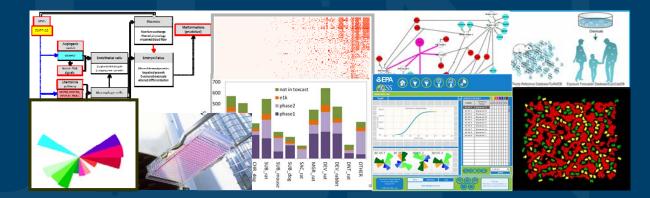


Update on the ToxCast Chemical Prioritization Project

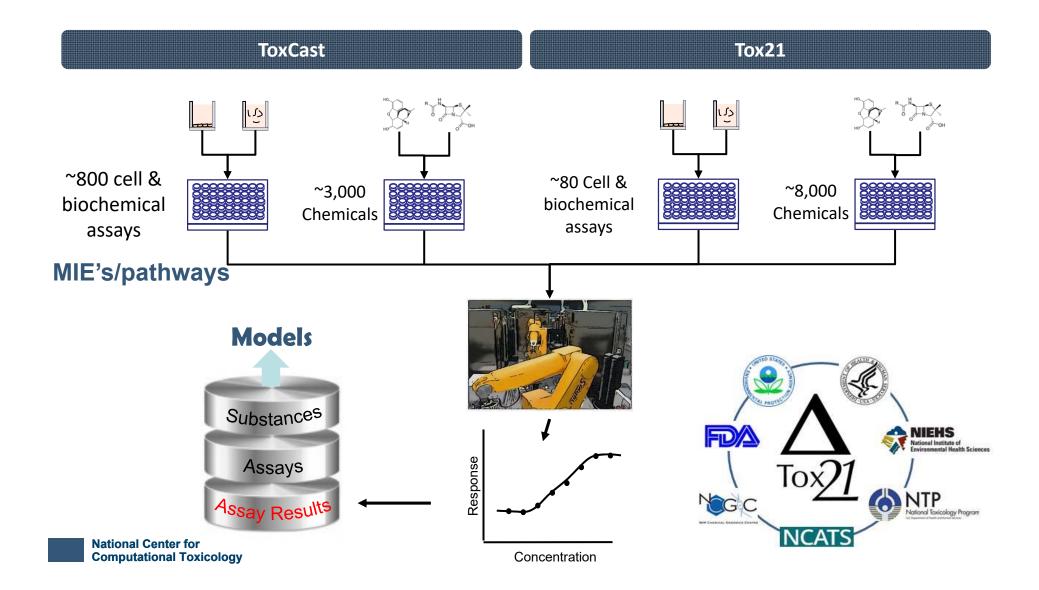


CBCRP Oakland, CA February 12-13, 2018

Keith Houck National Center for Computational Toxicology

The views expressed in this presentation are those of the author and do not necessarily reflect the views or policies of the U.S. EPA

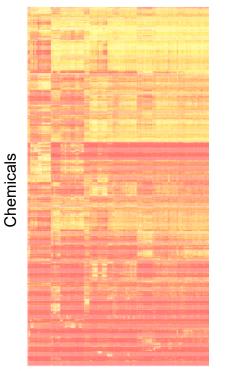




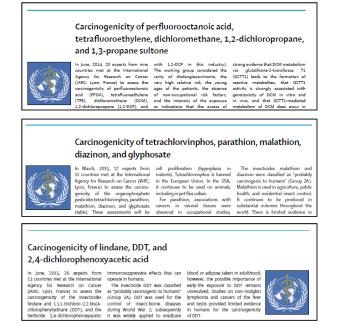


Broad Success Derived from High-Throughput Screening Approaches

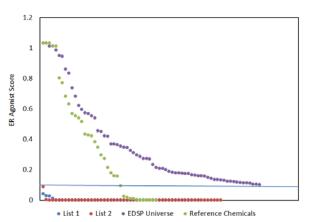
Group Chemicals by Similar Bioactivity and Predictive Modeling



Provide Mechanistic Support for Hazard ID Prioritization of Chemicals for Further Testing



IARC Monographs 110, 112, 113



FIFRA SAP, Dec 2014

Assays/Pathways

National Center for Computational Toxicology



What Are We Doing Now?



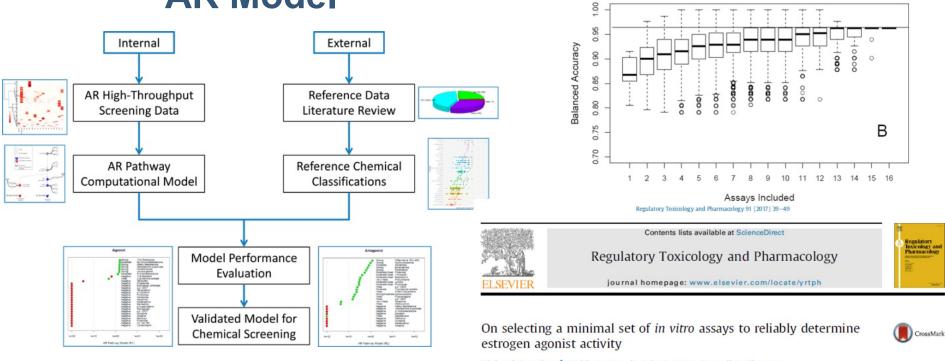
Continued EDSP Support



ER Model

Reference Chemicals

AR Model



pu

Richard S. Judson^{*}, Keith A. Houck, Eric D. Watt, Russell S. Thomas US. Environmental Protection Agency, RTP, NC, United States

Chemical Research in To<u>xicology</u>

Development and Validation of a Computational Model for Androgen Receptor Activity

Nicole C. Kleinstreuer, *[†] Patricia Ceger,[‡] Eric D. Watt,[§] Matthew Martin,[§] Keith Houck,[§] Patience Browne,^{||} Russell S. Thomas,[§] Warren M. Casey,[†] David J. Dix,[⊥] David Allen,[‡] Srilatha Sakamuru,[#] Menghang Xia,[#] Ruili Huang,[#] and Richard Judson[§]



National Center for Computational Toxicology

HPT Axis Targets

Assay Target						
OATP	TR					
MCT8	Duox					
Sulfation/Gluc	Deiodinases					
Agonists	NIS					
AhR	Pendrin					
Antagonists	TBG					
CAR	Thyroid Receptors					
PXR	ТРО					
Phase I	TRH Receptor					
Phase II	TSH Receptor					
Hepatic Metabolism	TTR					



Addressing Selected Criticisms of ToxCast Program

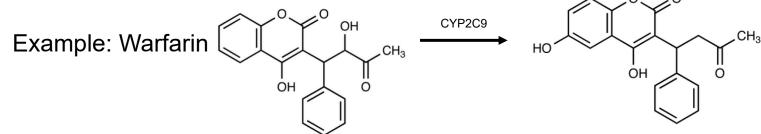
- You don't include metabolism in your *in vitro* assays
- You don't measure my favorite endpoint
- You don't cover all of biological space
- *In vitro* assays are not normal biology
- Assay (x) in your battery did not get the right answer for my chemical
- My assay disagrees with your assay (x), so your approach is flawed
- You can't test my favorite chemicals because of limitations in your methods (e.g., solvents, high LogP)
- Your assay descriptions to do not allow me to reproduce your results
- I get different answers when I analyze your data



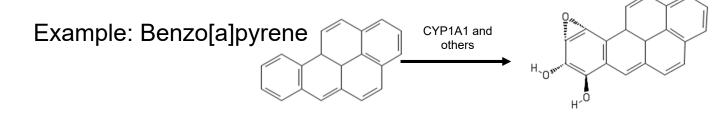
Why is Metabolic Competence Important for *in vitro* Assays?

Our existing *in vitro* assays have <u>limited or no metabolic capacity</u>. This leads to two problems:

1. Overestimation of chemical hazard *in vitro* if the parent compound is detoxified to a less toxic or non-toxic metabolite *in vivo*



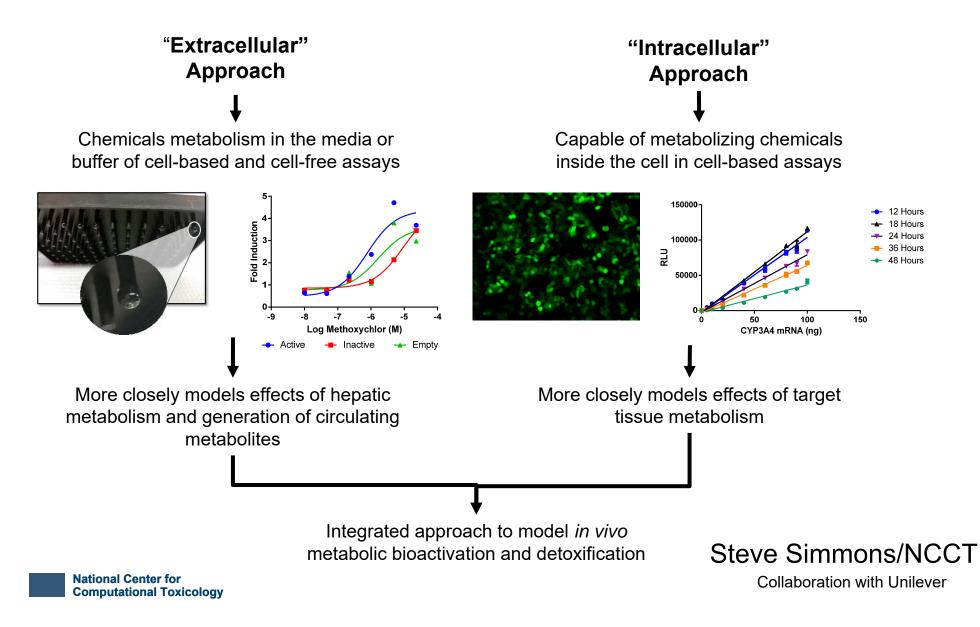
2. Underestimation of chemical hazard *in vitro* if the parent compound is activated to a more toxic metabolite *in vivo*



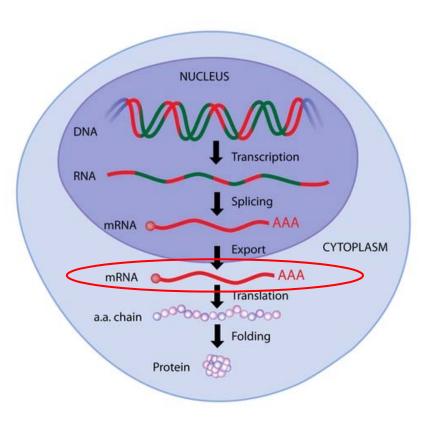
Steve Simmons/NCCT



Beginning to Address Metabolic Competence



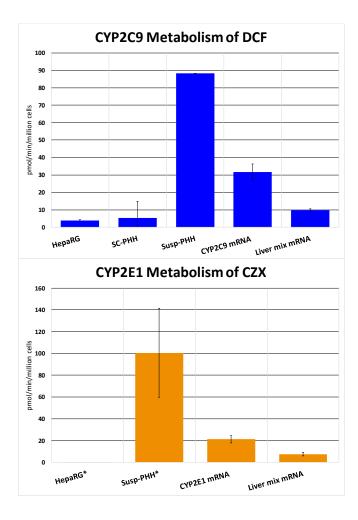
United States Environmental Protection Agency

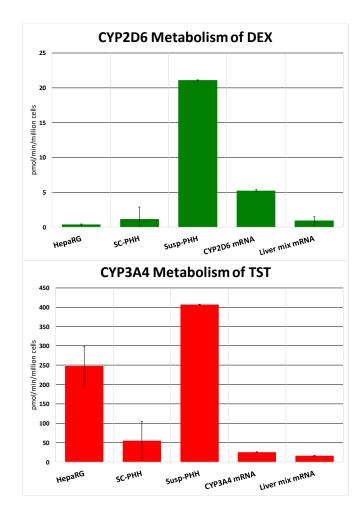


- Intracellular Metabolism with mRNA Transfection
 - Introducing xenobiotic-metabolizing enzyme (XME)-encoding genes back into cells with low/no expression is not a new idea
 - Plasmid transfection, electroporation, and various viral vectors introduce XME-encoding genes (DNA) back into cells under control of gene promoters that drive strong expression (transcription)
 - Transcription levels vary greatly between cell types and tightly controlled co-expression genes is difficult
 - Transfection of XME-encoding mRNAs is a novel approach that bypasses cellular transcription
 - Chemically-modified nucleotides and cap eliminate the toxicity traditionally seen with RNA transfection
 - Rapid XME expression and permits user to define composition and ratios of input mRNAs
 - Method development focused on cytochrome P450 (CYP) enzymes, responsible for phase I metabolism



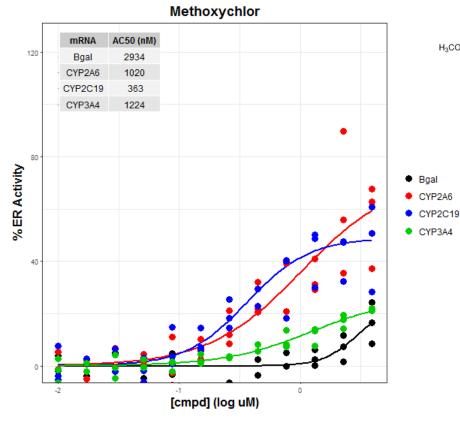
Comparison to "Gold-Standard" XM-Competent Cell Models

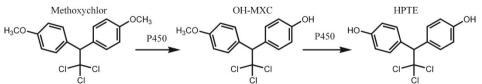






Deployment to ER Transactivation Assay

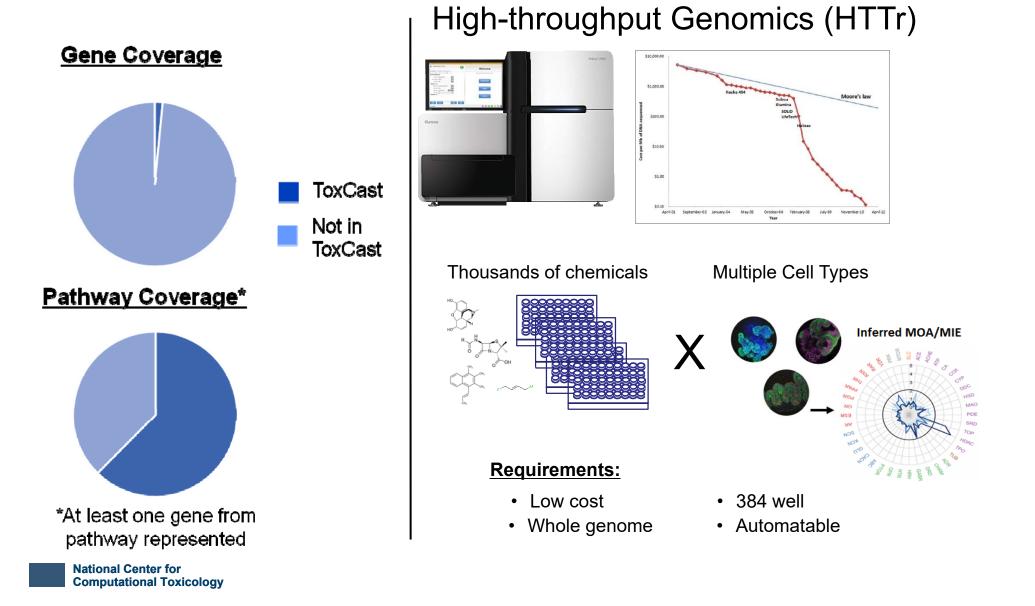




- Methoxychlor (MXC) has minimal ER agonist activity
- MXC is demethylated by certain human CYP450 enzymes to HPTE: 1A2, 2A6, 2C18, 2C19 > 2B6, 2C9
- HPTE is a more potent and efficacious agonist of ER
- VM7 cells (formerly BG1) transfected with CYPencoding mRNA or B-gal control for 6 hours (384w)
- Exposed to MXC (10nM 5µM) for 24 hours
- Activity normalized to maximal E2-induced activity (parallel wells on same plate)
- A minimal ER response was seen in cells transfected with B-gal or CYP3A4 mRNA
- A pronounced ER response was observed in cells transfected with CYP2A6 or CYP2C19



Beginning to Address Concerns for Increased Biological Coverage

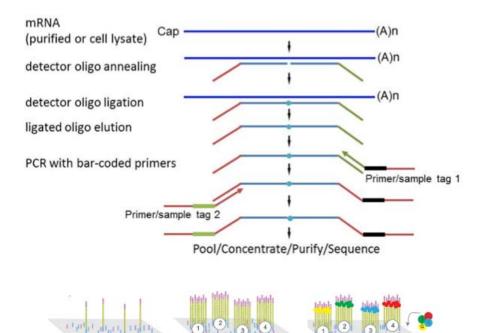




BioSpyder TempO-Seq

- Targeted RNA-Seq technology
- Whole transcriptome assay provides output on > 20,000 transcripts.
- Requires very low input (< 10 pg total RNA).
- Performed on "standard" PCR and Next Gen Sequencers.
- Compatible with purified RNA or cell lysates.

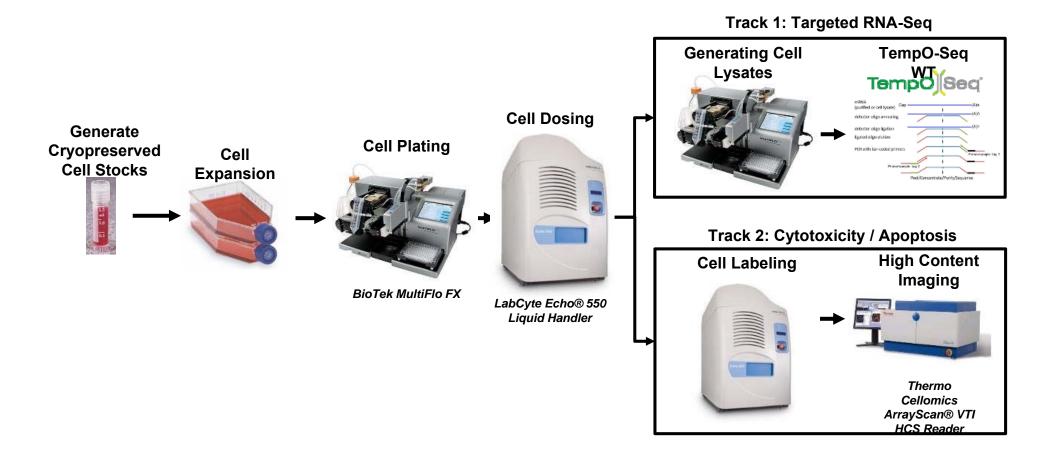




www.biospyder.com



HTTr Pilot: Workflow



Josh Harrill/NCCT

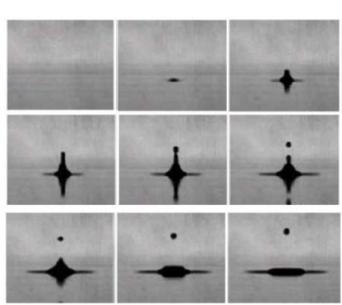


Acoustic dispensing technology:

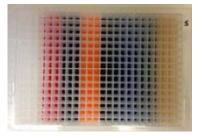
- Uses soundwaves to precisely transfer small quantities of liquid (nL) from source plate to test plate.
- Allows for randomization of test wells → mitigate potential edge effects without "losing real estate."



LabCyte Echo® 550 Liquid Handler



Source Plate



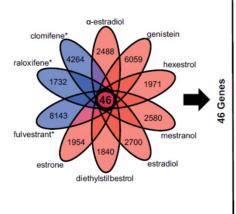
Test Plate

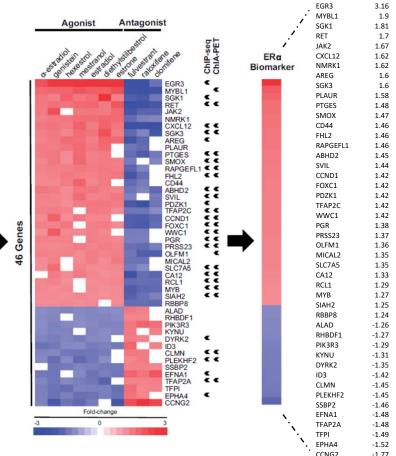




$\text{ER}\alpha$ Biomarker Signature

- Biomarker signature determined by consensus DEGs in MCF7 cells with various ERα agonists and antagonists.
- Can we use this to detect biologically meaningful signal in the BioSpyder data?



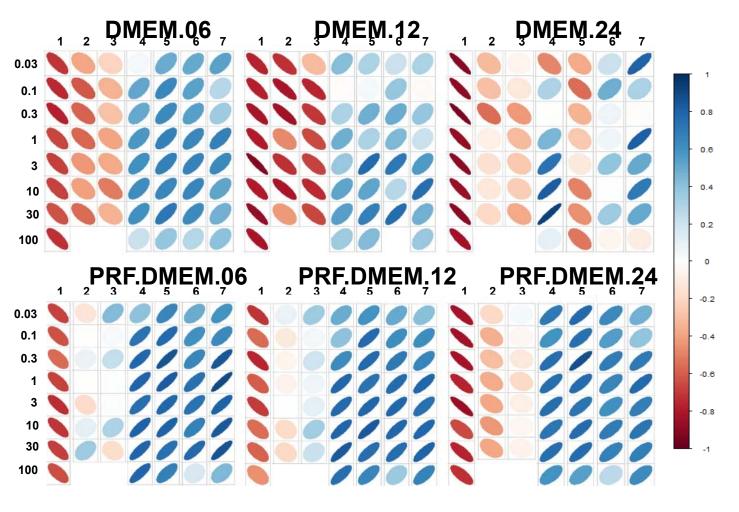


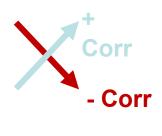
Ryan et al., 2016. Toxicol Sci. 2016 May;151(1):88-103.



Correlation with ERα Transcriptional Biomarker

	Chemical	MOA			
1	Fulvestrant	Antiestrogen (SERD)			
2	4- Hydroxytamoxife n	Antiestrogen (SERM)			
3	Clomiphene Citrate				
4	Bisphenol A				
5	Bisphenol B				
6	4-Nonylphenol, branched	Estrogenic			
7	4-Cumylphenol	1			







Pathway Enrichment

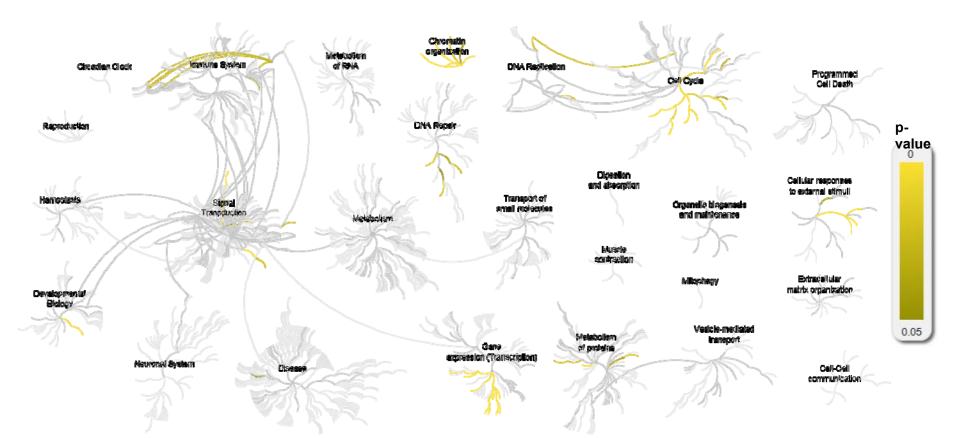
Numbers of Pathways Enriched

Chemical Name	MSigDB_C2	MSigDB_H	Reactome	Chemical Name	MSigDB_C2	MSigDB_H	Reactome
Ziram	1268	26	314	Propiconazole	20	1	2
4-Hydroxytamoxifen	1068	14	331	3,5,3'-Triiodothyronine	18	0	1
Cycloheximide	570	24	126	Fenofibrate	17	0	1
4-Nonylphenol, branched	533	7	127	Cyanazine	16	0	1
Amiodarone hydrochloride	524	12	136	Flutamide	10	0	1
Reserpine	523	11	80	Fulvestrant	9	1	0
Maneb	248	3	75	Cypermethrin	7	0	1
Rotenone	215	5	22	Lovastatin	6	0	0
Thiram	204	5	64	Simvastatin	5	0	0
4-Cumylphenol	198	4	27	Butafenacil	3	0	0
Bisphenol B	185	2	31	Vinclozolin	2	0	0
Fenpyroximate (Z,E)	183	5	14	Tetrac	2	0	1
Cyproterone acetate	166	5	4	Lactofen	2	0	0
Prochloraz	113	2	10	Cyproconazole	0	0	0
Clomiphene Citrate	68	3	0	Clofibrate	0	0	0
Nilutamide	56	0	29	PFOS	0	0	0
Trifloxystrobin	47	1	2	Simazine	0	0	0
Cladribine	47	0	71	Fomesafen	0	0	0
Bisphenol A	45	1	5	Troglitazone	0	0	0
Imazalil	41	0	4	PFOA	0	0	0
Pyraclostrobin	37	0	1	Atrazine	0	0	0
Farglitazar	22	1	0	Bifenthrin	0	0	0

- Heterogeneity in the amount and type of pathways enriched.
- Changing filtering stringency and BMD modeling strategy affects these results.



Network Mapping [Clomiphene Citrate]



- Reactome (v60) Pathway Hierarchy → Overlaid with enrichment scores based on probes with acceptable BMD model fit
- Highlights different areas of biology affected by a chemical

National Center for Computational Toxicology Josh Harrill, NCCT, unpublished



Connectivity Mapping Demonstrates Multiple Pathway Matches

0.00

-0.25

-0.50

-0.75

⁰5 −1.00

-1.25

-1.50

-1.75

-2.00 -

-3

HRN

-2

 $^{-1}$

0

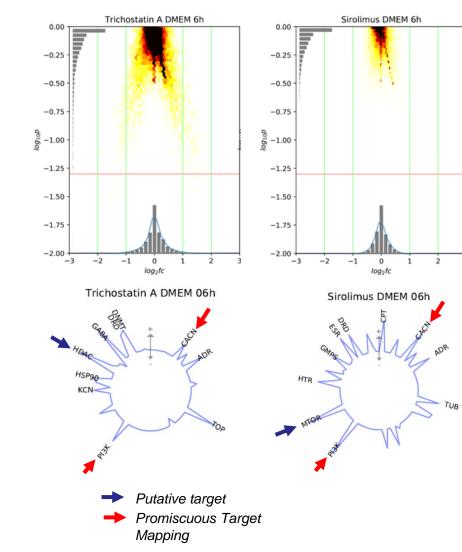
log₂fc

Genistein DMEM 06h

2

1

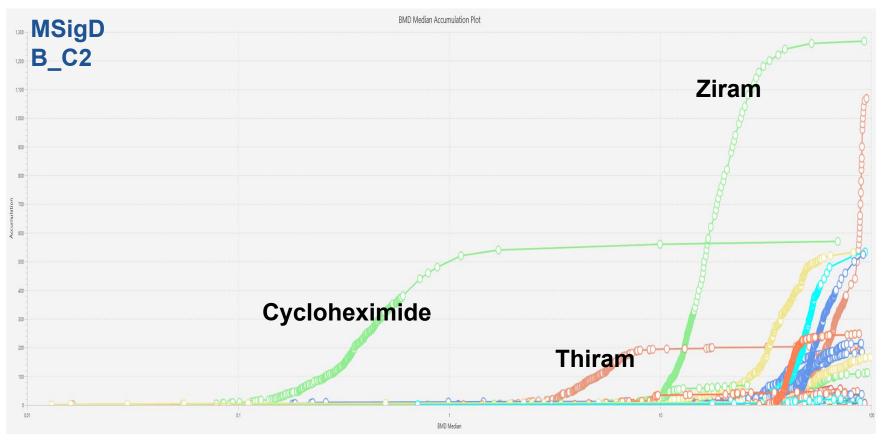
Genistein DMEM 6h



National Center for Computational Toxicology Imran Shah, NCCT, unpublished

- Differential gene expression observed with reference chemicals
- Putative targets identified using Connectivity Mapping
- Large degree of promiscuity of predicted targets observed
- Currently evaluating additional methods for MIE prediction





• Broad range of pathway level potency estimates and number of pathways affected across chemicals.



Cell Painting Phenotypic Screen Background

- Cell Painting (Bray et al., 2016, *Nature Protocols*): A cell morphology-based phenotypic profiling assay multiplexing six fluorescent "non-antibody" labels, imaged in five channels, to evaluate multiple cellular compartments and organelles.
- Key Features:
 - Non-targeted screening (i.e. target agnostic)
 - Tractable across different adherent cell lines
 - High content 100s 1000s of features measured at the cell level
 - Concentration-response analysis
 - Fingerprinting and clustering

Marker	Cellular	Lobaling Chamiatry	Labeling	Opera Phenix		
Warker	Component Labeling Chemistry		Phase	Excitation	Emission	
Hoechst 33342	Nucleus	Bisbenzamide probe that binds to dsDNA		405	480	
Concanavalin A – AlexaFluor 488	Endoplasmic reticulum	Lectin that selectively binds to α-mannopyranosyl and α-glucopyranosyl residues enriched in rough endoplasmic reticulum		435	550	
SYTO 14 nucleic acid stain	Nucleoli	Cyanine probe that binds to ssRNA	Fixed	435	550	
Wheat germ agglutinin (WGA) – AlexaFluor 555	Golgi Apparatus and Plasma Membrane	Lectin that selectively binds to sialic acid and N- acetylglucosaminyl residues enriched in the trans-Golgi network and plasma membrane		570	630	
Phalloidin – AlexaFluor 568	F-actin (cytoskeleton)	Phallotoxin (bicyclic heptapeptide) that binds filamentous actin				
MitoTracker Deep Red	Mitochondria	Accumulates in active mitochondria	Live	650	760	



Experimental Objectives & Design

Objectives:

- Replicate phenotypes observed by BROAD group (Gustaffdottir, Bray)
- Compare sensitivity across cell models.
- Identify reference chemicals for use as assay controls in screening applications.
- U-2 OS / MCF7
- 384-well plate
- 16 chemicals, 7 concentrations
- 3 technical replicates / plate
- 3 biological replicates

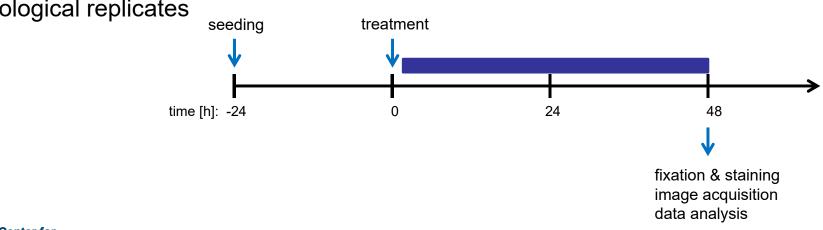


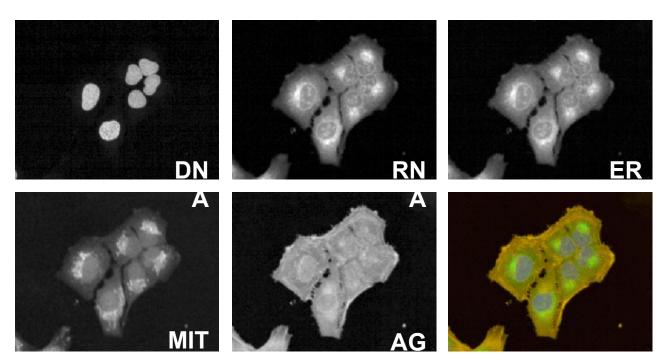


Image Acquisition

Image Acquisition

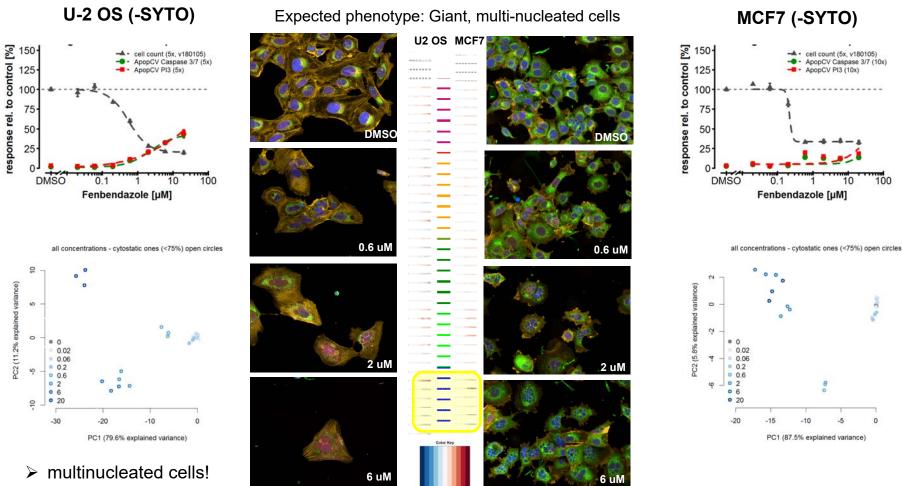
- Perkin Elmer Opera Phenix
- 20x Water Immersion Objective
- Confocal Mode, Single Z
- CellCarrier-384 Ultra Microplates







Fenbendazole



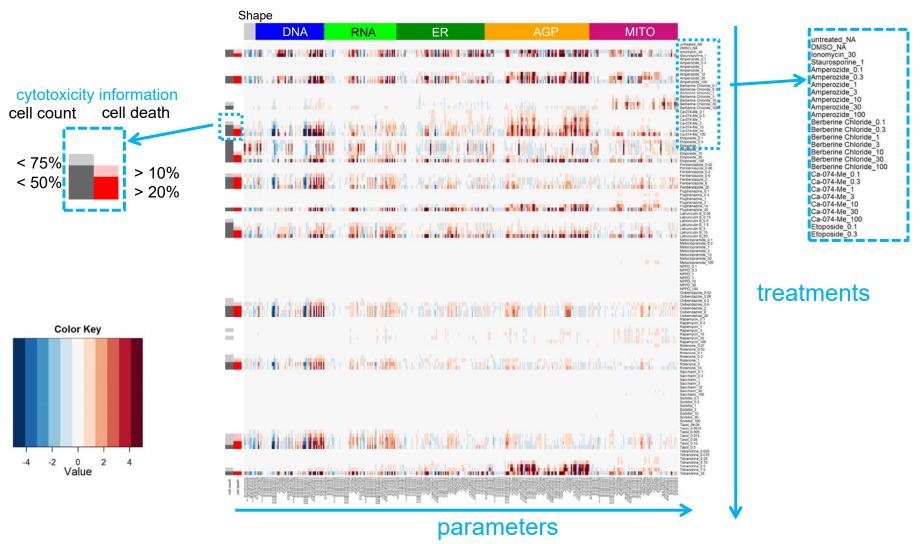
4 -2 0 2 4 Value

Josh Harrill, NCCT, unpublished

National Center for Computational Toxicology

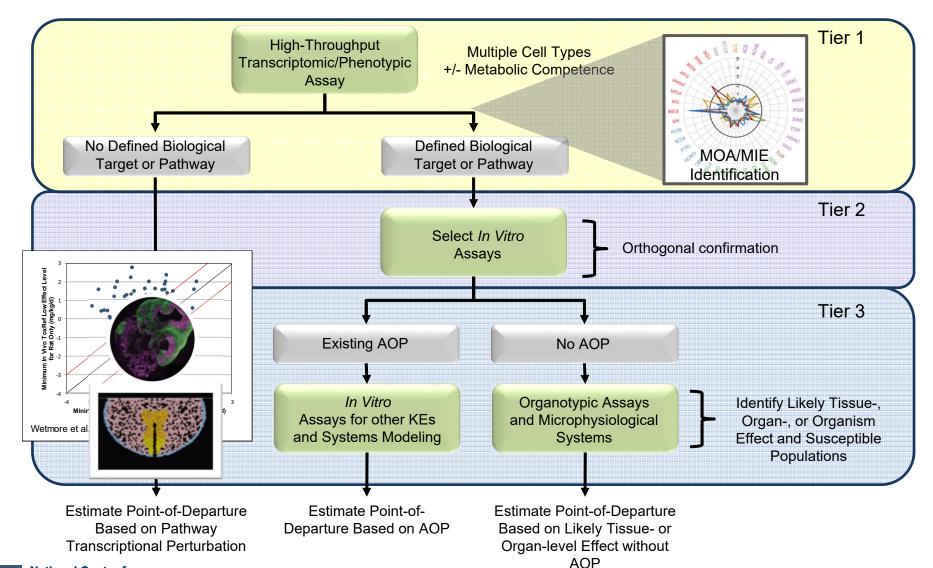


Results





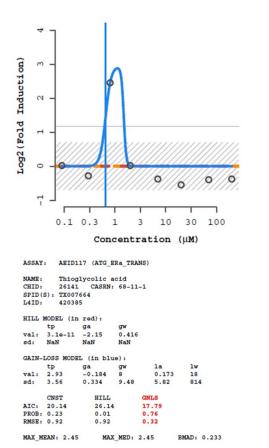
Framework for Integrating Hazard Components...



National Center for Computational Toxicology



Regulatory Applications Require More Focus on Quality and Transparency



COFF:	1.17	HIT-CALL:	1	FITC:	50	ACTP:	0.77	

FLAGS: Only one conc above baseline, active Borderline active

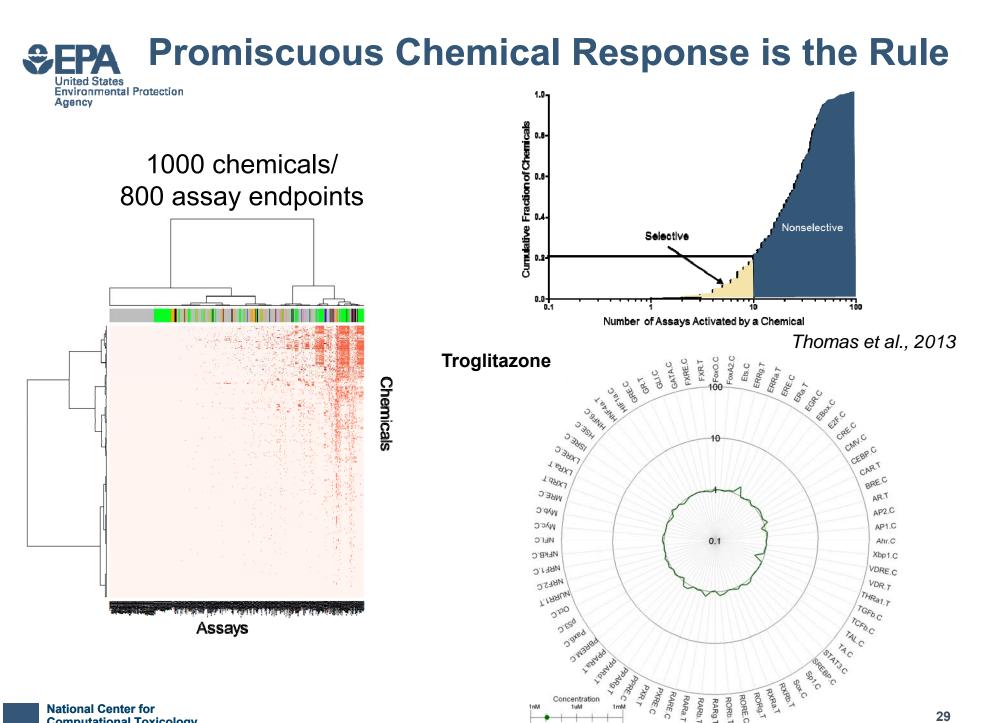
- Public release of Tox21 and ToxCast data on PubChem and EPA web site (raw and processed data)
- Publicly available ToxCast data analysis pipeline
 - Data quality flags to indicate concerns with chemical purity and identity, noisy data, and systematic assay errors
- Tox21 and ToxCast chemical libraries have undergone analytical QC and results publicly available
- Public posting of ToxCast procedures
 - Chemical Procurement and QC
 - Data Analysis
 - Assay Characteristics and Performance
- External audit on ToxCast data and data analysis pipeline
- Migrating ToxCast assay annotations to OECD 211 compliant format



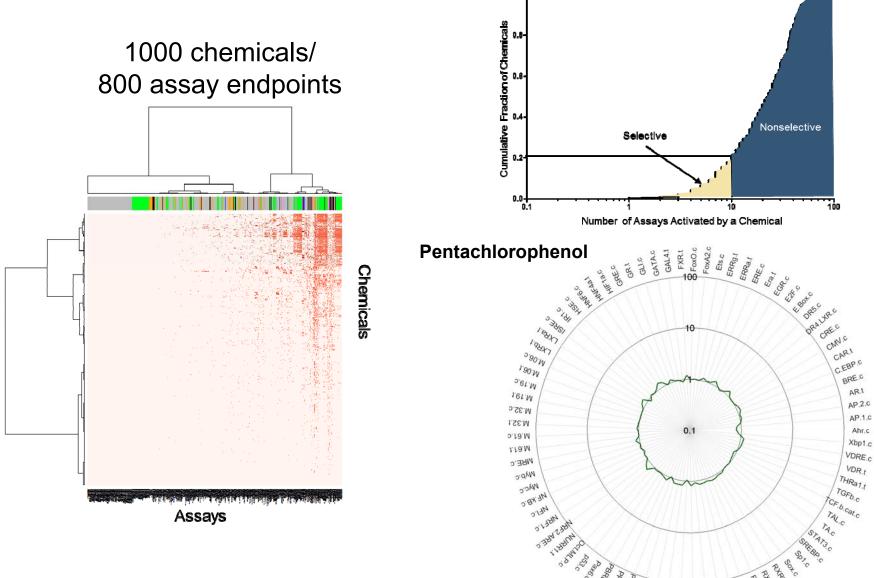
Effort to Provide Data Through Display and Decision Support Dashboards

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		retrois Properties					 Chemicals 	Dashboard: v2	Start Tutorial - Bioactivity Tab
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hhaara	L		25086-38-8	Eisphenol A/ Epichiorohydrin resin					
shboard	ג		25036-25-3	Bispherol A-bispherol A diglyoidyl ether polymer					
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						E NVS_NR_AR 10.0045	H NVS_NR_6ER 0.421	# Tex21_TH_LUC 59.7000	

EDSP21 Dashboard (https://actor.epa.gov/edsp1)







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RARb

PXR

PXR

"Rdy

Concentration

1uM

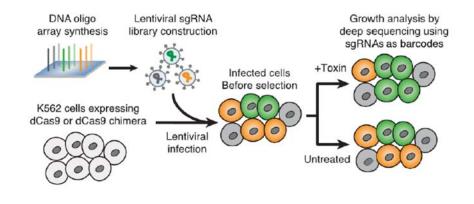


Functional genomics: Defining Relevancy

 Most chemicals have apparent polypharmacology—what is the critical/relevant MOA?

-Could use potency to define but this may not be linked to adversity

- -Transcriptomics is high content but function is generally inferred
- Functional genomics allows for bridging between genotype and phenotype
- Previously mostly used in prokaryotic systems such as S. cerevisiae
- Advent of CRISPR-Cas9 opens door for higher throughput applications in mammalian cells



Gilbert et al., Cell, 2014



Pilot Project

- Collaboration between University of Florida (Chris Vulpe) and USEPA (NCCT, Keith Houck)
- Funded by USEPA SMARTi award to Keith Houck and Audrey Bone
- Goal of the project is to test the feasibility of using CRISPR-Cas9 genome editing in human cells for screening environmental chemicals in a functional genomics toxicology format





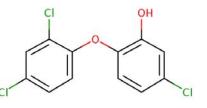
Chemical Selection

- Criteria
 - Mix of uses (pharmaceutical, pesticide, consumer, industrial)
 - -Well-characterized mechanisms of cytotoxicity
 - Mitochondrial toxicity
 - DNA damage
 - Oxidative stress
 - Microtubule disruption
 - Proteosome inhibition
 - Known cytotoxic in Tox21/ToxCast assays without metabolic activation

11 chemicals



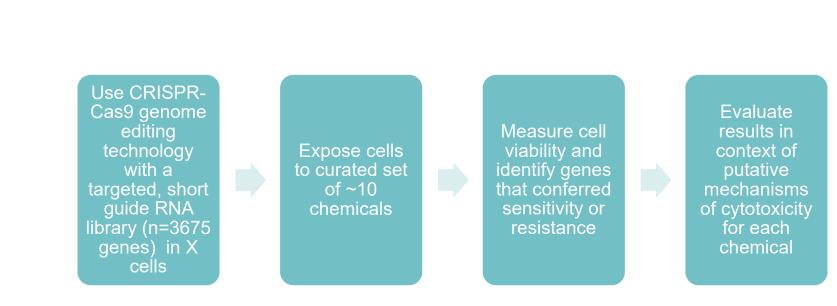
- -Triphenyltin chloride
- -Triglycidyl isocyanurate
- -Cytembena
- -Propargite
- -Octhilinone
- -Triclosan
- -Tralopyril
- -Dibutyltin dichloride
- -Malachite green
- Bisphenol A glycidyl methacrylate



Triclosan



Experimental Design





Ideas for ToxCast Assays for Prioritization of Carcinogens

Current

- Assays selected by commercial availability
- Broad bioactivity to cover all types of toxicity
- -Challenges
 - Chronic exposures
 - Many diseases
 - Epigenetic events
 - Evolutionary development/stochastic genetic effects key



CarciCast

- -Focus on key characteristics
- Best-in-class existing assays
- –Development may benefit from:
 - genome editing tools
 - complex/organotypic cell models
 - phenotypic screening

Thank You for Your Attention!

• EPA:

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IΠ

36

- Imran Shah
- Joshua Harrill
- Woody Setzer
- Richard Judson
- Rusty Thomas

EPA:

•

- Steve Simmons
- Danica DeGroot
- Johanna Nyffeler
- Stacie Flood
 - (ORAU)

• U of Florida:

- Chris Vulpe
- Abderrahmane Tagmount

NY STR. ATT.