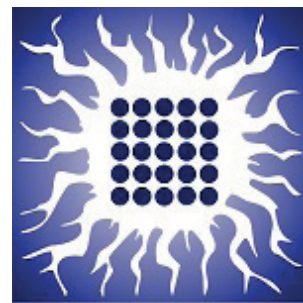


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PREFACE

The Belgrade Bioinformatics conference is a biennial event since 2016. This year, we are hosting the third **Belgrade Bioinformatics 2021 conference – BelBI2021**. The aim of the BelBI2021 is to provide a forum for exchange of knowledge and new ideas between scientists in the field, as well as, to include young scientists in this process and provide educational opportunities for them. Previously, we had the pleasure to welcome participants in Belgrade, but the situation with COVID-19 pandemic during 2020. made us postpone our conference and hold it this year as a virtual event. Nevertheless, the research presented in the abstracts available in this book is outstanding and it was an honor to edit it.

Several research institutions, faculties and scientific societies from Serbia have joined their forces to organize this international conference focused on different aspects of bioinformatics. Four Universities participated in the organization – Universities of Belgrade, Novi Sad, Niš and Kragujevac. The Conference is organized by the Vinča Institute of Nuclear Sciences – National Institute of the Republic of Serbia, University of Belgrade, as the the main organizer, and Faculty of Mathematics, University of Belgrade, Faculty of Biology, University of Belgrade, Institute of Molecular Genetics and Genetic Engineering University of Belgrade, Mathematical Institute of SASA and Serbian Society for Bioinformatics and Computational Biology, as co-organizing institutions, in cooperation with several other institutions and societies from Serbia.

This Book of Abstracts covers a wide range of various topics in bioinformatics, including Big data analytics, Machine learning in biological data analysis, Biological networks, Data mining methods and their applications in biology and medicine, Protein structure and function prediction, and much more. Special session of the BelBI2021 is dedicated to the bioinformatics in the field of COVID-19 analysis, which emerged as an immensely important research topic during the previous year, and these abstracts are also included in this book.

The Book of Abstract is printed as a Special Issue of *Biologia Serbica*, a journal published by the Faculty of Sciences, Department of Biology, University of Novi Sad, one of the Conference co-organizes, and thus, I would like to thank Prof. Željko D. Popović, Managing Editor, for all his effort to bring this enormous work successfully to the finish.

I would like to thank all members of the International Advisory, the International Program and the Local Organizing Committees for their efforts and help to make this event successful. Also, on behalf of the Local Organizing Committee, I would like to express my deepest gratitude to all attendees, and especially to all presenters for their interesting and much appreciated talks. In addition, we owe many thanks to the Ministry of Education, Science and Technological Development of the Republic of Serbia, as well as to the International Centre for Genetic Engineering and Biotechnology (ICGEB) that supported attendance of many students and early stage researchers. Also, the Local Organizing Committee is very grateful to all Conference's sponsors and donors, especially Factory World Wide d.o.o. and Seven Bridges Genomics, with the hope that they will be with us for many years to come.

This book contains 101 abstracts of presentations at the third Belgrade Bioinformatics 2021 conference – BelBI2021. Authors from 21 countries from almost all continents will present their work at the conference. There will be six keynote lectures, forty one invited lectures, twenty seven contributed talks and thirty two poster presentations.

Belgrade, June 2021.
Branislava Gemović
On behalf of BelBI2021

Differential gene expression analysis of heterotic groups' maize inbred lines under optimal conditions led to the identification of specific gene regulation under low-temperature

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Abstract

Finding new ways of improving crop quality, yield potential and abiotic stress tolerance are some of the most important pursuits in crop production today. As one of the biggest causes of yield and productivity reduction is climate change, specifically increasing temperatures and drought during the summer, a large number of strategies is focussed on lessening their negative effects. Cropping pattern changes include earlier sowing (early spring), when the temperatures are lower, as one of the most promising escape strategies for avoiding high summer temperatures. Thus, development of cold tolerant maize lines became an important goal. Comparative analysis of 46 maize inbred lines belonging to two different genetic backgrounds, one predominantly cold tolerant (marked as Non-Lancaster) and the other predominantly cold sensitive (marked as Lancaster) in the field, was done by whole transcriptome sequencing and differential gene expression (DGE) analysis. Plants were grown under optimal, greenhouse conditions and sampled after completing the V4 growth stage. Total RNA isolated from leaves of three plants per inbred line was used for cDNA library preparation by Illumina TruSeq Stranded RNA LT kit. Pair-end sequencing was performed on MiSeq Illumina sequencer using MiSeq Reagent kit, v2 (2 x 150bp). Data manipulation and analysis was performed using a custom-made bioinformatics pipeline that included high throughput sequence data quality control (using FastQC), removal of low quality reads (using Trimmomatic tool, version 0.32), transcriptome assembly and mapping (using Cufflinks, version 2.2.1), expression quantification (using CuffDiff) and DGE analysis (using BLAST2GO and GO analysis Toolkit and Database for Agricultural Community, agriGO v2).

DGE analysis revealed 77 differentially expressed genes (DEGs) between the Lancaster and the Non-Lancaster group, 21 of which were statistically supported for differential expression between the two groups and annotated as involved in abiotic stress responses in maize and other plant species. To test DEGs response to cold stress expression of a subset of seven DEGs in eight inbred lines (4 belonging to Lancaster and 4 belonging to Non-Lancaster genetic background) was analyzed under 24^h long exposure to low temperatures (6/4° C, 12^h photoperiod), with sampling being done 6^h and 24^h after beginning of the treatment, as well as after 48^h of recovery. Six DEGs showed different expression regulation dependent on cold exposure duration and genetic background. These findings imply differently regulated processes between the analysed Lancaster and Non-Lancaster inbred lines, contributing to their different cold response and adaptation, and will be further used for the development of cold tolerant hybrids.

Key words:

Transcriptomics, NGS, DEGs, maize, cold tolerance

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