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CONTEMPORARY REVIEW

Pluripotent Stem Cells in Developmental Toxicity Testing: A Review of Methodological Advances

Anthony L. Luz and Erik J. Tokar¹

Stem Cell Toxicology Group, National Toxicology Program Laboratory, Division of the National Toxicology Program, National Institute of Environmental Health Sciences, Research Triangle Park, North Carolina 27709

¹To whom correspondence should be addressed at Stem Cell Toxicology Group, National Toxicology Program Laboratory, Division of the National Toxicology Program, National Institute of Environmental Health Sciences, 111 TW Alexander Drive, Building 101, Room E-105, Research Triangle Park, NC 27709. E-mail: erik.tokar@nih.gov.

ABSTRACT

Millions of children are born each year with a birth defect. Many of these defects are caused by environmental factors, although the underlying etiology is often unknown. *In vivo* mammalian models are frequently used to determine if a chemical poses a risk to the developing fetus. However, there are over 80 000 chemicals registered for use in the United States, many of which have undergone little safety testing, necessitating the need for higher-throughput methods to assess developmental toxicity. Pluripotent stem cells (PSCs) are an ideal *in vitro* model to investigate developmental toxicity as they possess the capacity to differentiate into nearly any cell type in the human body. Indeed, a burst of research has occurred in the field of stem cell toxicology over the past decade, which has resulted in numerous methodological advances that utilize both mouse and human PSCs, as well as cutting-edge technology in the fields of metabolomics, transcriptomics, transgenics, and high-throughput imaging. Here, we review the wide array of approaches used to detect developmental toxicants, suggest areas for further research, and highlight critical aspects of stem cell biology that should be considered when utilizing PSCs in developmental toxicity testing.

Key words: pluripotent stem cells; teratogen; developmental toxicity.

Globally, approximately 8 million children are born each year with a birth defect. The causes of only 30% of these birth defects are somewhat understood, leaving the possibility that environmental factors could be playing a significant role (Weinhold, 2009). In support of this, in utero exposure to various environmental contaminants, including industrial solvents, metals, and pesticides have been implicated in causing birth defects in humans and in various mammalian models (reviewed in Stillerman et al., 2008). However, there are currently over 80 000 chemicals registered for commercial use in the United States, and there is limited human toxicity and exposure data for the majority of these chemicals (Judson et al., 2009). The prenatal developmental toxicity test, which utilizes pregnant mice, rats, or rabbits, is considered the definitive test to identify chemicals that may pose a risk to the developing fetus, and is regularly used to establish human exposure guidelines. However, these *in vivo* tests are both expensive and time-consuming, making it impractical to test all commercially used chemicals for developmental toxicity, thus necessitating the development of rapid, low-cost *in vitro* methods that can be used to detect potential developmental toxicants, and prioritize chemicals for further *in vivo* testing.

In response, researchers have developed myriad alternative methods for detecting developmental toxicants. These include the *in vivo* zebrafish embryotoxicity test (Chapin *et al.*, 2008), and the frog embryo teratogenesis assay (Bantle *et al.*, 1989), as well as the *in vitro* rat micromass (MM) test, the rat wholeembryo culture assay (WEC test), and the mouse embryonic stem cell (mESC) test (mEST) (Genschow *et al.*, 2002). Of these early embryotoxicity tests, the MM test, WEC test, and the mEST have all undergone thorough validation studies coordinated by the European Center for the Validation of Alternative Methods

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(ECVAM) (Genschow et al., 2002). Furthermore, these in vitro methods can all properly classify embryotoxic compounds with at least 70% accuracy (Table 1). However, the mEST is the only assay that does not require the sacrifice of pregnant animals, making it a more attractive method for developmental toxicity testing. Since its validation, the mEST has been used extensively by researchers to test the embryotoxic potential of a wide array of compounds, including metals (Stummann et al., 2007, 2008), nanoparticles (Di Guglielmo et al., 2010; Park et al., 2009), cosmetics (Chen et al., 2010), industrial chemicals (de Jong et al., 2009), pharmaceuticals (Eckardt and Stahlmann, 2010; Paquette et al., 2008), and a wide-variety of environmental contaminants (Kamelia et al., 2017; Kong et al., 2013; Zhou et al., 2017). Indeed, the widespread acceptance of the mEST by the toxicological research community over 15 years ago has triggered a burst of research in the field of stem cell toxicology and has led to the development of numerous in vitro assays that can be used to detect developmental toxicants. These methodological advances use mESCs and human embryonic stem cells (hESCs), spontaneous and directed ESC differentiation protocols, and cutting-edge technology in the fields of metabolomics, transcriptomics, transgenics, and high-throughput imaging. Here, we review the wide array of approaches used to detect developmental toxicants, as well as highlight critical aspects of stem cell biology that should be considered when utilizing ESCs in developmental toxicity testing.

CHALLENGES OF IN VITRO DEVELOPMENTAL TOXICITY TESTING

No in vitro assay can completely recapitulate the complexities of fetal development or the fetal-maternal interactions that occur in vivo. Many of the challenges involved in using ESCs for developmental toxicity testing have been recently reviewed (Kugler et al., 2017), and thus are only briefly highlighted here.

Fetal-Maternal Interactions

Pluripotent SCs can differentiate into nearly any cell type in the human body, including trophoblasts, which are placentaspecific epithelial cells (Gamage et al., 2016); however, the formation of mature placental tissue from PSCs has not been demonstrated. In vivo, the developing fetus is dependent upon the placenta for transfer of nutrients and gases from maternal blood. From a toxicological perspective, the placenta can play a role in transporting toxicants from maternal to fetal blood resulting in fetal exposure, or may act as a barrier, preventing fetal exposure. Recently, researchers have utilized placental BeWo cells to generate toxicokinetic data, and have demonstrated that incorporation of this data into the mEST can increase assay predictivity (Dimopoulou et al., 2018). Maternal metabolism can also play a role in the detoxification or toxification of teratogens. As minimal xenobiotic metabolism occurs in ESCs, it is likely that most proteratogens will be classified as false-negatives in ESC-based assays. To overcome this, metabolic activation systems (MAS) utilizing rat liver microsomes have been incorporated into the zebrafish embryotoxity test (Busquet et al., 2008) and the frog embryo teratogenesis assay (Fort et al., 1989) to great effect; however, MAS have yet to be incorporated into ESC-based assays.

Human Versus Mouse ESCs

To date, most developmental toxicity testing has been performed using mESCs (Table 2), and the implementation of Table 1. Alternative Models in Developmental Toxicity Testing

Model	Accuracy	References	
Mouse embryonic stem cell test	78%	Genschow et al. (2002)	
Rat MM test	70%	Genschow et al. (2002)	
Rat WEC assay	80%	Genschow et al. (2002)	
Zebrafish embryotoxicity test	72%	Chapin et al. (2008)	
Frog embryo teratogenesis assay	NA	Bantle <i>et al.</i> (1989)	

hESCs in developmental toxicity testing has been slow. Ethical and legal issues of performing toxicity testing with hESCs may be partially to blame. Historically, hESCs have been more difficult to culture than mESCs; however, advances in culturing techniques have eliminated this issue (Desai et al., 2015). The most apparent advantage of using hESCs instead of mESCs is to limit the possibility of false-negatives that may arise due to speciesspecific differences. However, it is yet to be demonstrated that hESC-based assays perform better than mESC-based developmental toxicity assays. Furthermore, species-specific differences are often due to in vivo differences in metabolism or toxicokinetics, which may not apply to in vitro assays. Finally, it is important to note that mESCs are more naïve than hESCs, meaning the molecular features of mESCs more closely resemble those of pluripotent cells in the early embryo, which may mean mESCs are a more appropriate model for early embryogenesis.

Embryonic Versus Induced Pluripotent

Induced pluripotent stem cells (iPSCs) are derived from somatic cells that are reprogramed back to an embryonic-like state. Although these cells are pluripotent, their use in developmental toxicity testing has remained limited. This may, in part, be due to the fact that many iPSC lines tend to have lineage bias towards the lineage of origin, which may be due to an incomplete reset of DNA methylation back to an "embryonic state" (Liang and Zhang, 2013). However, many commonly used ESC lines have also been shown to have lineage biases (Bock *et al.*, 2011; Tsankov *et al.*, 2015). Additionally, donor age, sex, race, and exposure history may all influence the toxicant response of iPSCs. Therefore, the true power of iPSCs may lie in the field of personalized toxicology, and in their utility to incorporate genetic diversity into *in vitro* developmental toxicology studies [reviewed in (Jennings, 2015; Liu *et al.*, 2017)].

Culture Conditions

Unsurprisingly, growing work has demonstrated that culture conditions can affect SC pluripotency and differentiation. Most notably, the international stem cell initiative (ISCI) compared 8 commonly used culture methods, and found only a few were capable of maintaining PSCs for at least 10 passages (Akopian et al., 2010). Furthermore, the ISCI has also reported subtle genetic differences, including alterations in DNA methylation and SNP occurrence, when they compared over 100 low- and highpassage PSC lines from 38 laboratories (International Stem Cell Initiative, 2011). More recently, Merkle et al. (2017) analyzed 140 PSCs lines and identified 6 mutations in the tumor suppressor P53. Furthermore, the allelic fraction increased with passage number suggesting the mutations confer selective advantage. These studies demonstrate that researchers need to carefully consider not only the culture system, but also limit PSC passage number to avoid the potential accumulation of mutations or epigenetic alterations that may increase assay variation.

Table 2. Stem Cell-Based Methods for	r Developmental Toxicant Screening
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Assay	Species	Duration (days)	Compounds in Test Set	Summary	References
mEST	Mouse	10	15-20	Accuracy: 78%–83%	Genschow et al. (2002), Paquette <i>et al</i> . (2008)
FACS-EST	Mouse	7	10	Accuracy: 100%	Buesen et al. (2009)
Molecular-EST	Mouse	4	65	Accuracy: 72%; Sensitivity: 76%; Specificity: 69%	Panzica-Kelly et al. (2013)
EBT	Mouse	10	21	Accuracy: 90.5%	Kang et al. (2017)
Untargeted metabolomics	Human	4	8	Accuracy: 88%; Sensitivity: 80%; Specificity: 100%	West et al. (2010)
	Human	3	11	Accuracy: 83%; Sensitivity: 92%; Specificity: 75%	Kleinstreuer et al. (2011)
Metabolomics (O/C ratio)	Human	3	13	Accuracy: 77%; Sensitivity: 57%; Specificity: 100%	Palmer et al. (2013)
High-throughput imaging	Human	3	71	Accuracy: 94%; Sensitivity: 97%; Specificity: 92%	Kameoka et al. (2014)
ReProGlo Assay	Mouse	1	17	Accuracy: 76%; Sensitivity: 71%; Specificity: 100%	Uibel et al. (2010)
Hand1-EST	Mouse	6	24	Accuracy: 83%; Sensitivity: 93%; Specificity: 63%	Suzuki et al. (2011)
Cmya-1-EST	Mouse	6	24	Accuracy: 92%; Sensitivity: 93%; Specificity: 87%	Suzuki et al. (2011)

Solvent Effects

Solvents used to solubilize hydrophobic compounds must be chosen carefully. Research has demonstrated that both ethanol and dimethyl sulfoxide (DMSO) can adversely affect pluripotency and differentiation of mouse and human PSCs. For example, DMSO ($\geq 0.1\%$) can reduce Oct4 expression and alter DNA methylation patterns in mESCs (Adler et al., 2006; Iwatani et al., 2006), and impair differentiation of hESCs (Czysz et al., 2015; Pal et al., 2012). Similarly, ethanol ($\geq 0.25\%$) can alter Oct4 expression in mPSCs (Adler et al., 2006), and alter DNA methylation, induce apoptosis, and impair neuronal differentiation in hESCs (Khalid et al., 2014; Nash et al., 2012). Given these low-dose solvent effects, final solvent concentrations should be kept low, and appropriate solvent controls should always be included.

PSC-BASED METHODS FR DEVELOPMENTAL TOXICITY TESTING

The mESCs Test and Assay Variations

The mEST was one of the first, and mostly thoroughly validated, ESC-based assays used to assess compounds for embryotoxicity (Genschow et al., 2002). Embryotoxicity is based on 3 endpoints: the ability of a compound to (1) impair differentiation of mESCs into contracting cardiomyocytes, and cause cytotoxicity in (2) undifferentiated mESCs, and in (3) differentiated 3T3 fibroblasts (Genschow et al., 2002) (Figure 1). Overall, the accuracy of the mEST is 78%-83% (Genschow et al., 2002; Paquette et al., 2008), and has been used extensively by toxicologists. However, the mEST has limitations. First, scoring cardiomyocyte beating is a subjective process that requires highly trained staff. Second, the assay is relatively low-throughput. Third, the mEST assumes that undifferentiated ESCs will be more sensitive than highly differentiated fibroblasts to developmental toxicants; however, exceptions to this assumption have led to the misclassification of methyl mercury, cadmium, and various arsenicals (Genschow et al., 2002; Stummann et al., 2008).

Given these limitations, a variety of modified versions of the mEST have been developed, although they have not been validated as thoroughly. For example, protocols have been optimized for embryoid body (EB) formation in 96-well plates to increase assay throughput (Peters et al., 2008), while fluorescent-activated cell sorting has been used to assess cardiomyocyte differentiation, thus eliminating subjectivity of scoring contracting cardiomyocytes (Buesen et al., 2009). Innovatively, Dimopoulou et al. (2018) incorporated placental BeWo b30 cells into the mEST, and demonstrated that the incorporation of placental transport velocity data can increase assay predictivity. A great deal of effort has also been expended to incorporate transcriptomics into the mEST (>50 studies published [reviewed in van Dartel and Piersma, 2011]). Of note, the molecular EST, in which expression of 12 developmentally regulated genes are assessed, reduced assay time from 10 to 4 days, and had a similar degree of accuracy (72%-83%) as the original mEST (Panzica-Kelly et al., 2012).

The transgenic EST. Transgenic mESCs that can be used to monitor cardiomyocyte differentiation have also been generated (Le Coz et al., 2015; Nagahori et al., 2016; Suzuki et al., 2011). In these models, luciferase expression is driven by either the Hand1 or Cmya1 promoters, both of which are considered indispensable for proper heart development. Importantly, the endpoint of cardiomyocyte beating is replaced with the rapid and highly quantitative endpoint of luciferase expression. Furthermore, both the Hand1-Luc and Cmya1-Luc assays have been shown to properly predict 83% and 92% of compounds, respectively.

The EB stem cell test. Recently, several groups have proposed that EB growth dynamics can be used to predict the embryotoxic potential of chemicals (Flamier et al., 2017; Kang et al., 2017; Warkus and Marikawa, 2017). Kang et al. (2017) demonstrate a strong correlation between EB area and cardiomyocyte beating, indicating that a reduction in EB size closely reflects cardiomyocyte differentiation. This led to the development of a novel mEST variation in which cardiomyocyte beating was replaced

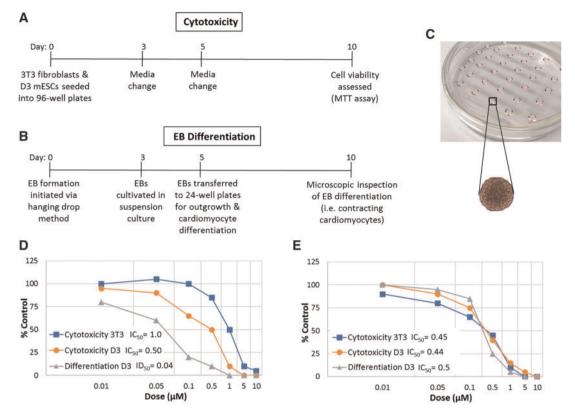


Figure 1. The mESCs test. A, Viability of pluripotent murine D3 ESCs and differentiated 3T3 fibroblasts is compared across an 8-point dose-response following 10 days of toxicant exposure. B, EBs are generated via the hanging drop method, and allowed to differentiate into contracting cardiomyocytes while being exposed for 10 days across an 8-point dose-response. C, EB formation via the hanging drop method. Compound concentrations that reduce cell viability (IC₅₀) and cardiomyocyte differentiation (ID₅₀) by 50% are calculated and input into the EST prediction model to determine the embryotoxic potential of the test compound. D, Hypothetical example of concentration-response curves for an embryotoxic compound that inhibits cardiomyocyte differentiation at non-cytotoxic concentrations. E, Hypothetical example of concentration response curves for a nonembryotoxic compound that only inhibits cardiomyocyte differentiation at cytotoxic concentrations.

with an EB size measurement, termed the EB stem cell test (EBT). The accuracies of the mEST and EBT were found to be similar (86.9% and 90.5%, respectively) when compared across a 21-compound test set. Although the EBT requires further validation, it may represent a significant advancement over the mEST, as it is more adaptable to high-throughput screening, as EB growth can be monitored using high-content imaging (HCI) devices.

Alternative differentiation models. Additional differentiation models have also been incorporated into the mEST in an attempt to expand the assays applicability domain. For example, Adler et al. (2008) developed a human EST to limit potential falsenegatives that may arise due to species-specific differences. Furthermore, many embryotoxic compounds can adversely affect skeletal development (an endpoint regularly monitored in in vivo developmental toxicity studies), which has led researchers to incorporate osteoblast differentiation protocols into the mEST (Chen et al., 2015; zur Nieden et al., 2010a,b). Finally, because the original mEST failed to properly classify the strong neurodevelopmental toxicant methyl mercury, numerous research groups have worked to incorporate neuron differentiation protocols into the mEST (Baek et al., 2012; Stummann et al., 2009; Theunissen et al., 2010), which have resulted in the proper classification of methyl mercury.

Metabolomics-Based Approaches

Metabolomics is the study of small molecules (metabolites) that are the end-product of various cellular processes, including

energy metabolism. This highly quantitative approach is being implemented in developmental toxicity testing, and has allowed researchers to identify small molecules that can serve as putative biomarkers of myriad diseases (Cezar et al., 2007; Palmer et al., 2013; West et al., 2010). Cezar et al. (2007) first established the utility of metabolomics in developmental toxicity testing by demonstrating that valproate, a neurodevelopmental toxicant, can alter the secretome of hESCs, affecting processes such as tryptophan and glutamate metabolism. In a follow-up study, hESCs were exposed to the ECVAM test set, and the secretome was analyzed using an untargeted metabolomics approach, which led to the identification of 8 small metabolites (dimethylarginine, aspartic acid, arginine, glutamate, GABA, malate, succinate, isoleucine) that correlated with teratogenicity (West et al., 2010). A predictive model was then generated that could accurately classify 88% (7/8) of drugs and 73% (8/11) of environmental toxicants in 2 separate blinded test sets (Kleinstreuer et al., 2011). More recently, it was found that a 12% reduction in the ornithine to cysteine (O/C) ratio in the secretome of hESCs following a 3-day exposure was predictive of developmental toxicity when compared with cell viability across a 9-point dose-response (Palmer et al., 2013). Although this approach could accurately classify 77% of compounds in a 13-compound test set, the overall sensitivity of the assay was low, as only 57% (4/7) of known teratogens were properly classified, while 100% of nonteratogens were correctly classified. Despite this high false-negative rate, changes in the O/C ratio have been used successfully to rank retinoid analogs based on teratogenic

potency using human iPSCs (Palmer et al., 2017). Furthermore, this metabolomics-based method is the only commercially available service that utilizes PSCs for developmental toxicity testing (www.stemina.com).

Spontaneous Differentiation of EBs

EBs are 3D aggregates of PSCs that spontaneously differentiate into all 3 embryonic germ layers (ectoderm, mesoderm, and endoderm), in a process that recapitulates many of the molecular events that occur throughout early embryogenesis (Weitzer, 2008). To test for developmental toxicity, Shinde et al. (2015) exposed differentiating EBs to teratogens throughout a 14-day differentiation window, and then assessed EB differentiation using transcriptomics and immunocytochemistry. Although the overall accuracy of this approach has not yet been established, several proof-of-principle experiments with cytosine arabinoside (Jagtap et al., 2011), thalidomide (Meganathan et al., 2012), valproic acid (Krug et al., 2013), and methyl mercury (Shinde et al., 2015) have demonstrated the validity of this approach. For example, thalidomide perturbed the expression of genes associated with limb and heart development (Meganathan et al., 2012), which coincides with clinical observations of thalidomide toxicity in humans.

Despite these promising characteristics, this assay is relatively low-throughput and does not utilize consistently sized or individually cultured EBs. This may prove problematic for highthroughput developmental toxicant screening, as EB size can influence PSC differentiation, likely due to reduced diffusion of nutrients and oxygen into the core of larger EBs, resulting in increased cell death and altered differentiation patterns (Moon *et al.*, 2014; Nath *et al.*, 2017). Furthermore, pooled EBs rapidly (within several hours) fuse, resulting in increased EB size, cell death, and altered differentiation (Dang *et al.*, 2002), which may also contribute to assay variability. However, advances in EB formation protocols may allow researchers to overcome these limitations (reviewed in Pettinato *et al.*, 2015).

Transgenic Reporter Strains

Early embryogenesis is primarily under the control of 6 signaling pathways—the Wnt/ β -catenin, transforming growth factor β (TGF-β), Notch, Hedgehog, receptor tyrosine kinase/Ras, and cytokine receptor signaling pathways. The crucial nature of these pathways is demonstrated by the fact that genetic manipulation results in embryonic lethality or developmental defects in mammalian models (Loebel et al., 2003). This has led to the development of several transgenic ESC lines that can be used to monitor pathway activity following toxicant exposure. For example, the ReProGlo Assay utilizes mESCs transfected with the SuperTopFlash luciferase reporter, which can be used to monitor Wnt signaling pathway activity following toxicant exposure (Uibel et al., 2010). In the initial validation study, the ReProGlo assay could properly classify 76% of compounds in a 17-compound test set. Although the low-cost and rapid (24-h) nature of the ReProGlo assay make it an attractive tool for developmental toxicant screening, follow-up studies have reported high falsenegative rates, suggesting the applicability domain of the assay needs to be better defined (Uibel and Schwarz, 2015). However, generation of additional transgenic lines capable of assessing the activity of the other signaling pathways (ie, Notch, Hedgehog, TGF-β, receptor tyrosine kinase/Ras, and cytokine receptor signaling) may help overcome this limitation when used in combination.

Another strategy used to generate transgenic ESC lines is to isolate ESCs from transgenic mouse models, which has led to

the generation of 2 transgenic mESC lines that can be used to monitor Wnt and TGF- β signaling (Kugler *et al.*, 2015, 2016). Both models have been tested with a small set of developmental toxicants (valproic acid, retinoic acid, and 6-aminonicotinamide), and reporter activity correlates well with subsequent cardiomyocyte differentiation assays, demonstrating the validity of these approaches. However, the overall accuracy of these models is yet to be tested.

High-Content Imaging

HCI, in combination with automated image analysis software, can allow researchers to rapidly screen large suites of compounds for biological activity. Utilizing this technology, Kameoka et al. (2014) directed hESCs to differentiate down the mesendoderm lineage in the presence of toxicants throughout a 3-day differentiation window. Cell viability and differentiation were then assessed by staining for DAPI and SOX17, an established mesendoderm marker. Teratogenic risk was based upon a compounds ability to reduce nuclear translocation of the SOX17 transcription factor. Impressively, 94% of pharmaceutical compounds (67/71), and 87% of environmental toxicants (13/15) with known in vivo outcomes were properly classified using this approach. Given the rapid (72 h) and automated nature of this approach, it represents a promising advancement in the field of stem cell toxicology; however, the requirement for expensive HCI systems may limit its widespread utility.

In Vitro Test Battery Approaches

Embryonic development is a highly complex process that no single in vitro assay can completely recapitulate. Furthermore, no single PSC-based assay will be able to detect development toxicants with 100% accuracy. This realization has led several groups to develop a battery of in vitro assays that can be used to screen chemicals for developmental toxicity. For example, the ReProTect study employed 14 in vitro assays, including the mEST, ReProGlo assay, and WEC discussed earlier. This test was designed to detect adverse effects on male and female fertility, and embryonic development (Schenk et al., 2010). Combined, the 3 in vitro assays properly classified >90% of compounds across 2 separate studies (Piersma et al., 2013; Schenk et al., 2010). Alternatively, Augustine-Rauch et al. (2016) optimized 3 in vitro assays, including the zebrafish embryo culture assay (ZEC), WEC, and the molecular EST, for screening pharmaceuticals for developmental toxicity. Overall, the individual predictivity of the 3 assays ranged from 73% to 82% for a 73-compound library. However, the main advantage of this approach was that it allowed the authors to detect toxicants with diverse mechanisms of action, and more clearly define the applicability domains of each assay. For example, the molecular EST and ZEC frequently misclassified hydrophobic compounds, and compounds with H1 receptor or GABAnergic activity, while the WEC could accurately classify these compounds. Overall, the suite of assays correctly predicted the teratogenicity of 64 out of 73 compounds (88%), while achieving 95% predictivity for the 21 known human teratogens included in the test set.

FUTURE DIRECTIONS

As with any new assay, validation is key to acceptance by the scientific community. To date, the mEST remains the most thoroughly validated ESC-based assay for developmental toxicant testing. Validated by ECVAM, the mEST was tested by 4 independently contracted laboratories against a blinded test set of 20 compounds with known *in vivo* outcomes (Genschow *et al.*, 2002). Importantly, this process allowed not only assay predictivity to be calculated, but also intra- and interlab variability. Despite the limitations of the mEST, the assay has been widely accepted and used by the toxicological research community, likely in part due to its thorough validation. Alternatively, many of the novel ESCbased assays discussed in this review have not undergone as thorough of a validation process, and are typically only tested for predictive capacity, while assay applicability domains remain poorly defined. Thus, further work is required to validate these cutting-edge approaches. However, it is also important to note that assay validation does not equate to regulatory acceptance, and to date, no SC-based assay is used to make regulatory decisions.

Due to limitations, no single in vitro assay will ever be able to detect developmental toxicants with 100% accuracy. Thus, it is critical that assay limitations are acknowledged and discussed so that more complete in vitro approaches to developmental toxicant screening can be developed. In particular, developing a battery of PSC-based assays may prove the best approach for in vitro developmental toxicity testing, as several studies have shown promising results (Augustine-Rauch et al., 2016; Schenk et al., 2010). However, it is necessary that assays chosen for inclusion in the battery are thoroughly validated, and are chosen such that the assays address the limitations of one another. For example, inclusion of the mEST and the ReProGlo assay, as done in the ReProTect study, may not be appropriate (Schenk et al., 2010), as the ReProGlo assay detects perturbations in Wnt signaling, but not other signaling networks critical to embryonic development. Instead, inclusion of multiple transgenic reporter strains designed to detect perturbations in the key developmental signaling pathways (ie, Wnt, Notch, TGF-β, receptor tyrosine kinase, cytokine receptor, and Hedgehog), in combination with assays that utilize spontaneously differentiating EBs (Shinde et al., 2015), or ESCs directed to differentiate down a specific lineage (Kameoka et al., 2014) may dramatically expand the applicability domain of the test battery and limit false-negatives. However, it will also be critical to address some of the more conspicuous limitations of PSC-based assays, such as lack of xenobiotic metabolism. This point may be especially important, as maternal metabolism can bioactivate benign compounds to teratogens, and these proteratogens would likely be misclassified as false-negatives by current PSC-based methods. Furthermore, zebrafish and frog teratogenesis assays have made good use of MASs (Busquet et al., 2008; Fort et al., 1989) that have potential to be applicable to PSC-based assays.

There is a growing push to use 3D cell culture models in toxicology, disease modeling, and drug discovery, as mounting evidence indicates that 3D in vitro systems are more analogous to in vivo events than cells grown in monolayer (reviewed in Ravi et al., 2015; Trosko, 2018). In response, myriad complex 3D in vitro organoid models have been generated using human PSCs, including intestinal (Leslie et al., 2015), kidney (Freedman et al., 2015; Takasato et al., 2015), liver (Takebe et al., 2013), lung (Dye et al., 2015), neural (Jo et al., 2016; Sandström et al., 2017) pancreas (Hohwieler et al., 2017), prostate (Calderon-Gierszal and Prins, 2015), and stomach organoids (McCracken et al., 2014). To date, these organoids have primarily been used for disease modeling and drug discovery; however, several promising studies suggest these models may be useful for investigating organ-specific developmental toxicity. For example, Calderon-Gierszal and Prins (2015) demonstrated that low-dose bisphenol A exposure can disrupt prostate organoid morphology and alter stem cell dynamics. Alternatively, Sandström et al. (2017) demonstrated that prototypical neurodevelopmental toxicants such

as methyl mercury and trimethyltin can cause increased astroglial reactivity in neurospheres generated from hESCs.

Although methodological advances have primarily focused on using ESCs for developmental toxicity testing *in vitro*, iPSCs may allow researchers to incorporate genetic diversity (ie, sex, ethnicity, age, etc.) into their studies (reviewed in Warren and Cowan, 2017). Indeed, several large cohorts of genetically diverse iPSCs have been derived, and are publicly available (Panopoulos *et al.*, 2017; Park *et al.*, 2017). Although, these genetically diverse cohorts have yet to be utilized for developmental toxicity testing, several studies have successfully utilized iPSCs to incorporate genetic diversity into cardiotoxicity testing. For example, iPSC-derived cardiomyocytes can recapitulate the penchant of patients to doxorubicin-induced cardiotoxicity.

Despite many challenges, a great deal of progress has been made in using PSCs for developmental toxicity testing, and this trend will continue with future research efforts and discoveries. In particular, many of the advanced PSC-based assays discussed in this review require further validation and standardization. Further standardization will help reduce variability between similar methods, and increase the reproducibility between different labs and lab settings, which will be ultimately be critical to improving our ability to predict *in vivo* developmental toxicants *in vitro*.

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