



4th EPI-CATCH Conference Epigenetic Mechanisms of Crop Adaptation to Climate Change

BOOK OF ABSTRACT

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PLANT
BREEDING IN
VIEW OF
EPIGENETIC
MECHANISMS
AND
TECHNOLOGICAL
ADVANCEMENTS



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АУТОНОМНА ПОКРАЈИНА ВОЈВОДИНА
ПОКРАЈИНСКИ СЕКРЕТАРИЈАТ ЗА
ПОЉОПРИВРЕДУ, ВОДОПРИВРЕДУ И
ШУМАРСТВО



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ВИСОКО ОБРАЗОВАЊЕ И
НАУЧНОИСТРАЖИВАЧКУ
ДЕЛАТНОСТ



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Analysis of differentially methylated DNA sequences in potato plants exposed to French marigold essential oil

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Volatile organic compounds (VOCs) are important for tropospheric chemistry and have diverse roles in ecosystems. Plants 'sense' VOCs to efficiently adapt and respond to their environment. Volatiles of neighboring plants through alternations in the receiver plant's physiology contribute to the induction of direct plant defense against pest organisms and elevate immunity status by translating plants to 'primed' status when they are ready for rapid and energy-efficient response to upcoming attacks. Induced epigenetic changes, on the level of DNA and histones, could be involved in this response. Plant essential oils (EOs) have shown promising prospects as novel priming inducers, but a little is known about their potential to induce previous epigenetic alternations. In this study, potato (*Solanum tuberosum* L.) plants were exposed to French marigold (*Tagetes patula* L.) EO during 3 consecutive days for 8h each day and samples were collected 10 days after EO removal. Whole-Genome Bisulfite Sequencing (WGBS) was used to identify EO-induced differentially methylated (DM) DNA sequences. Average methylation level of whole genome and every chromosome, percentage of cytosine methylation in CG, CHG and CHH contexts, number of selected DM elements (promoters, exons, introns, 3'UTR, 5'UTR, and intergenic regions), were analyzed at differential methylation ratio between control and treated samples. Functional annotation of DM genes was done with KEGG pathway maps and Gene Ontology categories, and associated DM genes were identified for upcoming analyses of gene transcription in potato plants challenged with different abiotic and biotic stress conditions.

Keywords: DNA methylation, whole-genome bisulfite sequencing, essential oil, defense priming