



NIEHS National Toxicology Program Tox21 Update

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ICCVAM Public Forum NIH Natcher Conference Room Center, Room D Bethesda, MD



25 May 2016



Tox21 Phase II – Expanded Screening



(2011 – Present)

Tox21 qHTS Phase II:

- 10K compound library (8,948 unique; 13,129 unique solution IDs), ~ 3,000 each from EPA, NTP, NCATS (drugs)
- Screened 3 times at 15 concentrations in each "quantitative High Throughput Screen" (**qHTS**) assay
- qHTS assays (~ 60 assays) focused on:
 - Nuclear receptor activation or inhibition
 - Cellular stress response pathways and cytotoxicity





Multiple workshops, webinars, meeting presentations, reports, publications, and websites for distribution of information rapidly and transparently to stakeholders

Data Released to Public as Rapidly as Possible

- via EPA Safer Chemicals Research website <u>https://www.epa.gov/chemical-research/research-evaluating-</u> <u>chemicals-adverse-effects</u>
- via PubChem (<u>http://pubchem.ncbi.nlm.nih.gov/</u>)
- via Tox21 Toolbox (http://ntp.niehs.nih.gov/results/hts/tbox/)
- via Tox21 Data Browser (<u>https://tripod.nih.gov/tox21/index</u>)

Transparent Data Processing and Analysis Pipeline

• Pay Attention to Warning Flags – Compounds & Calls

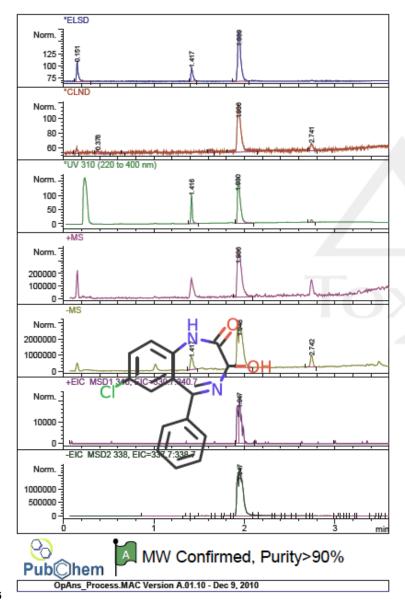


Quality Control of Tox21 Compounds



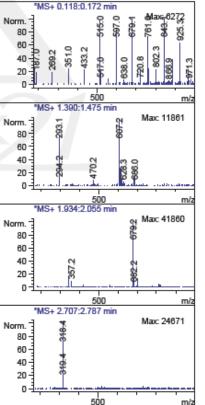
ID Tox21_400050 Plate Batch4-SP112429 Well P1-P-24 File SP112429-P24.D Inj Date: 26 Nov 13 2:54 pm

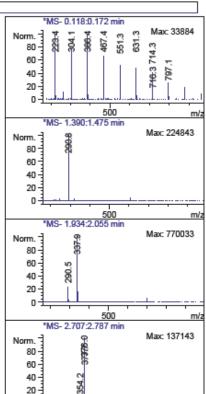
MF C14H13NO7S MW 339.0 Expected Conc: 3.00 mM



RT	Found	BLS %	UV %	BLS [mg/mL]	Adj [BLS]	[N mM]	Adj [CLN]	#N
0.15		16.2	0.0	0.21		0.11 mM		1.0
0.38		0.0	0.0			0.19 mM		1.0
0.65		0.0	0.0			0.01 mM		1.0
1.42		12.5	23.1	0.17				1.0
1.62		0.0	0.0			0.09 mM		1.0
1.92		0.0	0.0					1.0
1.93	Yes	71.3	74.9	0.85	2.52 mM	2.58 mM	2.58 mM	1.0
2.74		0.0	2.0			0.27 mM		1.0

Comment: Failed-Purity





500

0-



Tox21 Data Browser



1	A	4504
1	в	64
	ND	18
		5
	C	2
	D	0



4568 «	1 2 3	4 5 6 7	456 457 »	-
Structure	Tox21 ID	Name	QC Grade T0	QC Grade T4
ua~	Tox21_111726	Alclofenac	MW Confirmed, Purity > 90%	MW Confirmed, Purity > 90%
HO R CH	Tox21_201930	Acetaminophen	MW Confirmed, Purity > 90%	MW Confirmed, Purity > 90%
Tox21_200830		2-Acetylaminofluorene	MW Confirmed, Purity > 90%	MW Confirmed, Purity > 90%
ncfoffen	Tox21_200653	3-Amino-4- ethoxyacetanilide	MW Confirmed, Purity > 90%	MW Confirmed, Purity > 90%
H2-1-0	Tox21_200069	1-Acetyl-2- phenylhydrazine	MW Confirmed, Purity > 90%	MW Confirmed, Purity > 90%







- Increased use of computational models to predict toxicity and metabolism.
- Increased focus on human cells with known ability to metabolize chemicals
- Increased focus on genetic variation to understand susceptibilities - Toxicogenetics
- Increased use of stem cells (both embryonic and iPS) to investigate the effects of chemicals on developmental processes
- Enhanced testing of compounds in lower organisms (e.g. zebrafish, *C. elegans*)
- Expand our understanding of biology by developing and implementing a high throughput and low cost approach to measure the entire transcriptome – HT-Transcriptomics





Improving on Biological Coverage and Human Relevance



• Increased use of computational models to predict toxicity and metabolism.

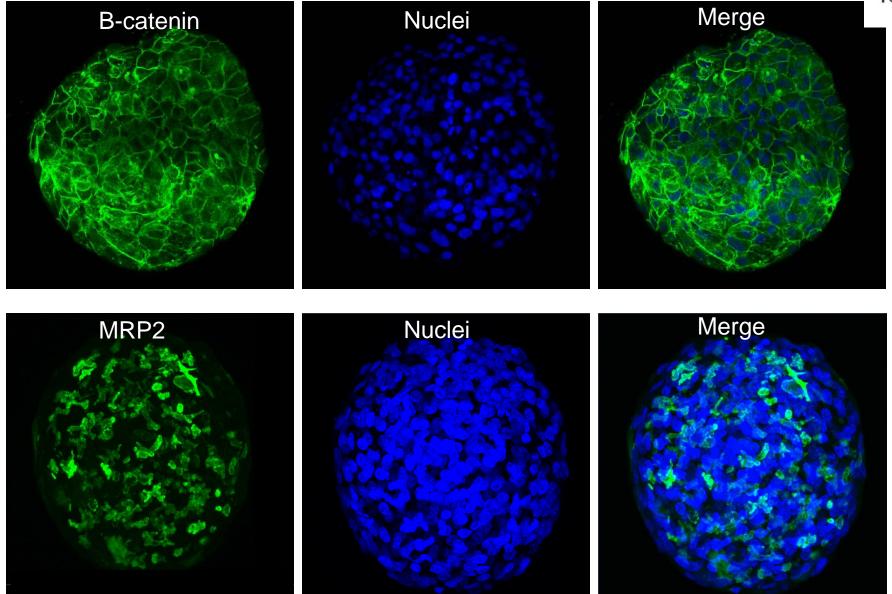
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Human HepaRG Polarized Spheroids





Sreenivasa Ramaiahgari and Steve Ferguson, NTP 100 um





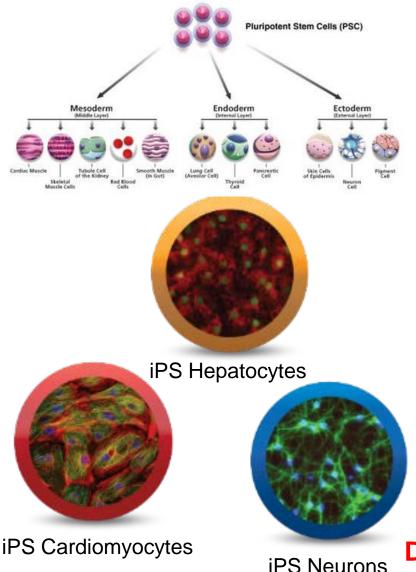


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Improving on Biological Coverage and Human Relevance



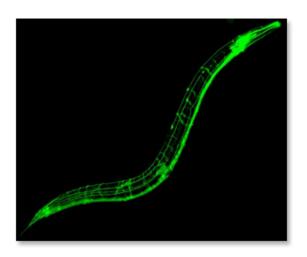
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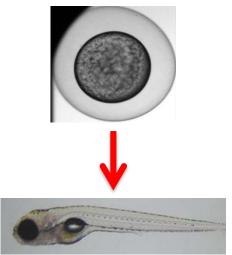
Distribute sets of reference compounds₁₀

Paules_2016









5 days

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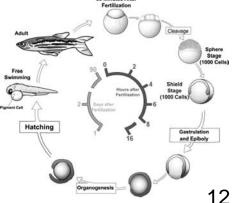
NTP Evaluation of Zebrafish for Tox21



SEAZIT – Systematic Evaluation of the Application of Zebrafish in Toxicology

- A multipronged, multi-year program for the systematic evaluation of the application of zebrafish in toxicology (SEAZIT) studies by the DNTP.
- Aims:
 - to provide the scientific basis on which to make a programmatic decision on the further use of zebrafish in toxicological screening of chemicals to which humans are exposed during development and into adulthood.
 - provide fundamental knowledge on the use of zebrafish in toxicology, which will support further research endeavors by the academic community.



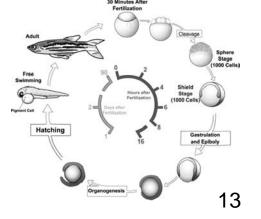


Contact: Nigel Walker, NIEHS/DNTP

SEAZIT – Systematic Evaluation of the Application of Zebrafish in Toxicology

NTP Evaluation of Zebrafish for Tox21

- Aims (cont.):
 - Determine the influence of various protocol parameters on distribution within the zebrafish during development and into adulthood.
 - Assess the developmental origins of health and disease in zebrafish.
 - Determine optimal methods for evaluating zebrafish data to link it to phenotypic outcomes in mammals.

















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The Assumption:

 Global "Omic" (Whole System) approaches can link perturbations with alterations in biological processes that result in toxicity and / or disease.

The Hypothesis:

- Alterations in the **transcriptome** following exposures can provide:
 - linkage between chemical exposures and adverse biological outcomes (signatures/biomarkers),
 - linkage between *in vitro* and *in vivo* model systems, and
 - linkage between *in vitro* models & human pathobiology





The Ideal Solution:

A rapid and low-cost High Throughput (HT) method to measure expression levels of ALL GENES

The Reality:

- At this time, whole transcriptome technologies are prohibitively expensive for HT applications.
 - Target cost of \$25 \$50 per sample.
- It will be necessary to focus on a **subset of genes** to use in a rapid, low-cost technology suitable for HT studies.





- **1. Diversity:** Capture the maximal expression variability and dynamics.
- **2. Co-Expression:** Capture the **Sentinel** genes with maximal coexpression information to represent members of nodes or networks.
- Maximal Pathway Coverage: Genes are included to ensure maximal biological pathway coverage.
 1500 Sentinel Genes Bioinformatically Selected – S1500
- 4. Inclusion of toxicity and disease related genes: Specific genes will be selected for their reported roles in toxicity-related and disease-related processes. Also include L1000 gene set from LINCS program.
- 5. "Extrapolatability": This property refers to the ability to extrapolate or infer or impute with some accuracy the expression changes in all genes from those observed in this reduced set of sentinel genes.





Develop Approach & Train on Rat Data Sets – Complete

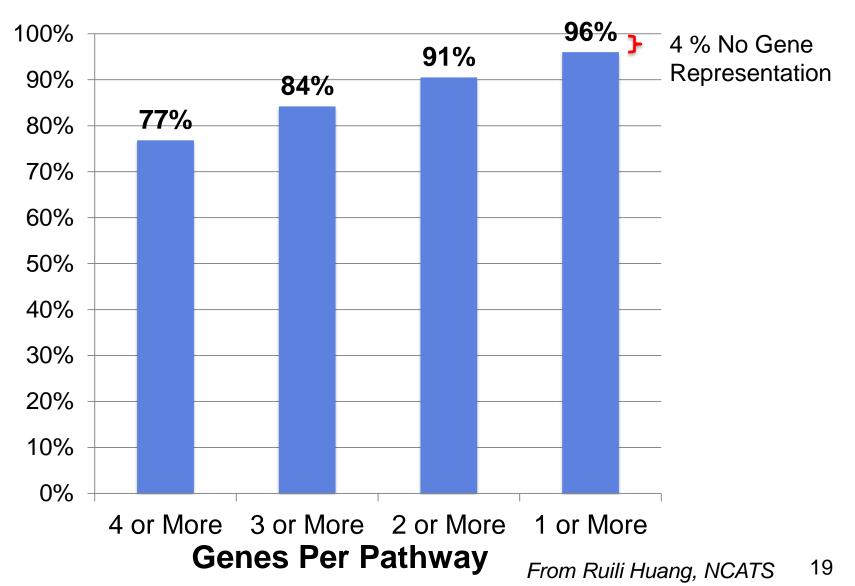
 Pathway Concordance between Extrapolated & Measured Data ~ 0.9

Generate Human "S1500+" Gene Set –

- Affymetrix microarray human data sets (HG-U133plus2) were downloaded from GEO and 3339 series were manually curated.
- Human gene expression data sets that passed curation were subjected to our hybrid bioinformatic gene selection process
- 1500 gene set identified bioinformatically in a strictly data-driven approach
- Additional genes were added from knowledge-based, nominated gene lists for a total of 2871 genes
- Human S1500+ Gene Set was released for public comment: <u>http://ntp.niehs.nih.gov/results/hts/s1500-gene-set/index.html</u>

Human S1500+ Evaluation - NCATS BioPlanet

• Hosts the universe of public, curated human pathways (2314 Pathways)



Where Are We Going with HT Transcriptomics?

Short Term

Application to Cell Systems used in Tox21 Phase II Assays with a subset of the 10k set of chemicals Application to Metabolically-Competent Human Cells (e.g. primary hepatocytes, 3D HepaRG spheroids, organoids) Application to Human iPS cells undifferentiated and induced to differentiate along specific lineages

Mid Term

Application to other species (rat, mouse, zebrafish, etc.) Application to NTP archived material from rat and mouse studies

Longer Term

Application of HT Transcriptomics to Human samples from molecular epidemiological studies and clinical studies





Biomolecular Screening Branch

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