

Coordinated by: InSphero

4-organ ADME/Tox chip TISSUSE

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4-organ chip (intestine, liver, neuronal, and kidney) build-up and blood flow simulation

Organ	Human Data*		Chip Data	
	Blood flow in L/min (L/min)	Ratio of blood flow in %	Simulation Proportion in %	Theoretical volumetric flow in $\mu\text{L}/\text{min}^{**}$
Portal system: Pancreas/intestine	64.3 (1.07)	35.3	35	10.6
Liver	82.0 (1.37)	45.2	45	13.6
through portal vein	~64.3 (1.07)	35.3	35	10.6
through hepatic artery	~17.7 (0.30)	9.9	10	3
Kidney	61.1 (1.02)	33.7	34	10.3
X	38.6 (0.64)	21.1	21	6.4
Total (arterial blood)	181.7 (3.03)	100	100	30.3

14 Days treatment with Haloperidol (3 μM)

Parent compound and metabolite profile. Distinct gene expression profiles.

Control D14 Haloperidol D14

Kidney Liver Neuronal Intestine

no signs of morphological changes

PgP inhibition

- Human ADME chip at 1:100,000 scale
- Accommodates gut, liver, neuro and kidney
- Metabolic competence to assess metabolite effects
- Barrier function (gut, kidney) stable over 14 days
- No signs of necrosis observed over 14-days culture
- Stable glucose, lactate and LDH values over 14d
- Increasing metabolite formation over time (HPP+)
- Only subtle effects observed upon HP-treatment

Reporter Zebra Fish Universiteit Leiden

Bjorn Koch Annemarie H. Meijer Hermann Spaank

Col2:mCherry reporter visualizes ceratohyal angle during craniofacial development

Hexanoic acid Conc. (μM)

0 250 500 1000

CS1 data, comparing effects of 13 compounds with chemical structures similar to valproic acid, and their relative potency in causing craniofacial developmental toxicity.

- Developmental toxicity cannot be investigated in simple cell culture assays, as it involves concurrent cell migration and differentiation processes
- The v-shaped ceratohyal cartilage around day 5-post fertilization is highly dynamic and therefore represents a sensitive readout for DART
- CS-1 compounds (VPA and analogues) could be sorted for their relative potency of inflicting developmental toxicity

Use of complex *in vitro* models for the study of complex drug-target and off-target interactions Universiteit Leiden

T. S. S. USE

- A full-liver model was established by combining PSC-derived parenchymal (Heps) and non-parenchymal (endothelial, macrophages, and stellate) cells, cultured in bioengineered hydrogel promoting hepatocyte differentiation
- After a 40-day differentiation process, liver typical morphology and function could be observed
- The model is suitable to induce a NASH like phenotype and to test anti-NASH drugs

- Steatosis affects >25% of worldwide population, but is mostly ignored in pre-clin. and clinical safety
- 3D liver models can be induced for steatosis, which affects lipid and xenobiotic metabolism on gene expression level and enzymatic activity
- The models allow compound testing for 7 days
- Steatosis shows altered sensitivity to classical DILI compounds, which partially could be explained by changes in CYP activity

Tissue-engineered iPSC-derived liver model Universiteit Leiden

Manoj Kumar Cath. Verfaillie

PSC-derived hepatocytes and NPCs are further differentiated and matured supported by engineered ECM scaffold and improved media.

iPSC-derived liver model KU LEUVEN

Tissue-engineered iPSC-derived liver models to simulate NASH for drug candidate testing

Modelling steatohepatitis/Fibrosis in HepMat

Oleic acid (OA) + Obeticholic acid (OCA) + Elafibranor (ELN)

Cell-type analysis reveals all major liver cell constituents, hepatocytes, endothelial cells, macrophages and mesenchymal cells

NASH-like phenotype could be partially reversed (fibrosis, inflammation) by Obeticholic acid and Elafibranor, both drugs currently under clinical investigation

Steatotic liver induction scheme sphero

aggregation resting induction induction reversion

Steato-DILI condition

Diseased liver model sphero

Monika Kijanska Agnieszka Pawlowska Wolfgang Moritz

Induction of steatotic phenotype upon lipid loading

Nile Red O staining, CO1 confocal imaging, MIP (lipids: red, nuclei: blue)

Lean, day 7 Diabetic/LDL, day 7

predominantly macrovesicular lipid droplets predominantly microvesicular phenotype

Altered gene expression profile relevant to drug metabolism

Up-regulated pathways: Extra-cellular matrices remodeling, Liver homeostasis and regeneration, Phase I metabolism (e.g. CYP3A5), Phase II metabolism (e.g. GSTA), Phase III metabolism (e.g. MRP2)

Down-regulated pathways: Lipid metabolism (Cholesterol, Steroids, Lipoprotein, Fatty acids), Phase I metabolism (e.g. CYP2C8, CYP1A1), Phase II metabolism (e.g. GSTA), Phase III metabolism (e.g. BSEP)

Steatosis affects CYP activities

Altered sensitivity to DILI cmpd

Chlorpromazine

Potential mechanism of observed hypersensitivity towards Chlorpromazine in steatotic liver microtissues

Contributing partners

Several advanced *in vitro* models were established at current TRL 4-8. They all represent heterotypic multicellular systems, providing metabolic and immune-competence in health and disease for better hazard identification and risk stratification.

