Influence and Control of SR Ca^{2+} Release

A crucial element in modeling EC coupling is the mechanism which luminal Ca^{2+} controls release. In the Shiferaw model, it was assumed that the amount of Ca^{2+} release is a phenomenological nonlinear function of the Ca^{2+} load which becomes steep for high loads (8). The origin of this nonlinear relationship, however, is not well understood. Calcium release from the SR is regulated by the ryanodine receptors (RyRs), which open upon a rise in the local cytosolic Ca^{2+} concentration (14). There is a growing body of experimental evidence showing that luminal Ca^{2+} regulates the sensitivity of the RyRs via the interaction of auxiliary proteins (triadin-1/junctin, T/J) with the luminal Ca^{2+} buffer calsequestrin (CSQN) (e.g., (15 17)). In particular, Györke

the equations and model parameters is given in the Appendix. In Elementary Ca^{2+} Release Unit Structure we describe the intracellular compartments and the various currents in our model. In Cell Architecture we briefly describe the geometry of ventricular myocytes, which we use to realistically implement our spatially extended model. Finally, in the sub-sections Luminal Gating and Luminal Buffering we present a new mathematical formulation of CSQN-mediated luminal gating and buffering that takes into account the transition from monomeric to dimeric forms of CSQN with increasing luminal free Ca^{2+} concentration.

Elementary Ca^{2+} Release Unit Structure

Excitation-contraction coupling, the process by which cardiac myocytes transform the membrane depolarization signal into cell contraction, is a complex process that spans multiple scales (44,45). Calcium ions (Ca^{2+}) enter the cell upon membrane depolarization, triggering discrete Ca^{2+} release events at the elementary CRUs of the SR, an intracellular store whose primary function is the sequestration and release of intracellular Ca^{2+}. These Ca^{2+} sparks (46,47) are highly localized in space ($\sim 1\,\mu$m) and time (~ 20 ms). The SR is a sac-like structure which forms a spatially dense network of interconnected tubules and cisternae. The tubular network is usually referred to as network SR (NSR), while the cisternae are referred to as junctional SR (JSR). These cisternae are localized in close proximity to the t-tubules, cell membrane invaginations that form a also a dense structure in ventricular myocytes (48). The cisternae are usually called dyads, and the space between a dyad and the sarcolemma is referred to as the

num er of LCC channe s er d ad wou d resu t in a more heterogeneous I_{Ca} current am itude er C , since different num ers of channe s cou d o en within some narrow time

$$k_{41} \quad \tau_u^{-1}. \tag{9}$$

where τ_u and τ are the characteristic unbinding (slow) and binding (fast) times, and $B_{C N}^0 \quad 400\,\mu M$ is the normal C N concentration and guarantees that $k_{14} \to \tau^{-1}$ for low c_J. We will choose these constants based on experimentally measured spark restitution curves. The transition rate from the open C N-unbound to the open C N-bound state is taken to be the same as the one from the closed C N-unbound to the closed C N-bound state, $k_{23} \quad k_{14}$. Finally, to satisfy detailed balance, $k_{12}k_{23}k_{34}k_{41} \quad k_{14}k_{43}k_{32}k_{21}$, we set the transition rate from the open C N-bound to the open C N-unbound to be

$$k_{32} \quad k_{41}k_{12}/k_{43}. \tag{10}$$

The value of the parameters can be found later in Table 10 and further details can be found in the Appendix.

We will model each dyad as having 100 channels. Each channel evolves stochastically, independent of the other channels in the dyad. However, to avoid keeping track of the $\sim 20,000 \times 100$ channels in the monte, we only keep

track in each dyad of the number of channels that are in each of the four states. As described in the Appendix, these numbers can be updated in each time-step in a way that is equivalent to individually evolving each channel. Therefore we are able to speed up the simulations a factor of ~ 20 (from 100 s and four L-type channels to the number of channels per state and four L-type channels).

A crucial feature of the model described above is that the transition rate from the C N-unbound to the C N-bound states depends dynamically on the luminal Ca^{2+} concentration through the dependence of the monomer concentration [M] on c_J. In Fig. 2 b we plot the fraction of monomers $\hat{M}$ (

of C N- ound channe s increases. hese channe s have a ower o en ro a i it , and therefore the s ark terminates short thereafter. u se uent , the J re s, and eventually the umina Ca^{2+} concentration ecomes high enough that the concentration of monomers decreases. C N un- inds from the /J com e of the channe s, and the d ad

of Fig. 7 we plot the averaged cytosolic Ca^{2+} concentration c_i (Eq. 1) as a function of time for a pacing period of $T = 220$ ms. In the bottom panel we show the proximal space Ca^{2+} concentration c_p as a function of time for a transversal line of dyads across the myocyte, indexed in the vertical axis. This panel shows that, even though there is well-defined whole-cell CaA, individual dyads do not necessarily reflect this, since, in the time interval shown, there are some dyads firing only in the beats with large c_i, some firing every beat, and some firing irregularly, examples of which are indicated with the horizontal arrows and marked as a, b, and c, respectively. The vertical arrows in the top panel indicate the time of pacing. In Fig. 8 a we show the maximum values of the averaged Ca^{2+} cytosolic concentration during steady state pacing for different pacing periods. A bifurcation to CaA appears when the pacing period is decreased at <

development of alternans. Inserting these expressions in Eq. 22 and linearizing, we obtain

$$\begin{pmatrix} \delta l_{n+1} \\ \delta f_{n+1} \end{pmatrix} = \begin{pmatrix} 1 & \partial_l R(1+\partial_l U) & \partial_f R(1+\partial_l U) \\ \partial_l g(1-\partial_l R)e^{-/\tau_u} & \partial_l g\,\partial_f R\,e^{-/\tau_u} \end{pmatrix} \begin{pmatrix} \delta l_n \\ \delta f_n \end{pmatrix}, \tag{23}$$

where the derivatives are evaluated at the values l, f. The condition for alternating growth of the perturbations is that the eigenvalue of the matrix in Eq. 23 with the largest magnitude is < -1 (for alternans, this eigenvalue is negative). This condition results in that alternans develop when

$$(1+\partial_l U)(\partial_l R - 1) + \partial_f R\,\partial_l g\,e^{-/\tau_u} > 1. \tag{24}$$

This equation is the key to understanding the relative contributions of steep release-load relationship, uptake, and recovery of CaN-bound channels. If we can neglect CaN-mediated effects, $\partial_f R \approx 0$, $\partial_l g \approx 0$, or $\tau_u \ll T$

u ator of   activit , which a ows us to investigate the ro e
of C   N in romoting C A. In Fig. 11 c we show the ma -

number of available channels, and vice versa. However, when the uptake is enough to reduce or eliminate the dependence of the diastolic content on the number of available channels in the previous beat, one can observe CaA without significant alternations in diastolic Ca^{2+} content as in Fig. 8 C.

Another important feature of our model is that, for the first time, it simulates a realistic number ($\sim$20,000) of diffusively coupled, physiologically detailed elementary release units, where each unit has a realistic ($\sim$100) number of

D ff _ f f _ a ace b e b e

prohibitive, since diffusive coupling between adjacent CaNs requires the simultaneous processing of gating dynamics. To reduce the computation time to reasonable levels, we do not simulate each individual channel in a given CaN, but rather keep track of the number of channels in a given CaN that are in each state. The number of states in the nth dyad in the open CaN-bound (3), open CaN-unbound (2), and closed CaN-unbound (1) are denoted $x_3^{(n)}$, $x_2^{(n)}$, and $x_1^{(n)}$, respectively (the number of CaNs in the closed CaN-bound state is $x_4^{(n)} = 100 - x_1^{(n)} - x_2^{(n)} - x_3^{(n)}$.) Henceforth we will omit the superscript (n). The release current I_r depends only on the fraction of states in the open states $P_o = (x_2 + x_3)/100$, rather than on which particular channels are in each state. Therefore, at each time step, we only need to compute the number of channels that make transitions from one state to another. Since we have the probabilities for the transition of an individual channel, the distribution of the number of channels making a transition from state j can be obtained from a multinomial distribution with the number of trials being the number of CaNs in state j and the probabilities of success being the probabilities of transition to another state given by the expressions in Eq. 55. We remark that, so far, this is an equivalent mathematical formulation of the process that requires, for the large number of CaN channels we consider, less computational effort. Further approximations allow us to increase the efficiency of the simulation. In practice, the probabilities of transition per unit time are small and we can treat transitions to different states as independent. For example, if at time t there are x_1 channels in the closed unbound state, the probability that x_{12} of these channels makes a transition to the open unbound state and x_{14} channels make a transition to the closed bound state in the time interval $[t, t + \Delta t)$ is

$$p(x_1, x_{12}, x_{14}) = M(x_1, k_{12}\Delta t, k_{14}\Delta t) , \qquad (56)$$
$$\approx B(x_1, k$$

7. Pruvot, E. J., and D. . osen aum. 2003. -wave a ternans for risk strati cation and prevention of sudden cardiac death. Curr. Cardiol. Rep. 5:350 357.

8. hiferaw, ., M. A. Watana e, A. Garinke, J. N. Weiss, and A. Karma. 2003. Mode of intracellu ar ca cium coing in ventricu ar m oc tes. Biophys. J. 85:3666 3686.

release sites in rat cardiac myocytes. Proc. Natl. Acad. Sci. USA. 95: 10984–10989.

48. Soeller, C., and M. B. Cannell. 1999. Examination of the transverse tubular system in living cardiac rat myocytes by 2-photon microscopy and digital image-processing techniques. Circ. Res. 84:266–275.

49. Flucher, B. E., and C. Franzini-Armstrong. 1996. Formation of junctions involved in excitation-contraction coupling in skeletal and cardiac muscle. Proc. Natl. Acad. Sci. USA. 93:8101–8106.

50. Franzini-Armstrong, C., F. Protasi, and V. Ramesh. 1999. Shape, size, and distribution of Ca^{2+} release units and couplons in skeletal and cardiac muscles. Biophys. J. 77:1528–1539.

51. Shannon, T. R., F. Wang, J. Puglisi, C. Weber, and D. M. Bers. 2004. A mathematical treatment of integrated Ca dynamics within the ventricular myocyte. Biophys. J. 87:3351–3371.

52. Mahajan, A., Y. Shiferaw, D. Sato, A. Baher, R. Olcese, L.-H. Xie, M.-J. Yang, P.-S. Chen, J. G. Restrepo, A. Karma, G. A., S. Z., and N. J. 2007. A rabbit ventricular action potential model replicating cardiac dynamics at rapid heart rates. Biophys. J. In press, published online at DOI:10.1529/biophysj.106.098160.

53. Bondarenko, V. E., G. C. L. Bett, and R. L. Rasmusson. 2004. A model of graded calcium release and L-type Ca^{2+} channel inactivation in cardiac muscle. Am. J. Physiol. Heart Circ. Physiol. 286:H1154–H1169.

54. Lovetti, S. J., A. Gaenke, Z. Lu, J. Weiss, and Y. Shiferaw. 2006. Factors required for graded calcium release in a simplified computational model of the dyadic junction: importance of junctional variation. Heart Rhythm. 3:64–65.

55. Parker, I., W. J. Zang, and W. G. Wier. 1996. Ca^{2+} sparks involving multiple Ca^{2+} release sites along Z-lines in rat heart cells. J. Physiol. 497:31–38.

56. Satoh, H., L. M. D. Delbridge, L. A. Blatter, and D. M. Bers. 1996.