Vol. 43 - No. 1 Special Edition 2021

Biologia Serbica

Department of Biology and Ecology,
Faculty of Sciences, University of Novi Sad, Serbia

BELBI 2021

Book of Abstracts
Belgrade BioInformatics Conference 2021
21-25 June 2021, Vinča, Serbia

http://ojs.pmf.uns.ac.rs/index.php/dbe_serbica/index

Biologia Serbica

JUNE 2021
Vol. 43 - No. 1 Special Edition

Biologia Serbica is formerly Review of Research, Faculty of Sciences, Biology Series (1971-2004), published by Department of Biology and Ecology, Faculty of Sciences, University of Novi Sad, Serbia

Aim and Scope

Biologia Serbica (BS) is an international scientific, peer-reviewed, open access journal that publishes original research articles, review articles, and short communications in all areas of biology.

Publisher

Department of Biology and Ecology
Faculty of Sciences
University of Novi Sad
Trg Dositeja Obradovića 2
21000 Novi Sad, Serbia
: +381 21 485 26 59
: +381 21 450 620
www.dbe.uns.ac.rs

Biologia Serbica is published biannually.

Printed by

"Sajnos"
Momčila Tapavice 2,
21000 Novi Sad
+381/21/499-461, +381/21/499-088
sajnosns@gmail.com

Date od publication: June 2018.

Subscription rates

Instructions available at
http://ojs.pmf.uns.ac.rs/index.php/dbe_serbica/index

ISSN 2334-6590

Biologia Serbica

Book of Abstracts
Belgrade BioInformatics Conference 2021

Volume 43 - No. 1
(Special Edition)
2021

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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 tolerante (marked as Non-Lancaster) and the other predominantly cold sensitive (marked as Lancaster) in the field, was done by whole transriptome 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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CIP – Каталогизација у публикацији
Библиотека Матице српске, Нови Сад 57
BIOLOGIA Serbica / editor-in chief Milica Matavulj. –
Vol. 34, no. ½ (dec. 2012) - . – Novi Sad : Faculty of Sciences, Department of Biology and Ecology, 2012-. –
Ilustr. ; 28 cm
Dva puta godišnje. – Je nastavak: Зборник радова Природно-математичког факултета. Серија за биологију = ISSN 0352 – 1788
ISSN 2334 – 6590 = Biologia Serbica
COBISS.SR – ID 275725831

ISSN 2334-6590

2021
Vol. 43 - No. 1 Special Edition

Biologia Serbica

ISSN 2334-6590