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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



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Abstracts

INTEGRATION OF METABOLOMICS AND TRANSCRIPTOMICS DATA REVEALS THE MOLECULAR BACKGROUND OF THE IRIDOID DIVERSITY WITHIN THE GENUS *NEPETA* (FAM. LAMIACEAE)

<u>Danijela Mišić</u>, ¹ Uroš Gašić, ¹ Branislav Šiler, ¹ Slavica Dmitrović, ¹ Marijana Skorić, ¹ Dragana Matekalo, ¹ Jasmina Nestorović Živković, ¹ Tijana Banjanac, ¹ Biljana Filipović, ¹ Milica Milutinović, ¹ Jelena Božunović, ¹ Neda Aničić, ¹ Luka Petrović, ¹ Tamara Lukić, ¹ Miloš Todorović

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Introduction: Recent intensive research on the genus *Nepeta* has resulted in increasingly accumulated information regarding the biosynthetic pathways and chemical evolution of iridoids; however, several intriguing aspects remain yet to be resolved. Our objective was to deeply investigate the molecular background of the diversity of iridoid compounds within the genus *Nepeta*, as well as regulative mechanisms of their biosynthesis.

Methods: Leaves of greenhouse-grown plants were analysed for the composition of iridoid aglycones (IAs) and iridoid glucosides (IGs) adopting non-targeted (UHPLC/LTQ Orbitrap MSⁿ, GC/MS) and targeted (UHPLC/DAD/(±)HESI-MS²) metabolomics approaches. Following RNA-Seq, transcriptomes of phylodiverse *Nepeta* taxa were searched for the presence/absence of iridoid-related biosynthetic genes. Co-expression patterns (qPCR) of biosynthetic genes and transcription factors were determined following plants' exposure to various environmental stresses.

Results: The comparison of metabolite composition among phylodiverse *Nepeta* taxa provided a systematic understanding of qualitative and quantitative composition of iridoids in leaves of the selected *Nepeta* taxa. Mining of RNA-Seq data in search for iridoid biosynthesis-related genes pointed to significant differences between taxa producing both IAs and IGs and those producing only IGs. Comparative metabolomics and gene co-expression analysis provided new information about mechanisms of regulation of iridoid biosynthesis.

Conclusion: Integration of data from several techniques analysed by different methods resulted in identifying key genes involved in the regulation of metabolic flux through the iridoid biosynthetic pathway and offered an explanation why some *Nepeta* taxa produce only IGs, while others produce both IAs and IGs. The obtained results pointed to new gene targets for improving iridoid production through biotechnology-based approaches.

Key words: Nepeta; iridoids; metabolomics; transcriptomics; gene co-expression analysis

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