MATHEMATICAL MODEL OF ELECTROMECHANICAL HEART CONTRACTILE SYSTEM

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Abstract: *An effort of the authors of this paper is to focus on heterogeneous pathological functions of a heart muscle, which result mostly in patient's death and they are not from views of physiology hitherto explained. One possible way leading to their clarification is application of suitable mathematical models describing myocard from look of ionic transport through membrane of heart cells. The paper is therefore focused on mathematical model of one heart myocyte, discuss its dynamic characteristics and possibilities of verification.*

Key words: *simulation, mathematical model, calcium, myocard.*

1. INTRODUCTION

In clinical practice is known all series of cases when run down, without apparent cause, to pathological function of a heart muscle, presenting itself like fibrillation, pledge or electromechanical dissociation, and which caused then the death of a patient. Generally with ref., that these reasons could be dynamic processes acting on membrane and submembrane level of myocardiac cells. This explanation is self apart crimp, because an exact description of these action requires biochemical and physiological metering, which are not currently feasible or proceed on condition which are not always in conformance with the reality.

Widespread method how to solve this phenomenon is application of mathematical models concentrated, by reason of simplicity of description, on very limitation function of myocard or its cells. Current mathematical models describe myocard from the two main views, electrical and mechanical (resp. biochemical-mechanical), eventually combine both of them, however at the expense of their simplicity.

More applicated - models of electrical heart activity feel myocard as a dipole and map its potential eventually its potential field which form (Czerwinska & Doros, 1999; Coveney & Highfield, 1990; Fozzard, 1986). They are relatively well verified and serve for detection especially static illness of heart muscle (for instance infarct).

Biochemical-mechanical models present myocard as joiner pulse pumps and describe its cells from view of ionic transport (Na+, K+, Ca2+, and so on). Their verification is very difficult, but thereby, that they are more close to dynamic action coursing on cellulate membrane, they have prospection of detection causes of dynamic illness of myocard (for instance above mentioned heart fibrillation).

Therefore we prepared here presented model of electromechanical heart contractile system (based on a proposal of the model's rough structure made by research team leaded by Prof. Dr. Med. habil. Dipl.-Ing. R. Poll from TU Dresden), which belongs, in present stage of development, among biochemical-mechanical, however we suppose its extension about control system i.e. electrical module (action potential).

2. DESCRIPTION OF MODEL AND ITS PROPERTIES

2.1 Method

Model is derived from kinetic formulas of chemical reactions of components of the actomyosin system. It feeds mathematical formulation of genesis of cross bridge between contractile proteins, actin and myosin, whose incidence is mechanical contraction of one cardiac cell.

Physical chemistry allows to these formulas to assign a system of ordinary, non-linear first-order differential equations with constant coefficients, which express dynamic properties of reversible or one-way chemical reactions. For example chemical reactions

$$[A]+[M-ATP]\xleftrightarrow{k_{TA},k_{-TA}}[A-M-ATP] \quad (1)$$

$$[A]+[M-ADP-P_i]\xleftrightarrow{k_{DPA},k_{-DPA}}[A-M-ADP-P_i] \quad (2)$$

answering to differential equation

$$\frac{d[A]}{dt}=-k_{TA}\cdot[A]\cdot[M-ATP]+k_{-TA}\cdot[A-M-ATP]- \quad (3)$$
$$-k_{DPA}\cdot[A]\cdot[M-ADP-P_i]+k_{-DPA}\cdot[A-M-ADP-P_i]$$

Alike for further (completely in Neumann & Novak, 1999).

The system of differential equations is possible to model and simulate in a suitable environment, for example in well-known Simulink.

2.2 Dynamic characteristics of the model

We have focused on calculation of model's equilibrium state attained for relaxed and contracted cardiomyocyte, stability of model in equilibrium state and conditionality.

Results of analyses have shown, that the model is stiff with quantity of linear loops. These characteristics are not surprising, because they were found at majority of mathematical model of biological systems (Czerwinska & Doros, 1999; Coveney & Highfield, 1990). Problem of stiff systems is in those that demand implicit methods of numerical integration with very high accuracy, i.e. minimal value of a sampling period. Linear loops present in model, for all that cause singularity of a Jacobi matrix, do not affect a quality of a simulation process.

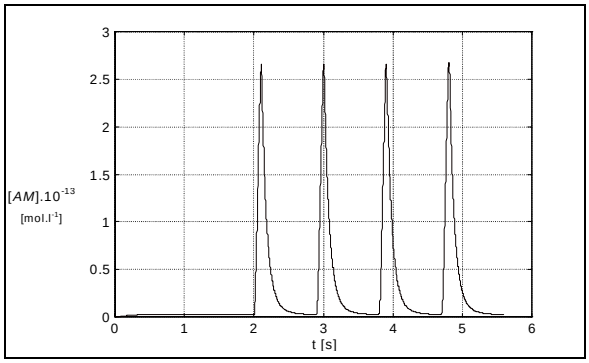
2.3 Initial conditions

Before starting of own simulation process initial conditions should be introduced – it means determined the starting point in a state space. In contradistinction to mathematical models of technical systems is situation much more complicated. It is not explicitly given time "zero" and, in addition, initial concentration of the state variables (complexes) are immeasurable, because they should reflect state in seven weeks old cardiomyocyte of a human fetus in the moment before the first heart contraction.

This reality we have gone round by option of zero initial conditions except complexes, whose concentration is in moment of relaxation of cardiomyocyte maximal. By suitable form of input signal we have achieved of transient action, so that model's response (set of transient characteristics) moves in state belongs to relaxed cardiomyocyte. It is evident, that described transitional action serves to compensation prenatal evolution of one cardiomyocyte.

3. RESULTS AND THEIR VERIFICATION

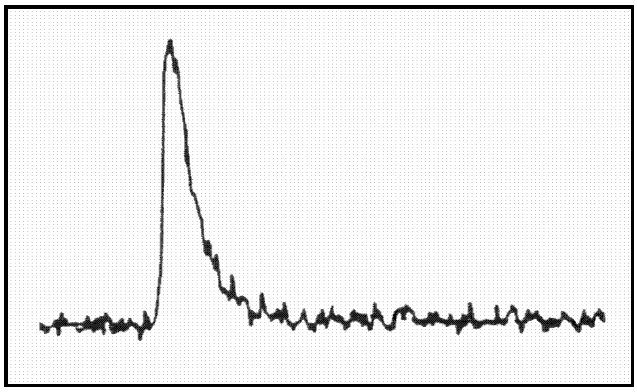
The result of simulation process is a set of charts representing transient concentration curves of a relevant complex - state variable (for example AM, see picture 1).



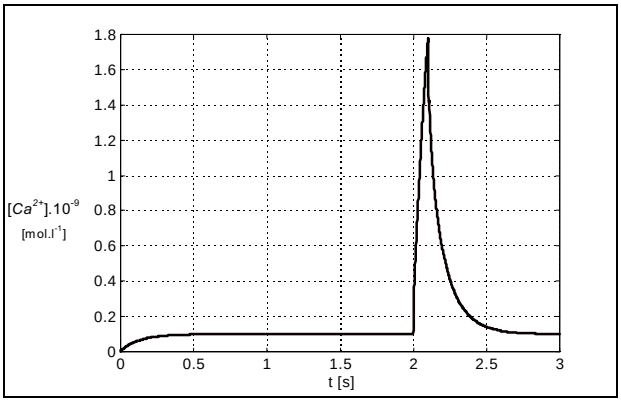
Pict. 1 - Concentration transient curve of the AM complex

Verification of model is very complicated from the two reasons. Firstly, present-day physiology has not reliable in vivo metering of intracellular concentration of all complexes modelled by us. Secondly, majority of measuring is orientated on concentration transient curves of calcium ion Ca2+, which are in addition indirectly based (for example fluorescent spectroscopy, Borovansky, 1997).

Nevertheless due to coincident structure of mammalian heart myocyte (the presence of a sarcoplasmic reticulum, Wier, 1980), is possible to perform visual confrontation of transitional calcium concentration curve of heart muscular fibre of rabbit (see pict. 2) with the result of simulation processes (see pict. 3). Although it is evident, that first version of our model does not work with stochastic character of ionic transport, which is perceptible from the picture 2, the model reaches very high level of conformance.



Pict 2 - Calcium transient curve measured in vivo on rabbit ventricle (Fozzard, 1986)



Pict. 3 – Result of simulation process

4. CONCLUSION

With regard to the structure of the model, in further work we would like to locate on finding of elements of a deterministic chaos, accurately formulate calcium transport through membrane into intracellular space and extend the model by equations describing the ATP metabolism in cardiomyocytes.

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