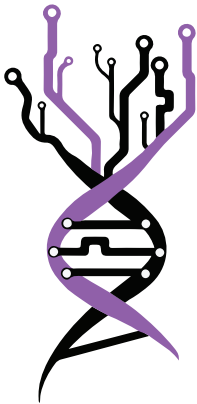


#BelBi2023 • Belgrade, Serbia

BOOK OF ABSTRACTS



4th Belgrade Bioinformatics Conference

HYBRID • 19 - 23 JUNE 2023

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Dr. Ivana Morić

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ISBN: 978-86-82679-14-1

belbi.bg.ac.rs

Title	4 th Belgrade Bioinformatics Conference BOOK OF ABSTRACTS
Publisher	Institute of Molecular Genetics and Genetic Engineering, University of Belgrade Vojvode Stepe 444a, Belgrade, Serbia https://www.imgge.bg.ac.rs/
Editors	dr. Ivana Morić dr. Valentina Đorđević
Technical editor	Dušan Radojević
ISBN	978-86-82679-14-1
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FOREWORD

Dear colleagues and friends,

The 4th Belgrade Bioinformatics Conference - BelBi2023, where many high-quality scientific contributions were presented, has just ended. With great thanks to all participants, we now proudly present a book of abstracts that both reflects the scientific abundance and diversity of the conference and serves as a reminder of a memorable event.

Several research institutions, faculties, and scientific societies from Serbia joined forces in organizing this international conference, which covered numerous topics in computational biology, bioinformatics, and biomedical and health informatics. The main goal of BelBi2023 was to foster contact between scientists, both early stage career and senior researchers, allowing them to share experiences and latest advances in their fields. We sincerely hope that BelBi2023 has served as a platform for researchers from around the world to meet, initiate new collaborations, and expand professional contacts, and that all of you would become a part of the growing BelBi community.

We are grateful and proud to have welcomed more than 250 researchers from 21 countries. We have had 28 scientific sessions, consisting of more than 60 lectures (including eight Keynote talks), 47 presented posters, as well as three workshops and one satellite event – COST action. We have also organized seven industry lectures, including the NGS Challenge,

two Meet the Expert Sessions, and one Business Coffee Break where ten start-up companies took part. And finally, the future BIO4 campus was presented and first panel on Serbia's resources for storage and analyses of genetic data was organized.

We would like to thank all the members of the International Advisory Board and the International Program Committee for their efforts and help in making this event a success. We are very grateful to the Ministry of Science, Technological Development and Innovation of the Republic of Serbia, SAIGE project, and UNDP-Serbia for their support. Finally, the Local Organizing Committee is very grateful to all the sponsors of the conference - BGI, Illumina & Elta'90MS, PacBio & East Diagnostics, ThermoFisher Scientific & Vivogen, Huawei, Labena, DSP Chromatography, RNIDS, Telekom Srbija, Alfa Genetics, Kefo and Superlab, hoping that they will stay with us for many years to come.

Looking forward to seeing you again at the 5th Belgrade Bioinformatics Conference.

Belgrade, July 2023

Dr. Valentina Đorđević
& *Dr. Ivana Morić,*
On behalf of BelBi2023
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Seven miRNAs potentially included in the chilling response of maize plants in early stages of development

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Micro RNAs (miRNAs) are known regulators of various processes in plants, including growth, development and stress responses. They achieve this through mRNA cleavage or translational inhibition, in a process called RNA interference. Herein, their role in chilling stress response in young maize seedlings (*Zea mays* L.) is examined, using high-throughput sequencing methods. Bringing light to all aspects of chilling stress response in maize is necessary since earlier sowing, during colder periods, is one of the most promising strategies of avoiding maize yield loss due to effects of climate change in these areas.

Sterilized seeds of two maize genotypes (tolerant - T and sensitive - S to low temperatures) were germinated in the dark for five days (optimal conditions), after which the 5-d old seedlings were exposed to chilling conditions for 6h (10° C). Samples for RNA isolation and cDNA library preparation were taken after the treatment ended, and single-end 50 bp sequencing was performed (Illumina® Novaseq 6000). The miRNAs were then filtered, mapped, identified and quantified using adequate bioinformatics tools; and the differential expression analysis was carried out using the DEGseq R package. The analysis was performed on 859 miRNAs, after previously executed TPM normalization using the MA-plot-based method with random sampling model (MARS). The threshold for significantly differential expression was set as the Bayesian adjusted p-value, or q-value < 0.01 and log₂ fold change > 1.

A total of 612 were expressed differentially, but only 55 miRNAs were common for both genotypes and at the same time differentially expressed between control and treatment conditions – 40 novel and 15 known. Half of the common miRNAs showed the same expression patterns in both genotypes, while the other half did not. Among them, seven known miRNAs showed opposing expression patterns between the genotypes (zma-miR167b-3p, zma-miR167e-3p, zma-miR159c-5p, zma-miR164g-3p, zma-miR166a-5p, zma-miR398a-3p, and zma-miR528a-3p). These miRNAs were shown to have a role in various abiotic stress responses, including drought, waterlogging, high salts – but not chilling. While the results point to their potential role in establishing chilling tolerance in maize seedlings, further research is necessary to confirm it and connect the miRNAs to their potential targets.

Keywords: maize, abiotic stress, chilling, high-throughput sequencing, miRNAs



ISBN: 978-86-82679-14-1