

Role of Heterogeneous Ionic Profiles in Atrial Fibrillation Propagation. A Population of Models Study

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Background: Atrial fibrillation (AF) is characterized by Wave Breaks (WB), it is a turbulent Action Potential (AP) propagation manifested as irregular electrical signals. Experimental data show heterogeneity regarding ionic profiles throughout the atrial tissue. In this study, the effect of the interaction of tissue with different ionic profiles is evaluated in terms of wave propagation.

Methods: An experimentally calibrated population of AF profiles based on the Koivumaki model was generated. Eight currents took random-sampled values between -75% and 150% of their original values. Ionic profiles fitting physiological biomarkers on 1Hz pacing protocols and capable of self-sustaining reentrant activity were evaluated. A bilayer rectangular mesh (160.000 nodes, diffusion $0.24 \mu\text{m}^2/\text{ms}$) was simulated including the basal model (left), one of the population models (right) and a transition zone (1 cm). A functional reentry was started on the basal region and the wave propagation to the altered region was classified as Continuous Propagation (CP) or WB (a).

Results: Preliminary results on 90 ionic profile simulations showed 38 CP and 43 WB patterns. For 9 ionic profiles (red dots in b) the rotor was dragged to the right, ending the reentry. Regarding ionic variations lower I_{K1} ($p=1.53 \cdot 10^{-10}$), I_{Na} , I_{CaL} ($p=0.04$), and higher I_{Kr} , I_{Kur} were associated with WB. Considering biomarkers at 1 Hz, higher Resting Membrane Potentials ($p=2.36 \cdot 10^{-10}$), longer AP Duration and larger AP Amplitude are associated with WB. Distributions of biomarkers prior to normalization ($X_N = (X-\mu)/\sigma$) in the 239 population were: $\text{APA} = 113.4 \pm 9.7 \text{ mV}$, $\text{APD}_{90} = 198.8 \pm 45.7 \text{ ms}$, $\text{RMP} = -77.5 \pm 2.3 \text{ mV}$, $\text{CV} = 32.1 \pm 4.6 \text{ cm/s}$.

Conclusions:

Populations of models allow simulating the arrhythmic role of physiological AF phenotypes. They will serve as a basis for personalized simulations able of predicting the efficacy of AF treatments.

