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CoMBoS2

Content

WELCOME SPEECH

Professor Dušanka **Savić-Pavićević**
President of the Serbian Society
for Molecular Biology

Dr. Melita **Vidaković**
President of the Steering Committee
of the Serbian Society for Molecular Biology

Dear colleagues and friends,

On behalf of the Serbian Society for Molecular Biology (MolBioS), we warmly welcome you to Belgrade for the Second Congress of Molecular Biologists of Serbia (CoMBoS2).

The congress is gathering almost 250 participants from 13 countries (Sweden, United Kingdom, Italy, Switzerland, USA, Australia, Hungary, Czech Republic, Romania, Montenegro, Croatia, Bosnia and Herzegovina, and Serbia).

The program covers various fields of Molecular Biology, including Molecular Biomedicine, Molecular Biotechnology and Molecular Cell Biology, and consists of plenary and invited lectures, the MolBioS award winner lecture, poster sessions and the project corner. Special attention is paid to students and young scientists through the MolBioS Student Session, flash presentations and workshops on state-of-the-art molecular biology methods.

We wish you to be inspired by exciting and outstanding lectures given by renowned scientists and experts, exchange ideas, find opportunities for new collaborations, and have good fun.

WELCOME TO

CoMBoS2

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IDENTIFICATION OF MICRO RNA FROM COMMON COPY NUMBER VARIANTS AS RISK FACTORS FOR CAKUT

Ivan Životić,[1] Kristina Mitrović,[1] Ivana Kolić,[1] Mariana Seke,[1] Maja Živković,[1] Aleksandra Stanković,[1] Ivan Jovanović[1]

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Introduction: Congenital anomalies of the kidney and urinary tracts (CAKUT) are a diverse spectrum of defects with complex etiology and not fully explained genetic background. miRNA-containing copy number variants (CNVs) are described as genetic risk factor for the disease development. We aimed to identify miRNAs with the maximum regulatory coverage of previously reported differentially expressed genes in CAKUT tissue compared to controls and bioinformatically characterize a set of these miRNAs which are located in common CNVs.

Methods: Differentially expressed genes were identified from ureter tissue transcriptome open data GSE83946 from 15 CAKUT patients and 7 healthy controls, generated in house previously. miRPathDB v2.0 was used for identification of miRNAs with maximum coverage of DEGs (miRNAs which complimentarily regulate all DEGs). Mapping of maximum coverage miRNAs onto common CNVs (frequency >0.2) was performed using UCSC genome browser and gnomAD database. miRNA mapping common CNVs were further bioinformatically analyzed using miRPathDB v2.0.

Results: In a maximum coverage set of 50 miRNAs interacting with DEGs in CAKUT, we have identified 3 miRNA genes located in the common CNVs (hsa-miR-663b, hsa-miR-3180-3p and hsa-miR-1302). Using Reactome database we identified all three miRNAs to be significantly enriched in the pathway Neuronal System: -log(p-value)>2.326 for hsa-miR-1302; -log(p-value)>1.556 for hsa-miR-3180-3p; and -log(p-value)>1.703 for hsa-miR-663b.

Conclusion: CAKUT is characterized with variable penetrability and expressivity and often followed with other comorbidities such as neurodevelopmental disorders. miRNAs involved in DEG networks and prone to CNV effects could present modulating factors of the disease phenotype. Further studies should provide additional evidence about hsa-miR-1302, hsa-miR-3180-3p and hsa-miR-663b involvements in CAKUT etiology.

Key words: CAKUT; CNV; microRNA; Microarray; Bioinformatic analysis

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