

Finite Element Modeling of Vasoreactivity Using COMSOL Multiphysics® Software

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Abstract

Regulation of vascular tone is a complex process that remains poorly understood. Here we present our recent efforts for the development of physiologically realistic model of an arteriole for the analysis of vasoreactivity in health and in disease. Our goal is to describe function at a macro scale level by integrating mechanisms at the subcellular/molecular level. The behavior of a cell component (i.e. current-voltage relationship of an ion channel) or a signaling pathway is described through mathematical formulations. Modeling integrates intracellular and cell membrane components into whole-cell models of calcium and membrane potential dynamics. Cellular models are coupled (i.e. through diffusion of ions and second messengers) and multi-cellular models of the vascular wall are generated, capable of investigating intercellular communication and signaling. We implemented individual endothelial (EC) and smooth muscle (SMC) cell models as 2 D rectangular domains using COMSOL Multiphysics® software. Electro-diffusion for the ionic species was taken into account. This allows implementation of voltage and concentration dependent membrane currents as boundary equations. The continuum models allows introduction of spatial distribution of cellular components and microdomains. EC and SMC models were coupled through homocellular and heterocellular gap junctions and the diffusion of NO (Figure 1) to form multi cellular vessel model. High-throughput gene expression data inform the model of changes in activity of a component (i.e. conductance of an ion channel, concentration of a protein, density of pumps and receptors) in hypertension, to appropriately modify model parameters. Thus, the outlined approach can be used to investigate cellular mechanisms underlying altered peripheral vascular resistance in hypertension.

Figures used in the abstract

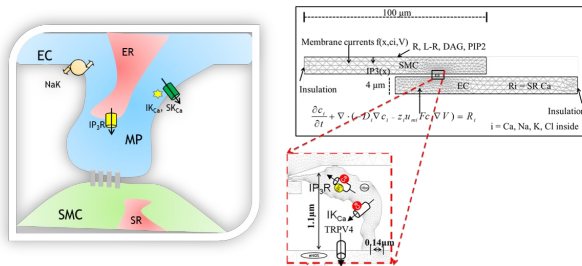


Figure 1