

CHROMATIN FEATURES AND EPIGENETIC-MEDIATED MECHANISMS IN HELIANTHUS ANNUUS L. IN THE CLIMATE CHANGE SCENARIO

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Drought as a major abiotic stress induces numerous, complex responses in plant cells. Those include gene expression alteration, accumulation of different metabolites, and synthesis of specific proteins. At molecular level, changes are under the control of complex regulatory pathways that include epigenetic mechanisms responsible for suitable and fast reactions to newly occurring stress conditions. Epigenetic modifications cause gene expression alteration through histone posttranscriptional modifications, DNA methylation, and small RNAs and lncRNAs expression. Some of these epigenetic modifications might pass on to the next generation, thus providing a good basis for a quicker response to drought stress. Revealing the epigenetic memory mechanisms involved in stress response could be of use in breeding programs for a prompt adaptation of plants to stress conditions. In the context of the Cropinno project, funded under the Europe Horizon Programme, our aim is to develop an exploratory research project dedicated to the implementation of multi-omics tools for increasing the climate resilience of sunflowers.

Hence, at the Serbian Institute of Field and Vegetable Crops (IFVCNS) 30 sunflower inbred lines were tested to create in *in vitro* conditions using PEG 6000 to obtain a smaller panel of genotypes for analyzing chromatin and

transcriptome changes induced by drought.

On a few selected sunflower genotypes, a global analysis both of transcriptome and selected histone modifications will be conducted in plants subjected to a progressive dehydration stress and a full recovery period that mimics the field conditions.

To gain insights into chromatin dynamics, ChIP-seq will be employed to analyze two histone modifications (H3K4me3 and H3K27me3) and the histone variant H2A.Z distribution to unveil their role in changing chromatin states in response to stress and investigate their associations with changes in the transcriptome. Moreover, through an integrated data analysis approach, we expect to identify many genes with stress-induced increase in both mRNA and H3K4me3/H3K27me3 levels that, after re-watering and recovery, could maintain a sustained expression.