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Serbian Society for Mitochondrial and Free Radical Physiology Bato Korac, Aleksandra Jankovic, Andjelika Kalezic

Dear Colleagues,

"Those who were fortunate to wake up this morning in Belgrade may believe that they have accomplished enough in their lives. To insist on more than this would be merely immodest" (Serbian poet and writer Dusko Radovic).

With these words, we would like to warmly welcome you to the virtual SFRR-E 2021 annual meeting "Redox Biology in the 21st Century: A New Scientific Discipline" from June 15-18, 2021, presented from Belgrade, Serbia.

Belgrade (Serbian: Beograd, meaning "white city") is the capital of Serbia and one of the oldest cities in Europe. It lies at the confluence of the Sava and Danube rivers, the position that defined Belgrade as the Door to Europe, the meeting point between East and West, North and South. In its 7000-year-old history, our city was demolished more than forty times, each time reborn and resurrected, like the Phoenix. Today, Belgrade unites diversity, creating a unique spirit of time. In the words of another Serbian writer, Momo Kapor: "Belgrade is not even in Belgrade, because Belgrade, in fact, is not a city; it is a metaphor, a way of life, a perspective on things".

There are a number of reasons one can say that the 21st century has given birth to a new scientific discipline – Redox Biology. And Redox Biology is also, like any other aspect of science and life, a perspective on things, with the cooperation of opposites in its basis. With a goal. Harmonized in health, out-of-balance in illness. Studying Redox biology: oxidants, antioxidants, redox active molecules and redox regulation is a multilayered endeavor to comprehend the complexity and uniqueness of this regulation. Understanding this complexity will allow for a greater understanding of biology and, life.

This Conference is an attempt to get to know more deeply the core of Redox Biology, the core of life.

With these warm thoughts, we are waiting to virtually meet you in June 2021.

On behalf of the Organizing Committee,

Bato Korac

Bata Karac



Belgrade Fortress



Church of Saint Sava



Nikola Tesla Museum







PP141

Hydroxyl radical scavenging potential of the late embryogenesis abundant proteins (LEA) proteins from *Ramonda serbica* – in silico approach

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Ramonda serbica Panc. is a resurrection plant that can survive long desiccation periods (extreme loss of cellular water). The accumulation of late embryogenesis abundant proteins (LEAPs) is a crucial step in desiccation tolerance mechanism. Based on in vitro studies, LEAPs can be involved in antioxidative defense, ion sequestration, structural stabilization of both membranes and enzymes during freezing or drying, while by forming intracellular proteinaceous condensates they increase structural integrity and intracellular viscosity of cells during desiccation. Here we investigated the antioxidative potential of LEAPs identified by de novo transcriptomics of R. serbica, based on their primary and secondary confirmation. In our previous work [1], we displayed the antioxidative capacity of 20 free proteogenic amino acids (FAA) through determining their hydroxyl radical (OH, generated in Fenton reaction) scavenging rate by using electron paramagnetic resonance. These results served as a basis for generating a model for prediction of 'OH scavenging activity for selected proteins. In addition, the model was built based on protein primary sequences, hydrophobicity, 3D structure and predicted solvent accessible area. Manually curated data for peptides and proteins with experimentally determined 'OH scavenging rate were used for training and testing. The model was fed into machine learning algorithm and 'OH scavenging potential scale was created using IC50 values. By applying our model, we classified 164 LEAPs according to their potential for 'OH scavenging. Further work will focus on the experimental evaluation of the obtained model by measuring of the rate of 'OH scavenging in the presence of recombinantly produced LEAPs.

Keywords: desiccation tolerance; electron paramagnetic resonance (EPR); intrinsically disordered proteins; machine learning; resurrection plants; secondary structure.

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