

Loo Lit Hsin Senior Principal Investigator









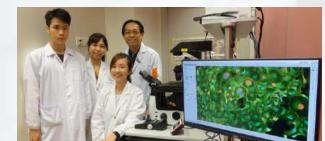




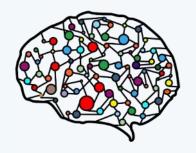
Complex Cellular Phenotype Analysis Group, BII



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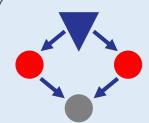






Phenotypic profiling and computational modeling

- Chemical/drug safety or efficacy assessments
- High-throughput Image-based Phenotypic Profiling
- Machine learning, data analysis, and assay automation



ToxMAD

Toxicity Mode-of-Action Discovery Platform

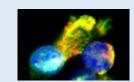
Assess chemical safety based on mechanistic reasoning

Bioimage Databases



Big bioimage data management, visualization, standardization, and analytics

Digital Medicine for Cancer



Data-driven cancer treatment and care

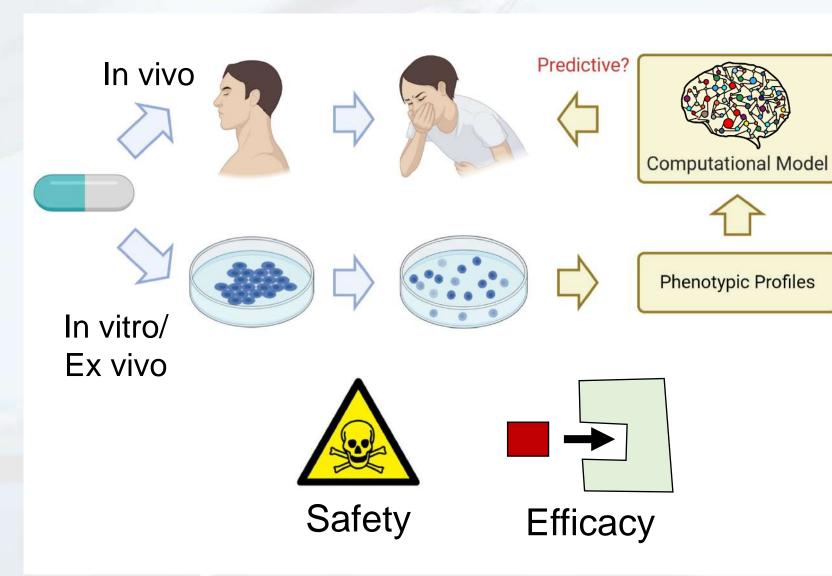




Building Predictive In vitro or Ex vivo Models for Chemical/Drug Safety or Efficacy Assessments







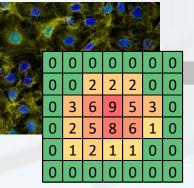




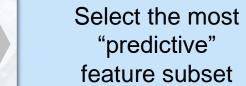
High-throughput Image-based Phenotypic Profiling (HIPP)



@



Measure **large** numbers of phenotypic features based on **general markers**





Build and evaluate computational models

Conceptually similar to "RNA expression profiling"

	Phenotypic Profiling	High-Content Analysis (HCA)
Number of measured phenotypic features	Very Large (~100s-1000s)	Small (<10)
How are the features designed and selected?	Automatically based on machine-learning algorithms	Manually based on known or expected mechanisms
What stains/markers are used?	General cell structures or biological processes	Specific structures or biological processes
Modes of action need to be defined a priori?	No	Yes
Can discover novel MoAs?	Yes	No





Proximal tubule cells exhibit distinct phenotypes when exposed to different chemicals

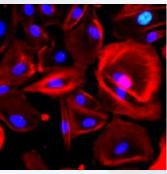






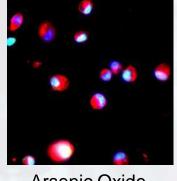
Non-PTC-Toxic reference chemicals

PTC-Toxic reference chemicals



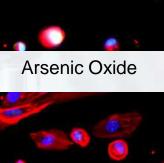


Water

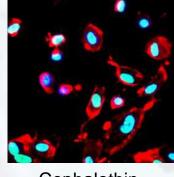




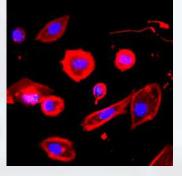




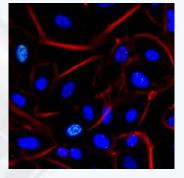
Tetracycline



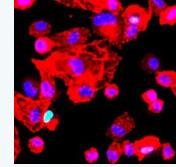
Cephalothin



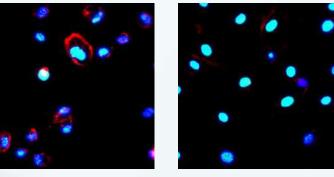
Bismuth Oxide



Paraquat



Potassium Dichromate



Cadmium Chloride **Gold Chloride**

Human PTCs were treated with 44 reference chemicals and stained with DNA, Actin, RelA/gH2AX

In collaboration with Dani Zink, SIFBI





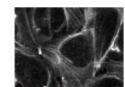
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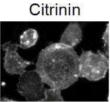


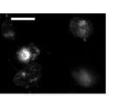
We performed phenotypic profiling ... 129 features

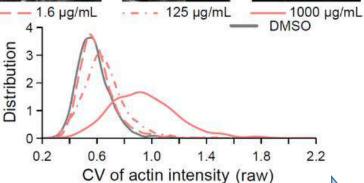


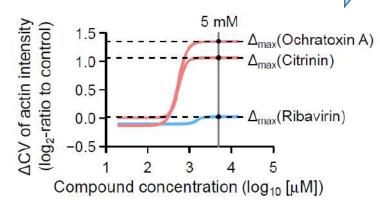


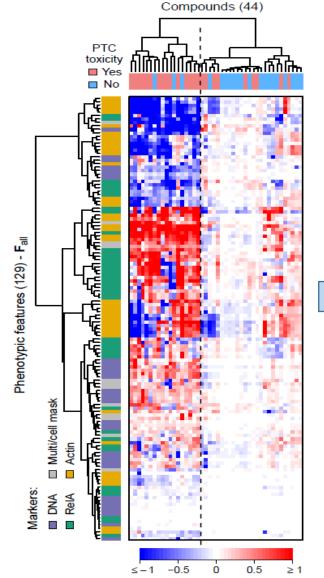






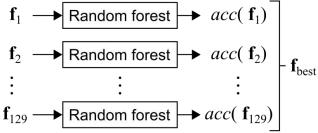


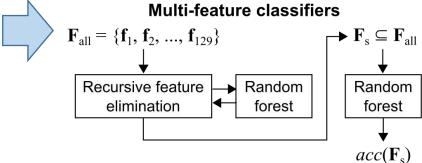




 Δ_{max} (log₂-ratio to control)

Single-feature classifiers





5 features based on DNA, actin, and γH2AX in HK-2 (89% accuracy)



[Su et al., Arch Tox, 2016]















Ran Su is now an Associate Professor at Tianjin University, China



In 2016, Drs. Loo and Zink have become the first from Asia to win the Lush Prize (Science Award), UK





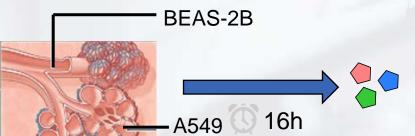








Building Lung Toxicity Model Using Phenotypic Profiling



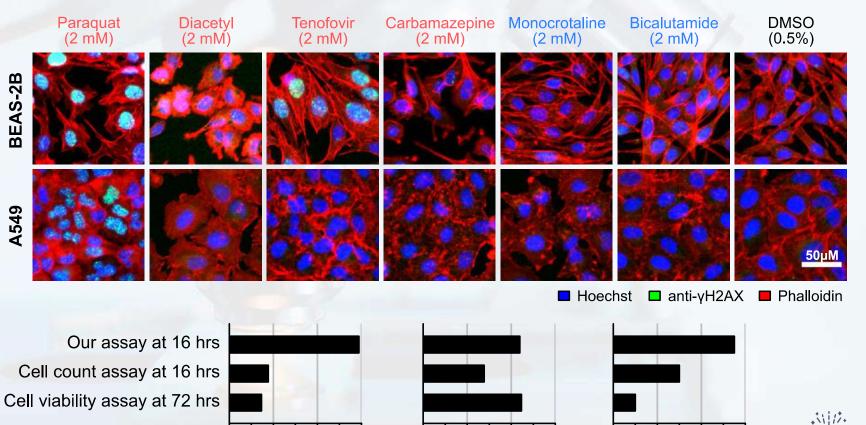
70

80

Balanced accuracy (%)

90

HIPPTox lung assays are more accurate and specific than standard cell count or viability assays



60

80

Sensitivity (%)

100



Joey Lee



80 100

60

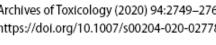
Specificity (%)

[Lee et al., Arch Tox, 2018]









IN VITRO SYSTEMS



Predicting direct hepatocyte toxicity in humans by combining high-throughput imaging of HepaRG cells and machine learning-based phenotypic profiling

Faezah Hussain¹ · Sreetama Basu² · Javen Jun Hao Heng¹ · Lit-Hsin Loo^{2,3} · Daniele Zink¹

Received: 12 November 2019 / Accepted: 5 May 2020 / Published online: 12 June 2020 © Springer-Verlag GmbH Germany, part of Springer Nature 2020

Abstract

Accurate prediction of drug- and chemical-induced hepatotoxicity remains to be a problem for pharmaceutical companies as well as other industries and regulators. The goal of the current study was to develop an in vitro/in silico method for the rapid and accurate prediction of drug- and chemical-induced hepatocyte injury in humans. HepaRG cells were employed for highthroughput imaging in combination with phenotypic profiling. A reference set of 69 drugs and chemicals was screened at a range of 7 concentrations, and the cellular response values were used for training a supervised classifier and for determining assay performance by using tenfold cross-validation. The results showed that the best performing phenotypic features were related to nuclear translocation of RELA (RELA proto-oncogene, NF-kB subunit; also known as NF-kappa B p65), DNA organization, and the F-actin cytoskeleton. Using a subset of 30 phenotypic features, direct hepatocyte toxicity in humans could be predicted with a test sensitivity, specificity and balanced accuracy of 73%, 92%, and 83%, respectively. The method was applied to another set of 26 drugs and chemicals with unclear annotation and their hepatocyte toxicity in humans was predicted. The results also revealed that the identified discriminative phenotypic changes were related to cell death and cellular senescence. Whereas cell death-related endpoints are widely applied in in vitro toxicology, cellular senescence-related endpoints are not, although cellular senescence can be induced by various drugs and other small molecule compounds and plays an important role in liver injury and disease. These findings show how phenotypic profiling can reveal unexpected chemical-induced mechanisms in toxicology.



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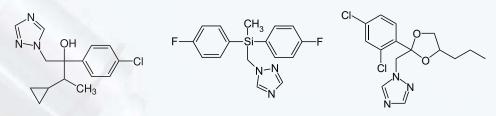


Example of how our models were used to assess fungicides









Cyproconazole

Flusilazole

Propiconazole

What are their relative bioactivities?





To validate our model, we also add in 3 negative controls: azole drugs known to have <u>low</u> kidney effects



[van der Ven et al., Chem Res Tox, 2020]

Ketoconazole

Voriconazole

Fluconazole



*

(4)



Our ranking of the chemicals agrees with predictions based on other toxicological endpoints made by RIVM



National Institute for Public Health and the Environment Ministry of Health, Welfare and Sport

Table 4. Potency Comparison^a

Toxicological domain	Prediction Models (n)	Targeted endpoints in prediction models	Flu	Pro	Сур	Ref
Cell functions	4	Dynamic cell state, mitochondrial function, metabolism, transporter functions	+	±	±	26-28
Endocrine perturbation, Mode of action screening	5	Endocrine profiling, nuclear receptors, G-protein-coupled receptors (aminergic/other)	±	±	±	26, 29
Endocrine perturbation, specific	8	Estrogen signalling pathway, estrogen receptor interaction, androgen receptor interaction, aromatase inhibition, steroidogenesis, thyroid hormone synthesis	++	+	+	30-37
Metabolic disorder	7	Glucose metabolism, adipocyte function, feeding behaviour	+	+	±	38, 39
Developmental toxicity	8	Developmental toxicity in rats, rabbits, zebrafish, C.elegans; vascular development	++	++	+	40-46
(Developmental) Neurotoxicity	6	Ion channel, transporters, enzymes, neuronal network activity, neurobehavior	+	+	±	26, 47 - 49
Hepatotoxicity	2	Hypertrophy, liver injury, proliferative lesions, oxidative stress	+++	++	+	50, 51
Nephrotoxicity	1	Renal proximal tubular cell toxicity	+++	+++	+	17
Genotoxicity	5	DNA damage, gene mutations, chromosomal aberrations, p53 activation and oxidative stress	-	-	-	9-11, 14, 15, 19, 20, 52, 53
Carcinogenicity	2	Nuclear receptor activity, cancer hazard prioritization (hallmark genes)	+	++	+	54, 55
LOAEL embryotoxicity			10	35	20	
LOAEL hepatotoxicity			2.4	121	25.3	
LOAEL carcinogenicity			384	108	13.2	
Acceptable Daily Intake (ADI)			0.007	0.07	0.02	







International case study on the use of in vitro bioactivity in risk-based chemical prioritization

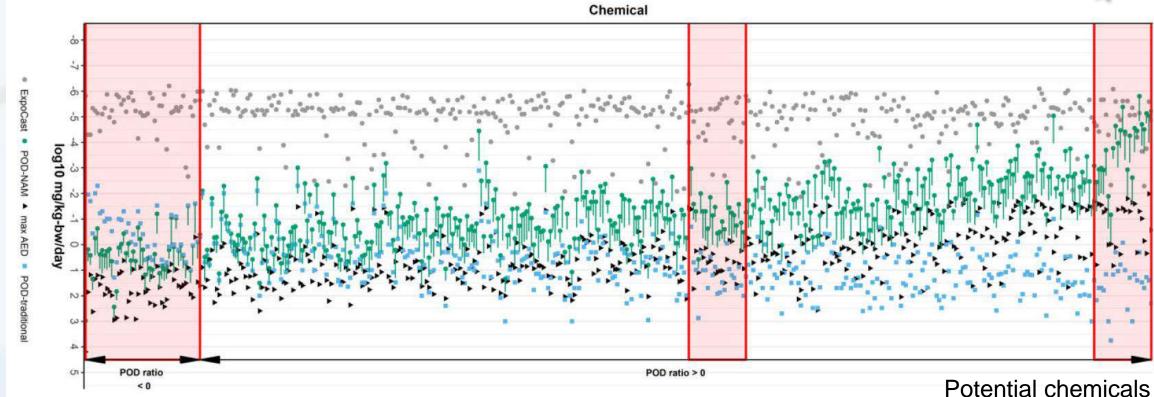


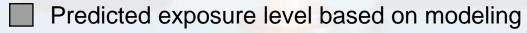
[Paul-Friedman et al., Tox Sci, 2020]

SOT Paper of the Year Award (Honorable Mention), 2020









PODs based on NAMs (ToxCast + HIPPTox)

PODs based on traditional animal models











of concern













Current safety assessments

Phenotypic endpoints



Future safety assessments

Mechanistic reasoning



ToxMAD is based on various A*STAR-developed in vitro and in silico technologies, and aim to rapidly and efficiently identify MoAs of chemicals (especially key molecular initiating events and cellular events leading to adverse outcomes)

Molecular initiating events

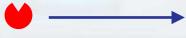
Key molecular/cellular events







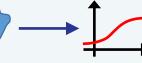












Sequence analysis

profiling

Metabolite 3D structure modeling

Virtual docking Chemogenomic profiling

profiling

Proteomic Transcriptomic profiling

Phenotypic profiling

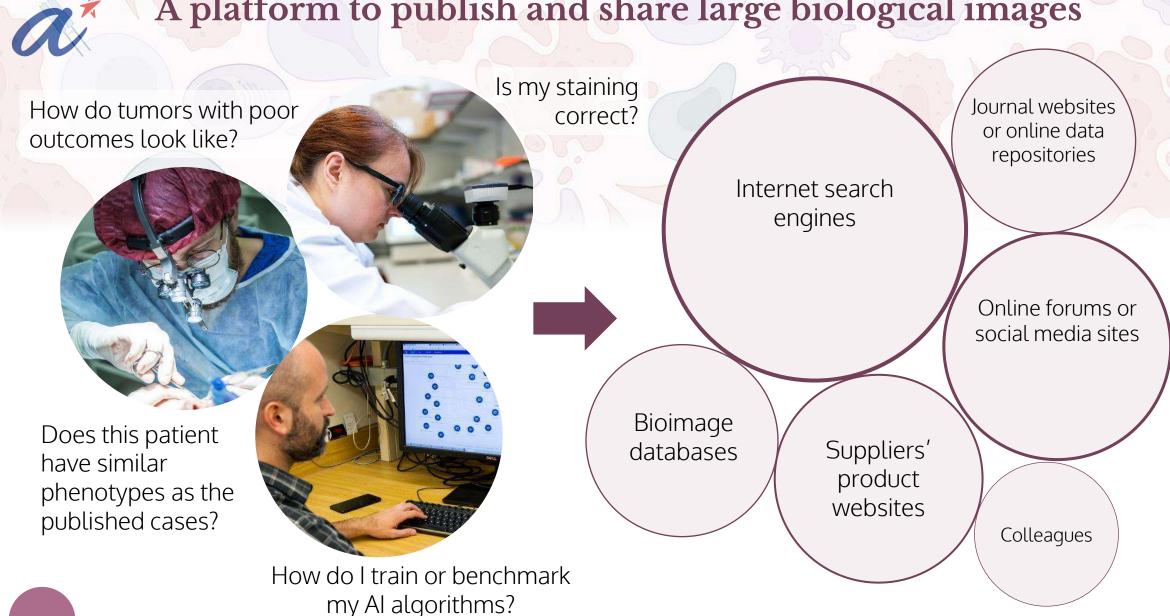
Immunophenotyping







A platform to publish and share large biological images













Standard or reference images of clinically-relevant immunofluorescence or immunotherapy markers (Users include researchers, pathologists, standard workgroup, and companies)

Reference and validate Interact and collaborate

Publish and share View and annotate





Institute of Molecular and Cell Biology



Singapore General Hospital

SingHealth

Immuno Atlas

Bioimage publishing and sharing portal (2021)

HistoPath Analytics (HPA) Platform

Online tissue image management and analysis platform (2019-2021)

cellXpress 2.0

Image processing engine in C++ (2011-2021)













CREATING GROWTH, ENHANCING LIVES



■ Samples collected for the case:

