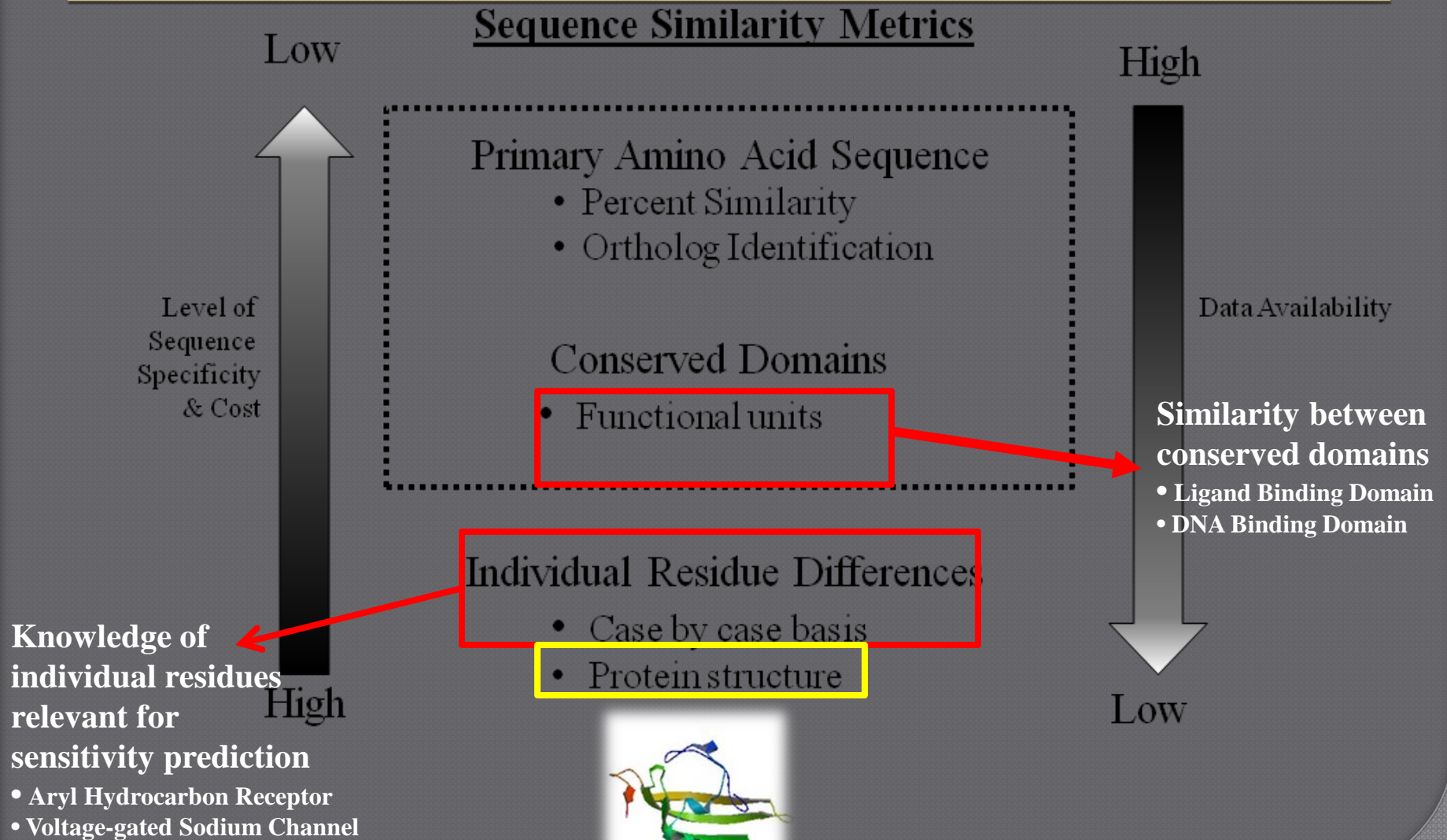
Molecular Initiating Event

Taking a Closer Look

Delving into sequence comparisons



Logic behind development



Conserved Domains: The Next Level

Original Query

Target Species: *Aedes aegypti*

Molecular Target: Voltage-gated para-like sodium channel


NCBI Accession: ACB37024.1

Bit Score: 4464

Total Conserved Domains: 4

Organism Class: Insecta

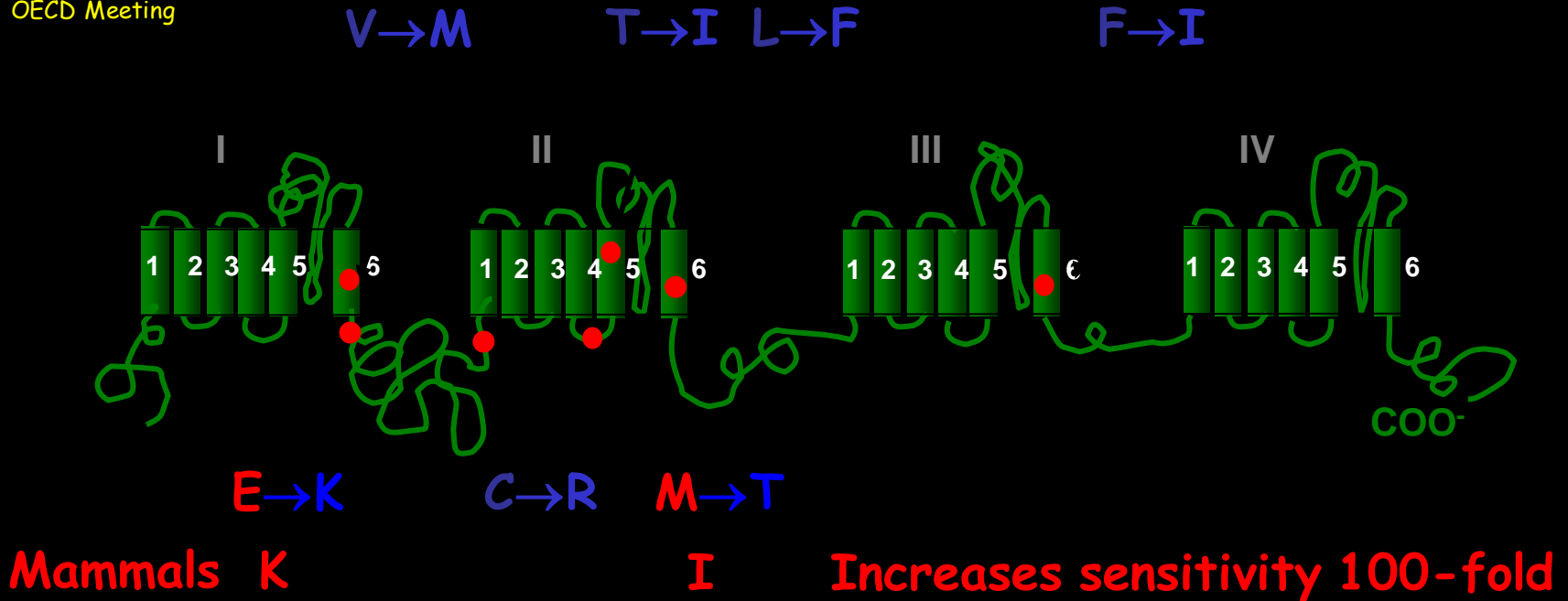


| Organism Class | Non-Target Species | Protein Name | Calculated % similarity | Common Domains | Conserved domain IDs | Domain type | Sequence coverage of conserved domains | Conserved Domain % Similarity |
|----------------|--|--------------|-------------------------|----------------|---|---|---|-------------------------------|
| Insecta |  <i>Apis mellifera</i> | paralytic | 73 | 3 | pfam11933 pfam08016 pfam00520 | Unknown function Polycystin cation channel Ion transport protein | 1-222, same 217-423, same 1-194, same | 61 92 93 |



Knowledge of individual residues

Slide from Tim Shafer
OECD Meeting



Resistance and sensitivity: Single amino acid residue substitutions

- Targeted mutagenesis
- Voltage clamp techniques

Targeted sequence comparisons


COBALT *Constraint-based Multiple Alignment Tool*
My NCBI 
[Home](#) [Recent Results](#) [Help](#)
[Sign In](#) [Register](#)



vs.

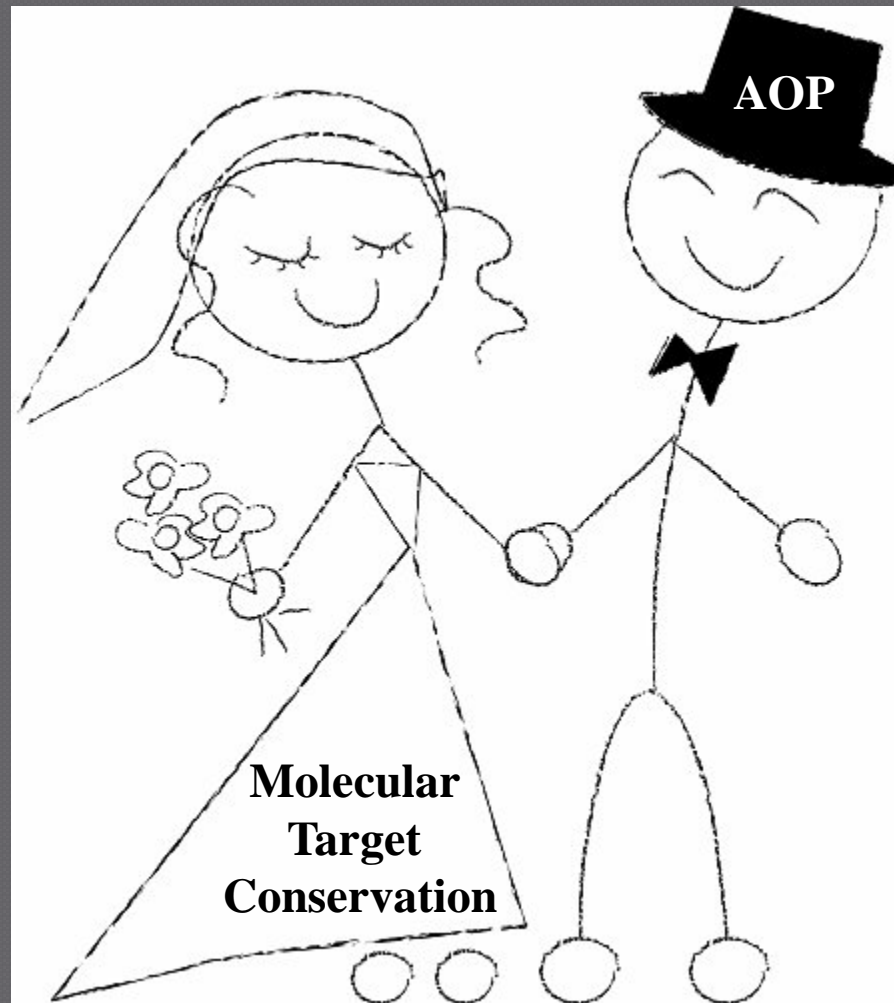


vs. Species A, B, C.....

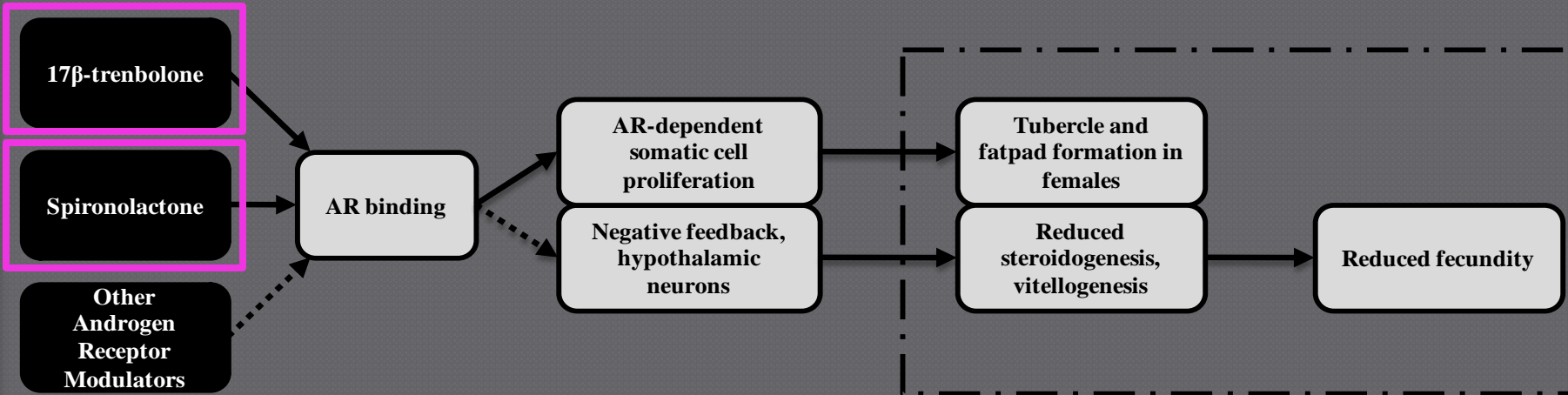
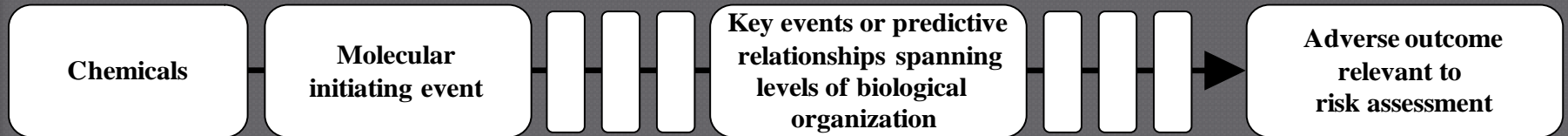
| | | | | |
|-------------------------------------|--------------------------|------|---|------|
| <input checked="" type="checkbox"/> | ACB37024 | 1651 | NMLTMTLDHYKQTDTFSAVLDYLNMFICIFSSSECLMKIFALRYHYFIEPWNLFDFVWVILSILGLVLSDLIEKYFVSPT | 1730 |
| <input checked="" type="checkbox"/> | ACV87000 | 1619 | NMLTMTLDHYQQTQTFSDVLDYLNMFIVIFTSECLMKIFALRYHYFKEPWNLFDFVWVILSILGLVLSDLIEKYFVSPT | 1698 |
| <input checked="" type="checkbox"/> | ACB37024 | 1731 | LLRVVRVAKVGRVRLRVKGAKGIRTLFFALAMSLPALFNICLLFLVMFIFAIFGMSFFMHVKYKSGLDDVYNFKTFGQS | 1810 |
| <input checked="" type="checkbox"/> | ACV87000 | 1699 | LLRVVRVAKVGRVRLRVKGAKGIRTLFFALAMSLPALFNICLLFLVMFIFAIFGMSFFMHVKDKSGLDDVYNFKTFGQS | 1778 |
| <input checked="" type="checkbox"/> | ACB37024 | 1811 | MILLFQMSTSAGWDGVLVDGIINEDECLPPDNDKGYPGNCGSATIGITYLLAYLVISFLIVINMYIAVILENYSQATEDVQ | 1890 |
| <input checked="" type="checkbox"/> | ACV87000 | 1779 | MILLFQMSTSAGWDGVLVDGIINEEDCQEPNNEIGYPGNCGSSTIGIAYLLSYLVISFLIVINMYIAVILENYSQATEDVQ | 1858 |

- Automate the process of querying a/multiple specific residue position/s
- Use knowledge for species susceptibility predictions
 - Hypotheses generation

Knowledge of molecular target conservation complements the AOP construct

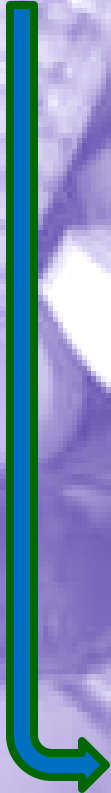


Established AOP



- Established mechanistic linkage with quantitative or semi-quantitative data
- Plausible linkage with limited data
- · - · - Predicted apical outcomes following AR activation in small fish





Humans

Acne



#ADAM

Hirsutism



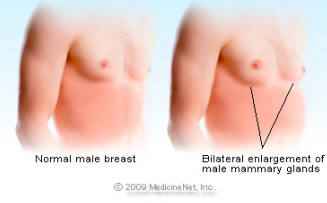
Chas. Eisenmann, Photo. 27th Bowery, N. Y.



Female Pattern Baldness

Side Effect

Gynecomastia



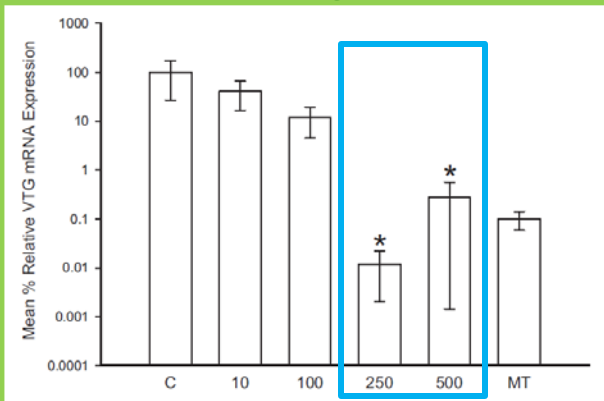
Normal male breast

Bilateral enlargement of male mammary glands

© 2009 MedicineNet, Inc.

Western Mosquitofish

Decrease Vitellogenin mRNA



Masculinization



♂

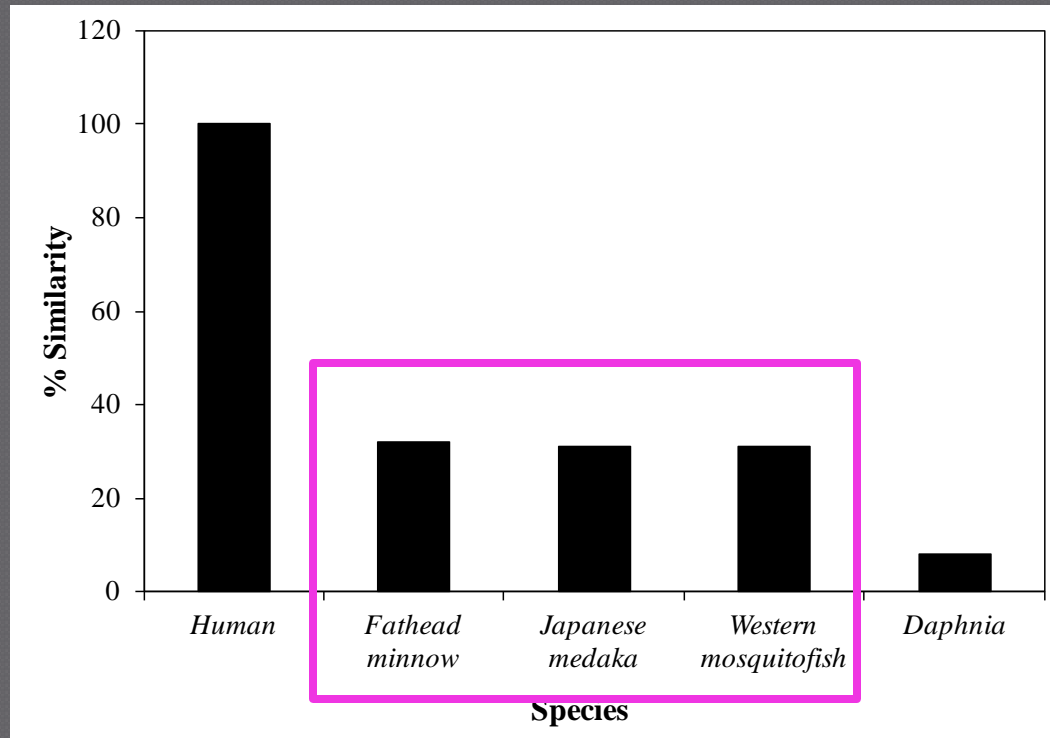
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Environmental Toxicology and Chemistry, Volume 30, Issue 6, pages 1376-1382, 2011

Observed Adverse Effect in Aquatic Species

Molecular Target Conservation: Species Susceptibility Prediction

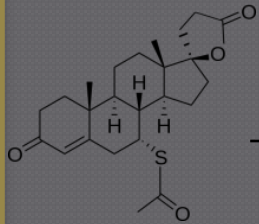


○ Hypothesis:

- Based on homology to the human androgen receptor
 - Small fish likely to be susceptible
 - Invertebrates unlikely to be susceptible

AR Activation in Small Fish

Spirolactone



Androgen Receptor Activation

Tubercle Formation



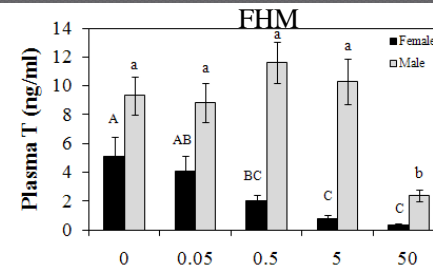
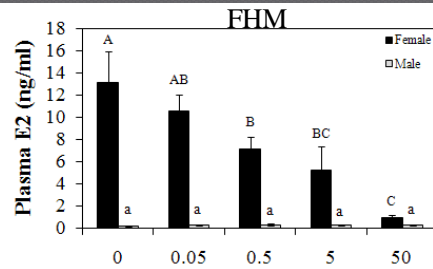
5 µg/L

Papillary Process Formation

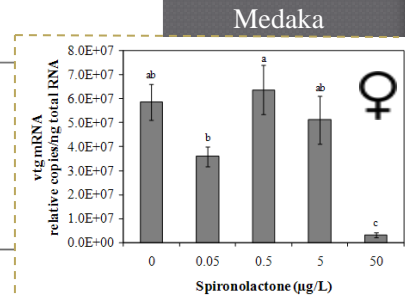
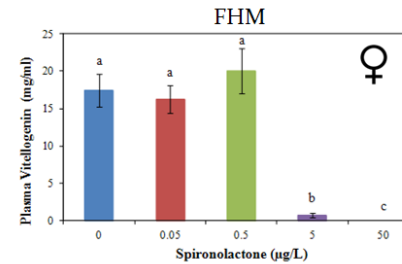
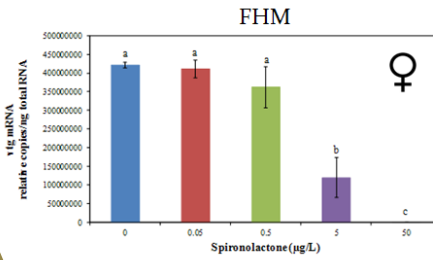


5 µg/L

Reduced Steroidogenesis



Reduced vtg expression/synthesis

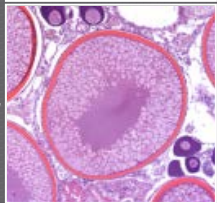


FHM
Reduced deposition of vtg in oocyte

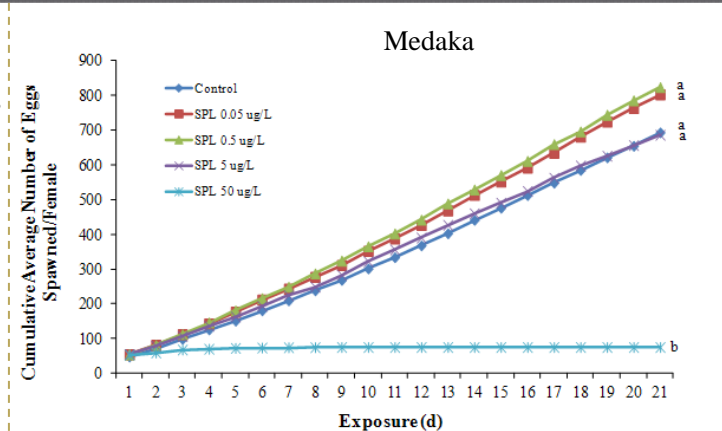
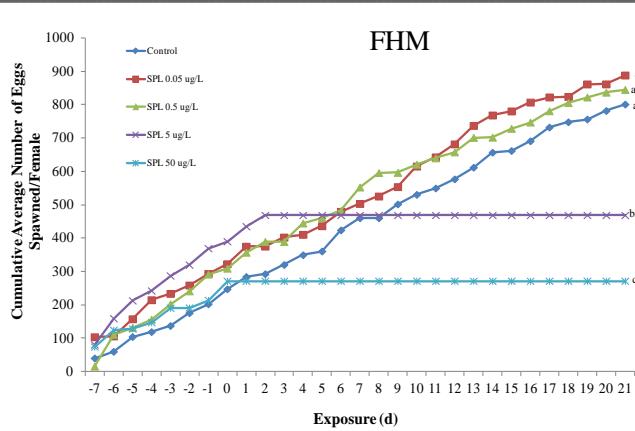
Control



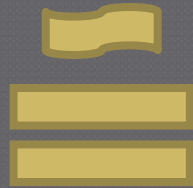
50 µg/L



Reduced Fecundity



Small fish species sensitive



Secondary Sex
Reproduction

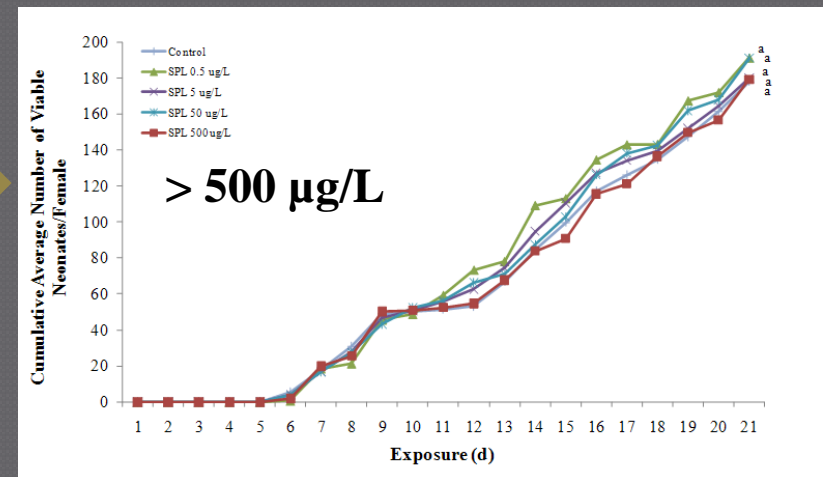
0.5 $\mu\text{g/L}$

5 $\mu\text{g/L}$



5 $\mu\text{g/L}$

50 $\mu\text{g/L}$





Key Findings

- ◉ Evidence that MIE conservation and knowledge of sequence similarity across species can be useful for defining taxonomic domain of applicability for AOP
- ◉ Consistency of AOP across small fish species
 - Predictable adverse effects
- ◉ Further examination of functional domains, individual residue queries, and protein structure between species may enhance predictive utility

Progress

○ Manuscripts:

- Molecular Target Sequence Similarity as a Basis for Species Extrapolation to Assess the Ecological Risk of Chemicals with Known Modes of Action. Submitted
- Cross species sensitivity to a novel androgen agonist of environmental concern, spironolactone. ET&C 2013. Published online

○ Sequence Similarity Tool:

- Transferrable tool
- Automated with capabilities described throughout talk
 - Primary protein sequence, conserved domains, and individual residue query capabilities



Current Analyses: Sequence Similarity Tool

- Honey bee sensitivity- focus on pesticide MIE nAChR
- Acetylcholine esterase
- Avian AOP for Conazoles – CYP51
- 27 Pharmaceutical case study
- Estrogen receptor-sequence similarity vs. binding of in vitro recombinant ER across species



Future Directions: Sequence Similarity Tool

◎ Test the predictive utility:

- Establishing quantitative relationships between target similarity and initiation of responses using comparative in vitro systems
- Confirmation that in silico predictions correspond with in vivo responses
- Use tool to provide cross-species insights as to ADME to support PBPK modeling

◎ Improve the tool: Develop automated computational methods for assessing tertiary structure across species

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