Mechanistic Systems Biology Modeling Applied to the Pre-Clinical Cardiac Safety Assessment of a Pharmaceutical Compound:

from Channels to Cells to Tissue

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An Integrative Modeling Process



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Cardiac Safety Assessment of Compounds

Potential for QT prolongation?

- One of the main reasons to withhold approval and withdraw drugs from the market
- Is associated with an enhanced risk for a specific ventricular arrythmia, which may lead to tachycardia (TdP), which may lead to death
- Very complex issue: many unknowns, multiple opinions, multiple risk factors, other important readouts for arrythmogenicity (TDR), integrated assessment of multiple endpoints to evaluate clinical risk (+range of expertise!)

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Pre-Clinical Cardiac Safety Assessment: Work flow on the Experimental Side



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Tiered Risk Assessment



* When there is a class or structural signal, subsequent nonclinical studies should include a representative positive control from that class

CARDIAC SAFETY INDICES •CSI = IC_{50u} / EC_{50d} •CSI = IC_{50u} / IC_{50d} $\bullet CSI = IC_{50u} / [Plasma]_{free}$ •CSI = IC_{50u} / [Myocardium] •Acceptable value = F[therapeutic class, benefit/risk factor, corporate policy, regulatory guidance]

Safety Margins



Drug concentration



Integrating Channel Responses

- I_{Kr}: often the only channel directly tested at early screening stage
- Drugs often affect other channels: I_{Ks}, I_{Ca-L}, late I_{na-sus}, all important in repolarization!
- ➢ I_{Kr} "red flag signal" → Mixed effects on other channels may worsen OR improve effects on APD and QT
- ➢ <u>NO</u> I_{Kr} "signal" → Doesn't imply one is necessarily "safe" at the APD or QT level!
- Spatial heterogeneity in channels, from endo- to mid- to epi-cardiac cells across ventricular wall
- Many other physiological variables
 heart rate, disease/genetic status, gender, nutrition, diurnal



CardioPrism[™] (Physiome – Novartis, 2002)



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CardioPrism[™] Platform: Basis for Integrated Models

Suite of cardiac cell models for multiple species built upon:

- > J.J. Rice (+ Ca²⁺ handling), M.S. Jafri, R.L. Winslow
- > D. Noble et al.
- > C. Antzelevitch et al.

Spatial aspects & integration at tissue level (modeling & experiments):

- > P.J. Hunter et al., Y. Rudy et al. (1-D "cable" model)
- C. Antzelevitch et al.
- > Physiome: A. Muzikant, C. Penland, G. Chen (based on previous work, Duke U.)

Compound entry: model assumes that the channel-specific ($IC_{50,x}$) and Hill Coefficient (*Nx*) characterize a sigmoidal dose-response relationship for the inhibition of current (*Ix* vs. *Ix,control*) as a function of [Drug] $I_x([Drug])$ 1

$$\frac{I_x([Drug])}{I_{x,control}} = \frac{1}{1 + \left(\frac{[Drug]}{IC_{50,x}}\right)^{N_x}}$$

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CardioPrism[™]: Drug A vs. Drug B



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CardioPrism[™]: (I) Development of New <u>Canine</u> Purkinje Fiber Model

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CardioPrism[™]: (I) Development of Canine Purkinje Fiber Model: Assumptions

- Mechanisms within the endocardial myocyte model are similar to those of canine Purkinje fiber
 - > Differences can be approximated by changing 14 conductance parameters
- Drugs act via a sigmoidal dose-response relationship to inhibit 6 currents (I_{Kr}, I_{Ks}, I_{to}, I_{Ca-L}, I_{Na-Ca}, I_{Na-sus})
 - These currents suffice to predict the action of a drug on ventricular myocytes and Purkinje fibers
- Dose-response parameters from HERG assay and Purkinje fiber parameter estimates can be used in ventricular myocyte models
- The chosen error functions are a good measure of the quality of fit of the model to action potential data

CardioPrism[™]: (II) Reverse-, then Forward-Engineering

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CardioPrism[™]: (II) Reverse-Engineering: Global Estimation Results

- Target shows location of best IC50 fits for I_{Na-sus} & I_{Ca-L}
- Clustered points are next best fits (simulations with errors less than twice the error of the best fit)

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Data Set: Drug A vs. Drug B HERG current is inhibited, but APs are not prolonged

Isolated canine Purkinje fiber
 paced at 0.5, 1.0 Hz,
 0.0, 0.1, 0.3, 1.0, 3.0, 10 μM

CardioPrism[™]: "Pure I_{Kr} Blocker" Hypothesis (Drug A & B) → Not good, but we knew this

Cells Coupled Through the Cable Model

CardioPrism[™]: "Pure I_{Kr} Blocker" Hypothesis (Drug A & B)

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CardioPrism[™]: Reverse-Engineering & Prediction of IC₅₀'s for late I_{Na-sus} and I_{Ca-L} Currents

- → Significant inhibition of I_{Na-sus}, I_{Kr}, I_{Ca-L} by both drugs
- → Dose-response estimates for key currents: important for AP repolarization

CardioPrism[™]: Forward-Engineering (I)

In contrast to pure I_{Kr} blockers, which prolong the action potential (severely so in M cells), Drug A & Drug B either do not affect or even shorten action potentials in isolated cells

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CardioPrism[™]: Forward-Engineering (II)

➢Pure I_{kr} blockers prolong the QT interval (left panel)

- Both drugs act to shorten the QT interval and reduce the amplitude of the T wave (at high doses there is also inversion)
- >At higher concentrations of Drug A (5-10 μ M), shortening of the QT interval reverses but remains less than control

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CardioPrism[™]: Forward-Engineering (III)

The difference in APD between isolated epicardial and M cells is, in this example, consistent with the TDR in the 1-D cable

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CardioPrism[™]: Conclusions, Drug A vs. Drug B

- Both compounds block multiple ion currents
 - Data and model indicate significant block of I_{Kr}, I_{Ca-L} and I_{Na-sus}
 - Stark contrast to "null-hypothesis" of pure I_{Kr} block
- No dose-dependent QT prolongation or increase in TDR
- Confidence intervals for Drug A smaller vs. Drug B
 - Confidence in predictions is better for Drug A

Experimental Confirmation

Fast I_{Na}

Drug A: $IC_{50} = 2.30 \ \mu M$ Late I_{Na}

Drug B: IC₅₀ = 4.48 μM

Data Set: Drug C HERG current is strongly inhibited, APD is prolonged

- IC₅₀ (hERG_{HEK293}) = 28.7 nM
 - IC₅₀'s also available for two metabolites and other compounds in same class
- Detailed AP study (parent + two metabolites)
 - Canine Purkinje Fibers: 2 frequencies, concentration range over 3 orders of magnitude
 - Parent + one metabolite are associated with APD prolongation, at >0.1 μM

CardioPrism[™] Conclusions, Drug C

- "*Pure I_{Kr} block*" hypothesis examined again
 - Single cell models
 - Tissue "cable" model
 - NOT satisfactory to explain observed AP's
- Reverse-engineering
 - Both global & local estimation routines could NOT find an IC₅₀ profile on the 6 candidate channels (I_{Kr}, I_{Ks}, I_{to}, I_{Ca-L}, I_{Na-Ca}, I_{Na-sus}) to interpret AP data for Drug C in a satisfactory fashion
 - Dose-dependent block of the 6 ion currents do not suffice to predict the action potential data for Drug C
- Need to formulate & test other hypotheses
 - Drug-induced potentiation (rather than inhibition) of channel currents?
 - Additional mechanisms in the Purkinje fiber?

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THANK YOU

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