Stem cell-derived models to improve mechanistic understanding and prediction of human drug induced liver injury

Citation for published version:

Digital Object Identifier (DOI):
10.1002/hep.28886

Link:
Link to publication record in Edinburgh Research Explorer

Document Version:
Peer reviewed version

Published In:
Hepatology

Publisher Rights Statement:
Author's final peer-reviewed manuscript as accepted for publication.
Stem cell-derived models to improve mechanistic understanding and prediction of human drug induced liver injury

Christopher Goldring (C.E.P.Goldring@liverpool.ac.uk) 1, Daniel J. Antoine (bs0u1156@liverpool.ac.uk) 1, Frank Bonner (frankbonner@focusbio.com) 2, Jonathan Crozier (jonathan.crozier@epaaind.eu) 3, Chris Denning (Chris.Denning@nottingham.ac.uk) 4, Robert J. Fontana (rfontana@med.umich.edu) 5, Neil A. Hanley (Neil.Hanley@manchester.ac.uk) 6, David C. Hay (davehay@talktalk.net) 7, Magnus Ingelman-Sundberg (Magnus.Ingelman-Sundberg@ki.se) 8, Satu Juhila (Satu.Juhila@orionpharma.com) 9, Neil Kitteringham (neilk@liverpool.ac.uk) 1, Beatriz Silva-Lima (beatrizlima@netcabo.pt) 10, Alan Norris (alan.norris@liverpool.ac.uk) 1, Chris Pridgeon (cpr@liverpool.ac.uk) 1, James A. Ross (J.A.Ross@ed.ac.uk) 7, Rowena Sison Young (Rowena.Sison-Young@liverpool.ac.uk) 1, Danilo Tagle (tagled@mail.nih.gov) 11, Belen Tornesi (m.tornesi@abbvie.com) 12, Bob van de Water (water_b@lacdr.leidenuniv.nl) 13, Richard J. Weaver (richard.weaver@servier.com) 14, Fang Zhang (Fang.Zhang@liverpool.ac.uk) 1, B. Kevin Park (B.K.Park@liverpool.ac.uk) 1

1 MRC Centre for Drug Safety Science, Department of Molecular and Clinical Pharmacology, University of Liverpool, Liverpool, UK
2 Stem Cells for Safer Medicines, London, UK
3 European Partnership for Alternative Approaches to Animal Testing (EPAA), Brussels, Belgium
4 Department of Stem Cell Biology, Centre for Biomolecular Sciences, University of Nottingham, Nottingham, UK
5 Division of Gastroenterology, Department of Internal Medicine, University of Michigan, Ann Arbor, MI, USA
6 Centre for Endocrinology & Diabetes, University of Manchester; Central Manchester University Hospitals NHS Foundation Trust, Manchester Academic Health Science Centre Manchester, UK
7 MRC Centre for Regenerative Medicine, University of Edinburgh, UK
8 Department of Physiology and Pharmacology, Karolinska Institutet, Stockholm, Sweden
9 R&D, In Vitro Biology, Orion Pharma, Espoo, Finland
10 Universidade de Lisboa, Faculty of Pharmacy, Lisbon, Portugal
11 National Center for Advancing Translational Sciences, National Institutes of Health, Bethesda, MD, USA
12 Abbvie Global Pharmaceutical Research and Development, North Chicago, IL, USA
13 Faculty of Science, Leiden Academic Centre for Drug Research, Gorlaeus Laboratories, University of Leiden, Netherlands
14 Institut de Recherches Internationales Servier (I.R.I.S), Suresnes, 92284, Cedex France

This article has been accepted for publication and undergone full peer review but has not been through the copyediting, typesetting, pagination and proofreading process which may lead to differences between this version and the Version of Record. Please cite this article as doi: 10.1002/hep.28886

This article is protected by copyright. All rights reserved.
Keywords:
hepatocyte, hepatotoxicity, cardiomyocyte, biomarker, de-differentiation

Contact Information:
Christopher Goldring, PhD, MRC Centre for Drug Safety Science, Department of Molecular and Clinical Pharmacology, Sherrington Building, Ashton Street, University of Liverpool, Liverpool, L69 3GE, UK; Tel +44 151 794 5979; Fax +44 151 794 5540; email C.E.P.Goldring@liverpool.ac.uk

List of Abbreviations:
DILI, drug-induced liver injury; ADR, adverse drug reaction; SC-HLC, stem-cell-derived hepatocyte-like cell; EPAA, European Partnership for Alternative Approaches to Animal Testing; NC3Rs, National Centre for the Replacement, Refinement and Reduction of Animals in Research; MRM, multiple-reaction-monitoring; CRISPR, clustered regularly-interspaced short palindromic repeats; iPSC, induced pluripotent stem cell

Financial Support:
CG\(^1\), DJA\(^1\), NK\(^1\), AN\(^1\), CP\(^1\), RSY\(^1\), FZ\(^1\) and BKP\(^1\) are supported by grants from the Medical Research Council (grant number MR/L006758/1) and the European Community under the Innovative Medicine Initiative project MIP-DILI [grant agreement number 115336].

FB\(^2\) is supported by Stem Cells for Safer Medicines (SC4SM).

CD\(^4\) is supported by EPSRC, BHF, Heart Research UK, Medical Research Council and National Centre for the Replacement, Refinement and Reduction of Animals in Research (NC3Rs).

RJF\(^5\) is a member of the Drug Induced Liver Injury Network (DILIN) a U01 cooperative agreement supported by the National Institute of Diabetes and Digestive and Kidney Diseases (U01DK065184).

NAH\(^6\) is supported by Wellcome Trust in addition to Stem Cells for Safer Medicines (SC4SM).

JR\(^7\) is supported by the Innovative Medicines Initiative Joint Undertaking under grant agreement n° 115439, resources of which are composed of financial contribution from the European Union’s Seventh Framework Programme (FP7/2007-2013) and EFPIA companies in kind contribution. This publication reflects only the author’s views and neither the IMI JU nor EFPIA nor the European Commission are liable for any use that may be made of the information contained therein.

MIS\(^8\) is supported by grants from The Swedish Research Council and from the European Community under the Innovative Medicine Initiative project MIP-DILI [grant agreement number 115336].

BvdW\(^13\) is supported by the EC FP7 project DETECTIVE (grant agreement n° 266838), the IMI MIP-DILI project (grant agreement n° 115336), and the Horizon2020 EU-ToxRisk project (grant agreement n° 681002).
Abstract

Current preclinical drug testing does not predict some forms of adverse drug reactions in humans. Efforts at improving predictability of drug-induced tissue injury in humans include using stem cell technology to generate human cells for screening for adverse effects of drugs in humans. The advent of induced pluripotent stem cells means that it may ultimately be possible to develop personalised toxicology to determine inter-individual susceptibility to adverse drug reactions. However, the complexity of idiosyncratic drug-induced liver injury (DILI) means that no current single cell model, whether of primary liver tissue origin, from liver cell lines, or derived from stem cells, adequately emulates what is believed to occur during human DILI. Nevertheless, a single cell model of a human hepatocyte which emulates key features of a hepatocyte is likely to be valuable in assessing potential chemical risk; furthermore understanding how to generate a relevant hepatocyte will also be critical to efforts to build complex multicellular models of the liver. Currently, hepatocyte-like cells differentiated from stem cells still fall short of recapitulating the full mature hepatocellular phenotype. Therefore, we convened a number of experts from the areas of preclinical and clinical hepatotoxicity and safety assessment, from industry, academia and regulatory bodies, to specifically explore the application of stem cells in hepatotoxicity safety assessment, and to make recommendations for the way forward. In this short review, we particularly discuss the importance of benchmarking stem cell-derived hepatocyte-like cells to their terminally-differentiated human counterparts using defined phenotyping, to make sure the cells are relevant and comparable between labs, and outline why this process is essential before the cells are introduced into chemical safety assessment.

Prediction of adverse drug reactions in the liver: why it is important, limitations of current in vitro models and how stem cells may prove useful in drug screening
Adverse drug reactions (ADRs) are a significant clinical problem, resulting in considerable patient morbidity and mortality and thus represent a major financial burden on healthcare systems. ADRs also represent a major challenge for the pharmaceutical industry leading to attrition of drugs in development and the withdrawal of drugs post-licensing. Amongst different forms of ADRs, the liver is particularly susceptible to drug toxicity; drug-induced liver injury (DILI) is the second highest cause of attrition and accounts for more than 50% of cases of acute liver failure.

The principal cause of these high attrition rates is the failure of current preclinical drug testing procedures to effectively predict idiosyncratic DILI in patients. This is true for in vitro models and even for in vivo models - a recent study that related the preclinical assessment of drugs with the occurrence of DILI in the clinic showed that between 38% (Medline database: 269 out of 710 compounds) and 51% (EMEA database: 70 out of 137 compounds) of drugs that subsequently caused liver injury in patients were not predicted from animal studies. Concerted worldwide efforts are therefore required to improve the assessment of hepatotoxic risk for new compounds. In Europe, the SEURAT (http://www.seurat-1.eu/pages/cluster-projects/scrtox.php) and MIP-DILI (http://www.mip-dili.eu/) consortia, and in the US, DILIN (http://www.dilin.org/) and iSAEC (http://www.saeconsortium.org/) are attempting to address this issue. The clinical manifestation of DILI indicates that it is a multi-dimensional and multi-faceted disease. Indeed, the diagnosis of DILI is largely based upon exclusion criteria. Although the use of currently available cell lines and primary human hepatocyte models has been able to correctly classify a number of DILI compounds as hepatotoxins, idiosyncratic DILI is inherently difficult to model in the laboratory, and therefore highly unlikely to be predicted by simplistic screening strategies, often based on single-cell models involving cell lines. Many approaches use liver-derived cancer cell lines, e.g. HepG2 and HepaRG, which may have value for identifying drugs lacking a propensity to cause idiosyncratic DILI (90-95% predictability), but perform less well for positive predictions (50-89%). Metabolically-competent freshly-isolated, or cryopreserved human primary adult hepatocytes are still considered to be the gold-standard single cell model of DILI. Nevertheless, human hepatocytes are difficult to source, they
are also costly and functionally variable (reflecting variation in the human population), they undergo severe stress during the isolation process and, critically, they rapidly lose key functions when cultured in vitro. Moreover, it is important to note that hepatocyte toxicity per se is not the sole cause of hepatotoxicity which, in the intact liver, may involve multiple different cell types including lymphocytes and macrophages. Yet it is reasonable to assume from the work of several groups, over many years, that a metabolically-competent hepatocyte will be an essential component of any model of hepatotoxicity in vitro. Thus, a robust and reproducible metabolically-competent hepatocyte-like cell derived from directly reprogrammed cells, or from pluripotent stem cells, would represent a major step forward for the development of a new generation of in vitro models.

The imperatives of industry and academia are driven by different model requirements. The priority for industry is a cost-effective and scalable high-throughput screening model that has direct input into ‘go/no go’ decision making during drug development, whilst academic scientists are driven by the need to understand hepatic physiology and the mechanistic basis of DILI. Hepatocytes derived from stem cells can, however, be central to both of these objectives. Whilst significant progress towards a functional hepatic phenotype has been made, it is clear that stem-cell-derived hepatocyte-like cells (SC-HLCs) still fall well short of recapitulating the full mature hepatocellular phenotype\(^\text{12-15}\).

Because of the importance and likely impact of developments in this field, scientists with expertise in preclinical and clinical hepatotoxicity and complex and novel forms of in vitro cell culture, representing industry, academia and regulatory bodies, assembled at a workshop at the University of Liverpool, under the auspices of the European Partnership for Alternative Approaches to Animal Testing (EPAA) (http://ec.europa.eu/growth/sectors/chemicals/epaa/index_en.htm) and the MRC Centre for Drug Safety Science (https://www.liverpool.ac.uk/drug-safety/). The purpose of the workshop was to specifically explore the application of stem cells in hepatotoxicity safety assessment, and to make recommendations for the way forward. This workshop follows the
EPAA/NC3Rs (National Centre for the Replacement, Refinement and Reduction of Animals in Research) (https://www.nc3rs.org.uk/) “Stem Cells in Safety Testing Forum” workshop that took place in 2013, with a mandate to provide a platform for permanent dialogue between research groups, to share experiences, problems, successes and opportunities.

**Current challenges in the use of stem cell-derived hepatocytes in the safety assessment of new chemical entities**

It is clear from a large number of studies\(^\text{[13, 14, 16-47]}\) (see Table 1) that hepatocytes generated from stem cells are not currently sufficiently mature to emulate an adult primary human hepatocyte, and that these cells are probably closer in phenotype to a fetal hepatocyte\(^\text{[12]}\). Many studies using SC-HLCs purport to demonstrate a hepatocyte-like phenotype but do not actually incorporate a physiologically-relevant benchmark (e.g. freshly-isolated human hepatocytes) and a non-physiologically-relevant benchmark (e.g. HepG2 cells); in addition, often very few markers of the hepatic phenotype are used and studies do not always employ quantitatively-relevant assays (e.g. mass spectrometry). Thus, inadequate benchmarking has hampered the field and there is likely significant value in identifying a common framework that might allow end users to readily interpret cell phenotype.

Despite the challenges in generating mature hepatocytes, SC-HLCs have recently been shown to retain the cytochrome P450 (CYP) expression profile (specifically CYP2C9 and CYP2D6) of the donor hepatocyte\(^\text{[48, 49]}\), yielding metabolism-specific toxicity for CYP2C9 (benzbromarone) and CYP2D6 (tamoxifen). This is highly relevant as the CYPs are key enzymes of Phase I drug metabolism, that play a key role in the chemical functionalization and eventual elimination of drugs from the body, but which also can yield significant intracellular concentrations of chemically reactive metabolites, leading to cellular and tissue damage of the liver, and therefore DILI (for a review of this area, see Park et al, 2011\(^\text{[50]}\).
The recent studies outlined above (48, 49) are particularly important as they suggest that modelling some forms of DILI (such as that elicited by benz bromarone or tamoxifen) using stem cell-derived hepatocytes may be possible, and that ultimately the challenges to generating a fully mature HLC will not always be insurmountable.

We consider that there are at least three major challenges to producing mature, physiologically- and pharmacologically-relevant hepatocytes from stem cells:

- Stem cell-derived hepatocytes must mimic several years of development in vivo.
- Like primary hepatocytes, the stem cell-derived hepatocyte phenotype is unstable currently in culture(51).
- At the moment, it is difficult to emulate the complexity of the liver, with its unique blood supply and exposure to relevant concentrations of intestinal products and nutrients in vitro. Development of three-dimensional culture systems that employ co-cultivation of all cell types found in the liver acinus is likely to be required if we are to recapitulate the liver in vitro(51, 52). Following on from this, it is important to remember that a hepatocyte is not a single entity but varies functionally according to the hepatic zone in which it is located. The consequence of this is that some hepatotoxins induce hepatocellular damage in a zone-specific manner and this has not yet begun to be addressed meaningfully in the stem cell field, as we focus our attempts on improving basic functional maturity of the SC-derived cells, but it will need to be considered.

Despite these challenges, there are many promising leads in development, e.g. the discovery of several small molecule inducers of the hepatic phenotype(53), and the finding that microbial-derived secondary metabolites to which immature hepatocytes are likely to be exposed to post-partum may induce a significant increase in maturity. A further paradigm comes from the exploitation of SC-HLCs for demonstration of efficacy; specifically, for the reversal of the hepatic alpha1-antitrypsin-deficient
phenotype, shown by Yusa et al\textsuperscript{(54)}. This study demonstrated restoration of alpha1-antitrypsin activity was possible on a “sufficiently” mature background, rather than one that was necessarily fully mature and identical to a freshly-isolated adult hepatocyte. Furthermore, a recent study by Ware et al\textsuperscript{(55)} suggests that DILI detection is possible using SC-HLCs in micopatterned co-cultures, in which cells mature to significant levels. It is worth remembering that the hepatocyte exhibits more individual functions (>500) than any of the other ~200 terminally differentiated cell types in the human body. Therefore it is perhaps not surprising that this cell is amongst the most challenging to mature, and we should still continue to explore the utility of hepatocyte-like cells as prototypes rather than await the final “product”.

\textit{Lessons learned from the use of stem cell-derived cardiomyocytes in detecting cardiotoxicity}

A parallel example, from which lessons can be learned, comes from the use of stem cells in the assessment of drug-induced cardiotoxicity – a primary cause of drug attrition. Cardiotoxicity, specifically QT prolongation, has already been successfully modelled using such cells\textsuperscript{(56-58)}. In comparison, there is only very recent evidence that SC-HLCs are able to recapitulate hepatotoxic events\textsuperscript{(49, 55)}. The difference between successful application of cardiac models compared with hepatic models may reflect the relative specificity of some forms of drug-induced cardiotoxicity, in contrast with the rather pleiotropic and diverse manifestations of hepatotoxicity, at the molecular, cellular, and tissular level\textsuperscript{(59)}. Cardiotoxicity often arises due to drug-induced electrical perturbation of the cell interfering with its contractile function\textsuperscript{(60)}. Here, the stem cell-cardiomyocyte model provides advantages over recombinant tumour models. Thus, the impact of drugs that cause simple single ion channel or complex multi-channel perturbation can be related to cardiomyocyte arrhythmias and abnormalities in contractility\textsuperscript{(61)}. In hepatotoxicity, however, there are myriad factors required to recapitulate toxicity, especially idiosyncratic toxicity where the immune system is
also implicated. This is compounded by inter-individual variation in expression of xenobiotic metabolism and transporter proteins in addition to the chemistry of each drug.

Whilst protocols to differentiate stem cells towards cardiomyocytes generate cells that are not fully mature\(^{(61)}\), these cells can recapitulate some facets of the cell phenotype required to produce specific forms of cardiotoxicity. This has prompted major international efforts to search for methods to further mature stem cell cardiomyocytes. Each incremental improvement made towards progressing the compliment of ion channels, regulatory pathways and structural proteins to the complete sets found in adult cells will dramatically increase the utility of stem cell cardiomyocytes. The demonstration that specific toxicological phenotypes can be mimicked by stem cell-derived cardiomyocytes allows the cell model to be considered “fit-for-purpose”. This raises the notion of using stem cell-derived hepatocytes that may be sufficiently mature for a specific toxicological assessment even though the cells may lack the full hepatic functionality with respect to drug metabolism, transporter expression etc. For example, where one or two cytochrome P450s (P450s), some relevant phase II enzymes, such as the glutathione transferases and UDP-glucuronyl transferases, and some Phase III proteins (influx and efflux transporters) are expressed at a set and reproducible % of a “typical” human hepatocyte, this cell may in some cases represent a significant and useful model in understanding specifically drug metabolism and possible metabolism-dependent toxicity.

**The Importance of Phenotypic Characterisation**

For the field to continue to move forward and develop liver cell models that are useful in prediction and mechanistic understanding of DILI, it is essential that the SC-HLCs are properly benchmarked against currently used and relevant human cells, especially fresh primary human hepatocytes and HepG2 cells (see Table 1 and Figure 1). Moreover, the phenotype of the HLCs must be as reproducible as possible, and they should be fully characterised, particularly with reference to the
pharmacological phenotype (using a defined panel of training compounds). It is also important that the cell model can provide a static point of reference that can be used to ascertain if real progress is being made. When assessing novel models of hepatotoxicity it is important to use functional assays employing quantitative mass spectrometry whenever possible, as this is now being routinely employed\(^{68, 62, 63}\) in order to determine the true phenotype of the model. A global proteomic analysis however may be the most appropriate way to characterise the cells, as this would represent a broad visualisation of the physiological phenotype of the cells. Similarity to freshly-isolated hepatocytes/tissue can be established through proteomics and targeted multiple-reaction-monitoring (MRM)-based mass spectrometric analysis of key proteins, such as CYP450s, transporters and intracellular signalling molecules and metabolic and cellular uptake profiles determined. Developments in mass spectrometric technologies mean that it is now possible to analyse small panels of proteins (for example 10-20 transporters or P450s) using MRM, in order to quantify proteins per cell at an absolute level\(^{64}\). This would ensure valid comparisons between currently used models and cells, as well as cells that are developed in the future. Given the inherent deficiencies in a transcriptomic-only approach, which are well-illustrated in a recent landmark paper reporting only a 39% correlation between mRNA and protein at a global level\(^{65}\), measuring mRNA levels is not recommended for cell characterisation purposes.

As part of a comprehensive assessment of HLC phenotype, recent developments in the field of hepatocyte-selective translatable biomarkers (e.g. miR122\(^{66}\)) might allow us to translate the response to chemicals between humans, model organisms and cells including SC-HLCs and it is likely that additional novel and selective biomarkers will be identified in the future using models such as SC-HLCs. This is an important area for industry which requires selective and translatable biomarkers of liver injury to monitor potentially hepatotoxic compounds in the clinic.

The recently developed concepts of adverse outcome pathways and points of departure\(^{67}\) in the field of systems toxicology should also be considered in the context of phenotyping the response to
chemical exposure of hepatocyte-like cells that express relevant proteins and pathways. To this end, cells expressing genetic reporters for key adaptive pathways such as Nrf2, PXR and NF-κB will be useful as a means for understanding the earliest events in the biological response to a drug. However, it is imperative that we develop ways to bridge our findings from these molecular investigations to what actually occurs in DILI in humans – the development of novel bridging biomarkers that allow extrapolation from *in vitro* test system to man will be invaluable in this endeavour. Another important development in relation to hepatocyte genotype and phenotype in DILI is the derivation of SC-HLCs with specific polymorphisms relevant to drug toxicology. Of particular interest in this regard is the developing use of CRISPR technology in SC-HLCs to edit, for example, genes relevant to drug metabolism and toxicity thereby providing a wild type cell and an almost identical cell with an alteration in drug metabolism and toxicological responses, respectively.

Finally, phenotypic characterisation may be assisted by a better understanding of the mechanisms contributing to de-differentiation or loss of phenotype. Consideration of the cellular complexity of the liver and the functional sophistication of a hepatocyte makes it unsurprising that the maintenance of a fully functional hepatocyte in culture is difficult to achieve. The cells have been removed from their neighbouring hepatocytes, disrupting their gap junctions and tight junctions which are important for their phenotype, as well as their juxtaposed non-parenchymal cells, which may also be responsible for the differentiated hepatocyte phenotype. Dedifferentiation is not a unique process to the liver; when cardiomyocytes are cultured, they also lose some of their *in vivo* phenotype, e.g. the t-tubules are lost, glycogen is accumulated and chromatin becomes dispersed *in vitro*. However, the key difference between hepatocytes and myocytes is the importance of the metabolic phenotype with respect to drug toxicity, and it is this function – particularly the phase I CYP450 capacity – that is most rapidly and profoundly depleted - and it is also this function, at a defined proportion of the activity present in human liver, that is essential in any *in vitro* model of a hepatocyte.
One area of research that could have a significant impact on attempts to re-establish a functional hepatocyte from stem cells, is the investigation of the precise cellular mechanisms underlying the de-differentiation process that occurs in hepatocytes once they have been removed from the liver.

Whilst the factors driving de-differentiation may not be identical to those that drive differentiation, it is likely that one or more pathways and processes uncovered through research into de-differentiation will be amenable for testing in differentiation experiments. If it is not understood how to maintain the dynamic and sophisticated machinery of a fully mature hepatocyte in vitro, it is likely to be difficult to capture the same phenotype in a stem cell-derived cell grown under similar conditions.

Summary and recommendations

- DILI is a complex, multi-dimensional disease, with variable phenotype between individuals, even for a single drug. There is essentially no ideal in vitro or in vivo model that recapitulates all of the potential features of this injury.

- The aspiration of the field is a “perfect” mature hepatocyte as it exists in a liver - this has not yet been achieved. Until it is, hepatocyte-like cells with known, quantifiable and reproducible proportions of the function of two widely-used standards, i.e. primary fresh human hepatocytes, and HepG2, will be valuable biological models to explore the physiological, pharmacological and toxicological response of hepatocytes to drug exposure.

- These “immature” cells should be explored as models of chemical perturbation using genetic reporters and biomarkers, with continual effort to relate findings to human DILI.

- Global proteomic analysis aligned with biological pathway analysis may be the most appropriate way to characterise HLCs – a small targeted panel of proteins will also help to compare cells for key proteins and functions using absolute quantitation by mass spectrometry. Crucially, this will advance the field by avoiding over-reliance on a small panel
of liver proteins, such as albumin, that may not be representative of a fully mature and functioning liver cell.

- It is likely that niche creation in vitro, deploying enhanced matrices\textsuperscript{(13)} and even 3D bioprinting\textsuperscript{(76)}, and incorporating other cell types such as endothelial cells\textsuperscript{(76, 77)} and Kupffer cells\textsuperscript{(78)} \textit{inter alia}, will mature and support hepatocyte function.

- A small panel of chemical benchmarks will be needed to probe the physiological, pharmacological and toxicological function of the cells, only once they have been properly phenotyped. There is little point in exposing HLCs to chemicals chosen as hepatotoxins in man unless we fully characterise the cells.

\section*{Bibliography}


Table 1. Summary of studies post-2007 of HLC-derivation from human pluripotent stem cells (adapted from Table 1 and Table 2, Kia et al (13) with modification). Note the limited number of Phase I and 2 phenotyping markers generally employed in the characterization of the HLCs.

<table>
<thead>
<tr>
<th>Reference</th>
<th>Method of stem cell differentiation</th>
<th>Culture format</th>
<th>Differentiation factors</th>
<th>Differentiation efficiency % ALB +ve HLCs (assay method)</th>
<th>PHENOTYPING: Phase I and II enzyme activity</th>
<th>Other comparators</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cai et al., 2007&lt;sup&gt;(14)&lt;/sup&gt;</td>
<td>hESC (H1, H9)</td>
<td>Monolayer, EB formation</td>
<td>AF V, AA, ITS, BMP2, FGF4, HGF, OSM, DEX</td>
<td>70 (ICC)</td>
<td>CYP2B6 (Fluorescence)</td>
<td>ND hESC</td>
</tr>
<tr>
<td>Ek et al., 2007&lt;sup&gt;(15)&lt;/sup&gt;</td>
<td>hESC (SA002, SA002.5, SA167)</td>
<td>Monolayer</td>
<td>Proprietary differentiation medium, FGF2</td>
<td>ND</td>
<td>CYP1A1 (Fluorescence)</td>
<td>0 ─</td>
</tr>
<tr>
<td>Söderdahl et al., 2007&lt;sup&gt;(16)&lt;/sup&gt;</td>
<td>hESC (SA001, SA002, SA002.5, SA034, SA121, and SA167)</td>
<td>Monolayer</td>
<td>Proprietary differentiation medium, bFGF</td>
<td>ND</td>
<td>GST (Fluorescence)</td>
<td>80 HepG2</td>
</tr>
<tr>
<td>Hay et al., 2008&lt;sup&gt;(17)&lt;/sup&gt;; Godoy et al., 2015&lt;sup&gt;(11)&lt;/sup&gt;; Cameron et al., 2015&lt;sup&gt;(10)&lt;/sup&gt;</td>
<td>hESC (H1)</td>
<td>Monolayer</td>
<td>AA, Wnt3a</td>
<td>90 (ICC)</td>
<td>CYP 1A2 (LC-MS-MS)</td>
<td>CYP1A2 (Luminescence) 100 CYP3A4 (Luminescence) 100</td>
</tr>
<tr>
<td>Shiraki et al., 2008&lt;sup&gt;(18)&lt;/sup&gt;</td>
<td>hESC (Khes-1)</td>
<td>Co-culture with M15 cell line</td>
<td>AA, BMP4, bFGF, HGF, DMSO, DEX, Ly294002</td>
<td>9 (ICC)</td>
<td>ND ─ ─</td>
<td></td>
</tr>
<tr>
<td>Agarwal et al., 2009&lt;sup&gt;(19)&lt;/sup&gt;</td>
<td>hESC (WA01, WA09)</td>
<td>Monolayer</td>
<td>AA, FGF4, HGF, BSA, OSM, DEX</td>
<td>67.4 (ICC)</td>
<td>ND ─ ─</td>
<td></td>
</tr>
<tr>
<td>Moore et al., 2009&lt;sup&gt;(20)&lt;/sup&gt;</td>
<td>hESC (H1)</td>
<td>Monolayer, EB formation</td>
<td>AA, Wnt3a, HGF, OSM, DEX</td>
<td>72.8 (ICC)</td>
<td>CYP 1A2 (Fluorescence)</td>
<td>ND hESC-derived HLCs in culture media of different components</td>
</tr>
<tr>
<td>Basma et al., 2009&lt;sup&gt;(21)&lt;/sup&gt;</td>
<td>hESC (H1)</td>
<td>Monolayer, EB formation</td>
<td>AA, FGF2, HGF, DMSO, DEX</td>
<td>55.5 (ICC)</td>
<td>CYP1A (Fluorescence)</td>
<td>CYP3A (LC-MS-MS) 30 ─</td>
</tr>
<tr>
<td>Song et al., 2009&lt;sup&gt;(22)&lt;/sup&gt;</td>
<td>hESC (H1), hiPSC (hFb-derived 3U1, 3U2)</td>
<td>Monolayer</td>
<td>AA, sodium butyrate, BMP2, BMP4, FGF4, HGF DMSO, DEX, KG, B27</td>
<td>60 (ICC)</td>
<td>CYP2B6 (Fluorescence)</td>
<td>ND hiPSC-derived versus hESC-derived HLCs</td>
</tr>
<tr>
<td>Duan et al., 2010&lt;sup&gt;(23)&lt;/sup&gt;</td>
<td>hESC (H9)</td>
<td>Monolayer</td>
<td>AA, BMP4, FGF2, BMP2, FGF4, HGF, OSM, DEX, KG, B27</td>
<td>75-90 (ICC, FACS)</td>
<td>CYP1A2 (LC-MS-MS)</td>
<td>CYP2C9 (LC-MS-MS) 60 CYP2D6 (LC-MS-MS) 95 CYP3A4 (LC-MS-MS) 90</td>
</tr>
<tr>
<td>Synergren et al., 2010&lt;sup&gt;(24)&lt;/sup&gt;</td>
<td>hESC (SA002, SA167, SA461)</td>
<td>Monolayer</td>
<td>AA, ITS, FGF1, FGF2, BMP2, BMP4, HGF, OSM, DEX</td>
<td>ND</td>
<td>ND ─ ─</td>
<td></td>
</tr>
<tr>
<td>Touboul et al., 2010&lt;sup&gt;(25)&lt;/sup&gt;</td>
<td>hESC (H9)</td>
<td>Monolayer</td>
<td>AA, BMP4, FGF2, FGF4, FGF10, HGF, EGF, retinoic acid, SB437152, Ly294002</td>
<td>80 (FACS)</td>
<td>ND ─ ─</td>
<td></td>
</tr>
<tr>
<td>Brolén et al., 2010&lt;sup&gt;(26)&lt;/sup&gt;</td>
<td>hESC (SA001, SA002, SA002.5, SA167)</td>
<td>Monolayer</td>
<td>AA, BMP2, BMP4, FGF1, FGF2, HGF, OSM, DEX, Wnt3a</td>
<td>ND</td>
<td>ND Spontaneously differentiated hESC-derived HLCs, HepG2</td>
<td></td>
</tr>
<tr>
<td>Ghodsizadeh et al., 2010&lt;sup&gt;(27)&lt;/sup&gt;</td>
<td>hiPSC (hFb-derived)</td>
<td>EB formation</td>
<td>AA, FGF2, HGF, DMSO, DEX</td>
<td>50 (FACS)</td>
<td>CYP2B6 (Fluorescence)</td>
<td>ND hiPSC</td>
</tr>
<tr>
<td>Liu et al., 2010&lt;sup&gt;(28)&lt;/sup&gt;</td>
<td>hESC (WA01, WA09), hiPSC (hFb-derived)</td>
<td>Monolayer</td>
<td>AA, FGF4, HGF, OSM, DEX</td>
<td>ND</td>
<td>CYP1A2 (Bioluminescence)</td>
<td>CYP3A4 (Bioluminescence) ND ─</td>
</tr>
<tr>
<td>Si-Tayeb et al., 2010&lt;sup&gt;(29)&lt;/sup&gt;</td>
<td>hESC (H9), hiPSC (hFb-derived)</td>
<td>Monolayer</td>
<td>AA, BMP4, FGF2, OSM, B27</td>
<td>80 (FACS)</td>
<td>ND ─ ─</td>
<td></td>
</tr>
<tr>
<td>Sullivan et al., 2010&lt;sup&gt;(30)&lt;/sup&gt;</td>
<td>hiPSC (hFb-derived)</td>
<td>Monolayer</td>
<td>AA, HGF, Wnt3a, DMSO, OSM, hydrocortisone, triptase phosphate broth, B27</td>
<td>70-90 (ICC)</td>
<td>CYP1A2 (Bioluminescence)</td>
<td>CYP3A4 (Bioluminescence) ND ─</td>
</tr>
<tr>
<td>Authors</td>
<td>Year</td>
<td>hiPSC Type</td>
<td>Differentiation Medium</td>
<td>Cell Culture Method</td>
<td>Confluency</td>
<td>Induction Proteins</td>
</tr>
<tr>
<td>----------------------</td>
<td>------</td>
<td>------------</td>
<td>------------------------</td>
<td>--------------------</td>
<td>------------</td>
<td>--------------------</td>
</tr>
<tr>
<td>Rashid et al., 2010</td>
<td>hiPSC (hFb-derived)</td>
<td>Monolayer</td>
<td>AA, BMP4, FGF2, HGF, OSM, Ly294002, CHIR99021 (GSK-3 inhibitor)</td>
<td>83 (FACS)</td>
<td>CYP3A4 (Bioluminescence)</td>
<td>ND</td>
</tr>
<tr>
<td>Zhang et al., 2011</td>
<td>hiPSC (hFb-derived)</td>
<td>Monolayer, EB formation</td>
<td>AA, BMP2, FGF4, HGF, KGF, OSM, DEX</td>
<td>60-80 (ICC, FACS)</td>
<td>CYP3A4 (Bioluminescence)</td>
<td>0.32</td>
</tr>
<tr>
<td>Bone et al., 2011</td>
<td>hiPSC (Shef1, Shef3)</td>
<td>Monolayer</td>
<td>FGF4, HGF, OSM, DEX, 1 m (GSK-3 inhibitor)</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Yiğdirkan et al., 2011</td>
<td>hiPSC (SA002)</td>
<td>Monolayer</td>
<td>Proprietary differentiation medium</td>
<td>ND</td>
<td>CYP1A2 (LC-MS-MS)</td>
<td>50</td>
</tr>
<tr>
<td>Chen et al., 2012</td>
<td>hiPSC (H9), hiPSC (hFb-derived)</td>
<td>Monolayer</td>
<td>AA, ITS, HGF, Wnt3A, OSM, DMSO, DEX</td>
<td>ND</td>
<td>CYP3A4 (Bioluminescence)</td>
<td>100</td>
</tr>
<tr>
<td>Cayo et al., 2012</td>
<td>hiPSC (FH patient JD fibroblast-derived)</td>
<td>Monolayer</td>
<td>OCT4, SOX2, NANOG, LIN28</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Schwartz et al., 2012</td>
<td>hiPSC (hFb-derived)</td>
<td>Monolayer</td>
<td>AA, BMP4, FGF2, HGF, OSM</td>
<td>80 (ICC)</td>
<td>CYP3A4 (Fluorescence)</td>
<td>100</td>
</tr>
<tr>
<td>Takayama et al., 2012</td>
<td>hES (H9), hiPSC (hFb-derived, MCRS &amp; 201B7)</td>
<td>Monolayer</td>
<td>AA, SOX17, HEX, BMP4, FGF4, LacZ, HNF4α, HGF, OSM, DEX</td>
<td>ND</td>
<td>CYP2C9 (Fluorescence)</td>
<td>&gt; 10</td>
</tr>
<tr>
<td>Choi et al., 2013</td>
<td>hiPSC (derived from AAT deficient patients)</td>
<td>Monolayer</td>
<td>B27, AA, FGF4, HGF, OSM, DEX</td>
<td>ND</td>
<td>CYP3A4 (Fluorescence)</td>
<td>80</td>
</tr>
<tr>
<td>Ramasamy et al., 2013</td>
<td>hESC (H1)</td>
<td>Monolayer &amp; 3D culture in Algimatrix plate</td>
<td>AA, DMSO, HGF, OSM</td>
<td>ND</td>
<td>CYP3A4 (Bioluminescence)</td>
<td>ND</td>
</tr>
<tr>
<td>Gieseck et al., 2014</td>
<td>hiPSC (hFb-derived)</td>
<td>Monolayer, 3D- single cell or Clump culture in RAFT system</td>
<td>AA, FGF2,BMP4, Ly294002, Hepatocyte-SFM</td>
<td>ND</td>
<td>CYP3A4 for 2D Day 35 (HPLC-MS)</td>
<td>4</td>
</tr>
<tr>
<td>Jia et al., 2014</td>
<td>hiPSC (from urine cells of HA patient)</td>
<td>Monolayer, EB formation</td>
<td>AA, FGF4, BMP2, HGF, KGF, OSM, DEX</td>
<td>64 (FACS)</td>
<td>CYP3A4, 1A2 (Fluorescence)</td>
<td>30</td>
</tr>
<tr>
<td>Avior et al., 2015</td>
<td>hESC (E3)</td>
<td>Monolayer</td>
<td>AA, B27, Wnt3A, HGF, DMSO, DEX, Fgf2, LCA, MK4</td>
<td>83 (FACS)</td>
<td>CYP3A4, 1A2 (Fluorescence)</td>
<td>25</td>
</tr>
<tr>
<td>Chien et al., 2015</td>
<td>hiPSC (from dental pulp stromal cells)</td>
<td>Co-culture with MEF, EB formation</td>
<td>AF V, AA, FGF4, BMP2, HGF, KGF, OSM, DEX, B27, miR122 (delivered by PU-PRI in CHC)</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
</tbody>
</table>

Abbreviations: AA, activin A; AF V, albumin fraction V; bFGF, human recombinant basic FGF; BMP, bone morphogenic protein; BSA, bovine serum albumin; CHC, carboxymethyl-hexanoyl chitosan; DEX, dexamethasone; DMSO, dimethyl sulfoxide; EGF, epidermal growth factor; FACS, fluorescence-activated cell sorting; FGF, fibroblast growth factor; GFP, green fluorescent protein; GSK, glycogen synthase kinase; Hepatocyte-SMF, hepatocyte serum free medium; HEX, hematopoietically-expressed homeobox protein; hESC, human embryonic stem cell; hiPSC, human induced pluripotent stem cell; HLCs, hepatocyte-like cells; HGF, hepatocyte growth factor; HNF4alpha, hepatocyte nuclear factor 4 alpha; ICC, immunocytochemistry; ITS, insulin-transferrin-selenium; KGF,
keratinocyte growth factor; LacZ, beta-D-glactosidase; Ly294002, phosphoinositide 3-kinase inhibitor; miR122, microRNA 122; ND, not determined; OCT, octamer-binding transcription factor; OSM, oncostatin M; PU-PEI, biodegradable polyurethane-graft-short-branch polyethylenimine; qRT-PCR, quantitative real time polymerase chain reaction; SB431542, inhibitor for activin receptor-like kinase receptors ALK5, ALK4 and ALK7; SOX, sex determining region Y-box; Wnt3a, wingless-type MMTV integration site family, member 3a