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CLIMATE CHANGE IMPACT ON EPIGENETIC PLANT RESPONSES

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Drought-coping epigenetic mechanisms in sunflower

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Drought is the leading cause of agricultural production loss, with 75% of the world's harvested land sustaining yield losses due to this major abiotic stress. According to global climate models, drought conditions are expected to worsen as droughts will grow more severe and prolonged as a result of climate change. Production of sunflower, the fourth most important oil crop, is affected by drought, hence breeding for drought tolerance presents a major task for breeders. So far, the majority studies were oriented toward understanding changes drought causes on morphological, physiological and more recently, on genomic, transcriptomic and proteomic level. Epigenetic mechanisms of drought tolerance in sunflower are still to these days unrevealed. At the Institute of Field and Vegetable Crops several drought tests are being developed for detecting drought tolerant sunflower genotypes from our vast collection. *In vitro* tests with PEG6000 and rhizothron testing allows detecting genotypes tolerant at early stages of sunflower development, while pot tests in walk-in-chambers enables detection of tolerant sunflower in the flowering stage. We will analyze differentially expressed non-coding sRNAs and lncRNAs and their target genes between the most drought tolerant and least drought tolerant genotype for the identification of epiQTLs that can be used in sunflower breeding programs. Additionally, mild drought stress mimicking field conditions is applied to plants grown in pots at early stage of development, to investigate chromatin dynamics during stress application and after recovery from the stress.

Keywords: drought, *Helianthus annuus* L., epiQTLs, sRNAs, lncRNAs

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