The reprogramming of somatic cells to a pluripotent state by a mixture of a few transcription factors will certainly be considered one of the major biological advances of the 21st century. The finding that these induced pluripotent stem cells (iPSCs) can give rise to every cell type in the body quickly triggered an explosion of interest in using patient-specific iPSCs and their differentiated derivatives to model simple and complex clinical presentations of disease.

Remarkable advances have been made in reprogramming technologies beyond the stable integration of 4 core genes (Oct4, Sox2, Klf4, and c-Myc) originally described by Takahashi and Yamanaka in 2006 for mouse cells and soon reproduced from human cells. Although the integrated viruses and transgenes become transcriptionally silenced during reprogramming, insertional mutations and residual transgene or virally induced gene expression may interfere with differentiation or alter subsequent cell phenotypes, leading to questions of whether iPSCs and their derivatives truly reflect a patient’s own cells. To circumvent these issues, newer nonintegrating, virus-free, and vector-free methods have been developed. Importantly, the technology for iPSC creation from patient-derived cells has proven robust in that iPSCs can be effectively derived from many tissues, even from elderly and sick individuals, enabling the derivation of a wide range of patient-specific cells more than just the past few years. These advances now set the stage for modeling...
disease to decipher basic mechanisms, predicting toxic drug effects, matching a drug therapy to an individual patient, and discovering new drugs for a variety of disorders.

Despite such progress, there are significant challenges to implementing large-scale drug screens using iPSC-based models of human disease. The initial problem of directing large-scale production of particular cell types under simplified and defined conditions is being solved for cardiomyocytes and vascular endothelial and smooth muscle cell lineages. Nonetheless, many substantial hurdles must still be overcome. Among these include variability in iPSCs derived even from a single patient, such as could be caused by imperfect reprogramming. The variability in the disease phenotype among iPSC isolates, even from a single patient, can be so great as to mask differences between iPSCs from affected versus unaffected individuals. Second, in order for a screening campaign to be predictive, any in-dish phenotype must be demonstrated to be relevant to the clinical issues surrounding disease treatment and/or management. It is easy to envisage that the need for highly specialized cells or a complex cellular context, such as interactions between multiple cell types or 3-dimensional architecture, could hamper reproducing the disease phenotype in a culture well. Thus, the correct cell type(s) must be produced and interact appropriately in the cell culture assay. Perhaps less obvious is that many diseases take years to manifest in patients and might not be apparent in the developmentally immature cells derived from patient iPSCs, particularly in the relatively short time interval from pluripotent cell to differentiated derivative used in the laboratory experiment or high throughput screen.

Here we review the derivation of cardiovascular disease-specific iPSCs and progress toward recapitulating clinically relevant disease phenotypes in high throughput formats, with particular focus on how iPSC technology can improve the probability that drugs will be clinically effective through the development of realistic human cardiovascular disease models. In addition, we discuss the challenges to be overcome before the potential of iPSC models can be fully exploited for the elucidation of disease processes, as well as drug toxicity, targets, and mechanisms of action.

**iPSC-based Cardiovascular Disease Modeling: From Patient to 384-Well Plate**

In principle, the ability to generate iPSCs from patients will permit the production of unlimited numbers of any cardiovascular cell type needed to model disease. Moreover, natural polymorphisms in the population that confer susceptibility to disease or sensitivity to drugs (eg, drug-induced long QT-2) can be isolated, and the differentiated derivatives of the pluripotent cells can, in principle, be used to model the phenotype (Figure 1). Most disease phenotypes, however, will manifest only in differentiated cells and not in the iPSCs themselves, which are analogous to the pluripotent cells of the peri-implantation embryo. Fortunately, the directed differentiation of cardiovascular cell types is becoming increasingly efficient, at least for heterogeneous populations of cardiomyocytes and vascular endothelial and smooth muscle cells, thanks to protocols that recapitulate normal development (eg, References 9–12). Other reviews in this series summarize the generation of patient-specific iPSCs and recent advances in optimizing the production of different cardiovascular cell types.

A number of iPSC lines have been isolated from patients with a broad range of genetic cardiovascular diseases (Table 1). In most cases, the relevant cell types, cardiomyocytes and smooth muscle cells, have been produced from these patient iPSCs and reported to recapitulate key aspects of the disease phenotypes. For instance, long QT and Timothy syndrome patients exhibit prolonged QT intervals on electrocardiography, and cardiomyocytes derived from patient-specific iPSCs showed increased duration of action potentials when measured by single-cell intracellular recording. Similarly, a recent study investigated the phenotype of cardiomyocytes derived from LEOPARD syndrome patient iPSCs and found the cells

![Figure 1. Use of induced pluripotent stem cell (iPSC) technology for drug discovery.](http://circres.ahajournals.org)
<table>
<thead>
<tr>
<th>Disease Name</th>
<th>Genetic Cause</th>
<th>Clinical Presentation</th>
<th>Disease Mechanism</th>
<th>Cell Type Made</th>
<th>Phenotype Displayed in iPSC-Derived Cells</th>
<th>Drug Testing Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Arrhythmogenic right ventricular cardiomyopathy/dysplasia</td>
<td>Plakophilin-2 L614P</td>
<td>Syncope and sudden death; frequently adolescent/young adult onset; fatty or fatty fibrous replacement of myocardium with thinning of the right ventricular wall</td>
<td>Desmosomal dysfunction</td>
<td>CMs</td>
<td>Reduced expression of plakophilin-2 and plakoglobin; evidence of myofibril disorganization; elevated lipid content relative to control CMs when exposed to adipogenic differentiation media</td>
<td>Nifedipine-inhibited contraction; isoproterenol increased contraction rate</td>
</tr>
<tr>
<td>CPVT-1</td>
<td>RyR2 p.F2483I</td>
<td>Stress-induced ventricular tachyarrhythmia, syncpe, and sudden cardiac death in children and young adults</td>
<td>Diastolic Ca²⁺ leak from the sarcoplasmic reticulum</td>
<td>CMs</td>
<td>Higher amplitudes and longer durations of spontaneous Ca²⁺ transients; Ca²⁺ release events after repolarization; abnormal Ca²⁺ response to phosphorylation induced by increased cAMP levels</td>
<td>None</td>
</tr>
<tr>
<td>CPVT-1</td>
<td>RyR2 S406L</td>
<td>Same</td>
<td>Same</td>
<td>CMs</td>
<td>Catecholaminergic stress induces elevated diastolic Ca²⁺ concentrations, reduced sarcoplasmic reticulum Ca²⁺ content, DADs; increased frequency and duration of elementary Ca²⁺ release events</td>
<td>Dantrolene restored normal Ca²⁺ spark properties and rescued the arrhythmogenic phenotype</td>
</tr>
<tr>
<td>CPVT-1</td>
<td>RyR2 M4109R</td>
<td>Same</td>
<td>Same</td>
<td>CMs</td>
<td>Similar to above, but also evidence of early after depolarizations (EADs)</td>
<td>None</td>
</tr>
<tr>
<td>CPVT-2</td>
<td>CASQ2 D307H</td>
<td>Ventricular arrhythmias causing sudden death in young individuals</td>
<td>Intracellular Ca²⁺ mishandling caused by delayed depolarization (DADs)</td>
<td>CMs</td>
<td>Immature cardiomyocytes with less organized myofibrils, enlarged sarcoplasmic reticulum cisternae and reduced number of caveolae; DADs; Oscillatory arrhythmic prepotentials; After-contractions and diastolic [Ca²⁺]i rise</td>
<td>None</td>
</tr>
<tr>
<td>Familial dilated cardiomyopathy</td>
<td>TNNT2 R173W</td>
<td>Ventricular dilatation, systolic dysfunction, progressive heart failure and dilated cardiomyopathy.</td>
<td>Decreased Ca²⁺ sensitivity and ATPase activity which cause force production impairment</td>
<td>CMs</td>
<td>Reduced beat rate; Compromised contraction Abnormal sarcomeric α-actinin distribution; Altered regulation of Ca²⁺</td>
<td>Metoprolol improved sarcomeric organization</td>
</tr>
<tr>
<td>Duchenne muscular dystrophy</td>
<td>DMD Deletion of exons 45–52</td>
<td>Dilated cardiomyopathies and/or cardiac arrhythmias</td>
<td>Cell death caused by extracellular Ca²⁺ influx</td>
<td>VSMCs, ECs, fibroblasts</td>
<td>Calponin sequestration, premature senescence phenotypes, DNA damage phenotypes associated with vascular ageing</td>
<td>None</td>
</tr>
<tr>
<td>Hutchinson Gilford Progeria</td>
<td>LMNA C1824T</td>
<td>Premature ageing leading to myocardial infarction</td>
<td>Disorganization of nuclear lamina and loss of heterochromatin</td>
<td>VSMCs, ECs, fibroblasts</td>
<td>Calponin sequestration, premature senescence phenotypes, DNA damage phenotypes associated with vascular ageing</td>
<td>None</td>
</tr>
</tbody>
</table>

(Continued)
<table>
<thead>
<tr>
<th>Disease Name</th>
<th>Genetic Cause</th>
<th>Clinical Presentation</th>
<th>Disease Mechanism</th>
<th>Cell Type Made</th>
<th>Phenotype Displayed in iPSC-Derived Cells</th>
<th>Drug Testing</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>LEOPARD syndrome</td>
<td>PTPN11</td>
<td>Hypertrophic cardiomyopathy</td>
<td>Pathogenesis unknown</td>
<td>CMs</td>
<td>CMs are larger, have a higher degree of sarcomeric organization and preferential localization of NFATC4 in the nucleus compared to normal CMs</td>
<td>None</td>
<td>19</td>
</tr>
<tr>
<td>Long QT-1</td>
<td>KCNQ1</td>
<td>Delayed repolarization; Arrhythmias; Polymorphic ventricular tachycardia</td>
<td>Prolonged ventricular repolarization due to mutation in repolarizing potassium channel KCNQ1</td>
<td>CMs</td>
<td>Longer and slower repolarization velocity; Abnormal subcellular distribution of R190Q KCNQ1; Reduction of outward K+ current</td>
<td>Isoproterenol induced EAD was prevented by Propranolol, simulating clinical LQT1</td>
<td>15</td>
</tr>
<tr>
<td>Long QT-2</td>
<td>KCNH2</td>
<td>Same</td>
<td>Significant reduction of the rapid component of the delayed rectifier potassium current (IKr) due to mutation affecting the pore-forming region of the potassium channel KCNH2</td>
<td>CMs</td>
<td>Prolongation of the action potential duration; Reduction of potassium current I\textsubscript{K}\textsubscript{r}; EADs</td>
<td>Nifedipine: complete elimination of EADs; pinacidil: abolished EADs; Ranolazine: pronounced anti-EAD effect at both cellular and multicellular level</td>
<td>16</td>
</tr>
<tr>
<td>Long QT-2</td>
<td>KCNH2</td>
<td>Same</td>
<td>Same</td>
<td>CMs</td>
<td>Same</td>
<td>Nicorandil and PD118057: action potential shortening and reduction of EADs; E4031: induced EADs; isoprenaline induced EADs was blocked by Nadolol and Propranolol, simulating clinical treatment</td>
<td>18</td>
</tr>
<tr>
<td>Long QT-8 (Timothy syndrome)</td>
<td>Cav1.2</td>
<td>ECG features of bradycardia, ventricular and atrial conduction slowing, exhibits aspects of both LQT-3, and Brugada syndrome</td>
<td>Mutation causes impairment of voltage-dependent inactivation of Cav1.2</td>
<td>CMs</td>
<td>Irregular contractions; excessive Ca\textsuperscript{2+} influx; Prolonged action potentials; irregular electric activity; abnormal Ca\textsuperscript{2+} transients</td>
<td>Roscovitine normalized the Ca\textsuperscript{2+} defects and improved channel inactivation</td>
<td>17</td>
</tr>
</tbody>
</table>
| SCN5A overlap syndrome    | SCN5A         | ECG features of bradycardia, ventricular and atrial conduction slowing, exhibits aspects of both LQT-3, and Brugada syndrome | Significant reduction in upstroke velocity of the action potential and longer action potential duration | CMs            | Significant decrease in I\textsubscript{Na} density and upstroke velocity; a larger persistent I\textsubscript{Na} leading to an increased persistent I\textsubscript{Na}

CM indicates cardiomyocyte; CPVT, catecholaminergic polymorphic ventricular tachycardia; DAD, delayed afterdepolarizations; EAD, early afterdepolarization; EC, endothelial cell; ECM, extracellular matrix; GAA, α-glucosidase; I\textsubscript{Na}, rectifier potassium current; I\textsubscript{Kr}, sodium current; rhGAA, recombinant human acid alpha-glucosidase; TGF, transforming growth factor; TNNT2, troponin T type 2; and VSMC, vascular smooth muscle cell.
to be enlarged, possibly reflecting the hypertrophic cardiomyopathy characteristic of these patients.\textsuperscript{19} In addition, vascular smooth muscle cells from iPSCs generated from Hutchinson-Gilford progeria patients were found to undergo premature senescence, suggesting that the cultures recapitulated aspects of the vascular defects seen in these patients.\textsuperscript{20,21}

Impressive as observing disease phenotypes in a dish seems at first blush, it is important to question the extent to which they mirror the clinical presentation of the patient so that drugs developed based on the in vitro model will elicit a salutary response in people. In this regard, it is important to bear in mind that human embryonic stem cell (hESC) and iPSC-derived cardiomyocytes are quite immature electrically, metabolically, and mechanically. Thus, they do not express the same complement of structural proteins and ion channels, nor would be expected to exhibit the same energetics, as their counterparts in the heart of an adult or even a child. As summarized,\textsuperscript{22,23} human induced pluripotent stem cell (hiPSC) and hESC cardiomyocytes are characterized by their small size, poorly organized myofilaments, and a punctate and uniform distribution of gap junctions that would influence action potential propagation. In addition, immature pluripotent-derived myocytes show ion channel differences that cause slower action potential kinetics (typically dV/dt is \textlt; 20 V/s as compared with adult ventricular myocytes with dV/dt of 100–150 V/s), a less well-developed sarcoplasmic reticulum making contractility dependent on Ca\textsuperscript{2+} entry rather than internal sarcoplasmic reticulum stores, and a relatively depolarized maximum diastolic potential and a slow phase IV depolarization that confer persistent automaticity and develop a negative, rather than positive, force-frequency relationship. Although not extensively studied to date, the metabolism of pluripotent stem cell-derived cardiomyocytes is expected to resemble that of fetal cardiomyocytes, which rely predominantly on glucose rather than fatty acids as an energy source, as do adult cardiomyocytes,\textsuperscript{24,25} although increased mitochondrial content and the capacity for oxidative metabolism distinguish hESC-derived cardiomyocytes from pluripotent progenitors and positively affect their differentiation.\textsuperscript{26,27}

As a consequence of their embryonic nature, iPSC-derived cardiomyocytes as produced currently are not capable of being completely accurate models of diseases that occur only in the physiological context of mature cardiomyocytes, and the same is true for other cardiovascular derivatives, albeit less strikingly. Even if the patient iPSC-derived cells exhibit an altered in-dish phenotype relative to normal cells, the phenotype might involve a different set of signaling and genetic pathways from those operating in the patient’s own cells, giving rise to a mimic rather than an accurate model of the disease. This presents a serious problem for drug discovery, because the all-important ancillary proteins and pathways that modulate the disease in the cells of the patient, and, hence, constitute high-value drug targets, could be quite different. Therefore, in-depth analysis of the disease model is necessary to be certain that it accurately mirrors the clinical presentation of the disease.

Clearly some diseases will be easier to model than others. iPSC-derived channelopathies might represent good candidates for drug development, because the mutated proteins themselves are likely to be reasonable drug targets for treating disease, and their cell autonomous and monogenic nature facilitate assay development. As an example, 2 recent reports investigated whether the iPSC-derived cardiomyocytes reproduce the phenotype of patients experiencing catecholaminergic polymorphic ventricular tachycardia type 1, which is caused by mutations in the cardiac ryanodine receptor type 2 gene (\textit{RYR2}) and is characterized by stress-induced ventricular arrhythmia that can lead to sudden cardiac death in young individuals with structurally normal hearts. The cardiomyocytes generated from patient iPSCs, with different mutations, showed increased propensity to generate spontaneous Ca\textsuperscript{2+} sparks in response to catecholaminergic stimulation and increased susceptibility to delayed after depolarizations,\textsuperscript{26–31} similar to the physiology of mutant \textit{RYR2} receptors in transgenic mice and transgenic mice, and the increased propensity for \(\beta\)-adrenergic triggered arrhythmias in response to exercise and stress.\textsuperscript{32–34}

Although animal models continue to be important for understanding disease mechanisms, they have limitations that might be overcome through the use of human cellular models. In particular, many transgenic mouse models of genetic diseases do not faithfully reflect the human pathophysiology. For example, the spontaneous hematopoietic failure that characterizes human Fanconi anemia patients is not mirrored by mouse models but does develop in differentiating iPSC cultures.\textsuperscript{35} In the heart, discrepancies between the pathophysiology of transgenic models and the human clinical presentation reflect different ion channel types and distribution, resulting in faster heart rate and shorter action potential duration of the mouse, as well as the differences in cardiac anatomy, such as vastly greater wall thickness. Although large animals might pose better disease models, creating transgenic versions of Dolly the sheep with human disease-causing mutations is exceptionally challenging,\textsuperscript{36} and although useful for later stage testing, do not advance target identification or in vitro drug screening. Thus, the early examples of iPSC-based cardiovascular disease models suggest that they are capable of bridging the gap between cell-based studies and animal models with clinical experimentation, which is costly and not generally amenable to mechanistic and target identification studies. Although the recent studies involved monogenic rather than polygenic disorders, presumably because of their relative simplicity, the same strategy and concerns should be relevant to polygenic disease. Regardless of the disease, it is essential that the cellular context, complete with relevant cell type and disease-associated profiles of gene and protein expression, plus the intracellular signaling pathways that influence the disease manifestation, match those in the clinical presentation to ensure that the model expresses appropriate targets for pharmaceutical intervention.

Modeling the vascular manifestations of Marfan syndrome (MFS) is a good illustration of contextual relevance. MFS is caused by mutations in the gene encoding fibrillin-1 (\textit{FBN1}). Although the fibrous connective tissue disorders of MFS were originally attributed to structural weakness of fibrillin-rich extracellular matrix, the pathological manifestations are now thought to involve enhanced bioavailability of transforming growth factor (TGF)-\(\beta\), explaining the resemblance to
MFS-related disorders such as MFS-type II and Loeys-Deitza syndromes, caused by elevated signaling through mutated type 1 and type 2 TGF-β receptors. Enhanced TGF-β signaling was reported recently in mesenchymal cells derived from MFS iPSCs and ESCs and also shown to underlie their spontaneous chordogenic differentiation, in contrast with normal iPSC/ESC-derived mesenchymal cells that require exogenous TGF-β chondrocytes. Although consistent with the skeletal manifestations of MFS, they do not model the potentially lethal thoracic aortic aneurysm that is closely associated with smooth muscle dysfunction. Moreover, the site-specific localization of thoracic aneurysm, as for regional susceptibility to calcification and atherosclerosis, is thought to be linked to the particular developmental origin of vascular smooth muscle cells (VSMCs), which by fate-mapping studies are known to arise from a remarkable diversity of mesenchymal populations in the embryo. Therefore, relevance of an in-dish phenotype for the vascular MFS phenotype most likely requires recapitulating the VSMC defect. In this regard, the recent article by Cheung et al is important because it described methods that recapitulate the developmental sequence of events to produce 3 distinct types of aortic VSMCs from iPSCs: aortic root VSMCs, derived from the lateral plate mesoderm via the secondary heart field; the ascending aorta and arch, which come from neural crest cells that emanate from the lateral border of hindbrain neuroectoderm; and the descending aortic VSMCs that originate from the somitic mesoderm. Each population exhibits distinct responses to cytokines, including differential activation of matrix metalloproteinase 9 and tissue inhibitor of metalloproteinase 1, in response to interleukin 1β that is likely to be relevant to the phenotypic modulation seen before aortic aneurysms in animal models. Given that VSMCs of diverse origin respond differentially to physiological stimuli, the clinical presentation of MFS would be best modeled in neuroectoderm-derived VSMCs, because these are analogous to ascending aorta and arch, where the Marfan phenotype is most prominent. Therefore, these cells seem likely to reflect the appropriate cellular context and, hence, the repertoire of potential drug targets.

**Discovery of Disease Mechanisms and Potential Drug Targets**

A few groundbreaking studies have probed iPSC-based cardiovascular disease models with small molecules, natural products, and biologics (Table 1), clearly demonstrating the feasibility of using disease-in-dish assays to evaluate drug responses. For example, Jung et al found that Dantrolene, which binds to the amino terminal region of RYR2 and restores interdomain interaction critical for the closed state, alleviated the arrhythmic behavior of catecholaminergic polymorphic ventricular tachycardia type 1 iPSC-derived cardiomyocytes. Similarly, the application of Ca2+-channel blocker Nifedipine and K ATP channel opener Pinacidil shortened the action potential duration and abrogated early after depolarizations in iPSCs-derived long QT-2 mutant cardiomyocytes. Although none of the reported iPSC-based studies have evaluated more than a few drugs, these early studies clearly show that the assays can discriminate drug effects, even if translation to clinic will require much more testing than in the immature and monocultured cardiomyocytes. Can iPSC-derived cells be used in high throughput? Moderate throughput screens of mouse and human embryonic stem cell-derived cells have been effective in identifying compounds that promote cardiogenic mesoderm from stem cells and others that target Wnt and TGF-β pathways to control cardiac cell differentiation, and primary neonatal rat cardiomyocytes have been used in a moderate throughput screen that identified microRNAs (miRs) that control hypertrophy. Although encouraging, the studies to date have been low-to-moderate throughput and, therefore, have not overcome the formidable hurdles to true high throughput screening (HTS) of hiPSC-based disease models. These include producing the desired and potentially rare cell types for disease modeling reproducibly and in adequate quantity, purity, and quality for HTS. Procedures for bioreactor process development, cell banking of primary and differentiated derivatives, and protocols for robotic automation must be devised. Importantly, the assay readout must have sufficient dynamic range to reliably distinguish disease from control states. Moreover, variability among iPSC line isolates must not be so great as to obliterate a difference between disease and normal states. Implementation of large-scale screening of >2 million compounds has been described using mouse embryonic stem cell-derived neuronal cells, yielding compounds that potentiate a particular glutamate receptor subtype. Adapting large-scale approaches to iPSC-based human disease models will accelerate their adoption for drug screening.

These issues are addressed during assay development and ultimately dictate whether the assay can be screened in true high throughput (up to millions of compounds) versus a low or moderate throughput capacity, such as for validating hits or studying their mechanisms of action (typically 1000–50000 wells). Readouts for cellular assays (Figure 2) can be whole well measurements, such as by a plate reader (eg, a gene promoter directing luciferase). This is the most common format and is referred to as HTS. Alternatively, high content screening (HCS) is the analysis of images acquired by automated microscopy, which is capable of providing multiple parameters of features, such as cell morphology, protein or gene expression, lipid accumulation, and so forth, reported for either the whole well or on a cell-by-cell basis. In addition to reading out subcellular details, single-cell (cytometric) analysis has the advantage of quantifying the number of cells exhibiting some trait, and this can be a more robust readout than scoring the overall level of activity. In addition, the rapid assessment of cells over time enables physiological responses on a whole well basis and is commonly used to measure calcium responses to G protein-coupled receptors by instruments such as the Fluorometric Imaging Plate Reader (Molecular Devices Corp). Recently, high content imaging and physiological recording are merging with the development of automated means to optically record cellular responses on a cell-by-cell basis at fast (33–100 Hz) rates. An iPSC-based screening assay, assuming it is capable of finding drug candidates that will translate effectively into clinically meaningful activity in patients, can in principle be used in primary screening to discover compounds with novel targets and/or molecular mechanisms of action (MMOAs).
MMA is defined as the biochemical mechanism through which a drug affects its target(s) to elicit a functional response in the cell (e.g., the precise effects on kinetics, stability/ degradation, protein modification, or redox processes of the target). Because an iPSC-based disease screen would most likely be a black box phenotypic assay, meaning that there is no preconceived hypothesis regarding target or MMA, it could theoretically be harnessed to reveal novel targets and MMAAs that are unlikely to emerge from target-based screening. However, phenotypic assays have 2 primary disadvantages that need to be addressed. First, knowledge of the target and MMA of active compounds aids in the subsequent medicinal chemical optimization of drug leads. Therefore, identifying the relevant macromolecular targets of the small molecule leads will likely become a priority but is often extraordinarily challenging (see below). Second, complex disease model screens are expected to have less throughput and to be more costly than comparatively simple target-based approaches, especially if they involve multiple cell types, complicated or prolonged differentiation and culture conditions, and image-based readouts, despite advances in HCS and automated microscopy. Although not precluding using iPSC-based disease assays as primary screens, these limitations prompt the question of whether a disease-in-dish screen should be intended to identify novel targets or drug leads. In other words, should the immediate intention be knowledge or drug discovery?

To finely characterize the molecular mechanisms of disease and bring potential drug targets into focus, pursuing the knowledge discovery path from a primary screen through to target identification and characterization of the drug’s MMA requires satisfying 2 conditions. First, the cellular context of the assay must contain drug targets relevant to ameliorating human disease. Second, there must be a robust means to identify and validate the cellular macromolecules targeted by the screen hits. The molecular disturbances that are the root cause of the disease phenotype may not necessarily be the same as the cellular macromolecules that could be pharmacologically targeted to alleviate disease symptoms. For instance, effective treatment of long QT caused by human ether-à-go-go related gene (hERG) mutations might involve small molecule targeting of a current other than the rectifier potassium current. Similarly, in contrast to antisense or RNA interference therapies, the potential targets by which a small molecule might treat cardiomyopathies caused by structural alterations in troponin T type 2 or Duchenne muscular dystrophy because of truncated dystrophin are unknown but might be revealed through studying cardiomyocytes derived from patient-specific iPSCs. As another example, iPSC models of Pompe disease might aid in discovering and characterizing small molecules that target signaling proteins to boost expression of the mutated acid α-glucosidase, as well as alter its bioavailability or trafficking, for those patients who can make protein, in addition to directly targeting GAA (e.g., acting as a small molecule chaperone to restore its shape or function). Thus, the cell type used in the assay must have as close a range of signaling pathways and proteins as the cells affected in the patient. More complex formats, such as involving 3-dimensional engineered tissues or hard-to-obtain cell types that match the

**Figure 2.** High throughput assay readouts. High throughput screening (HTS) readouts measure parameters of entire wells, such as luciferase or fluorescence, and readout by a plate reader (left). Monitoring whole well fluorescence or luminescence over time is also feasible (not shown). In contrast, high content screening (HCS) is based on the quantification of images and has the potential to report multiple parameters on a cell-by-cell (cytometric) basis, such as cardiomyocyte hypertrophy (middle). Kinetic imaging cytometry is the quantification of fluorescent probes over time and enables cell-by-cell analysis of physiological responses, such as for Ca2+ transients recorded under spontaneous or stimulated conditions, exemplified by the effect of an arrhythmogenic drug (right). (Illustration Credit: Ben Smith).
clinical presentation, might be prohibitively costly or unfeasible for HTS. For these reasons, it is logical to consider pursuing an iterative process that uses smaller scale, moderate throughput screens of phenotypic assays against functional and chemical genomics libraries (see below) to unveil disease-modifying cellular processes and macromolecular targets. Subsequently, validation of key processes and potential druggable targets can be accomplished through rescreening of additional and selective agents to eventually yield a refined network of cell signaling proteins and/or gene hierarchies that modulate disease phenotypes (Figure 3). The resulting cell signaling proteins can then be entered into a conventional target-based drug discovery pipeline.

**Chemical Genomics**

In the target-centric model of drug development, the pipeline begins by screening a biochemical or cell-based assay against a large chemical library to identify compounds that modulate a predetermined target of interest. Compounds are not tested for efficacy in actual disease-relevant assays until considerably later and often not against human disease until phase II clinical trials. Although this approach has been very successful over the past decade in developing drugs against well-characterized targets, it carries the risk that drugs that emerge from satisfying the constraints of target and MMOA may not be effective therapeutically, and this has been proposed to contribute to the high rate of drug candidate attrition, as discussed in Swinney and Anthony and Kola and Landis. By contrast, it is hoped that iPSC disease-in-dish technology will provide a means to introduce the patient-relevant context at the earliest stages of drug discovery and development (Figure 3). This would have 2 main advantages. First, it should be possible to obtain ef- ficacy and toxicity data before the nomination of compounds for costly animal and human testing and, second, the ability to directly identify novel disease-relevant targets through a chemical genomics or functional genomics approach.

Chemical genomics is the evaluation of the genome by screening phenotypic assays against libraries of small molecules followed by deconvoluting the cellular targets of the hits. Functional genomics is conceptually similar but involves libraries of nucleic acids or proteins (eg, small interfering RNAs [siRNAs], miRs, or expressed open reading frames) rather than a chemical library. Chemical and functional genomics are analogous to classic forward genetic screening by mutagenesis and have the power to dissect mechanisms of human disease, especially when combined with iPSC technology and a systems biology approach to building a signaling and genetic network among the cellular targets of the screen hits.

Chemical and functional genomics, therefore, are powerful tools to uncover disease mechanisms and to reveal novel druggable targets for treatment. The disease-in-dish assay is inherently phenotypic, meaning that the end point is an alteration in morphology, behavior, or physiology of cells in culture, rather than the direct biochemical activity of the target protein. Unlike target-based assays, which typically pose a single particular protein as a target for screening, phenotypic assays present a plethora of potential cellular macromolecules that could be targeted to elicit a desired cellular response. Phenotypic assays are generally more complex and costlier to develop and execute than target-based assays. Consequently, phenotypic assays are often reserved as secondary assays to evaluate hits from traditional target-based screening, although they are generating considerable interest as a means to cast a broad net for novel classes of therapeutic targets.

Phenotypic screening of complex bioassays has been successful and has exploited stem cell assays and even whole
organism screens.54,55 Indeed, primary screening of phenotypic assays in the pharmaceutical company setting has led to the initial discovery of a number of new small molecule drugs, in particular, first-in-class new molecular entities (NMEs). The calcium receptor allosteric activator Cinacalcet56 and the N-type calcium channel blocker Ziconotide57 are examples of drugs that resulted from phenotypic screens with little or no previous knowledge of the MMOA. In addition, phenotypic screens have also elucidated MMOAs for established targets that, in turn, led to additional small molecule drugs.51 More recently, a phenotypic assay for aberrant mitosis led to the discovery of Monastrol, which targets the motor protein Eg5 and is a promising antineoplastic agent.58

The fact that the target of a phenotypic assay is not known beforehand influences the choice of the molecular library for screening (Table 2). Primary HTS drug discovery campaigns often evaluate 300,000 to 100,000 small molecule compounds, typically without replicates, necessitating a high dynamic range, extreme assay robustness, and low cost.59,60 On the other hand, screens designed to probe pathways and targets, typical of chemical and functional genomics studies and well suited to the knowledge discovery mission of academia, are generally moderate throughput, on the order of 1000 to 50,000 wells. Because the cost in terms of effort and resources is relatively low, such assays can be performed in replicate to accommodate the higher level of assay noise often encountered in phenotypic assays. Whole genome RNA interference, miR screens, and many small molecule library screens are examples of low or moderate throughput screens.

Small molecule screen libraries fall broadly into 2 categories, diversity oriented and focused. Compound diversity collections bind many protein classes and are often used in phenotypic screens when the target is unknown. The tradeoff in using diversity collections is that any one molecule has a low probability of being active) for an excellent discussion see a recent article by Stockwell60), and identifying the target remains extraordinarily challenging (see below). Focused libraries, in contrast, are oriented toward specific classes of druggable targets and are constructed based on knowledge of the topology of chemicals that bind particular proteins. For iPSC-based screening assays, these might be focused on structures known to modulate the activity of protein classes hypothesized to result in clinical benefit to patients with a particular disease. Focused libraries can also be assembled to probe the involvement of proteins that mediate particular cell signaling or other cellular processes (eg, collections of kinase inhibitors and pathway modulators to probe signal transduction pathways), permitting chemical genomic dissection of disease mechanisms. Such libraries have been used to reveal mechanisms of cardiomyocyte differentiation,42 but they are constrained by the limited set of proteins that they affect in the cell. New strategies are being developed to circumvent the limitations of traditional libraries. Among the most interesting is the idea of biological activity space, exemplified by a library of chemical structures tailored to affect tumor proliferation assembled based on the structure-activity relationships of hits from antiproliferation screens of 60 tumor cell lines.51

The number of small molecules is cosmologically vast, yet only a fraction are feasible to synthesize and considered likely to yield good drugs.59 For this reason, diversity libraries contain compounds from the intersections between chemical properties that historically have defined oral absorption, distribution, metabolism, and excretion properties (space and drug likeness) and particular structural and physicochemical properties that define high-affinity, functional interactions with individual target classes. These compounds tend to target proteins with topologically defined drug-binding pockets, such as enzymes, G protein-coupled receptors, kinases, nuclear receptors, and ion channels,52 leaving many biologically interesting proteins, such as transcription factors, scaffold proteins, and structural proteins, largely unexplored.60,63 It is thought that there are >1,000,000 total human proteins, including splice variants, posttranslational modifications, and somatic mutants,64 greatly overshadowing the calculated 3000 to 10,000 so-called druggable proteins and the ∼500 proteins targeted by our current pharmacopeia, although few small molecules can be considered completely selective, and not all proteins would make good drug targets.52,65 Thus, typical drug discovery libraries, however vast, only scratch the surface of protein diversity within the cell.

A related issue with using a drug discovery (diversity) library for phenotypic screening is that progressing from hit to a novel target remains serendipitous. A common approach for identifying the targets of small molecules is to affinity capture proteins from cell lysates using a compound tethered to a solid matrix, followed by mass spectrometry analysis and subsequent identification of the binding proteins. The challenges of the chemical proteomics approach lies in promiscuity of

**Table 2. Library Design and Screening Goals**

<table>
<thead>
<tr>
<th>Library Type</th>
<th>Size</th>
<th>Type Description</th>
<th>Pros</th>
<th>Cons</th>
<th>Suitable for</th>
</tr>
</thead>
<tbody>
<tr>
<td>Diversity</td>
<td>$10^9$ to $10^8$</td>
<td>Small molecule</td>
<td>Immediate drug discovery</td>
<td>High cost target ID difficult</td>
<td>Drug discovery</td>
</tr>
<tr>
<td>Focused</td>
<td>$&lt;10^6$</td>
<td>Small molecule</td>
<td>Restricted target coverage Target ID easier</td>
<td>Restricted target coverage</td>
<td>Drug discovery Target identification</td>
</tr>
<tr>
<td>Chemical genomics</td>
<td>$&lt;10^4$</td>
<td>Small molecule</td>
<td>Target ID easy</td>
<td>Not drug discovery</td>
<td>Knowledge discovery Target identification</td>
</tr>
<tr>
<td>Functional genomics</td>
<td>$&lt;10^4$</td>
<td>siRNA, shRNA, miR, ORF</td>
<td>Target ID easy</td>
<td>Not drug discovery</td>
<td>Knowledge discovery Target identification</td>
</tr>
</tbody>
</table>

Different library designs carry distinct advantages and disadvantages and should be matched to the intent of the screen as well as to considerations of scale and cost. ID indicates identification; miR, microRNA; ORF, open reading frame; shRNA, short hairpin RNA; and siRNA, small interfering RNA.
hits from diversity libraries coupled with poor sensitivity of the pull-downs, although new mass spectroscopic techniques might improve the target identification beyond current capabilities.56 Alone, the technology cannot distinguish between proteins that merely bind from those that are relevant for the activity of the small molecule in the cell. The problem is that there can be high-affinity chemical-protein interactions with proteins that are irrelevant for the activity and lower affinity interactions with higher abundance proteins that obscure the relevant target.

Because of the difficulties inherent in identifying targets of hits from diversity library screens, we contend that it is more efficient to screen disease-in-dish assays against libraries of molecules for which the targets can be readily identified and then to move the targets through a process of in vivo validation and ultimately into the conventional drug discovery pipeline, as opposed to directly use a black box assay in a primary screen of a diversity library (Figure 3). Libraries for target and pathway characterization compose signaling pathway modulators (eg, kinase inhibitors), known drugs, and other well-characterized bioactive molecules. These libraries are potent tools for the molecular dissection of disease mechanisms and might aid in revealing novel therapeutic targets but are not designed for the direct discovery of NMEs. An example of small-scale screening is to test prescribed drugs against patient iPSC-derived cells to tailor a therapy to a particular patient class. On a larger scale, chemical and functional genomics screens can be coupled to systems biology to unveil basic disease mechanisms that might ultimately lead to novel drug targets. HTS screens for these novel targets can then be developed to discover new drugs (Figure 3).

Functional Genomics, RNA Interference, and MicroRNA Screening

Oligonucleotide libraries offer an alternative to chemical libraries for probing cardiovascular or other disease phenotypes. RNA interference (siRNA or short hairpin RNA [shRNA]) technology has proven to be a powerful reverse genetic method to evaluate the function of candidate genes, and even screen entire genomes, for the identification of pathway components that govern a variety of complex processes, such as proteins that sustain pluripotency in embryonic stem cells.67,68 RNA interference functions by introducing a double-stranded siRNA or shRNA into the cell to target cognate mRNAs for degradation by the RNA-induced silencing complex (RISC). siRNA and shRNA libraries are commercially available for human and other genomes and provide a means to predict the physiological and biological consequences of pharmacological target inhibition.

Although siRNAs and shRNAs are synthetic tools designed to target single mRNA species (although selectivity is not assured), miRs are endogenous, ≈22-nucleotide single-stranded RNAs that directly bind and suppress multiple mRNA targets. For instance, miR-223 is estimated by proteomics to affect >200 targets in neutrophils alone,69 and an estimated 60% of the total proteome is under direct control by miRs.70 Even more striking, miRs often block the expression of multiple proteins that govern the same biological process.

miR-486, for instance, blocks the production of multiple proteins that mediate phosphatidylinositol-3-OH kinase–AKT signal transduction.71 Similarly, miR-133a1 and miR-133a2 were found to negatively regulate multiple smooth muscle genes in cardiomyocytes, consistent with their role as mediators of serum response factor.72 miRs bind mRNAs through Watson-Crick base pairing of their seed sequence to the 3’ untranslated regions or, less commonly, the coding region. By governing translation, they fine tune nearly every normal and pathological process examined.73,74 In cardiovascular biology, miRs control early embryonic development and adult disease, exemplified by the essential roles of miR-1 and miR-133 in heart development75,76 and miR-21 and miR-208a in cardiac remodeling after myocardial infarction76,77 and metabolism.78 A large portion of the proteome is regulated by relatively few miRs; there are only ≈1500 human miRs in the human genome (www.mirbase.org), making libraries of oligonucleotide miR mimics an efficient means to elucidate disease-modifying mechanisms, regardless of whether a particular miR identified through such an approach is normally involved in the disease. Indeed, recent screening of oligonucleotide miR mimics has led to the discovery of miRs that govern formation of cardiogenic progenitors,79 cardiomyocyte cell cycle entry,80 and cardiomyocyte hypertrophy.81 miRs discovered through screening can be matched to candidate targets through computational and biochemical approaches. Computational algorithms are based on the sequence alignment of the miR seed sequence to the 3’ untranslated region of candidate target genes.81,82 The various software packages differ in the methods used to increase specificity, most commonly by exploiting nucleotide composition rules of the putative binding site(s), structural accessibility, or evolutionarily conservation of location of recognition elements within the 3’ untranslated region. The interactions between miRs and their bona fide targets have been hard to model because sequences surrounding the recognition site affect recognition, as does cellular context that can include untranslated region-binding cofactors that influence site accessibility (reviewed in Reference 73), making computational approaches alone too error prone for use as a sole means of target identification. To complement these deficiencies, investigators have turned to biochemical strategies, such as cataloging the proteins or transcripts that are depleted by overexpression of a particular miR, or direct determination of mRNAs that are brought into the RISC. For example, immunoprecipitation of RISC using antibodies against Argonaute 2 protein, the component of RISC that selects the miR strand to be base paired to the target mRNA, is effective in pulling down target mRNAs in multiple settings (eg, References 83–85). When combined with RNAseq, this approach can yield comprehensive insight into context-dependent targets of overexpressed miRs.86,87 In our laboratory, we use bioinformatics tools to link predicted targets of active miRs, along with interacting proteins, into networks that are then tested and refined by evaluating the effects that selective inhibition (by siRNA or selective small molecule inhibitors) of key network nodes has on the original assay readout. In this way, miRs and other functional and chemical genomics screen data can be translated into information about
signaling and genetic cascades that control or modulate a disease state. In addition to interrogating pathological mechanisms to identify drug targets, screening of miRs for activity in disease-in-dish assays might provide knowledge of miR function that could lead to the development of therapeutics that mimic or target miR function. Potential RNA-based therapeutics are composed of antisense RNA, ribozymes, RNA decoys, aptamers, siRNA, shRNA, and miRs that are distinguished not only by their structures and chemical compositions but also by their targets and mechanisms of action. Of these, siRNAs, shRNAs, and miRs exploit RISC-mediated targeting of mRNAs discussed above, and >20 candidate siRNAs, shRNAs, and miR therapeutics have been evaluated in clinical trials. These include vascular targets, for instance, siRNAs to VEGFA (Bevasiranib, Opko Health) and VEGFR1 (AGN-745, Allergan) were evaluated in clinical trials for age-related macular degeneration (Opko Health: phase I [NCT00722384] and phase II [NCT00259753]; Allergan: phase I/II [NCT00363714] and phase II [NCT00395057] trials). Unfortunately, both failed to achieve desirable clinical endpoints for reasons that have been linked to nonspecific activation of Toll-like receptors that potentially could be alleviated by chemical modification of the backbone and enhanced delivery. The first anti-miR candidate therapeutic miravirsen, a chemically modified oligonucleotide designed to inhibit miR-122, has recently advanced to a phase II trial (Santaris Pharma: NCT01020402) to treat chronic hepatitis C virus infection. There have not yet been clinical trials of miRs or anti-miR therapeutics for heart disease, although numerous miRs can be considered as potential therapeutic targets.

Cardiotoxicity and Arrhythmogenicity Testing
A valuable near-term opportunity for applying iPSC-derived cardiomyocytes in the drug discovery pipeline is to screen for cardiotoxic and arrhythmogenic effects. Drug-induced cardiotoxicity is difficult to predict and consequently remains a major factor for drug failure during development and even withdrawal after market launch, adding to the high cost of drug development. Many recent failures involve fatal ventricular tachyarrhythmias, including the rare Torsade de Pointes. Torsade de Pointes is commonly related to inhibition of the delayed rectifier potassium current, which is mediated by the human ether-a-go-go related gene (hERG/KCNH2) and KCNE2 channels that are responsible for action potential repolarization. Highly predictive assays involving whole heart or slice preparations and in vivo animal testing remain the standard for preclinical safety pharmacology, and extensive testing in humans occurs during phase III clinical trials. Assays that are currently of sufficient throughput for use in the early stage discovery, when drug candidates emerge, typically focus on single channels such as hERG and use tumor cell lines, such as automated patch-clamp recording of hERG-expressing Chinese hamster ovary cells. hESC- and hiPSC-derived cardiomyocytes, despite their electric and mechanical immaturity, nonetheless recapitulate many complexities of human heart muscle cells. Hence, they offer a quantum leap over tumor cell lines and can be used at the earliest stages of drug discovery. Moreover, it should also be possible to use the pluripotent stem cell-derived cardiomyocytes to test for other cardiotoxic liabilities, such as cardiomyopathies caused by certain anticancer drugs, that would not be readily detected in noncardiomyocytes.

A limitation of intracellular or patch-clamp recording for safety pharmacology is inadequate throughput for early stage testing. Multiple electrode array devices have been explored as an alternative to single-cell recording, yet, although the throughput is greater, it is still restrictive and the electrode arrays are costly. Intracellular calcium measured by fluorescent probes or by patch-clamp recording of calcium current \( I_{Ca} \) has been reported to be highly predictive of cardiotoxicity and arrhythmogenicity because it integrates the electrophysiological and signaling events leading to muscle contraction. To improve throughput, automated platforms are being developed for high throughput acquisition of Ca\(^{2+}\) and voltage dynamics using fluorescent reporters in contracting cardiomyocytes from hESC and hiPSC sources with sufficient throughput for early stage drug testing and primary screening. The instrument described in Cerignoli et al records from all cells within each field of view simultaneously and analyzes results on a cell-by-cell basis, enabling detailed analysis of individual cells or subsets gated by kinetic parameters (Figure 2).

One of the most appealing aspects of using hiPSC-derived cardiomyocytes in assessing risk is that cells can be prepared from individuals demonstrated to be susceptible to drug-induced arrhythmias, such as Torsade de Pointes. In principle, the predictive power of such a panel of cells, at least for detecting cell autonomous disturbances, could outstrip that of clinical testing given the relatively low incidence of susceptible individuals in the general patient population. Clinically relevant arrhythmia, especially re-entry–based clinical arrhythmia, depends not only on appropriate channel types and distribution but also on complex regional differences in electrophysiological properties within the ventricular wall that can be altered by pathology. Absolute QT intervals of isolated myocytes are not very predictive for arrhythmia incidence, and multifactorial methods may be more predictive. Interestingly, Matsa et al observed that cardiomyocytes from a long QT-2 patient and her asymptomatic carrier (mother) iPSCs showed more evidence of arrhythmias when sparsely plated cells were measured by single-cell patch-clamp recording than when field potentials were measured from more dense aggregates by multiple electrode array, which revealed arrhythmia in the patient but not the asymptomatic mother, perhaps indicating a stabilizing effect of noncardiomyocytes and suggesting that assessing complex populations might be better than isolated cardiomyocytes at predicting arrhythmia. Thus, the challenge of how to model complex electrophysiological phenomena using patient-specific iPSC-derived cardiomyocytes remains significant but, if solved, could greatly increase the predictive power of in vitro testing. Peering further into the future, a better understanding of the mechanisms that drive maturation, coupled with the development of materials that reproduce the 3-dimensional structure of myocardium, should enormously increase the use
of pluripotent stem cell-derived cardiomyocytes for assessing cardiotoxicity of new drugs.

Conclusions and Prospects

iPSC-based disease models represent a powerful new tool for drug discovery, with promising applications for primary phenotypic screening, elucidation of novel targets, and physiological assays for evaluating cardiotoxicity and optimization of patient-specific therapies. Although limited in scope, groundbreaking studies have shown that it is possible to elicit disease-relevant phenotypic changes in response to drugs, supporting the view that iPSC models can recapitulate genetically inherited disorders and be used for phenotypic screening. However, a number of major questions regarding the application of the iPSC cardiovascular disease models remain to be answered. Most importantly, to what extent will physiological studies on iPSC derivatives predict the effect of a drug on the clinical condition, in particular given that the cells might not be precisely the right cell type responsible for the disease, are maintained in vitro, and possibly exhibit an immature physiological response to the drugs? For example, the drugs shown by Itzhaki et al. to be effective in an iPSC-based long QT-2 model, Nifedipine and Pinacidil, would not be considered clinically at these doses because they would decrease vascular tone and be unacceptably hypotensive. It would be unrealistic to expect that small molecules found active in iPSC-based disease models in vitro would be immediately and consistently applicable to disease in humans; thus, devising additional disease-relevant assays remains an important challenge of the development process. Nonetheless, early indications suggest that iPSC-based disease models can make predictive primary screens and, by also enabling more clinically relevant secondary assays, will be an effective entry point to tailoring drug treatments or discovering NMEs.

Phenotypic assays are increasingly implemented in the pharmaceutical company setting not only for secondary assays and in mechanistic studies but also for primary screening. When used for primary screening, they represent a neoclassic alternative to target-based approaches because they mirror practitioner experience as the classical means of discovering compounds. Whether phenotypic approaches can reverse the trend toward fewer innovative new approved drugs per increasing investment in drug research and development and offset the anticipated revenue loss because of patent expirations remains uncertain. However, a recent report by Swinney and Anthony, who analyzed NMEs between 1999 and 2008, concluded that phenotypic screening outstripped target-based approaches for first-in-class small-molecule NMEs 28 to 17, but target-based bested phenotypic for screening follower small-molecule NMEs, 53 to 30. Phenotypic assays also showed a broader range of MMOAs than did target-based assays. This suggests that recapitulating the cellular context in a phenotypic assay increases the likelihood of developing a successful drug against a novel target and/or with optimal MMOA, increasing the efficiency of the drug discovery and development process. Therefore, the ability to generate iPSCs from patients with diseases of characterized and uncharacterized etiologies represents an unprecedented and powerful resource, because it is now theoretically possible to generate large numbers of organ-specific cell types to produce more realistic disease models.

More research is needed to harness the potential of iPSCs. First, by working out methods for directing the differentiation of disease-relevant cell types, including solving the problem of producing cells that recapitulate adult disease without the (possibly many year) latency to overt clinical presentation. Second, it will be important to develop improved methods for recreating the 3-dimensional architecture of vascular and myocardial tissue. This will be a tremendous advance that will certainly aid in creating representative physiological models (eg, to study substrates for arrhythmia and for measuring physical and other properties relevant to myocardial hypertrophy and heart failure) and lead to more realistic assays. Finally, improved proteomic methods for the identification of the protein targets of drugs from black box phenotypic assays are needed to help advance compounds through the development pipeline. Pursuing these challenges will introduce the patient context to the earliest stages of the drug pipeline, thereby broadening the scope of target and MMOA diversity and promising to increase the efficiency and productivity of drug discovery.

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Disclosures

M.M. has ownership interest in ChemRegen, Inc, and is a consultant/advisory board member of Vala Sciences. E.W. has ownership interest in ChemRegen, Inc.

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