MODELLING THE GATING OF THE CARDIAC RYANODINE CHANNEL

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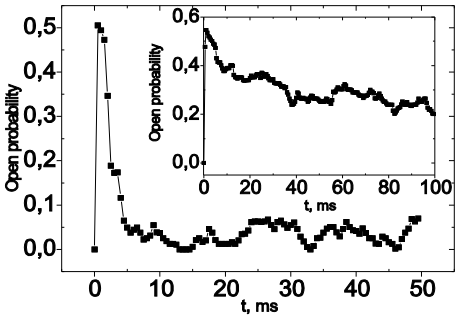
Simple physically-reasonable electron-conformational model was proposed [1,2] to describe the ryanodine receptor channel (RyR) gating in a cardiac cell. Each RyR is modelled with a single open and a single closed electronic state, described in frames of s=1/2 pseudo-spin formalism. Apart from the fast electronic degree of freedom, the RyR channels are characterized by a slow conformational coordinate, which specifies the RyR channel conductance. The sarcoplasmic (SR) load is incorporated into the model through the conformational stress. The RyR channel in such a model represents a particular version of so called spin-boson systems. Even being isolated it was shown to reveal both regular and chaotic dynamics[3]. The RyR gating in a cell implies i) Ca^{2+}-induced electronic transitions between two branches of a conformational potential with a probability set by the both *cis*-Ca_{SS} concentration and effective temperature, ii) a conformational Langevin dynamics, iii) quantum tunneling and thermal transitions. We have performed a series of computer simulations of a single RyR stochastic gating both under steady-state conditions and different stimuli aimed to reproduce all the features observed in lipid bilayer experiments, and elucidate the role of different transition mechanisms and control parameters. For illustration in Figure we demonstrate the short-decay time RyR response to Ca^{2+} spike (0.2 ms) induced both by Ca-dependent and Ca-independent transitions. Ensemble average is constructed from 81 individual episodes. Inset shows the long-decay time response due to only Ca-dependent transitions and Langevin dynamics.



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