To predict the safety of a drug at an early stage in its development is a major challenge as there is a lack of in vitro heart models that correlate data from preclinical toxicity screening assays with clinical results. A biophysically detailed computer model of the heart, the virtual heart, provides a powerful tool for simulating drug–ion channel interactions and cardiac functions during normal and disease conditions and, therefore, provides a powerful platform for drug cardiotoxicity screening. In this article, we first review recent progress in the development of theory on drug–ion channel interactions and mathematical modelling. Then we propose a family of biomarkers that can quantitatively characterize the actions of a drug on the electrical activity of the heart at multi-physical scales including cellular and tissue levels. We also conducted some simulations to demonstrate the application of the virtual heart to assess the pro-arrhythmic effects of cisapride and amiodarone. Using the model we investigated the mechanisms responsible for the differences between the two drugs on pro-arrhythmogenesis, even though both prolong the QT interval of ECGs. Several challenges for further development of a virtual heart as a platform for screening drug cardiotoxicity are discussed.

**LINKED ARTICLES**

This article is part of a themed section on Chinese Innovation in Cardiovascular Drug Discovery. To view the other articles in this section visit [http://dx.doi.org/10.1111/bph.2015.172.issue-23](http://dx.doi.org/10.1111/bph.2015.172.issue-23)

**Abbreviations**

AE, allosteric effector; APD, action potential duration; APD_{90}, APD at 90% repolarization; APs, action potentials; BCL, basic cycle length; CV, conduction velocity; CVR, conduction velocity restitution; ERP, effective refractory period; GR, guarded receptor; HH, Hodgkin–Huxley; I_{CaL}, L-type Ca\(^{2+}\) current; I_{Ks}, delayed rectifier K\(^{+}\) channel current; I_{Ktof}, fast component of the cardiac transient outward current; I_{Na}, Na\(^{+}\) channel current; LQTs, long QT syndrome; MR, modulated receptor; QTc, corrected QT interval; VW, vulnerable window; WL, wavelength

**Tables of Links**

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These Tables list key protein targets and ligands in this article which are hyperlinked to corresponding entries in [http://www.guidetopharmacology.org](http://www.guidetopharmacology.org), the common portal for data from the IUPHAR/BPS Guide to PHARMACOLOGY (Pawson et al., 2014) and are permanently archived in the Concise Guide to PHARMACOLOGY 2013/14 (Alexander et al., 2013a,b).
Introduction

The development of a new drug from its discovery to final market approval takes, on average, about 10 years and costs over ~$1 billion (DiMasi et al., 2003). Some drugs (e.g. cisapride) have had to be withdrawn due to their undesirable side effects, such as cardiotoxicity (Hondeghem et al., 2011). Withdrawal of a cardiotoxic drug is not just a waste of time and money for the pharmaceutical industry, but may also impose serious risks to a patient’s life. Therefore, predicting the side effects of a drug at an early stage of its development is of utmost importance as regards drug safety assessments (Pollard et al., 2010).

One of the most dangerous potential side effects of a drug is pro-arrhythmic effects arising from an interaction between drug molecules and cardiac membrane ion channels. A contemporary biomarker for predicting a drug’s safety is based on its effect on the corrected QT interval (QTc) of the ECG (Friedrichs et al., 2005): a drug that prolongs the QTc is regarded as having a great potential for triggering severe pro-arrhythmic events. As the delayed rectifier K\textsubscript{r} channel (Kr) provides a major repolarizing current that determines the cellular action potential duration (APD) and, therefore, the QT interval of an ECG, testing the effects of a drug on I\textsubscript{Kr} is normally performed as a preclinical screening to predict any potential risks of the drug. However, in most cases, drug-induced arrhythmia risk is not solely due to inhibition of I\textsubscript{Kr}, neither do all drugs that prolong the QTc interval induce arrhythmia. In fact, drug-induced arrhythmias may result from complex interactions between a drug and cardiac electrophysiology, including tissue’s excitability, refractoriness and spatial dispersion of ventricular repolarization. In some cases, where a drug acts (directly or indirectly) on multiple transmembrane ion channels simultaneously (i.e. combined actions on K\textsubscript{r}, Na\textsuperscript{+} and L-type Ca\textsuperscript{2+}-channels) (Hondeghem et al., 2001; Gintant, 2012), the mechanisms involved in the pro-arrhythmic effects of a drug are even more complex. Consequently, the assessment of a drug’s safety that is confined to preclinical screening for actions on I\textsubscript{Kr} or clinical QT interval is unlikely to be effective. Hence, novel methods are required to evaluate the complicated actions of a drug on cardiac activities for the assessment of drug cardiotoxicity.

In recent years, there have been rapid advances in the development of biophysically detailed computer models of the heart for simulating its electrical and mechanical dynamics (i.e. the virtual heart) (Clayton et al., 2011; Henriquez, 2014). The virtual heart has been extensively implemented as a cardiac electrophysiological platform for investigating the functions of the heart during various physiological, pathological and pharmaceutical conditions (Clayton et al., 2011; Henriquez, 2014). Recently, it has attracted attention as an appliance for quantitatively evaluating drug safety (Mirams et al., 2012).

In this review, we first present recent progress in the mathematical modelling of the drug–ion channel interactions in cardiac tissue. We then propose a family of biomarkers that can be used to quantitatively characterize the actions of a drug on cardiac electrical activities at the cellular and tissue level. To illustrate the suitability of the virtual heart as a screening strategy, we used computer models of the human ventricle to simulate and quantify the effects of cisapride and amiodarone on ventricular activities and pro-arrhythmic substrates. Finally, we discuss several challenges that need to be considered for the future development of a whole heart model as a platform for screening drug safety.

Theory for the interaction between ion channels and drugs

Mathematical models for ion channels

Two approaches have been used for mathematical modelling of the functions of cardiac membrane ion channels. One is the Hodgkin–Huxley (HH)-type model (Clayton et al., 2011; Henriquez, 2014), in which voltage and time-dependent gating variables are used to describe the properties of an ion channel, with activation and inactivation processes being assumed to be independent. For instance, the fast sodium channel current can be described by (Noble, 1960; 1962; Kohl and Noble, 2009; Kharche et al., 2011):

$$I_{Na} = g_{Na}m^2h(j(V_m - E_{Na}))$$  \hspace{1cm} (1)

where $I_{Na}$ is the sodium channel current; $g_{Na}$ the maximal channel conductance; $m$ the voltage- and time-dependent activation variable; $h$ and $j$ the fast and slow inactivation variables, respectively; $V_m$ the cell membrane potential; and $E_{Na}$ the reversal potential of the channel (for model details, please see Appendix A).

The other is the Markov chain type of ion channel model that allows for detailed descriptions of the specific channel states and the transitions between them (Iyer et al., 2004; Rudy and Silva, 2006; Clancy et al., 2007). Transitions between states can be dependent on voltage, temperature and drug concentration. So far, detailed Markov chain models have been developed for several cardiac membrane ion channels, including the transient outward K\textsubscript{r} current $I_{to}$ ($I_{Kr,1}$ and $I_{Kr,2}$) (Iyer et al., 2004), $I_{Na}$ and $I_{K}$ ($I_{K}$ and $I_{Ks}$) (Rudy and Silva, 2006).

Theory for a drug’s interaction with ion channels

Receptor theory is an important framework for mathematical modelling of pharmacological actions of cardiac ion channels. With this theory, a receptor model is based on the known laws of physical chemistry for describing the binding of drug molecules to cellular receptors, which can be divided into three categories (Kenakin, 2004) as listed below.

Theory of simple pore block. The ‘simple pore block’ theory assumes that drug molecules continuously access the ligand-binding site of the ion channel receptor and the affinity of the drug molecule for the receptor is independent of time and cardiac membrane voltage (Starmer et al., 1994). With this theory, the effects of a drug on blocking an ion channel can be simulated using a blocking factor $k$ that reduces the maximum conductance of the target ion channel. Mathematically, $k$ is expressed as:

$$k = \frac{1}{1 + \left(\frac{[D]}{[C_{50}]}\right)^m}$$  \hspace{1cm} (2)

where $[D]$ is the drug concentration, $[C_{50}]$ is the drug concentration that reduces the maximum conductance of the target ion channel by 50%, and $m$ is the Hill coefficient.
The simple pore block theory has been widely used for simulating drug action on cardiac electrical activities. For example, Starmer et al. (1994) implemented the theory to investigate the mechanism by which a drug blocking potassium channels suppressed the responses of cardiac cells to premature stimuli. Later on, Starmer et al. (1995) also implemented the theory to investigate the anti-arrhythmic effects of potassium channel blockade.

**Theory of state-dependent block.** The ‘state-dependent block’ theory is based on the dynamic properties of ion channels. There are two subcategories, the modulated receptor (MR) theory (Hille, 1977) and the guarded receptor (GR) theory (Starmer et al., 1984).

Both the MR and GR theories assume that the association and dissociation processes of a drug molecule are dependent on time and cellular membrane potential. However, the MR theory proposes that a drug can bind to the drug receptor regardless of the state of the targeted ion channel, and its binding affinity in each state is different. In contrast, the GR theory hypothesized that the affinity of drug binding to a particular conformation of an ion channel is constant, and the access of the drug to the binding site is limited due to alterations in the ion channel conformation.

Based on the MR theory, Hondeghem and Katzung (1977) proposed an HH type of model for simulating the action of lidocaine and quinidine on \( I_{Na} \). In this model, the \( Na^+ \) channel model had closed (R), active (A) and inactivated (I) states, and the drug had the same affinity to block each of them, as shown in Figure 1A. Thus, a mathematical model for the \( I_{Na} \) was represented as:

\[
I_{Na} = g_{Na}(1 - B) m \, n h (V_m - E_{Na})
\]

**Figure 1**
Schematic illustration of the modulated receptor theory and guarded receptor theory on the HH type of \( Na^+ \) ion channel. Figure adapted from Comtois et al. (2008). (A) Modulated receptor model proposed by Hondeghem and Katzung (1977) with transition rates from unblocked to blocked channels \( (k) \) and from blocked to unblocked \( (\ell) \). (B) Guarded receptor model with affinity to the inactivated and activated states (Starmer and Grant, 1985).

\[
\frac{dD}{dt} = k_i [D] (1 - B) + l_i B
\]

where \( k_i \) and \( l_i \) are the association and dissociation rates. For details of this model and parameters, please see Appendix A.

**Theory of allosteric effect.** The ‘allosteric effector’ (AE) theory differs from the ‘state-dependent block’ theory in that the AE theory considers that drugs act as allosteric effectors to alter the transition dynamics of the targeted ion channels instead of simply blocking them. A recent study has implemented the AE theory, together with the MR and GR theories and Markov chain model of ion channel gating kinetics to illustrate how class I anti-arrhythmic drugs, lidocaine and flecainide, affect ventricular rhythms by inducing functional changes in the dynamics of \( Na^+ \) channels (Moreno et al., 2011).

**Modelling the interactions between drug and ion channels**

**Na\(^+\) channel and drug interaction**

The \( Na^+ \) channel plays an important role in generating cardiac electrical action potentials (APs) (i.e. it is a major determinant of the maximal upstroke velocity of the AP and cardiac excitability) and ensuring AP conduction in the cardiac tissue. Drugs that target \( Na^+ \) channels have been widely used for treating various cardiac diseases (Corrias et al., 2010).

Mathematical modelling of the interaction between the \( Na^+ \) channel and drugs can be dated back to 1977 when Hondeghem and Katzung (1977) pioneered the study to investigate the anti-arrhythmic properties of the cardiac \( Na^+ \) channel blockers, lidocaine and quinidine, using the MR theory. Later on, Starmer et al. (1987; Starmer, 1987) developed a GR-based model for simulating the actions of lidocaine on the cardiac \( Na^+ \) channel and investigated the mechanisms by which the anaesthetics affect cardiac excitability (Starmer, 1987; Starmer et al., 1987). Recently, using the same GR-based model, Starmer et al. (2003b) investigated the effects of \( Na^+ \) channel blockade on the refractory period of cardiac excitations.

Models for simulating interactions between drugs and Markov chain model of \( Na^+ \) channels have also been developed. In their study, Clancy et al. (2007) developed a Markov chain model for the \( \Delta KPQ \) mutant \( Na^+ \) channel that is associated with variant 3 of long QT syndrome (LQTS). The model presented the \( \Delta KPQ \) mutant channel with drug-binding sites for the open and inactivation states of \( Na^+ \) channels for simulating the actions of mexiletine and lidocaine. Recently, Moreno et al. (2013) developed another Markov chain type of \( Na^+ \) channel model, with eight states representing drug bound effects, eight discrete background states representing the non-affected channel conformations and another four states describing \( Na^+ \) channel bursting...
Potassium channel and drug interaction

The $I_{\text{Kr}}$ activates during the plateau phase of the AP and plays an important role in AP repolarization (Sanguinetti and Tristani-Firouzi, 2006). The $K_{\text{v}11.1}$ (also known as hERG) channel is considered to be the most widely targeted potassium channel in arrhythmic pharmacological therapy.

Using a previous model of $I_{\text{Kr}}$ developed by Silva and Rudy (2005), Sale et al. constructed two Markov chain models for representing hERG 1a/1b and hERG 1a channels (Sanguinetti et al., 1995; Trudeau et al., 1995; Smith et al., 1996). Their modelling results showed that the time course of E-4031 for blocking heteromeric 1a/1b channels was slower than that for blocking homomeric 1a channels (Sale et al., 2008), which suggested that specifically disrupting hERG 1b channel function was expected to reduce cardiac $I_{\text{Kr}}$ and enhance drug sensitivity.

Drug molecular binding to channel states with different conformations or a distinct affinity presents complex behaviours. In a recent study, Romero et al. (2014) investigated in silico the drug/channel interactions by systematically altering the transition rates in the Fink et al. (2008) Markov chain model of human hERG ($K_{\text{v}11.1}$) channels. By incorporating the drug–channel model into the O’Hara et al. (2011) model of human ventricular APs, they showed that drugs with disparate affinities to conformational states of the $K_{\text{v}11.1}$ channel played an important role in increasing a tissue’s susceptibility to acquired LQT. Independently, Di Veroli et al. (2014) developed a mathematical model of $K_{\text{v}11.1}$ channels to study drug safety with different binding configurations. Based on experimental data on the effect of the antipsychotic clozapine on hERG channel blocking and unblocking kinetics, Hill et al. (2014) proposed an hERG channel model with kinetically distinct binding states of the drug to open and inactivation states. Their modelling data effectively illustrated the interaction between clozapine and hERG channels in acquired LQT (Hill et al., 2014).

The fast component of the cardiac transient outward current, $I_{\text{To}}$, plays an important role in the early phase of repolarization. A Markov chain type of formulation of $I_{\text{To}}$ with consideration of the effects of different $I_{\text{To}}$-specific block states (drug bound to the three closed states and the open state of $I_{\text{To}}$) on mouse ventricular AP has also been developed (Zhou et al., 2012).

Calcium channel and drug interactions

L-type Ca$^{2+}$ channels constitute a main Ca$^{2+}$ entry pathway into the cell and play an important role in cardiac excitation (Corrias et al., 2010). Pharmacological therapies targeting the cardiac $I_{\text{Ca,L}}$ have also been widely considered in practice.

Markov chain models for representing the $I_{\text{Ca,L}}$ have also been developed in previous studies (Hund and Rudy, 2004). These models have been implemented to investigate the effect of β-adrenoceptor stimulation on ventricular arrhythmogenesis in association with LQT (Faber and Rudy, 2007; Faber et al., 2007).

Multichannel and drug interactions

Drugs targeting multiple membrane ion channels may be effectively anti-arrhythmic. Computer modelling provides a tool for theoretically exploring the actions of a drug targeting multiple ion channels (Martin et al., 2004; Qu and Weiss, 2005; Bottino et al., 2006). It has been shown by a simulation study that a putative compound that blocks the three ion channels, which mediate $I_{\text{Ca,L}}$, $I_{\text{Ca,L}}$, and $I_{\text{Kr}}$, had better anti-arrhythmic effects than one that only blocks the $I_{\text{Kr}}$ (Mirams et al., 2011).

Some other advances in simulation of the interaction between a drug and the various ion channels are summarized in Appendix B.

Assessment flow for the action of a drug in silico

The electrical activity of the heart results from the coordinated actions of cardiac systems operating at many physiological sites, including subcellular, ion channel, cellular, tissue and organ levels. Therefore, a comprehensive assessment of drug safety has to be conducted at all of these levels. This imposes a major challenge, if not impossible, for conventional experimental preclinical drug safety screening. However, it can be achieved by computer models of the heart. In this regard, we propose an assessment flow for evaluating the actions of a drug at the cellular and tissue levels using computer models of the heart as illustrated in Figure 2.

In the following section, as illustrated, we present simulation results to demonstrate the application of computer models for evaluating the actions of cisapride and amiodarone on cardiac electrical activities at the cellular and tissue levels.

Computational evaluation of the effects of cisapride and amiodarone

Cisapride and amiodarone are both known to prolong the QT interval of the ECG, yet they have different effects on cardiac arrhythmogenesis. Cisapride, an $I_{\text{Ca,L}}$ blocker, has been withdrawn from the market due to the high risk for it to induce torsades de pointes leading to fatal cardiac arrhythmias. However, amiodarone, a multichannel blocker that simultaneously affects the channels that mediate $I_{\text{Ca,L}}$ and $I_{\text{Kr}}$, has been found to be effectively safe and anti-arrhythmic. It is unclear why the two drugs, while both increasing QT interval, have different actions on arrhythmogenesis. In this section, we used a biophysically detailed computational model of the heart to investigate the effects of the two drugs on the characteristics of cardiac electrical activities at the cellular and tissue levels.

Single-cell simulations of cisapride and amiodarone

Choice of single-cell AP model. The well-established ten Tusscher and Panfilov (2006a) models of the human ventricu-
lar APs were chosen in this study as they have been well validated to simulate electrical APs of human ventricular endo-, middle- and epicardial cells.

Modelling drug–channel interaction. To simulate the actions of cisapride and amiodarone, we implemented the simple pore block theory, by which the maximal channel conductance of the targeted channel(s) was reduced by various percentages according to the dose of the drug (Table 1). For cisapride, the channel conductance of \( I_{Kr} \) was reduced to 70 and 60% of its original values in control condition for a low (150 nM) and a high dose (300 nM) respectively (Wilhelms et al., 2012). For the amiodarone case, the channel conductances of \( I_{Kr} \) and \( I_{CaL} \) were reduced to 43 and 85%, respectively, for a low dose (presumably 1 μM), and to 15 and 66% for a high dose (presumably 3 μM) based on experimental data (Nishimura et al., 1989; Kodama et al., 1999).

Effects on cellular APs. Figure 3 shows the simulated effects of cisapride (Figure 3Ai,Bi) and amiodarone (Figure 3Aii,Bii) on human epicardial ventricular APs at low (left panels) and high doses (right panels). Simulation suggested that both drugs did not markedly affect the AP amplitude, resting potential or \( \frac{dV}{dt_{\text{max}}} \), but both prolonged the APD at 90% repolarization (APD90). This latter effect on the APD was dose-dependent. At low doses, cisapride and amiodarone prolonged the epicardial APD90 by 12 and 13 ms, respectively, which was changed to 16 and 11 ms at high doses. Such a dose-dependent APD prolongation is consistent with the

Table 1
Scaled ion channel conductance due to actions of cisapride and amiodarone at low and high doses

<table>
<thead>
<tr>
<th>Conductivity</th>
<th>Cisapride</th>
<th>Amiodarone</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>Low dose (%)</td>
<td>High dose (%)</td>
</tr>
<tr>
<td>( G_{Kr} )</td>
<td>70</td>
<td>60</td>
</tr>
<tr>
<td>( G_{CaL} )</td>
<td>100</td>
<td>100</td>
</tr>
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</table>

Figure 2
Assessment flow chart for testing drug actions using hierarchical levels of computer models including ion channel, cellular and tissue levels. The actions of a drug on cardiac electrical activity at cellular and tissue levels can be characterized by analysing their effects on a family of biomarkers.
clinically observed increase in the QT interval induced by the two drugs.

There are no experimental data from human ventricular cells with which to compare our simulation data. However, our simulation results are qualitatively comparable with experimental data obtained from other species. For cisapride, the simulated APD prolongation was in fair agreement with experimental observations from canine (Di Diego et al., 2003) and from rabbit (Varro et al., 1996; Nakagawa et al., 2010) ventricular cells. Experimentally, it was found that 0.2 $\mu$M cisapride prolonged the canine epicardial APD$_{90}$ by 9.45 ± 6.4% at a basic cycle length (BCL) of 500 ms (Figure 3Ci). Our simulation (Figure 3Ci) showed that a low dose (0.15 $\mu$M) and a high dose (0.3 $\mu$M) prolonged the APD$_{90}$ by 3.88 and 5.18%, respectively, which were close to the experimental data. Quantitative differences between the simulation and experimental data may reflect species differences between the human and canine or the rabbit hearts. The observed dose-dependent APD prolongation is also consistent with the experimental data of Fossa et al. (2004) from the guinea pig heart.

For amiodarone, experimental data from rabbit epicardial ventricular cells showed that 5 $\mu$M amiodarone prolonged the APD by 6.63 ± 2.76% at a BCL of 400 ms (Nakagawa et al., 2010). This is also close to our simulation data of 4.20 and 3.56% for low (1 $\mu$M) and high dose (3 $\mu$M) respectively (Figure 3Cii). In simulation, we observed that the APD prolongation decreased with an increased dose of amiodarone, which is consistent with the experimental data of Wu et al. (2008) from the rabbit heart.

Simulation using the other two types of cell models (i.e. the middle and endocardial cell models) showed qualitatively similar results to the epicardial cell model. Results are summarized in Table 2.

Simulation results showed that there were subtle differences between the two drugs with regard to their dose-dependent actions on APD. For cisapride, the APD prolongation increased with an increased dose. But for the amiodarone, the APD prolongation decreased with an increased dose. Such different dose-dependent actions of the two drugs on APD prolongation may be attributable to the different ion channels that they target: cisapride only inhibited $I_{Kr}$ whereas amiodarone inhibited both $I_{Kr}$ and $I_{CaL}$. In order to test this hypothesis and investigate the functional effects of blocking $I_{CaL}$, further simulations were performed with different percentages of $I_{CaL}$ blocking (10–70%), together with basal blocking of $I_{Kr}$ by cisapride at low (by 30%) and high (by 40%) doses (Figure 3Ai,Bi), and basal blocking of $I_{Kr}$ by amiodarone at low (by 57%) and high (by 85%) doses (Figure 3Aii,Bii). (Hereafter, simulations were also performed for characterizing the effects of the combined block of $I_{Kr}$ and $I_{CaL}$ on other characteristics of cardiac electrical activities.) It was shown that blocking $I_{Kr}$ alone prolonged the APD. However, when both $I_{Kr}$ and $I_{CaL}$ were blocked, the APD was prolonged when

**Figure 3**
Simulation of actions of cisapride and amiodarone on human epicardial ventricular APs with comparison to experimental data. Effects of a combined action of blocking of $I_{Kr}$ by the two drugs at high and low doses together with different blocking of $I_{CaL}$ (from 10 to 70%) were also shown. (Ai, Aii) Actions of cisapride and amiodarone at low doses. (Bi, Bii) Actions of cisapride and amiodarone at high doses. (Ci, Cii) Comparison of simulated APD prolongation results to experimental data for cisapride (Di Diego et al., 2003) and amiodarone (Nakagawa et al., 2010).
A low percentage of \( I_{CaL} \) was blocked but shortened when a high percentage of \( I_{CaL} \) was blocked. These simulation results explain why a high dose of amiodarone produces a smaller APD prolongation as compared with a low dose.

**Effects on APD and ERP restitution curves.** Measuring the action of a drug on the APD and effective refractory period (ERP) restitution curve can help to understand the rate-dependent actions of the drug on cellular APD and ERP, which form important biomarkers for characterizing the effects of a drug. To compute the APD restitution and ERP curves, we followed the same methods as used in our previous studies (Zhang and Hancox, 2004; Zhang et al., 2008).

Figure 4 shows APD restitution curves computed from epicardial cells at control and low and high doses of cisapride and amiodarone. Effects of a combined block of \( I_{Kr} \) by the two drugs at high and low doses together with the different blocking of \( I_{CaL} \) (from 10 to 70%) are also shown. (A) low dose of cisapride; (B) high dose of cisapride; (C) low dose of amiodarone; (D) high dose of amiodarone.

### Table 2

<table>
<thead>
<tr>
<th>Endo</th>
<th>APA (mV)</th>
<th>dV/dt\text{max} (mV·ms(^{-1}))</th>
<th>APD(_{90}) (ms)</th>
<th>ΔAPD (ms)</th>
<th>APA (mV)</th>
<th>dV/dt\text{max} (mV·ms(^{-1}))</th>
<th>APD(_{90}) (ms)</th>
<th>ΔAPD (ms)</th>
<th>APA (mV)</th>
<th>dV/dt\text{max} (mV·ms(^{-1}))</th>
<th>APD(_{90}) (ms)</th>
<th>ΔAPD (ms)</th>
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<td>396</td>
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<td>–</td>
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<tr>
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<td>32</td>
<td>129</td>
<td>405</td>
<td>320</td>
<td>11</td>
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ΔAPD is equal to the difference between the APD\(_{90}\) of control condition and that of a drug dose action in the same cell type.
In comparison with the control, cisapride and amiodarone prolonged the APD90 for all the stimulus intervals tested (400–2000 ms), producing steeper APD restitution curves as shown by increased maximal slopes of the curves. This suggested an increased propensity of the two drugs for generating AP alternans leading to arrhythmogenesis (Karagueuzian et al., 2013).

In comparison with amiodarone, the cisapride APD restitution curves were steeper, illustrating an even higher propensity for the induction of alternans. With regard to the combined action of I_{CaL} blocking together with the basal blocking of I_{Kr} by the two drugs, APD restitution curves became flatter with an increased level of I_{CaL} block. This suggested that a drug such as amiodarone (which has a combined action on I_{CaL} and I_{Kr}) is superior to a drug such as cisapride that only blocks I_{Kr} for suppressing the development of AP alternans, a predisposing factor for arrhythmogenesis.

Simulation data also showed that both cisapride and amiodarone prolonged ERPs for all the considered range of BCL (200–2000 ms) (data not shown).

**Multicellular tissue simulations of cisapride and amiodarone**

*Transmural ventricular tissue model.* A multicellular model of transmural ventricular tissue was constructed by incorporating the ten Tusscher and Panfilov (2006a) model into a reaction diffusion partial differential equation as in our previous studies (Zhang and Hancox, 2004; Zhang et al., 2008). The model was used to quantify the actions of cisapride and amiodarone on cardiac conduction and its vulnerability to arrhythmogenesis.

**Effects on conduction velocity (CV) restitution.** At the multicellular tissue level, an important biomarker for characterizing the actions of a drug on cardiac excitation wave propagation is the CV and its rate dependence, that is, the CV restitution curve (CVRC). Figure 5 show the results of the computed CVRC in control and cisapride and amiodarone conditions. It was shown that at low pacing rates with a BCL greater than 600 ms, neither cisapride (Figure 5A,B) nor amiodarone (Figure 5C,D) had any noticeable effects on the measured CV, either at low or high doses. However, at high pacing rates with a BCL smaller than 600 ms, the two drugs decreased the CV. The decreased CV at high pacing rates was attributable to reduced tissue excitability due to increased ERP.

Blocking I_{CaL} in addition to the basal block of I_{Kr} by the two drugs resulted in a slight decrease in the CV at low pacing rates, but a marked increase in the CV at high pacing rates as compared with conditions when only the basal I_{Kr} was blocked.

**Effects on excitation wavelength (WL).** The excitation WL is another biomarker to characterize the action of a drug on cardiac excitation waves. A drug that increases the WL is believed to be anti-arrhythmic, whereas a drug that shortens the WL is regarded as being pro-arrhythmic as it allows limited cardiac tissue to accommodate multiple wavelets of excitation waves underlying fibrillations.

Figure 6 shows the computed wavelength restitution curve from the epicardial cell model in control and cisapride (Figure 6A,B) and amiodarone (Figure 6C,D) conditions at low and high doses. In contrast to the CV (Figure 5), the WL...
Figure 6
Computed wavelength restitution curves of cardiac excitation waves in control and cisapride and amiodarone conditions. Effects of a combined action of blocking of $I_{Kr}$ by the two drugs at high and low doses together with different blocking of $I_{CaL}$ (from 10% to 70%) are also shown. (A) low dose of cisapride; (B) high dose of cisapride; (C) low dose of amiodarone; (D) high dose of amiodarone.

In the control condition, the VW was 14.3 ms. In the cisapride condition, the WL was increased to 15.2 and 15.7 ms for low and high dose respectively. For the amiodarone condition, the VW was about 15 ms for both low and high doses.

As compared with the cisapride condition, the measured VW in the amiodarone condition was smaller, suggesting a less pro-arrhythmic effect of amiodarone. Furthermore, the measured VW remained almost constant at low and high dose of amiodarone, rather than in the case of cisapride, where the measured VW was greater at high doses than at low doses. A smaller VW of amiodarone may be attributable to its combined action on both $I_{Kr}$ and $I_{CaL}$.
I\textsubscript{Kr} and I\textsubscript{CaL} compared to one targeting I\textsubscript{Kr} only. These results provide insights into understanding why amiodarone is less likely to have pro-arrhythmic effects than cisapride.

**Effects on ECG.** Effect of a drug on the QT interval of ECG has been used as an index to characterize the safety of the drug in practice. The effects of a drug on the characteristics of a pseudo-ECG can also be computed in the model. In simulations, the pseudo-ECG was computed as an integral of spatial gradient of membrane potential at all positions on the strand from a virtual electrode located in the extracellular space following the methods used by other studies (Gima and Rudy, 2002; Zhang and Hancox, 2004).

Figure 8 shows the results of simulated ECGs under control and cisapride and amiodarone conditions at low and high doses (Figure 8, left panel). It was shown that both cisapride and amiodarone prolonged the QT interval of ECG. Amiodarone increased the amplitude of the T wave at a low dose, but such an increased T-wave amplitude became insignificant at a high dose. Cisapride did not show any noticeable effects on the T-wave amplitude. In simulations, cisapride prolonged the QT interval by 7.50 and 8.75% for low and high dose, respectively (Figure 8, right panel), which was in fair agreement with experimental data that showed a 8.74 ± 5.28% prolongation in the QT interval by 0.2 μM cisapride in the canine heart (Di Diego et al., 2003); amiodarone at low
and high doses prolonged the QT interval by 10.94 and 12.81%, respectively, which was also fairly close to the 24.63 ± 6.72% QT interval prolongation by 5 μM amiodarone in the rabbit (Varro et al., 1996).

Effects on initiation and maintenance of re-entrant excitation waves. Re-entrant excitation waves are believed to be associated with cardiac tachycardial arrhythmias or fibrillation. Further simulations were performed to investigate the effects of cisapride and amiodarone on the initiation and maintenance of re-entrant excitation waves in a three-dimensional realistic model of human ventricles developed in our previous studies (Adeniran et al., 2011). In order to evaluate the effects of cisapride and amiodarone on re-entry initiation and maintenance, the lifespan of the re-entry and power spectrum of electrical activity recorded from a local site of the ventricle were computed.

The results are shown in Figure 9 for control (Figure 9Ai–Aiii), and high doses of cisapride (Figure 9Bi–Biii) and amiodarone (Figure 9Ci–Ciii). In the control case, re-entry was initiated and sustained as shown by the snapshots of excitation pattern in the ventricle (Figure 9Ai). The electrical activity recorded showed rapid spontaneous ventricular excitation (Figure 9Aii) with a dominant frequency of 4.84 Hz (Figure 9Aiii). With the high dose of cisapride, re-entry was also initiated and sustained (Figure 9Bi), with rapid spontaneous ventricular electrical activity (Figure 9Bii), but the excitation was slowed down with a dominant frequency of 4.17 Hz as compared with the control condition (Figure 9Biii). However, with the high dose of amiodarone, re-entry was self-terminated shortly after initiation (Figure 9Ci–Ciii). Consistent with the actions of these two drug effects on arrhythmogenic effects elucidated at the cellular and tissue levels, at the three-dimensional organ level, cisapride increased susceptibility to initiation and maintenance of re-entry, but amiodarone, by terminating re-entry, was anti-arrhythmic.

Discussion

Biophysically detailed and well-validated computer models of the heart have shown excellent promise as an alternative preclinical cardiotoxicity screening tool. Since the pioneering work of Denis Noble (1960), many complex and precise cardiac cell models have been developed in the last few decades for various species and different cell types, which form a fundamental basis for the virtual physiological heart (Kohl and Noble, 2009; Clayton et al., 2011). The virtual heart has attracted increasing attention for its application in drug development and assessment (Xie et al., 2014). With the use of the virtual heart, the effects of a drug on cardiac electrical activities can be quantitatively characterized at different levels, thus providing a better assessment of the safety profile of a drug as compared with the conventional use of QT prolongation or effects on I_{Kr}.

Mechanistic insights into the actions of cisapride and amiodarone

Our simulation results showed that cisapride, an hERG channel blocker, prolonged cellular APD, steepened the APD and ERP restitution cures, increased a tissue’s vulnerability to arrhythmogenesis and sustained but slowed down re-entrant excitation waves. However, although amiodarone, a combined channel blocker of hERG and L-type Ca^{2+} channels, also prolonged cellular APD, it steepened the APD and ERP restitution curves to a lesser degree, reduced the tissue’s vulnerability to arrhythmogenesis and most importantly terminated re-entrant excitation waves as compared with cisapride. These data explain why amiodarone is safer than cisapride as an anti-arrhythmic treatment. Furthermore, our simulations showed that such a difference in the two drugs can be

Figure 9

Initiation and maintenance of re-entry in a three-dimensional realistic model of human ventricles under control (A), high cisapride (B), amiodarone (C) conditions. (Ai, Bi, Ci) Snapshots of conduction pattern of ventricular re-entry. (Aii, Bii, Cii) Time series of electrical activity recorded from a local site in the ventricle. (Ci, Cii, Ciii) Power spectrum of the recorded electrical activities.
attributable to the blocking effect of amiodarone on $I_{CaL}$ in addition to the blocking of $I_{Ks}$.

**Future challenges**

Although advances have been made in the last few decades in modelling drug–channel interactions and cardiac electrophysiology, there are still some challenges ahead for implementing the virtual heart model for drug safety assessment. Firstly, more studies are needed to develop biophysically accurate models for simulating the interactions between drug molecules and ion channel receptors. This requires not only further development of theories on the interaction between drug and channel(s) but also detailed experimental data on the kinetics of a drug’s actions. A complete set of such experimental data will help to derive and validate mathematical equations and parameters for the drug–channel interaction model. Secondly, well-validated models for simulating different cell types of the human heart in normal physiological and various pathological conditions are needed. A complete set of these cell models can be incorporated into the whole heart model for simulating the actions of the drug on the electrical activities of the whole heart conduction system, not just in a localized region of the heart such as the ventricle. This whole heart model can be used to answer questions such as ‘is a drug that is effective for anti-ventricular fibrillation safe for atioventricular node conduction?’ Thirdly, cardiac arrhythmogenesis is associated with autonomic modulations, and so are the drug-induced cardiac arrhythmias. Therefore, it is necessary to incorporate the actions of autonomic regulations on the cardiac models for simulating the actions of drugs and their interactions with the heart during changes in autonomic systems. In addition, recently there are some new developments in structure-based virtual drug screening (Villoutreix et al., 2008), as well as simulations of drug–ion channel interactions based on protein structures (Silva et al., 2009; Silva and Rudy, 2010; Nekouzadeh and Rudy, 2011). How to incorporate such microscale models into a large-scale whole heart model for simulating and evaluating the actions of a drug is also a challenge.

**Conclusion**

A biophysically accurate, detailed and well-validated model of the heart provides a powerful platform for quantitative assessment of a drug’s safety. The platform integrates independent and distinct physical results from toxicological experiments, such as assay and patch clamp data, into a whole heart model based on detailed data from cellular electrophysiology, electro-anatomical mapping and MRI/CT structural imaging. The whole heart model can be further integrated into a three-dimensional human torso model, forming a multiscale physical platform allowing one to simulate the action of a drug on body surface ECGs (as shown in Figure 10). With these computational tools, the functional effects of a drug can be thoroughly analysed at the cellular, tissue and organ levels by a family of corresponding cardiac electrophysiological properties (i.e. biomarkers), from which the safety of the drug can be fully assessed.

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Author contributions

H. Z. conceived and designed the experiments. Y. Y. and C. L. performed the experiments; Y. Y., X. B., C. L., K. W. and H. Z. wrote the manuscript.

Conflict of interest

None.

References


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Appendices

Appendix A: Details of mathematical equation of \( I_{Na} \) in HH and Markovian chain formats

In the HH format, \( I_{Na} \) model is based on the Luo and Rudy (1994b) model, which is given by:

\[
I_{Na} = g_{Na} m^3 h (V - E_{Na}) \quad \text{(A1)}
\]

\[
E_{Na} = (RT/F) \ln ([Na^+]_o/[Na^+]_i) \quad \text{(A2)}
\]

For \( V \geq -40 \text{ mV} \):

\[
\alpha_h = \alpha_i = 0.0 \quad \text{(A3)}
\]

\[
\beta_h = 1/(0.13 \{1 + \exp[(V + 10.66)/-11.1]\}) \quad \text{(A4)}
\]

\[
\beta_i = 0.13 \cdot \exp(-2.535 \times 10^{-7} V)/(1 + \exp[V + 32]) \quad \text{(A5)}
\]

For \( V < -40 \text{ mV} \):

\[
\alpha_h = 0.135 \cdot \exp[(80 + V)/-6.8] \quad \text{(A6)}
\]

\[
\beta_h = 3.56 \cdot \exp(0.079 V) + 3.1 \times 10^4 \cdot \exp(0.35 V) \quad \text{(A7)}
\]

\[
\alpha_i = [-1.2714 \times 10^5 \cdot \exp(0.2444V) - 3.474 \times 10^3 \cdot \exp(-0.0439V)] \cdot (V + 37.78)/(1 + \exp[0.311 \cdot (V + 79.23)] \quad \text{(A8)}
\]

\[
\beta_i = 0.1212 \cdot \exp(-0.01052V)/(1 + \exp(-0.1378(V + 40.14))] \quad \text{(A9)}
\]

\[
\alpha_m = 0.32(V + 47.13)/(1 - \exp[-0.1(V + 47.13)] \quad \text{(A10)}
\]

\[
\beta_m = 0.08 \cdot \exp(-V/11) \quad \text{(A11)}
\]

In the Markovian chain format, the \( Na^+ \) channel is based on the three states of the \( Na^+ \) channel: resting (R), activated (A) and inactivated (I).

**MR representation of state-dependent drug action**

The sum of blocked channels (B) is given by the following:

\[
B = R' + A' + I' \quad \text{(A12)}
\]

\[
A = m^3 h j \quad \text{(A13)}
\]

\[
A' = m^3 h j \quad \text{(A14)}
\]

\[
R = h j - A \quad \text{(A15)}
\]

\[
R' = h j - A' \quad \text{(A16)}
\]

\[
I = 1 - B - h j \quad \text{(A17)}
\]

\[
Y = B - h j \quad \text{(A18)}
\]

\[
k_r = 0.4 \text{ ms}^{-1} \cdot \text{M}^{-1}, k_h = 1.0 \text{ ms}^{-1}, k_A = 5 \times 10^{-4} \text{ ms}^{-1} \cdot \text{M}^{-1},
\]

\[
l_A = 1.5 \text{ ms}^{-1}, k_B = 5 \text{ ms}^{-1} \cdot \text{M}^{-1},
\]

\[
l_I = 2 \times 10^{-3} \text{ ms}^{-1}, \text{and } \Delta V = 30 \text{ mV}
\]

**Guarded receptor representation of drug action**

The model was proposed by Starmer et al. (1991b), with details as the following:

\[
\frac{dB}{dt} = k_A[D]m^3 h j(1 - B_A - B_i) - I_A e^{-0.039} B_A \quad \text{(A19)}
\]

\[
\frac{dB}{dt} = k_I[D]m^3 h j(1 - B_A - B_i) - I_I e^{-0.039} B_I \quad \text{(A20)}
\]

\[
I_{Na} = g_{Na} m^3 h j(V - E_{Na}) \quad \text{(A21)}
\]

\[
I_{Na} = g_{Na}(1 - B_A - B_i) m^3 h j(V - E_{Na}) \quad \text{(A22)}
\]

Simulations of lidocaine action were obtained with a binding rate \( k_A = 1370.0 \text{ ms}^{-1} \cdot \text{M}^{-1} \) and an unbinding rate \( l_A = 1.3 \times 10^3 \text{ ms}^{-1} \) for the open state and a binding rate \( k_I = 60 \text{ ms}^{-1} \cdot \text{M}^{-1} \) and an unbinding rate \( l_I = 2.3 \times 10^{-4} \text{ ms}^{-1} \) for the inactivated state.
### Appendix B: List of some advances in simulation of ion channel–drug interactions

#### Table B1
Major models for simulating drug screening

<table>
<thead>
<tr>
<th>Model</th>
<th>Ion channelopathy</th>
<th>Using in simulating drug screening</th>
</tr>
</thead>
<tbody>
<tr>
<td>The Fitzhugh model (Fitzhugh, 1961)</td>
<td>$I_{Na}$ channel</td>
<td>(Starmer et al., 1994; Starobin et al., 1996)</td>
</tr>
<tr>
<td>The Beeler–Reuter model (Beeler and Reuter, 1977)</td>
<td>$I_{Na}$ channel</td>
<td>(Starmer et al., 1991a; 2003a,b)</td>
</tr>
<tr>
<td>The Ebihara–Johnson model (Ebihara and Johnson, 1980)</td>
<td>$I_{Na}$ channel</td>
<td>(Starmer et al., 2003a,b)</td>
</tr>
<tr>
<td>The Luo–Rudy model (Luo and Rudy, 1994a,b)</td>
<td>$I_{Na}$ channel</td>
<td>(Clancy and Rudy, 2002; Cimponeriu et al., 2003; Kapela et al., 2005; Terrenoire et al., 2005; Trenor et al., 2005; Clancy et al., 2007; Ahrens-Nicklas et al., 2009; Saiz et al., 2011)</td>
</tr>
<tr>
<td>The Ramirez–Nattel-Courtemanche model (Courtemanche et al., 1998; Ramirez et al., 2000)</td>
<td>$I_{Na}$ channel</td>
<td>(Kneller et al., 2005; Tsujimae et al., 2007; Comtois et al., 2008; Aguilar-Shardonofsky et al., 2012; Colman et al., 2014)</td>
</tr>
<tr>
<td>The Shannon–Bers model (Shannon et al., 2004)</td>
<td>$I_{Na}$ channel</td>
<td>(Wu et al., 2011)</td>
</tr>
<tr>
<td>The Hund–Rudy model (Hund and Rudy, 2004)</td>
<td>$I_{Na}$ channel</td>
<td>(Cardona et al., 2010; Aguilar-Shardonofsky et al., 2012)</td>
</tr>
<tr>
<td>The Tusscher model (ten Tusscher et al., 2004; ten Tusscher and Panfilov, 2006a)</td>
<td>$I_{Na}$ channel</td>
<td>(Fredj et al., 2006; Sale et al., 2008; Mirams et al., 2011)</td>
</tr>
<tr>
<td>The ten Tusscher–Panfilov model (ten Tusscher and Panfilov, 2006b)</td>
<td>$I_{K}$ channel</td>
<td>(Dux-Santoy et al., 2011)</td>
</tr>
<tr>
<td>The O’Hara–Rudy model (O’Hara et al., 2011)</td>
<td>$I_{Na}$ channel</td>
<td>(Moreno et al., 2013)</td>
</tr>
</tbody>
</table>