DESCRIPTION FOR THE GENERAL PUBLIC

Cardiac arrhythmias affect 0.1% adults under the age of 55 years and as many as 9% of people over the age of 80 years, constituting one of the biggest challenges of modern cardiology. Their pharmacological and invasive treatment is still characterised by unsatisfactory results. One of the reasons for his is still the incomplete knowledge of the nature, metabolism, or even the origin of particular elements of the electrical conduction system.

The scientific aim of the study is to delineate proteomic characteristic of human electrical conduction system nodes and surrounding heart tissue by comparing the protein profile of six regions of human heart: (1) the sinoatrial node, (2) cavoatrial junction, (3) atrioventricular node, (4) right atrial appendage vestibule, (5) working myocardium of the right atrium and (6) working myocardium of the right ventricle in the population of young healthy adults using modern proteomic analysis techniques.

Our study will be conducted on up to 15 human heart specimens, collected during routine forensic medicine autopsies. Organs will be collected from healthy young adults (18-40 years old). With the use of microsurgical techniques and under the control of the operational microscope, 6 samples will be taken from each heart. The proteomic analysis will be carried out using two methods. In the first step, the samples will be subjected to quantitative and qualitative “shotgun” analysis using Isobaric Tag for Relative and Absolute Quantitation (iTRAQ). Subsequently, in order to confirm the significance of the observed results, the second analysis will be performed using the Western blot technique.

The quantitative and qualitative proteomic analysis will allow to obtain a comparative view of the molecular structure of examined tissues. It will show the differences and similarities in the levels of specific proteins between the electrical conduction system nodes and tissue that surrounds them directly, as well as working atrial and ventricular myocardium in people without a history of cardiac arrhythmias and other cardiovascular diseases. These results will provide an introduction to the attempt to identify the unique “signature” of the cardiac electrical conduction tissue, which in the future will allow the identification and proteomic mapping of the entire cardiac electrical conduction system along with additional conduction paths and ectopic focus.

The recognition of the proteomic characteristics of the human electrical conduction cardiac system will help understand its origin and development. Knowledge of the proteomic profile of the sinoatrial and atrioventricular node is also interesting because it can be successfully used to develop effective treatment and diagnostic methods of arrhythmia or testing the effectiveness of antiarrhythmic drugs. The discovery of protein markers of the electrical conduction tissue may allow the identification of additional pathways and ectopic stimulation spots in the patients with cardiac arrhythmias and thus will contribute to a deeper understanding of the nature of these conditions.