Finding the Rhythm of Sudden Cardiac Death

New Opportunities Using Induced Pluripotent Stem Cell–Derived Cardiomyocytes

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Abstract: **Sudden cardiac death is a common cause of death in patients with structural heart disease, genetic mutations, or acquired disorders affecting cardiac ion channels. A wide range of platforms exist to model and study disorders associated with sudden cardiac death. Human clinical studies are cumbersome and are thwarted by the extent of investigation that can be performed on human subjects. Animal models are limited by their degree of homology to human cardiac electrophysiology, including ion channel expression. Most commonly used cellular models are cellular transfection models, which are able to mimic the expression of a single-ion channel offering incomplete insight into changes of the action potential profile. Induced pluripotent stem cell–derived cardiomyocytes resemble, but are not identical, adult human cardiomyocytes and provide a new platform for studying arrhythmic disorders leading to sudden cardiac death. A variety of platforms exist to phenotype cellular models, including conventional and automated patch clamp, multielectrode array, and computational modeling. Induced pluripotent stem cell–derived cardiomyocytes have been used to study long QT syndrome, catecholaminergic polymorphic ventricular tachycardia, hypertrophic cardiomyopathy, and other hereditary cardiac disorders. Although induced pluripotent stem cell–derived cardiomyocytes are distinct from adult cardiomyocytes, they provide a robust platform to advance the science and clinical care of sudden cardiac death. (*Circ Res*. 2015;116:1989-2004. DOI: 10.1161/CIRCRESAHA.116.304494.)**

Key Words: cardiovascular diseases ■ death, sudden, cardiac ■ drug discovery ■ induced pluripotent stem cells

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Nonstandard Abbreviations and Acronyms

AP	action potential
APD	action potential duration
CPVT	catecholaminergic polymorphic ventricular tachycardia
FPD	field potential duration
hERG	human ether-à-go-go-related gene
iPSC-CM	induced pluripotent stem cell–derived cardiomyocyte
MEA	multielectrode array
SCD	sudden cardiac death
TdP	torsades de pointes

Sudden cardiac death (SCD) refers to death from an unexpected circulatory arrest, usually caused by a cardiac arrhythmia occurring within a brief time period of the onset of symptoms.[1] This condition is a common cause of death in patients with various forms of structural heart disease, genetic mutations, or acquired disorders affecting cardiac ion currents. Because of the lack of a uniform definition and systematic autopsy evaluations, the epidemiology and incidence of SCD are not accurately known, but the latter is believed to range between 184 000 and 462 000 cases per year in the United States.[2] The subset of SCD patients without coronary or structural heart disease represents a substantial minority of cases that are difficult to identify and treat. Despite advances in risk stratification and elucidating mechanisms of SCD in patients without structural heart disease, significant knowledge gaps exist in the pathophysiology and risks associated with the individual disorders for this profile. There is a wide range of platforms to evaluate arrhythmic disorders leading to SCD, encompassing studying individual ion channel behavior to organism-level electrophysiology data. Induced pluripotent stem cell–derived cardiomyocytes (iPSC-CMs) offer a novel modeling platform for studying these disorders. Furthermore, iPSC-CMs have a tremendous potential in advancing arrhythmia science and the clinical care of patients at risk for SCD. In this article, we explore potential applications of iPSC-CMs in the study of SCD in the context of the range of experimental platforms available.

Sudden Cardiac Death

Patients at risk of SCD are divided into 3 broad categories: (1) those with known structural heart disease, such as coronary artery disease, left ventricular dysfunction, or hypertrophic cardiomyopathy (HCM) that predisposes them to the development of arrhythmias; (2) those without structural heart disease but who harbor an underlying genetic predisposition to the development of arrhythmias; and (3) those with no known predisposing factors who develop SCD in response to exogenous or acquired factors, most commonly drugs or metabolic disturbances.[3,4]

Those with structural heart disease form the largest group of patients with SCD and are more likely to present with symptoms and to have traditional risk factors for SCD.[3,5] Noninvasive cardiac imaging has the potential to identify those patients if they are successfully screened, but there is no evidence to support population-level screening for SCD. Nevertheless, tools are available to screen a subset of the population who are at high risk for SCD, such as those with coronary artery disease, postmyocardial infarction, or cardiomyopathy.

Patients who have SCD without structural heart disease tend to be younger, asymptomatic individuals, and sometimes even elite athletes.[4,6] These patients may or may not have a family history of SCD, and SCD is often the initial presentation of their disease. This group represents 5% to 10% of the total cases of SCD and is a challenging group to identify and risk stratify. Efforts to identify screening tools for this population have proven arduous.[7] The majority of these patients have underlying genetic cardiac ion channel disorders that predispose them to arrhythmic death.[8] Even in the absence of family history, these individuals commonly have a genetic

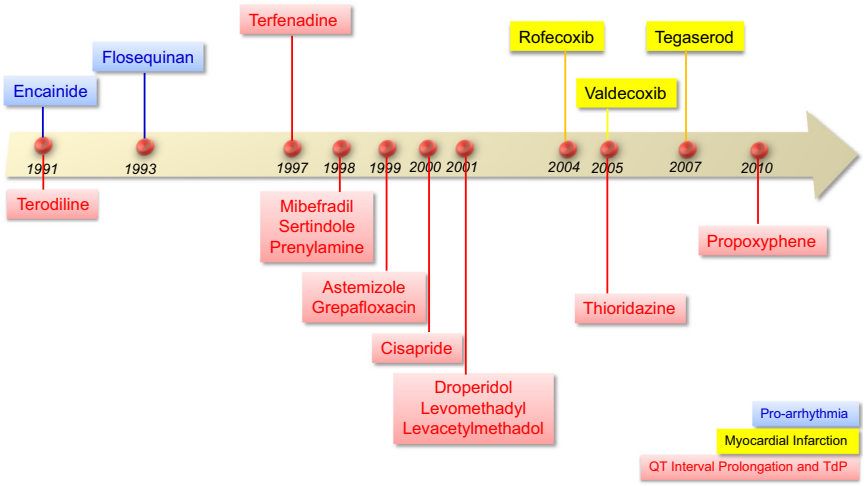

Figure 1. Examples of drugs that have been withdrawn because of cardiac safety issues. Drugs withdrawn because of proarrhythmic effect include Encainide (1991) and Flosequinan (1993). Drugs withdrawn because of their potential to induce a myocardial infarction include Rofecoxib (2004), Valdecoxib (2005), and Tegaserod (2007). Drugs withdrawn because of QT interval prolongation effect and possible torsades de pointes (TdP) include Terodiline (1991), Terfenadine (1997), Mibefradil (1998), Sertindole (1998), Prenylamine (1998), Astemizole (1999), Grepafloxacin (1999), Cisapride (2000), Droperidol (2001), Levomethadyl (2001), Levacetylmethadol (2001), Thioridazine (2005), and Propoxyphene (2010).

component contributing to their risk of SCD. The variable expression in the absence of affected relatives could be because of environmental triggers, germ line mutations, or modifier effects of polygenic disorders.

Drugs given to patients for a variety of purposes can cause cardiac arrhythmias and SCD. Drug-induced arrhythmia and SCD continue to be a significant concern in drug safety testing and have been a major reason for postmarketing drug warnings or drug withdrawal (Figure 1).[9] In fact, the assessment of the potential risk of developing drug-induced torsades de pointes (TdP) arrhythmia, by measuring drug effects on a surrogate marker (such as the QTc interval), is a mandatory component of drug testing before approval.[10] Individuals who develop drug-induced arrhythmias may have an underlying genetic or structural heart disease that predisposes them to developing arrhythmias, but these arrhythmias may also be observed in patients with no known abnormalities.[11–14] A low-event rate often delays awareness of the toxicity until data from large clinical trials or even postmarketing data are available. QT testing during drug development has been used to assess arrhythmia risk. This approach carries a high sensitivity but a low specificity for predicting arrhythmogenesis.[15–17] This has led to a marked reduction in approval of drugs with unrecognized potential liability to cause arrhythmias. For example, drugs with possible favorable benefit-to-risk profiles that could potentially address major unmet medical needs have been discontinued from development solely on the basis of a QT-prolonging effect.[18] This concern has led to a major ongoing effort to directly measure a drug's propensity to cause proarrhythmia instead of relying on the QT interval, which remains a low-specificity surrogate.[19]

SCD without structural heart disease constitutes an important cohort of patients with SCD, and the spectrum of pathology underlying those cases remains an elusive and active area of scientific inquiry. The broad spectrum of pathologies leading to SCD has led to an equally extensive set of research tools to study these disorders. Here, we will present traditional platforms available to study diseases predisposing to SCD, by highlighting the role of patient- and disease-specific iPSC-CMs as a novel platform with significant scientific and clinical potential in studying disorders related to SCD. The discussion of platforms available to study arrhythmic disorders will be conducted in the context of studying inherited or acquired disorders leading to SCD.

Platforms for Studying Arrhythmic Disorders Predisposing Patients to SCD and Cardiac-Safety Assessment of Drugs

The available platforms to study arrhythmic disorder and tailoring drug therapy include (1) organism level (clinical studies and animal models), (2) organ and tissue level (Langendorff technology, cardiac slices, and Purkinje fibers), and (3) cellular and molecular level (cardiomyocyte study, cardiac ion channels study, and iPSC-CMs).

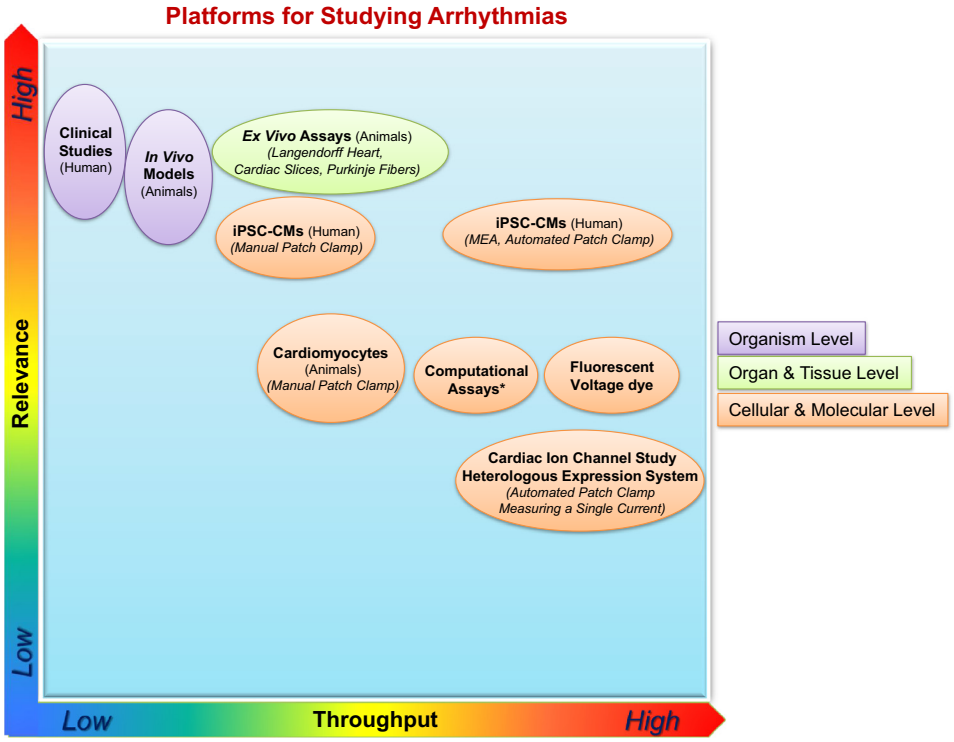

Figure 2. Platforms to assess arrhythmic disorders predisposing to sudden cardiac death and proarrhythmia liability of drugs. Organism-level platforms include human clinical studies and in vivo animal models that could evaluate QT interval and TdP. The relevance of human and animal testing paradigms might not be high with respect to specificity. Organ- and tissue-level platforms are mainly animal ex vivo assays, which include Langendorff technologies, cardiac slices, and Purkinje fibers. Cellular- and molecular-level platforms include human induced pluripotent stem cell–derived cardiomyocytes (iPSC-CMs) using manual and automated patch clamp and multielectrode arrays, animal cardiomyocytes using manual patch clamp measurement, fluorescent voltage dye, and computational assays. The relevance and throughput are approximate. *In silico proarrhythmia assessment would have more clinical relevance if the comprehensive in vitro proarrhythmia assay initiative is successful.[19] Reprinted from Heijman et al[20] with permission of the publisher.

In the following section, the existing platforms used to assess arrhythmic disorders predisposing patients to proarrhythmia liability of drugs[20] (as listed in Figure 2) and to SCD are reviewed briefly. The relevance and throughput for tailoring drug therapy are discussed.

Organism Level

Clinical Studies

The study of human subjects is central to understanding inherited and acquired human arrhythmic disorders. Resting, ambulatory, and exercise electrocardiographic findings are important in the diagnosis and management of inherited arrhythmic disorders.[21] Such data from clinical studies have helped define the diagnostic features, natural history, and treatment strategies of arrhythmic disorders and drug-induced arrhythmias long before these entities were defined on a genetic and cellular level.[22–24] Nevertheless, such ECG findings often have variable sensitivity and specificity in diagnosing these disorders.[25,26] Also, the relatively small number of patients with inherited arrhythmic disorders is often a barrier to creating large prospective clinical studies to guide risk stratification and therapy.[1]

Similarly, electrocardiographic evaluation via surface ECG and ambulatory rhythm monitoring is an integral component of the clinical assessment of cardiac safety of all compounds in development.[27] These platforms provide information on drug-induced effects from cardiac electrophysiology, including cardiac repolarization,[28] conduction defects, and incidence of arrhythmic events. The duration of ventricular depolarization and repolarization is shown as the QT interval on an ECG. QT interval prolongation has been associated with a potentially fatal arrhythmia, TdP.[29] However, a prolonged QT is now recognized to be sensitive but not specific for drug-induced proarrhythmia. In addition, ethical and regulatory standards limit the experimentation and testing that can be done in humans and recommend that animal data of safety be validated before initial human drug testing.[10] Thus, human clinical studies remain an important component of studying arrhythmic disorders, but technical and logistical challenges associated with such studies necessitate reliance on other models to elucidate the mechanism and risks of arrhythmia.

Animal Models

Animal models play a critical role in studying hereditary arrhythmic disorders and characterizing a drug's potential for proarrhythmic and cardiotoxic effects before human administration. The need to define possible toxicities before experimental drugs are given to humans led to the adoption of animal model-based arrhythmia research using small animals, such as mice, rats, and rabbits. Similarly, hereditary arrhythmia studies extensively rely on mouse models by taking advantage of the relative ease of creating genetically modified small-animal strains that allow disease-specific modeling.[30] Despite some degree of homology between many aspects of mouse and human cardiomyocytes, there are major fundamental electrophysiological and contractile differences between rodents and large mammals that limit the extrapolation of data generated from these models to humans. For example, the resting heart rate in mice is much higher than that of humans, and calcium-handling properties of mouse myocytes differ significantly from those of human myocytes.[31–35] Most importantly, the ion channels responsible for determining action potential (AP) duration (APD; and QT interval) in the mouse are not identical to those that determine APD in human myocytes. By comparison, large animal models, such as dogs,[36] pigs,[37] sheep,[38] and primates,[39] have long APDs that more closely resemble human organ structure and function.[40] Compared with the mouse model, humans and large animal models are more similar in heart rate,[36,41] APD and repolarization mechanisms, contractile filament isoforms, ion channels, and ion pumps,[11,18,19,42] all of which increase the validity of inferences made based on studies in large animal models for early stage clinical trials.[43] However, despite the superior recapitulation of human cardiac physiology, translational failures still occur with large animal models, and no animal model system can fully replace human clinical trials.[44] This is likely due to a host of factors, including interspecies variations in ion channel function,[44] the relatively youthful state of animals used in research, and differences in drug metabolism between animals and humans.[45]

Organ and Tissue Level

The Langendorff technology, which uses an explanted perfused heart, allows access to all functional and electric properties of an isolated heart. Limitations of this system include the absence of systemic neurohumoral regulation and the difficulty in maintaining normal function for prolonged periods.[46] Cardiac slices preserve the functional syncytium properties of native myocardium to provide a platform for measuring signal propagation and conduction velocity. This model system bridges the gap between cellular and organ-level assays. A limitation is the lack of natural electric and mechanical cycles of the native heart because of the absence of natural pacemakers. However, this can be an advantage in the studies that require the exclusion of the influence of natural pacemakers.[47] Furthermore, isolated cardiac tissue is only characteristic of the defined regions from which they are taken, such as Purkinje fiber and papillary muscle. This is especially useful in identifying regional specific electrophysiology effects of a disorder or a drug.[48–50] However, these models do not capture organ-level contributions or systemic contributions to arrhythmic disorders, including structural heart disease, autonomic tone, or adrenergic stimulation.[51] This strengthens the relevance of organism-level models over organ-level and tissue-level models. Naturally, all of these depend on the questions being asked, and the strategy should be to ensure that the model system used is best suited to answer the questions being posed. A combination of appropriate approaches is usually better than any single model alone in defining the nature of complex arrhythmias or the basis of drugs with complex electrophysiological effects.

Cellular and Molecular Level

Cardiomyocytes and Cardiac Ion Channels

Investigating primary ventricular cardiomyocytes allows a detailed study of ion channel behavior associated with physiological and pathophysiological functions of single cells. The difficulty in performing high-throughput drug screening in

human-like ventricular cardiomyocytes led to the adoption of heterologous expression models, such as introduction of the human ether-à-go-go-related gene (hERG), which is a gene (KCNH2) that codes for a protein known as $K_v11.1$, the α-subunit of a potassium ion channel. The hERG channel mediates the rapid delayed rectifier potassium current (I_{Kr}) and can be overexpressed in human embryonic kidney 293 or Chinese hamster ovary cell lines.[52,53] Isolated hERG inhibition has been shown to play an important role in TdP risk assessment in animals and in humans; mutations of this gene prolong the APD, and affected patients are prone to SCD.[54] The hERG inhibition cellular screening assay is used at the early stages of drug development because of the high throughput and low cost of the platform, especially when screening a large number of compounds. However, it has similar drawbacks as human QT testing because the drug-induced hERG block, although relatively sensitive, is not specific enough for predicting TdP. Some drugs that inhibit hERG at exposures reached in humans do not affect ventricular APs or result in TdP risk (despite APD/QT prolongation) because of the concomitant effect on other ion currents in addition to I_{Kr}. The specific effects of drug-induced perturbations on multiple ionic channels (eg, I_{Kr}, late I_{Na}, and $I_{Ca,L}$) likely explain why some QT-prolonging drugs are not always proarrhythmic. One notable example is verapamil, which inhibits hERG in vitro but does not cause QT prolongation in vivo because of its additional calcium channel–blocking properties.[17] Although it inhibits hERG in vitro and causes QT prolongation, ranolazine is similarly free from proarrhythmia likely due to its additional late I_{Na} channel–blocking properties.[55] The traditional gold standard is to measure I_{Kr} in these heterologous expression systems by manual patch clamp, which is low throughput. Automated patch clamp systems with medium to high throughput therefore provide a better balance between productivity and data quality. Our conclusion is that the assessment of arrhythmia risk of a new drug by screening against a single-cardiac ion channel is likely to lead to discarding potentially useful drugs while allowing others that can induce arrhythmias to move forward.

Induced Pluripotent Stem Cell–Derived Cardiomyocytes

More recently, iPSC-CMs have emerged as a new model capable of recapitulating many properties of human cardiomyocytes in vivo.[56] Human iPSC-CMs express major cardiac ion channels naturally found in the human heart. The cells are made by reprogramming human somatic cells into pluripotent stem cells (PSCs) with transcription factors identified from embryonic stem cells. The transcription factors are introduced into the somatic cells by viral transduction or nonviral transfection, or as soluble proteins.[57] The resultant iPSCs can be specifically differentiated into iPSC-CMs.[58] The differentiated cardiomyocytes are beating cells that express many human cardiac ion channels and sarcomeric proteins.

A major advantage of the platform is that iPSC-CMs express the set of encoded cardiac genes that are not necessarily expressed by the original donor somatic cell (eg, skin fibroblasts or peripheral blood mononuclear cells). Thus, in a case of an ion channel disorder, iPSC-CMs may express the abnormal ion channel gene and recapitulate the electrophysiological abnormalities associated with the disorder. This has proven especially useful in studying inherited cardiac disorders because a virtually unlimited supply of cardiomyocytes expressing the phenotype encoded by a particular variant can be created. The platform has been used to study multiple inherited cardiac disorders, demonstrating good correlation with predicted adult human cardiomyocyte behavior.

The use of single-cell animal cardiomyocyte models is limited by different ion channel expression profile that may cause different electrophysiological response to drugs compared with human cardiomyocytes.[59,60] Similarly, hERG cellular transfection models have limitations in predicting drug toxicity–related prolongation of ventricular repolarization.[61,62] Nevertheless, iPSC-CMs, although by no means a surrogate of adult ventricular myocytes, express a more complete panel of human cardiac ion channels associated with drug-induced cardiotoxicity.[63,64] With its higher degree of homology with human cardiomyocytes, iPSC models may provide a more comprehensive evaluation of ion channel function, AP features, and arrhythmic potential compared with animal cardiomyocyte or heterologous transfection models.[63,65–68]

A major strength of iPSC-CM models is the ability to create a disease-specific system to develop therapeutics specifically targeted for that disorder and to define disease-specific drug toxicity. Although single-cell recording by conventional electrophysiology techniques is generally low throughput, newer single-cell approaches using automated patch clamp and multicellular recordings with multielectrode arrays (MEAs) have largely compensated for the differences in throughput and relevance.[69–72] In addition, genetically encoded fluorescent voltage indicators are reported to faithfully demonstrate transmembrane potentials in iPSC-CMs. This new platform can be used in serial phenotyping of differentiating cardiomyocyte populations and in screening for drug-induced cardiotoxicity.[73]

Limitations of iPSC-CMs

It is important to note that iPSC-CMs, like any platform, have several limitations in modeling cardiac disorders. First, iPSC-CMs are single-cell models of cardiac disease and lack the complexity of cardiac tissue. Multicellular iPSC-CM models might resolve some of these problems, and some of these have shown promise in studying inherited and acquired disorders.[74,75] Another issue is that iPSC-CMs differentiate into heterogeneous patches of atrial-like, ventricular-like, and nodal-like precursors within the same preparation.[76] The development of newer systems with chamber-specific or region-specific cells would improve the available models.[77,78] Finally, as in the case with tissue-level models, iPSC-CMs may not capture the complex organ-level or systemic interactions that could influence cardiac disorders.

Furthermore, iPSC-CMs are surrogates, not replicates of human adult cardiomyocytes; in particular, there are differences in ion channel and sarcomeric protein expression profile that suggests that the cells are less mature than native adult myocytes.[79] Important work has shown the possibility of advancing the maturity of the cell types, but at present, iPSC-CMs remain closer in morphology to fetal cardiomyocytes.[74,80,81] This is especially important given that ion channel function, AP properties, and arrhythmic potential will all be influenced by the cellular maturity and ion channel expression

profile. In other words, instead of assuming that they have analogous expression to adult human cardiomyocytes, iPSC-CMs must be carefully screened for expression of a gene of interest and the phenotype output signal. These limitations must be considered when drawing parallels to adult human myocyte physiology. Thus, iPSC-CMs are by no means a perfect model or a substitute for other science models of arrhythmia or human clinical testing. Instead, they represent a novel tool that can bridge some of the gaps between animal-based models and adult human cardiomyocytes.

Electrophysiology Platforms

The electrophysiology platforms to study arrhythmic disorders and cardiac-safety assessment using cellular preparations will be discussed in detail as follows. Many of these platforms can be used to investigate iPSC-CMs and other cellular models as well (Figure 3).

Conventional Patch Clamping

Conventional patch clamp electrophysiology can be used to measure AP properties (current clamp) or in-depth biophysical properties (voltage clamp) of cardiac myocytes. Parameters including APD, beating rate, mean diastolic potential, and V_{max} are easily measured with current clamp techniques. Individual families of ion channels can be characterized with cell voltage clamp techniques. The cardiac ventricular AP is divided into 5 phases (0–4) and is mediated by the coordinated opening and closing of sodium, calcium, and potassium channels.[82–85] Phase 4 of the AP is the resting membrane potential that results from high K^+ conductance because of inward rectifying K^+ (I_{K1}) channels. Voltage sensitive Na^+ and Ca^{2+} channels are closed at the resting potential but remain available to activate with depolarization. The arrival of the depolarizing conducted AP causes the rapid opening of the inward Na^+ current (I_{Na}) and the upstroke (phase 0) of the AP. L-type Ca^{2+} ($I_{Ca,L}$) channels begin to activate during phase 0 of the AP. Phase 1 (initial repolarization) of the AP occurs immediately after the peak of depolarization, resulting from closure (inactivation) of the Na^+ channels and opening (activation) of the transient outward potassium current (I_{to}). Phase 2 of the AP is the plateau phase during which the membrane potential changes slowly because of a balance between inward Ca^{2+} current through the L-type calcium channels and the outward K^+ current through rapidly (I_{Kr}) and slowly (I_{Ks}) activating delayed rectifier K^+ channels.

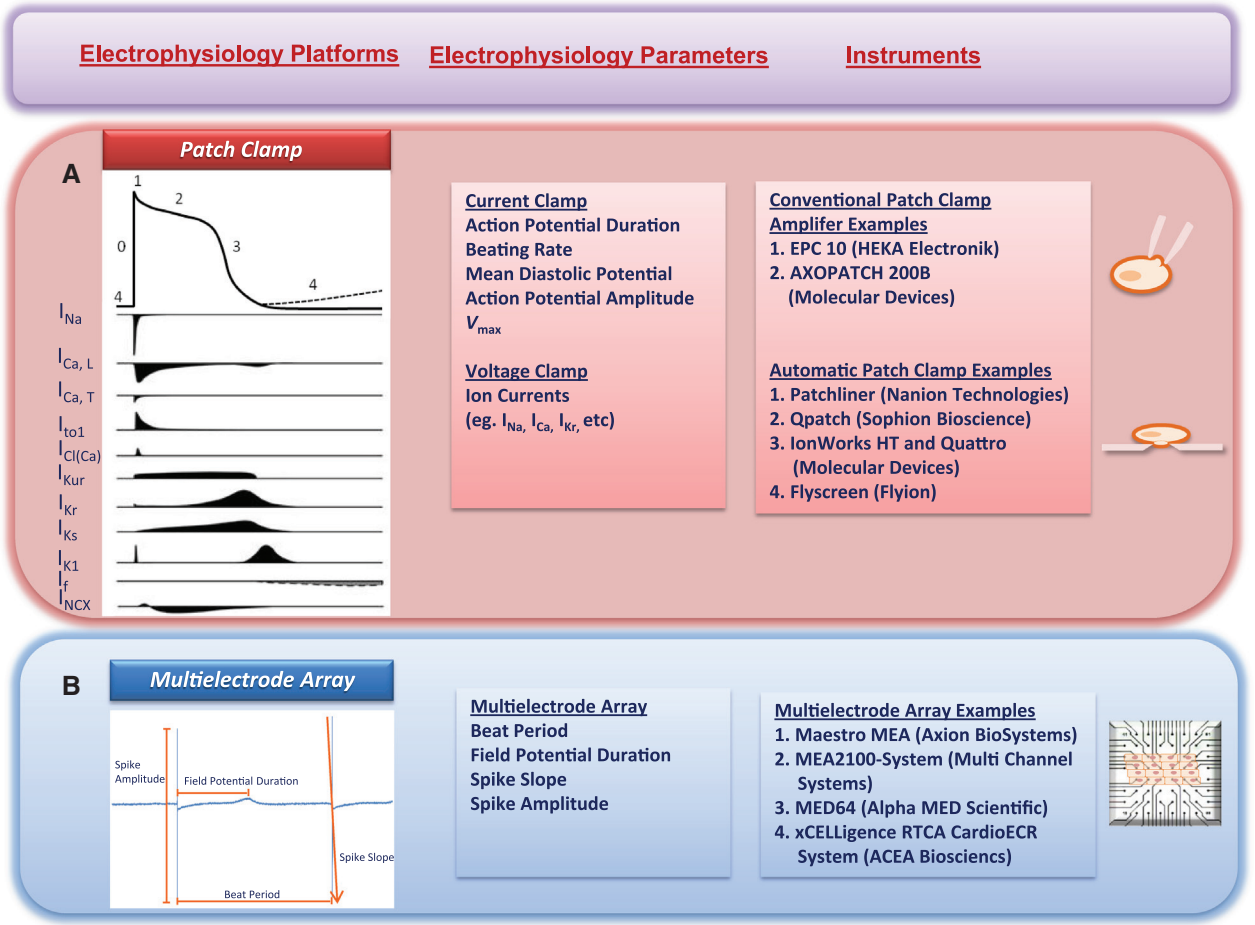

Figure 3. The electrophysiology platforms to study arrhythmic disorders and cardiac-safety assessment using induced pluripotent stem cell–derived cardiomyocytes. **A**, Patch clamp. Raw trace, parameters (action potential duration, beating rate, mean diastolic potential, action potential amplitude, V_{max}, and multiple ion currents), and instrument examples. **B**, Multielectrode array. Raw trace, parameters (beat period, field potential duration, spike slope, and spike amplitude), and instrument examples. Reprinted from Hoekstra et al[82] with permission of the publisher.

Phase 3 of the AP is the final repolarization phase that occurs when repolarizing K^+ currents (including the I_{Kr}, I_{Ks}, and I_{K1}) sum to repolarize the membrane potential and re-establish the resting potential (phase 4).[86]

The cardiac AP is a complex process that involves many different ionic currents, all of which are highly regulated. Prolongation of the APD can result from reduction of repolarizing currents or increase in depolarizing currents. It is known that patients with genetic defects that cause prolongation of the APD are prone to SCD. Therefore, studying the effects of new drugs on APD could lead to useful approaches for predicting arrhythmia risk. In our view, these types of studies should be performed in adult cardiomyocytes with APDs similar to those of human cardiomyocytes.

Cells from patients with mutations that are known to be at risk of SCD can now be studied. Patient-specific iPSC-CMs exhibit distinct in vitro disease phenotypes associated with the patients from which they were derived.[63] They can be used as models to study various disease phenotypes in affected patients. In addition, iPSC-CMs from normal humans could be used to identify drugs that have proarrhythmic properties, mainly by examining effects on APD morphology. However, increases in APD alone may not accurately predict arrhythmia risks of certain drugs. Additional approaches, such as comprehensive in vitro proarrhythmia assay initiative (CiPA),[19] might provide more substantial predictive value. The CiPA initiative adopts an integrated in vitro/in silico paradigm that emphasizes the repolarization changes that promote early afterdepolarizations, which are linked to TdP proarrhythmia.

In summary, patch clamp electrophysiology is considered the gold standard for detailed biophysical studies of ion channels. It can be useful to define the detailed molecular basis of proarrhythmic drugs or ion channel mutations. However, these single-cell approaches are labor intensive, and selective ion channels must be studied while others are blocked. These requirements make voltage clamp approaches in intact cardiac myocytes a low-throughput approach for drug screening.

Automated Patch Clamp

Because of the low throughput and technically challenging nature of manual electrophysiology of intact cardiac myocytes, a series of devices to automate conventional patch clamp assays were developed in the 1990s, including the Robocyte,[87] AutoPatch and RoboPatch,[88,89] and OpusXpress 6000A.[90] Automated electrophysiology platforms provide a relatively high efficiency assessment of compounds against a single-ion channel expressed in traditional cell lines (eg, human embryonic kidney 293 and Chinese hamster ovary) and in iPSC-CMs. The automated system requires large numbers of dissociated cells, with strict consistency and robustness of ion channel expression to achieve good reproducibility. Although substantial data can be obtained with these automated approaches, the human embryonic kidney 293 and Chinese hamster ovary cell systems cannot recapitulate the complexity of intact cardiac myocytes. In addition, the automated techniques do not work well with adult cardiomyocytes because of their shape and fragility. Recently, the planar-array patch clamp has further improved the efficiency by coordinating parallel multiwell plate or chip recordings.[91,92] These systems automatically integrate the steps of cell giga-ohm sealing, perfusion handling, and stable recording. Some of these systems have been validated for drug safety evaluations, including Patchliner,[93] IonWorks Quattro, PatchXpress, QPatch, and IonWorks HTS. In such platforms, the number of data points that can be assessed depends largely on the type of plates used by the study.

Multielectrode Arrays

MEA technology provides noninvasive, long-term recordings of extracellular field potentials generated by electrically active cells.[94,95] The synchronous beating of a cultured cardiac myocyte monolayer preparation in vitro has some electric patterns that are related to the ECG in vivo. The MEA may be most useful when used not only to evaluate the electrophysiological properties of cardiomyocytes but also to correlate them with tissue networks. A series of MEAs including Maestro MEA, MEA2100-System, MED64, and xCELLgence RTCA CardioECR System have been developed. MEAs can be used to study AP propagation rates and the APD. Field potential duration (FPD) in MEA systems can be used to evaluate proarrhythmic effects of drugs. It represents the time between the upstroke of the AP and final AP repolarization. FPDs reflect similar properties as the QT interval on the surface ECG. FPD prolongation is associated with QT prolongation, which has important predictive value for cardiac safety. MEAs have the advantage of measuring electric behavior for longer time frames. The spontaneous electric activity can be measured to investigate chronotropic drug effects. MEAs can also be used to detect effects of drugs on the conduction of the AP within the monolayer. As mentioned earlier, a limitation of this approach is that the myocytes used often have an immature electrophysiological phenotype that limits translation of results to the adult heart.

Computational Modeling

In silico structure–affinity models of ion channels have emerged as a possible quick estimate of hERG affinity and other predicted electrophysiological models.[96] These models provide a relatively efficient and inexpensive option to obtain a general prediction of a drug based on high-throughput data before launching the high-cost preclinical assessments. Encouragingly, the development of computer simulation methodologies has been reported to predict hERG-blocking and I_{Na}-blocking effects with whole-heart simulations,[97] making it possibly more relevant to clinical studies. However, it should be noted that the prediction certainty of this new technology relies largely on the accuracy of the underlying experimental data used to build the model.

In silico arrhythmia modeling can also be used to predict proarrhythmia by using existing data on a drug's effect on specific ion channels. When in silico platforms integrate multiple ion currents, the models are better in predicting proarrhythmia than using hERG alone.[98,99] Many evolving concepts are being evaluated in the modeling process, including using data from >2 or 3 channels, dose–response characteristics, and possibly kinetics of channel block. In silico arrhythmia modeling is a major focus of the evolving comprehensive in vitro proarrhythmia assay initiative, which uses an integrated nonclinical in vitro/in silico paradigm.[19] Promising modeling approaches

Table. Summary of Major Efforts Using iPSC-CM to Model Hereditary Arrhythmic Disorders, Platforms Used to Study Disorders and Most Significant Findings of Modeled Disorders

Disorder	Study	Gene (Variant/s)	Platforms			Drug Testing
			Patch Clamp	MEA	Fluorescent-Based Calcium Imaging	
LQT1	Moretti et al (2010)[100]	*KCNQ1* (p.R190Q)	Prolonged APD Slower repolarization $\downarrow I_{Ks}$ current density I_{Ks} activation shifted toward more positive voltages and deactivation being decelerated	…	…	Isoproterenol and propranolol
	Egashira et al (2012)[101]	*KCNQ1* (p.C1893del)	$\downarrow I_{Ks}$	Prolonged FPD EADs and arrhythmia	…	E4031, chromanol, isoproterenol, propranolol
	Wang et al (2014)[102]	*KCNQ1* (p.R190Q, p G269S, and p.G345E)	Prolonged APD EADs	…	…	Nifedipine
LQT2	Itzhaki et al (2011)[103]	*KCNH2* (p.A614V)	Prolonged APD EADs, $\downarrow I_{Kr}$	Prolonged FPD EADs	…	E4031, cisapride, nifedipine, pinacidil, ranolizine
	Matsa et al (2011)[104]	*KCNH2* (p.G1681A)	Prolonged APD, EADs	Prolonged FPD, EADs	…	E4031, isoprenaline. nicorandil, nadolol, PD-118057, propranolol
	Lahti et al (2012)[105]	*KCNH2* (p.R176W)	Prolonged Ventricular APD $\downarrow I_{Kr}$	Prolonged FPD	…	E4031, cisapide, erythromycin, isoprenaline, sotalol
	Wang et al (2014)[102]	*KCNH2* (p.A614V)	Prolonged APD EADs	…	…	Nifedipine
LQT3	Terrenoire et al (2013)[106]	*SCN5A* (p.F1473C)	Right shift in Na^+ channel inactivation and faster recovery from inactivation Normal I_{Kr}	…	…	Mexiletine
	Ma et al (2013)[107]	*SCN5A* (p.V1763M)	Prolonged APD Larger late Na^+ current Na^+ channel Steady state inactivation shifted toward more positive potentials	…	…	Mexiletine
LQT8	Yazawa et al (2011)[108]	*CACNA1C* (p.G406R)	Prolonged APD, DADs Reduced voltage-dependent inactivation L-type calcium channel	…	Ca^{2+} elevations larger, more prolonged and irregular	Roscovitine
CPVT	Itzhaki et al (2012)[109]	*RYR2* (p.M4109R)	DADs	…	Irregular calcium release events	Flecainide forskolin, isoproterenol thapsigargin
	Fatima et al (2011)[110]	*RYR2* (p.T7447A)	…	…	Smaller SR Ca^{2+} stores More sensitive gain of Ca^{2+} Induced Ca^{2+} release Longer Ca^{2+} sparks Diastolic Ca^{2+} overload	Bay-K 8644, di-butryl cAMP, isopreoterenol
	Novak et al (2012)[111]	*CASQ2* (p.D307H)	Longer APD, DADs, oscillatory prepotentials	…	Delayed after-contractions	Isopreoterenol
	Jung et al (2012)[112]	*RYR2* (p.S406L)	…	…	Abnormal Ca^{2+} handling Increased diastolic Ca^{2+} concentration Ca^{2+} sparks characterized by: higher Ca^{2+} spark amplitude Higher full width at 50% peak amplitude and decay time Higher decay time Prolonged plateau phase of calcium transients	Dantrolene

(*Continued*)

Table. Continued

Disorder	Study	Gene (Variant/s)	Platforms			Drug Testing
			Patch Clamp	MEA	Fluorescent-Based Calcium Imaging	
HCM	Lan et al (2013)[71]	*MYH7* (p.R663H)	DADs	…	Irregular calcium cycling Elevated (diastolic) intracellular calcium concentration Smaller SR Ca^{+} release events	Isoproterenol, propranolol, verapamil, lidocarine, mexiletine, ranolazine
Other	Liang et al (2013)[63]	*KCNQ1* (p.G269S), *MYH7* (p.R663H), *TNNT2* (p.R173W)	Longer APD of LQT lines EAD in LQT DAD in HCM No effect of verapamil on APD Alfuzosin prolonged APD Increased EAD and DADs in LQT and HCM iPSC-CMs, respectively, in response to cisapride	…	…	Alfuzosin cisapride, nicorandil, verapamil
	Braam et al (2013)[113]	*KCNH2* (p.G1681A)	I_{Ks}, I_{Kr}	Drug-induced prolonged FPD	…	Bepridil, diltiazem dofetilide, levcromakalim, moxifloxacin, sotalol, sparfloxacin, terfenadine, verapamil, JNJ303, HMR1556

APD indicates action potential duration; DAD, delayed afterdepolarization; EAD, early afterdepolarization; FPD, field potential duration; HCM, hypertrophic cardiomyopathy; LQT, long QT syndrome; and iPSC-CMs, induced pluripotent stem cell–derived cardiomyocytes.

are evolving, and their appropriate validation with human conditions will be increasingly important.

Fluorescent Voltage Dyes

Considering the laborious nature of conventional electrophysiological recordings and strict cell quality requirements of automated patch clamp, platforms based on fluorescent voltage dyes have emerged as a high-throughput alternative. In addition, these dyes can be applied to organ-level approaches, such as Langendorff, making them more relevant to clinical studies. However, some optical voltage indicators have phototoxicity, which limits the recording time and degrades signal quality.[100]

Applying Electrophysiology Platforms to iPSC-CMs in Disorders Leading to SCD

Multiple studies have used iPSC-CMs to study arrhythmic disorders. These efforts have ranged from studying disease-specific models to investigation using iPSC-CMs from normal patients in screens for drug toxicity.[115] We highlight some of the major efforts in the field above (Table).

Long QT Syndrome

The first arrhythmic disorder to be modeled using iPSC-CMs was long QT syndrome. This disease is characterized clinically by a prolonged QT interval on ECG, which predisposes patients to an unstable ventricular arrhythmia (eg, TdP). There are >10 loci associated with long QT syndrome, with each locus being associated with a specific subtype that has unique ion channel derangements and clinical features.[116]

Moretti et al[100] reprogrammed fibroblasts from a patient with a *KCNQ1* variant that is associated with type 1 long QT syndrome to create iPSCs and subsequently differentiated them into iPSC-CMs. The authors found that the resulting iPSC-CMs recapitulated multiple features of type 1 long QT syndrome including reduced I_{Ks} currents, prolongation of APD, and increased incidence of spontaneous arrhythmias. A similar approach was undertaken by Matsa et al[104] and Itzhaki et al[103] in studying type 2 long QT syndrome. These studies were also notable for confirming that FPD, as well as APD, was prolonged and validated the use of MEA to study tissue-level phenotype in iPSC-CM models.

Type 3 long QT syndrome was modeled using iPSC-CMs from patients harboring *SCN5A* mutations by 2 groups, with both models showing good correlation with the clinical phenotype.[106,107] The study by Terrenoire et al[106] recruited a subject with a novel *SCN5A* variant predisposing the subject to type 3 long QT syndrome, while also carrying a rare variant in *KCNH2* that was of unclear clinical significance. The authors investigated the electrophysiological significance of this variant by studying the I_{Kr} current using voltage clamp and observed no abnormality, thus concluding that the patient's presentation was secondary to the identified *SCN5A* variant without any contribution from the *KCNH2* variant. A similar method was applied by Davis et al[117] in studying mice harboring a complex *SCN5A* variant (*SCN5A*$^{1798insD/+}$), which encodes a sodium channel that exhibits combined characteristics of gain- and loss-of function. Such studies may provide a framework to investigate complex electrophysiology disorders or overlap syndromes. Specifically, these are disorders that do not fit into the classical channelopathies, often harboring features of >1 disorder.[107] More human studies are needed to validate the practice of functional testing of iPSC-CMs in overlap syndromes, including those caused by sodium channel variants.

Timothy syndrome, also known as type 8 Long QT syndrome, is another inherited arrhythmic disorder associated with syndactyly, immune deficiency, and autism. Yazawa et al[108] created a model of the L-type calcium channel (Cav1.2) disorder using iPSC-CMs that mirrored the abnormal calcium homeostasis and increased arrhythmia associated with the disorder. Another successful model of long QT syndrome was recently published by Wang et al[102]; the group created iPSC-CM models of types 1 and 2 long QT syndrome using zinc finger nuclease (ZFN) genome editing of pathogenic variants into wild-type iPSC. The advent of newer genome-editing technology, such as transcription activator–like effector nuclease (TALEN) and clustered, regularly interspaced, short palindromic repeat (CRISPR)/clustered, regularly interspaced, short palindromic repeat associated gene 9 (Cas9) system technology, allows for highly targeted genome editing with minimal effect on nontargeted sites of the genome.[110]

The above genome-editing techniques would be particularly useful in evaluating the functional significance of variants of uncertain significance (VUS) uncovered during genetic testing (Figure 4). The classification of such variants usually relies on published human studies, in silico models, or animal models of the variant in question or similar variants. Instead of using a known disease causing variant, as was done by Wang et al,[102] investigators can study a VUS thought to be associated with long QT syndrome and evaluate the electrophysiology of the derived iPSC-CMs. Before attempting such a strategy, 2 criteria must be fulfilled: (1) iPSC-CMs must show stable and reliable expression of the encoded gene and protein similar to that of adult cardiomyocytes and (2) iPSC-CMs must provide a reliable phenotype signal of the encoded protein that can be measured and has been shown to correlate with clinical disease.

Catecholaminergic Polymorphic Ventricular Tachycardia

Several studies have evaluated the ability to model catecholaminergic polymorphic ventricular tachycardia (CPVT) using an iPSC-CM model. CPVT is an arrhythmic disorder characterized by ventricular tachycardia provoked by exercise or catecholamine surges. It is a disorder of cardiac calcium homeostasis often caused by variants in calcium regulation genes, such as ryanodine receptor 2 and cardiac calsequestrin.[116] The first model of CPVT by Itzhaki et al[109] created iPSC-CMs from a patient heterozygous for a ryanodine receptor 2 variant. Using patch clamp techniques, the authors found an increased incidence of delayed afterdepolarizations in response to adrenergic stimulation. Furthermore, the authors used dye-based calcium imaging to demonstrate abnormal calcium transients in CPVT iPSC-CMs, validating the long-standing hypothesis of the mechanism of arrhythmia of the disorder.[120]

Other Models

There have been multiple efforts to model other inherited cardiac disorders that are associated with a risk of SCD. These include familial dilated cardiomyopathy,[121] arrhythmogenic right ventricular dysplasia,[78,122,123] LEOPARD syndrome,[124] and Friedreich Ataxia.[125] However, none of the studies primarily focused on the arrhythmic potential of the disorder.

Future Directions

Mechanisms of Disease

The ability to study a human-beating cardiomyocyte cellular model was limited before optimization of cardiac differentiation of pluripotent stem cells because the primary tissue fails to survive adequately in vitro.[126] As demonstrated by the models above, iPSC-CMs now offer the opportunity to study the cellular pathophysiology of arrhythmic disorders. The above models were concordant with known hypotheses of the underlying mechanism of the respective disorders (Table). Furthermore, Lan et al[71] were able to validate less common mechanistic hypotheses in HCM. HCM is an inherited cardiac disorder clinically associated with ≥1 of the following: a mild to severe increase in muscle wall thickness, left ventricular cavity obstruction, and SCD.[127] How these mutations in contractile filaments cause electrophysiological disturbances that promote sudden death has been studied.[128,129] Lan et al[71] created a model of the disorder and demonstrated relative hypertrophy of myocytes in response to adrenergic stimulation. Furthermore, the authors showed that HCM iPSC-CMs exhibited abnormal calcium handling and increased diastolic levels of calcium that were associated with an increase in delayed afterdepolarizations. This work was important in confirming the hypothesis that HCM is an arrhythmic disorder at a cellular level, independent of the degree of muscular hypertrophy or intracavitary obstruction in vivo.

Drug Testing

An emerging role for iPSC-CMs is in the field of drug testing, namely testing for arrhythmic toxicity of compounds. Currently, hERG channel cellular transfection models serve as the standard platform for testing proarrhythmia toxicity. However, recent studies have highlighted a superior potential for iPSC-CMs in this field.

Liang et al[63] compared iPSC-CM models and a hERG channel-transfected cell model, which is the current standard of pharmacological drug testing, to predict drug toxicity. The authors were able to demonstrate the superiority of iPSC-CMs in stratifying appropriate toxicity potentials of verapamil and alfuzosin. Furthermore, the study showed that there is a spectrum of toxicity dependent on the host genetic background; for example, iPSC-CMs from patients with long QT syndrome were more predisposed to hERG-mediated toxicity compared with iPSC-CMs from control healthy patients. Similarly, Navarrete et al[130] demonstrated that iPSC-CM drug-induced arrhythmia can be documented by MEA.

The concept of variable individual predisposition to arrhythmic toxicity, especially as it relates to TdP and the hypothesis of repolarization reserve, posits that a degree of repolarization current redundancy exists between I_{Ks} and I_{Kr} currents.[131] The individual degree of repolarization reserve is likely dictated by a combination of genetic and environmental factors; the population heterogeneity of such factors likely explains the differential responses to QT-prolonging drugs in individual patients. This was nicely demonstrated by Braam et al,[113] who used iPSC-CMs to confirm the repolarization reserve hypothesis. The authors used MEA to assess iPSC-CM effects of 9 different antiarrhythmic drugs

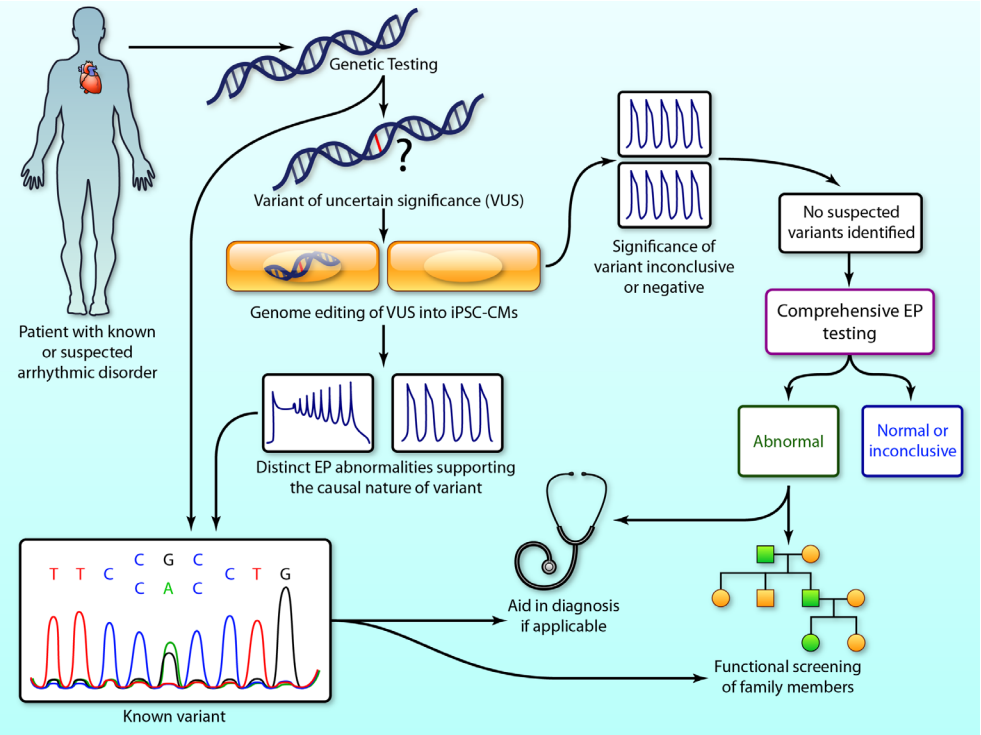

Figure 4. Potential role for iPSC-CMs in evaluation of patients with known or at risk for arrhythmic disorders. Clinical genetic testing attempts to identify a rare variant in genes commonly associated with arrhythmic disorders. When a known variant is identified, this may aid the clinical diagnosis and genetic screening can be offered to family members to identify those at risk for developing the disorder. If a variant of uncertain significance (VUS) is identified, genome-edited lines with VUS can be developed, and cellular EP testing can be done on the resultant iPSC-CMs to detect electrophysiological abnormalities and compare them to proband iPSC-CMs. This may help re-characterize the VUS as possibly disease causing and place it in a similar category as a known variant. In cases where EP testing of the VUS is negative or inconclusive or no variants are identified on genetic testing, one can ignore the genetic component and use iPSC-CMs as the cellular functional testing platform (EP study in a dish). iPSC-CMs from the proband would be created and undergo comprehensive EP testing; abnormalities thus identified may be used to aid in the diagnosis and management of the patient. Furthermore, family members could be offered the opportunity to have iPSC-CMs generated and screened for their arrhythmic predisposition. Much like genetic testing, iPSC-CM testing may not identify all arrhythmic abnormalities, and those patients are left to rely on clinical testing and screening (Illustration credit: Ben Smith).

on FPD. The authors note that the I_{Ks} blockers, HMR1556 and JNJ303, had minor effects on FPD. However, when the compounds were coadministered with sotalol (I_{Kr} blocker) or in type II long QT syndrome cells (genetically reduced I_{Kr}), the cells experienced a marked prolongation of FPD. The above studies support the versatility of iPSC-CMs as a platform for more comprehensive drug studies because of a broader recapitulation of adult ventricular myocyte ion channel expression compared with animal or cellular transfection models.

Efficacy testing is likely to be more challenging because of morphological differences between iPSC-CMs and adult myocytes and the fact that antiarrhythmic responses are often accompanied by competing proarrhythmic effects that sometimes are only unmasked in vivo.[132] Furthermore, many arrhythmic disorders, such as arrhythmogenic right ventricular dysplasia and Brugada syndrome, are thought to depend on multicellular and tissue level phenomenon that potentiates lethal arrhythmic events.[78,133] However, multiple investigators have shown consistent drug responses that are comparable with human cardiomyocyte responses in types 1 to 3 long QT syndrome and CPVT (Table). Thus, some evidence exists to use this platform for disease-specific toxicity and efficacy testing. Larger studies are needed to validate the adoption of this platform for use in toxicity screening at the population level.

Drug Discovery

Because the electrophysiological and contractile phenotype of iPSC-CMs is similar to that of normal human cardiomyocytes, they are valuable research tools for drug discovery. Many of the studies modeling cardiac disorders have relied on known therapeutic or toxic drug responses as part of their repertoire of recapitulation of disease phenotype. However, 1 study took a prospective approach by testing a novel drug on iPSC-CMs. Jung et al[112] used iPSC-CMs made from a CPVT patient with a ryanodine receptor 2 variant to test the therapeutic efficacy of dantrolene. This old drug is often used to treat malignant hyperthermia and, in this case, was able to successfully abate the calcium-handling abnormalities and delayed afterdepolarizations seen in CPVT iPSC-CMs. This study suggests that a high-throughput electrophysiology platform using iPSC-CMs can be used to test the therapeutic and toxic potential of large chemical libraries in specific diseases and the general population.[134]

Clinical Testing of Patients With SCD

Our understanding of inherited cardiac disorders has evolved with advances in genomic sequencing. For instance, it is now

recognized that some of the variability in risks associated with inherited cardiac disorders is specific to the causative variant and modifier loci.[116] Clinical genetic testing has proven to be a useful adjuvant tool to aid in diagnosis and management of some arrhythmic disorders. Furthermore, identifying a causative variant offers the ability to screen family members at risk for the disorder (Figure 4). Unfortunately, with the exception of long QT syndrome, genetic testing yields causative variants in less than 50% of cases. Furthermore, clinical genetic testing often yields variants of uncertain significance that are rare variants with unclear causal relationship with the observed clinical phenotype. Thus, in a large proportion of families with genetic arrhythmic disorders, we lack the ability to screen at risk members and possibly aid in the management of known affected individuals.

iPSC-CMs have the potential to serve the role of a personalized medicine tool that can alleviate some of the limitations of our current approach. This owes to iPSC-CMs' advantage of being donor specific, that is, having the ability to recapitulate the genetic information of the original donor. As mentioned above, iPSC-CMs are not adult myocytes, and to use the platform in any investigational capacity, the following criteria must be met: (1) the gene in question must be functionally expressed, (2) the phenotype observed must be reliably measured, and (3) the phenotype measured must be comparable with adult cardiomyocytes to provide adequate clinical correlation or predictive ability. To date, multiple independent investigators have identified electrophysiological abnormalities in iPSC-CMs that support criteria 1 and 2 but not definitively criterion 3 (Table). Population-level studies are needed to prospectively test the sensitivity and specificity of iPSC-CMs as a diagnostic or a risk stratification tool.

Validation of disease-specific electrophysiological characteristics of iPSC-CMs would enable the use of iPSC-CMs as an electrophysiology study in a dish platform. Using genome-editing methods, such as ZFN,[102] TALEN,[135] and CRISPR/Cas9 system,[119] this approach can be used to test the likelihood of candidate variants being disease causing (Figure 4).[102] Furthermore, this approach may prove useful in aiding the diagnosis of complex cases in which current clinical criteria fail to definitively make a diagnosis. In addition, in cases that are clinically or genetically idiopathic, iPSC-CMs may provide vital clues as to the electrophysiological abnormalities underlying the disorder at hand. If abnormalities are indeed identified, iPSC-CMs derived from individual family members could serve as a valuable screening tool analogous to genetic testing (Figure 4). Even if population studies prove iPSC-CMs to be reliable in diagnosing multiple disorders, this platform, similar to clinical genetic testing, will serve as an important adjuvant tool to aid the management and not define it.

Conclusions

Most of the heterogeneous disorders that lead to SCD in the absence of major structural heart disease share the common pathways of predisposition toward lethal arrhythmias. Multiple platforms have been used to study these disorders, ranging from cell-based to organism-based platforms, each providing important contributions to the field. Recently, the human iPSC-CM model has emerged as a novel beating cardiomyocyte model that provides several detailed and high-throughput methods of electrophysiology assessment. This platform has already been used to elucidate several inherited and acquired rhythm disorders and has shown excellent recapitulation of electrophysiology phenotype and drug efficacy and toxicity profile. With these advantages, iPSC-CMs are expected to provide valuable contributions to the science and clinical practice of arrhythmic disorders leading to SCD.

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