



# **BOOK** of **ABSTRACTS**

## **4<sup>th</sup> INTERNATIONAL CONFERENCE ON PLANT BIOLOGY (23<sup>rd</sup> SPPS Meeting)**



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**Faculty of Biology, University of Belgrade**

**BOOK OF ABSTRACTS**  
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## Chilling induced stress sRNAs in maize plants in early stages of development

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Small non-coding RNAs (sRNAs) have an important role in regulating plant gene expression, both in developmental processes and stress responses, through RNA interference or silencing. sRNAs respond to environmental stressors in manners dependant on the type of stress, tissue and genetic background. Herein, their role in chilling stress response is examined in young maize seedlings (*Zea mays* L.) of two inbred lines of contrasting chilling tolerance, using high-throughput sequencing methods. Understanding this response is critical since one of the most promising strategies of avoiding maize yield loss due to climate change is earlier sowing, during periods of suboptimal temperatures. Sterilized seeds of the two lines, marked as LT (tolerant), and LS (sensitive), were germinated in the dark for five days (optimal conditions), after which the 5-d old seedlings were exposed to chilling conditions for 24h (temperature: 10/8 °C; photoperiod: 12/12h). Samples for RNA isolation were taken after 6h and 24h of treatment. After the cDNA library preparations were finished, single-end 50 bp sequencing was performed (Illumina® Nova-seq 6000). sRNAseq analysis was performed using a custom pipeline that included quality control, mapping, known miRNA alignment and novel miRNA prediction and quantification. This is an ongoing research and a selection of results will be presented. On average 81% of sRNA reads were successfully mapped and belong to the class of microRNAs (miRNAs). Some of the sRNAs appear to be differentially regulated depending on the genotype and the chilling conditions, but more research is needed to verify their potential role in this process.

**Keywords:** maize, abiotic stress, chilling, NGS, sRNAs

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